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Dipòsit Legal: L.153-2015

<http://hdl.handle.net/10803/285530>



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POLYUNSATURATED FATTY ACIDS IN AMYOTROPHIC LATERAL SCLEROSIS

ROLE OF DHA, PEROXIDATIVE MODIFICATIONS
AND SEXUAL DIMORPHISM

by

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October, 2014



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CERTIFY:

That the work presented here, entitled **“Polyunsaturated Fatty Acids in Amyotrophic Lateral Sclerosis: Role of DHA, Peroxidative Modifications and Sexual Dimorphism”** was developed by Daniel Cacabelos Barral, B.Sc. Chem., under our supervision and was aimed to fulfil the requirements for the degree of Doctor at the University of Lleida following the PhD Program entitled “Estudis Avançats en Ciències Biomèdiques”.

Hereby, to confirm this, we sign in Lleida, September 23rd, 2014

Dr. Manel Portero Otín

Dr. Reinal Pamplona Gras

Financial support by the Spanish Ministry of Health (PI08-1843, PI11-01532 and PI13-00584) by the Catalanian Government (2009SGR-735) and by the Spanish Ministry of Science and Innovation (CENIT Program; BFU2009-11879/BFI, and AGL2006-1243). DC received a predoctoral fellowship from the Spanish Ministry of Health(PI08-00707).

ABSTRACT

In the present work we focus into the potential relevance of PUFAs in some models and human samples from patients suffering amyotrophic lateral sclerosis (ALS). Due to its pathological implication, oxidative stress was our first goal. We started from simple oxidative methodology screening to search for an antioxidant substance (among 21 different candidates) available in a Mediterranean diet. The results demonstrated high heterogeneity in carbonyl (measured by DNP) accumulation, regarding the oxidative source, substrate suffering it and the antioxidant structure. Further, thanks to GC/MS and LCQTOF, we detailed the protection over specific accrual of protein and lipid peroxidation markers as well as lipid profile modifications (as % of total fatty acids -FA) in oxLDL thanks to those dietary compounds. Moreover, we demonstrated its *in vitro* relevance, in terms of survival, when two cell lines (HMEC-1, HepG2) were treated with this oxidized (and protected) compounds, and finally address *in vivo* importance of those findings, demonstrating decreased carbonyl and oxidative accumulation in hamsters under an atherogenic diet supplemented with antioxidants. Once described the protective effect of antioxidants and specific signatures found regarding lipid oxidation markers, we extend the study focusing in different ALS samples. From previous work, we demonstrated an altered docosahexaenoic acid (DHA) composition in different location for patients suffering sporadic ALS. Hence, we thought necessary to define whether the enzymatic machinery aimed to synthesize DHA from its precursors, are affected in sALS. Interestingly, we found a tissue specific variation (spinal cord *vs* cortex), compatible with our previous FA results. Further, thanks to immunohistochemistry, differential involvement was unveiled for motor neurons (MN) and surrounding glia. Therefore, trying to depict cellular contribution, we switch to a neuronal model (N2A under oxidative stressors and/or aggregation-prone-TDP-43) and a tissular one (OT). There, we showed decreased desaturase ($\Delta 6$) and drebrin expression as well as increased DHA synthesis and an unreported inverse correlation of drebrin loss and aberrant p-TDP-43 expression under oxidative conditions in the cell culture. In the OT model, lipidomic analysis showed specific accretion of 8-iso-PGF_{2 α} and NPD1 as well as increased DHA (and dramatically decreased precursors) and reduced AA concentrations (GC measured). Analysis of slice O₂ consumption showed decreased O₂ levels under excitotoxic treatment and alleviation by antioxidant (tocopherol) addition. Treatment of OT slices with Ω -3 precursors (better than final products) and DHA plus tocopherol ameliorated MNs number. Finally, we wanted to disclose PUFA's implication and phenotype of an animal model (SODG93A) under a dietary intervention with opposed FA unsaturation levels. Not surprisingly, FA profile was difficult to be altered in nervous system, although subtle specific variations were found. More importantly, differences in survival and clinical manifestations, UPR (Ubiquitin inclusions), mt-DNA (8-oxo-dG) and protein oxidative modifications revealed sex as a relevant factor in lipid handling for this model. Hence, whereas male under a low PUFA diet showed increased survival, females lack this beneficial outcome. Last but not least, we wanted to dig deeper regarding this sexual dimorphism. For this purpose, we focused in mitochondria and analyzed spinal cord oxygen consumption, oxidative damage to proteins and lipid profile along disease progression and also in a neuronal model (N2A overexpressing SODG93A, treated with 17 β -estradiol). We could demonstrate a clear sexual implication, with females having late onset clinical symptoms concomitant to an upgraded mitochondrial function and lower protein and mitochondrial damaged proteins compared with males. Finally, to further confirmed steroid potential as a protective element in disease progression, *in vitro* estradiol pretreatment of N2A showed increased oxygen consumption, with no relation with the mitochondrial complex expression.

RESUMEN

En el trabajo que aquí se presenta se ha profundizado en la relevancia que los ácidos grasos poliinsaturados (PUFA) puedan tener en el tratamiento de la esclerosis lateral amiotrófica (ALS). Dada su implicación en el desarrollo de la patología, el estudio del estrés oxidativo asociado fue uno de nuestros primeros objetivos. Para ello hemos empezado por un cribado metodológico simplista, tratando de encontrar una sustancia antioxidante (entre 21), biodisponible en una dieta Mediterránea equilibrada y que fuese capaz de reducir un daño oxidativo generado desde diversos frentes (medido como acumulación de carbonilos) y sobre diferentes sustratos. Los resultados demostraron una alta heterogeneidad, dificultando así la elección de un único antioxidante. Aún así, gracias a la GCMS y la LCQTOF pudimos detallar la acumulación específica diferenciada de marcadores de daño oxidativo proteico y daño lipoxidativo producido cuando partículas de lipoproteínas de baja densidad (LDL) son oxidadas bajo la acción de diversos compuestos. Además se pudo objetivar el cambio en la composición lipídica de estas LDL (medida como % del total presente) y su relevancia biológica *in vitro*, medida en términos de supervivencia, cuando se exponen a dos líneas celulares (HMEC-1, HepG2). Por último se demostró la importancia *in vivo*, puesto que se pudo observar una menor acumulación de productos carbonílicos en hámsters alimentados con una dieta aterogénica, pero suplementada con antioxidantes. Una vez se demostró el papel jugado por estos antioxidantes en la acumulación diferenciada de productos de oxidación, extendimos el estudio a muestras y modelos de ALS. En trabajos previos habíamos evidenciado una composición tisular diferenciada en diversas localizaciones del sistema nervioso en pacientes diagnosticados de ALS. Por ello consideramos interesante el estudio de la expresión de la maquinaria enzimática necesaria para la síntesis lipídica. De un modo destacado, pudimos ver de nuevo una variación tisular, compatible con niveles reducidos de docosohexaenoico (DHA), y gracias a la inmunohistoquímica también se observaron diferencias entre las motoneuronas (MNs) y la glia circundante. Así pues, para poder revelar las aportaciones diferenciales de los distintos tipos celulares, utilizamos una línea celular (N2A) a la que sometíamos a diferentes estresores (daño oxidativo y sobreexpresión de una versión de TDP-43 que causa agregados) y a un cultivo tisular de médula espinal (OT), dónde se produce una muerte progresiva y selectiva de las MNs. Tras estos experimentos, observamos un descenso tanto en la expresión de la $\Delta 6$ desaturasa como de drebrin (marcador presináptico) tras la sobreexpresión de TDP-43, así como una mayor síntesis de DHA y una correlación inversa entre la pérdida de drebrina y la expresión de pTDP-43 bajo condiciones de estrés oxidativo. Por otro lado, en el modelo OT, el análisis lipídomico reveló la acumulación específica de 8-iso-PGF_{2α} y NDPD1 (posiblemente en respuesta a un incremento del daño oxidativo) así como el aumento en la concentración de DHA (con un descenso muy marcado de sus precursores) y el descenso de araquidónico. Quisimos analizar también el consumo de oxígeno, tanto en tejido intacto como permeabilizado, pudiendo observar como la excitotoxicidad reducía considerablemente su capacidad y como ésta era, en parte, rescatada con el uso de tocoferol. Además, el tratamiento del OT con precursores Ω -3 mejoró también el número de MNs. Por último, quisimos caracterizar la implicación que los PUFA dietarios podrían tener en un modelo animal bien conocido (SODG93A). No fue sorprendente encontrar que el perfil lipídico en el sistema nervioso fue muy difícil de alterar. Aún así, se observaron diferencias en supervivencia, en el devenir clínico, la respuesta UPR (con acumulaciones de Ub), el daño al DNA mitocondrial (8-oxo-dG) y modificaciones oxidativas en las proteínas y cómo éstas tenían un grado de afectación diferencial cuando considerábamos el sexo de los animales. Esto es, mientras que los machos sometidos a una dieta baja en PUFAs de cadena larga demostraron una mayor supervivencia, en las hembras no se

apreció mejoría. Por último, pero no menos importante, quisimos profundizar más respecto a este dimorfismo. Centrándonos en la mitocondria, pudimos hacer un seguimiento del consumo de oxígeno a lo largo de la enfermedad, el daño oxidativo a proteínas y el perfil lipídico. Por lo tanto pudimos demostrar una clara implicación sexual, siendo las hembras las que más tarde comienzan su manifestación clínica, con mejores funciones mitocondriales asociadas a un menor daño oxidativo. Finalmente, la relevancia del papel protector de los estrógenos se pudo comprobar *in vitro*, mediante el pretratamiento con 17β -estradiol en la línea N2A que sobreexpresa SOD1G93A, relacionado con la ALS familiar, proponiéndose el estradiol como un nuevo elemento que juega un papel relevante en el desarrollo de la enfermedad.

RESUM

En aquest treball s'ha intentat profunditzar en la possible rellevància dels àcids grassos poliinsaturats (PUFA) en el tractament de l'esclerosi lateral amiotròfica (ELA). Atesa la seva implicació en el desenvolupament de la patologia, l'estudi de l'estrès oxidatiu associat fou un dels primers objectius. Per això, es va començar amb un cribratge metodològic simplista, intentant trobar una substància antioxidant biodisponible en una dieta mediterrània equilibrada i que fos capaç de reduir el dany oxidatiu generat des de diferents fronts i sobre diferents substrats. Els resultats van demostrar una alta heterogeneïtat, dificultant així l'elecció d'un únic antioxidant. Malgrat això, mercès a tècniques de GC-MS i LC-QTOF, es va poder detallar l'acumulació específica diferenciada de marcadors de dany oxidatiu proteic i dany lipoxidatiu produït quan partícules de lipoproteïna de baixa densitat (LDL) s'oxiden per l'acció de diversos compostos. A més, es va poder objectivar el canvi en la composició lipídica d'aquestes LDL i la seva rellevància in vitro, mesurada en termes de supervivència, quan es cocultiven amb les línies cel·lulars. Per últim, es va demostrar la importància in vivo, atès que es va observar una menor acumulació de productes carbonílics en hàrmsters alimentats amb una dieta aterogènica suplementada amb antioxidants. Un cop es va demostrar el paper d'aquests antioxidants en l'acumulació diferenciada de productes d'oxidació, es va estendre l'estudi a mostres i models d'ELA. En treballs previs s'havia evidenciat una composició tissular diferenciada en diverses localitzacions del sistema nerviós central en pacients d'ELA (respecte l'àcid docosahexaenoic (DHA), depleció en medul·la espinal i acumulació en còrtex). Per aquesta raó es va considerar interessant l'estudi de l'expressió de la maquinària enzimàtica necessària per la síntesi lipídica. D'una manera destacada, es va poder veure de nou una variació tissular, compatible amb nivells reduïts de DHA i, per tècniques d'immunohistoquímica, es van observar diferències entre les motoneurons i la glia circumdant. Per tant, per poder revelar les aportacions diferencials dels diferents tipus cel·lulars, es va utilitzar la línia cel·lular N2A, sotmesa a diferents estressos (dany oxidatiu i sobreexpressió d'una forma de TDP-43 que causa agregats) i un cultiu tissular de medul·la espinal, en el que es produeix una mort progressiva i selectiva de les motoneurons. Es va observar un descens en l'expressió de FADS2 i de drebrina, un marcador sinàptic, així com una major síntesi de DHA i una correlació inversa entre la pèrdua de drebrina i l'expressió de TDP-43 sota condicions d'estrès oxidatiu. Per altra banda, en el model organotípic, l'anàlisi lipídica va revelar l'acumulació específica de 8-isoPGF_{2α} i NDPD1, així com l'augment de la concentració de DHA i el descens molt marcat dels seus precursors a més del àcid araquidònic. Es va mesurar també el metabolisme oxidatiu, observant-se que l'excitotoxicitat reduïa considerablement la seva capacitat i, en part, es rescatava amb l'ús de tocoferol. A més, el tractament dels cultius organotípics amb precursors d'àcids grassos n-3 va millorar el nombre de motoneurons. Per últim, es va caracteritzar la implicació dels PUFA dietaris en un model animal d'ELA. Malgrat que el perfil lipídic del sistema nerviós central era difícil d'alterar, es van observar diferències en supervivència, fenotip clínic, resposta al malplegament de proteïnes (UPR) amb acumulació d'ubiquitina, dany en el DNA mitocondrial i modificacions oxidatives en les proteïnes, amb un grau d'afectació diferencial quan es considerava el sexe dels animals. En aquest sentit, mentre que els mascles sotmesos a una dieta baixa en PUFA de cadena llarga van mostra una major supervivència, en les femelles només va apreciar cap efecte millora. Per profunditzar en el dimorfisme sexual en ELA, i especialment la disfunció mitocondrial, es va analitzar mitjançant respirometria d'alta resolució la medul·la espinal durant tot el desenvolupament de la malaltia. Es va revelar una clara diferència de gènere, amb una manifestació clínica més tardana en femelles que correlaciona amb una millor conservació de la funció mitocondrial i un menor dany oxidatiu. El possible paper protector dels estrògens es va

demostrar in vitro mitjançant el pretractament amb estradiol de cèl·lules N2A que sobreexpressen una forma de SOD1 humana mutada associada a l'ELA familiar (G93A-SOD1).

*Os meus pais,
a miña irmá,
a minmesmo*

Unas cuantas verdades que ya dijeron otros,...

La duda es la base de todo conocimiento.

Aristóteles

Mide lo que sea medible y haz medible lo que no lo sea.

*Todas las verdades son fáciles de entender, una vez descubiertas.
El caso es descubrirlas.*

Galileo Galilei

True ignorance is not the absence of knowledge, but the refusal to acquire it.

Science is always seeking, not a real discovery. It is continuous travelling for never arrival.

Karl Popper

Books permit us to voyage through time, to tap the wisdom of our ancestors.

There are many hypotheses in science that are wrong. That's perfectly alright; it's the aperture to finding out what's right. Science is a self-correcting process. To be accepted, new ideas must survive the most rigorous standards of evidence and scrutiny.

Carl Sagan

On the whole, human beings want to be good, but not too good and not quite all the time.

George Orwell

Cuando creíamos que teníamos todas las respuestas, de pronto, cambiaron todas las preguntas.

Mario Benedetti

Existe al menos un rincón del universo que con toda seguridad puedes mejorar, y eres tú mismo.

El secreto de la genialidad es el de conservar el espíritu del niño hasta la vejez, lo cual quiere decir nunca perder el entusiasmo.

Aldous Huxley

La religión explica los miedos del hombre, la ciencia descubre las verdades de la naturaleza, la ciencia es para valientes.

Anónimo

Agradecimientos,

Well, bueno, ben, bè ... Por fin me toca a mí!

Como es de rigor, pero además en este caso de verdad, me gustaría comenzar agradeciendo el calor y conocimientos que mis directores Manel y Reinald me han brindado, sin su apoyo esto hubiese sido imposible. Gracias Maestros!

Pero el grupo era una familia numerosa, muy extensa, por la que he ido viendo pasar mucha gente en estos años. Desde el principio, M^a Josep y Viki ya estabais por ahí, menudas charlas arreglamundos nos echamos en la mesada o en la cola del rancho por 2,12 leuros en el Santamaria, y los cafeses en el Kemdefer o en la Caseta... y cómo me olvidare de todo lo que aprendí para poder llevar la “colonia” de ratones, las inmunes y el dichoso confocal, el OT y demás técnicas! También estaba ya por allí el “socio fundador” Joan Prat, recuerdo felizmente el día que encontramos una foto de los tres Manel, Reinald y él haciendo butifarras o que se yo... Muchos de mis compis ya son doctores, pero los comienzos conociendo la ciudad y sus recovecos nocturnos y descubriendo el mundo de la ciencia (y sus recovecos aún más oscuros ;) de la mano de Katia, Alba y Mariona son inolvidables. También andaban por allí el David y la Nuria -de aquellas todavía becaria de Calderó- y al poco llegaron la Saray, Mery y Jessica para darnos más apoyo, que buena falta hizo ;) . Pobre Jessica como la hacía sufrir con las bestias, pero bueno, le gustó ... y se pudo quedar por el estabulario! Y al poco llego Jordi, siempre muy callado (pero por dentro se partía!), y tuve la suerte de compartir dos de sus pasiones (o tres si contamos el buen comer) a mitocondria y el monte, que tantas alegrías (!) me han dado. Y el Huget, Claro que si! Lo veía de prácticas con la M^a Angeles y lo fuimos llevando al lado (que no cuarto) oscuro fisiopato-ilógico... y cayó. Que pisazo teníamos... éramos la envidia del vecindario, jeje...días de vino y rosas!! Un abrazo para el Gus! Creo que fue mi segundo Octubre cuando apareció por aquí un cuate que nos conquistó con su saber hacer, buen humor y su “exo-estomago”; grande Chamaco! ... Dulces recuerdos de congresos de médicos, a todo *Nutren*... historias preburbuja inmobiliaria y crisis... *snif*... DeLorenzo con la nutrigenómica por la casa y el Ribera con su radar! Y mientras iban viniendo gentes de estancias: el José y la Pilar de los madriles, el Jorge del grupo de Aurora Pujol (la Ione y el Stéphane después), la griega, el francés, los mexicanos (estos no pararon de llegar). Al ratón el Jose se pudo traer a la moza y vino una nueva pieza neuro- mitocondrial, la Ana y sus buenos embutidos de la querida extrema y dura... y como el Jose tenía debilidad, y era cosa de Annas (con una o dos enes), pues al poco también se vino p’acá la mejor Allmacellenca que conozco, *Uber Alles!* ;). Al tiempo, como ya habían pasado unos años sin “esclavos extranjeros”, fichamos a un cubano, y cuando pensábamos encontramos a un macizo negrote, nos vino el Omarito “café con leche”! Pobre heredero de la “colonia” de gran corazón y mejor conversación! Unas buenas escapadas nos hemos hecho! Y con la Rosana y la Liliana se completó la cuadrilla, por ahora, quedando el grupo compuesto por médicos, biólogos /bioquímicos, químicos, farmacéuticos, nutricionistas tecnólogos alimentarios y hasta ingenieros, madre mía que lío! Es pura suerte que nos entendamos! Y las nuevas generaciones pisan fuerte, la Rosana misma, anda que no le pega al cromatógrafo la tía!, y el Pascual y la Lara y quién sabe quién más pasaran por acá. Solo espero que puedan disfrutar y aprender a su costado, como yo he hecho.

Y las risas que nos echamos con los de BioQuímica!... No sé..., el hecho de estar tan cerca, ahí enfrente...pero lo suficientemente lejos también... Vero, Armando, Stef, MaAlbe y tod@s los becari@s de estancias que pasaron por allí, mimadriña! ... pero con todos congeniábamos... No fueron malos años, no! Myriam, no quedara muy bien, puesto que aun la tendrás que juzgar, pero que sepas que esoy encantado de los éxitos que te han brindado fuera, tú lo vales y lo mereces, animo! Lleida estará siempre aquí en nuestro corazón (y Álvaro también, jeje)...y que sepáis que el tipo del On the Rocks os hecha mucho de menos! Creo que Quim Ros me reservará un trocito de poyata, aunque también descansara al no verme tanto “revoloteando entre sus becarias”. Yo ya lo echo de menos... Y las Rosas? Saludos a la Sta.

Decana, que me animo a calificar de amiga, Rosa Soler y las nuevas generaciones con AnaG y Nuria (y Rosa -la mujer del Sera y por supuesto de Roser y nuestros comienzos en el estabulario) y como no recordar als molt honorables presidents (Elia y David, herederos de una dinastía de justos representantes ;)) y los buenos momentos vividos (las grandes patxangas al futbol con Elia y los mano a mano de likor café con David... o era al revés) y mi compi de piso por unos meses, Saravanan, y Ambika... hay el idilio con la India ... Indilio! El Bupesh abrió la brecha y anda que no ha habido éxito! Cuantas buenas gentes he podido conocer, que rica comida y cultura me brindaron, Hiren y Rinku, Charumathi, Arindan y Upasana, Depsheeka y Venki y Disha, un abrazo chavalada!

De la segunda planta recuerdo muy gustosamente a Sara, Xenia y Eli que la pelearon conmigo y pude disfrutar sus defensas de tesis, así como alguna que otra cenuki ..., y al Dr Esquerda y Anna Casanovas que me ayudaron al poco de llegar con el microscopio y la perfusión de los pobres "voluntarios". Y del rock que se montan la Marta y Montse ni hablamos, no? Suerte que tienes Javi ;) . Del grupo de Loreta, con los que compartimos cuartucho algunos años, además del Bupesh no me quiero olvidar de Antonio y por supuesto de las mocicas: la rubia platino, compi hortolana y afines aficiones, Alba, y la morocha rizada albaceteña de profundos abrazos, que camina a Santiago más a menudo que yo, Bea, un beso a t@s, maj@s!

De la tercera, como olvidar el grupo mindundi y las competis de disfraces de carnavales que nos hacíamos con los del Arnau!! Muchos ya se han ido (Martí y Carme, Rita, Marcellí, Galal o Seba), pero otros aun siguen por aquí (Paco-quillo!, Jordi, Eloy, Marta, Sonia o Neus C) han vuelto hace poco (Serafi and family, Neus P) y parece que no han pasado los años o refrescan con sangre nueva (Irene y Noel)... y el grupo de Carme Espinet, con Peter, Anton y Gerard, donde luego vino a parar el Egea con sus becarios... la Catherine (cuantas veces habre firmado en tu nombre, salerosa ^^) la Mariajo (y sus melocotones-de comer;-)) y la Disha y, cómo no, la técnico mas viajera y con la que siempre puedes conversar, la Imma. Como olvidar la tarta que pasó tantos años en el arcón-congelador! (bueno si hubiese un historial de lo que allí ha habido, Dios!), poco más y se viene al IRB como uno más!

Este último año, ya recluso con la escritura de los papers y el ladrillo tesil, tuve la oportunidad de conocer a otra ilustre cubana, Idalmis, e intimar un poco más con Serafi, una suerte más que la vida me ha dado! Cuántas veces hemos desahogado las penas y arreglado el mundo con lixivados germánicos fermentados por levaduras y destilados revolucionarios! Gracias majetes!

No puedo dejarme fuera a gente como Isu o Berta, y las buenas conversaciones que nos echamos en cultivos y a los currantes de secretaria de IRB. La gente de conserjería, sin duda a Emeterio, Fini, Trillo (el seleccionador) y María, Mónica y Montse los informáticos Josep y Toni y demás gentes de secretaría (David, Yolanda y Sandra), con sus buenos días y tardes siempre podías contar, y a veces hasta una sonrisa ;) Y por supuesto con el siempre excelentísimo e impecable servicio de limpieza, desde la Charo, Marcia o Daniela, pasando por Ani, Aisa y Loli, siempre estaban por ahí para amenizar cuando las tardes se hacían noches. Un gusto haberlas conocido! Algunos más que recuerdo,... el "gran jefe" de la biblioteca, Roland, Ánimo!, sin duda los maestros del estabulario Emilià y Manolo y los siempre eficientes JR y Joan ... Y otros que ya se han marchado, pero cerca Marina, Esteban, Maya o Alejandra...

Mención especial me gustaría hacer a una gran compañera y amiga que me temo lo será lo que me quede de vida, la Colman. No sé qué decir que no intuyas, mas que fue una suerte haberme encontrado contigo y lo bien que nos caímos. Siempre p'alante leona! No sé que más decirte, porque sabés boluda que siempre era sho el que te pedía consejo! Muchos éxitos y un abrazo al Ahmed, otro león también, y a mi familia postiza Argenta; la Carlota y el Chingol (que gloria de personas de verdad!!) Alois, Alexia y su bichito y a papa Colman y lo bien que disfrutó de la vida. Abrazos para todos! Malditos, me pegaron el gusto por el asado lento y el mate o un Malbec en buena compañía! Y siguiendo por el cono sur, como olvidarme al Gualano

y M^aAlbe, dos corazones que no paran de bombear pensando en los demás, un placer chavales, que la vida les sonría! Y si hablamos de corazones y cono sur, me toca hablar de la Noe también, un recuerdo para ti, guapisísima, allá donde estés, estate bien y se buena!

And I would like also to thank the people in Norway. Lippid Gruppe kindly welcomed me a made my short stay in Bergen comfortable and very successful. Rolf, Bodil, Lena, Eline, Kari Wiliams, Pavol, Natalya, ... thanks to everyone up there!

Pero por suerte mi paso por Lleida fue largo y tuve la oportunidad de mezclarme con otras buenas almas que me entretuvieron para que esta tesis fuera tan larga como ha sido, y yo feliz! Quiero recordar a Iñaki (Mc Mardigan), que está justo hoy de cumple, y emigrado de nuevo en London, gran aventurero rapitense y mejor ser humano, sabio. Así como el frente variado que he ido atrayendo a los Pirineos: Gonzalo (alpinista trovador) y Ana (por muchas cosas...y la portada, gracias!), Pintor (gracias por las correcciones, las escapadas montaÑeras y, en general, que decir, la amistad desde la guardería!), Dopo (que viajes macho! Solo se vive una vez, pero que bien que la pasemos oiga, gracias por los mejores veranos de mi vida), Patmos (gracias por conocer tu familia villafranquina, y que bien que te veré por Ou, a patear O Courel y tomar botillo!!), Oier (Sr concejal euskaldune, a sus pies), Dani y Carol (viticultores rompiendo la velocidad del sonido!), els veïns Oriol y Mariona (bon viatge xiquets) Nodar y Truji, (ya papas dior mio!! Os veo con la mochila-niño), Fariña, Pow, Jimmy Po (y respectivas señoras, jeje), Anita, Paula (y respectivos maridos, juju), Zintia, Pauliña ... las gentes de Pontevedra, miña casiña, meu lar, ... Juanin, Ansel, Javiere, Toñil, Berni y vicesberzas ... bueno para el frente galaico podría hacer otra tesis así que agradecidos quedáis con este brindis: por todos los LK que no me pude tomar con vosotros, ya nos iremos actualizando!

También quisiera mencionar a una buena generación de estudiantes de medicina (Jesús, Samu, Cris, Paul, Jeong-Hu, Pili, Gonzalo, Clara, Ibai ...) que, cuando todavía no era muy cantoso que me juntase con ellos (ahora ya me ven como bicho raro, o yo quizás ya no pego...), me acogieron, permitiéndome prolongar un poco más mis mejores años universitarios. Muchas gracias por la compañía, el equipo de fútbol la facultad, las fiestas, los asados, las eskiadas... y, bien pensado, no está mal tener unos cuantos amigos médicos, que todos nos avejentamos!

Por último quixera dedicarlle unhas verbas á miña familia. Os meus país, que me deron a vida e as ferramentas para afrontala e que incondicionalmente axudaronme a apoiaronme nas miñas decisións, ese compromiso e ese amor que me destes espero me fixeran bo rapaz, con iso xa sería dicir moito. Gracias porque moitas veces tivestes que elixir entre vos e os vossos fillos, e nunca o dudastedes. Ademáis, agora mesmo apetécame moito pasar una tempadiña convosco y disfrutares de esta vida adulta que, como una parte mais do percorrer, teño o gusto de compartir con quen ma regalou. Así que xa sabes irmanciña, María, e certo que temén levamonos ben nas distancias, e que moitos días xuntos son como una bomba para nos, pero ben sabes o que che quero, e por un tempo xa é hora de tornares a casiña, pola miña parte estarei por ahí unha tempada, e sabes que alí sempre es (mais ben sodes, Miguel e mais ti ;)) benbidos. E os meus avos (Constantino e Carmen e mais Feliciano e Asunción), que tanto loitaron e que tiven a sorte de coñecer polo menos algún tempo. Aínda que agora so disfruto da compañía de Asunción, labrega emigrada tamén polo ben dos seus fillos, como tantos outros! pero esta e a miña! ... Mans tinguidas de terra traballada, ollos espertos que coñeceron boas persoas e percorreron mundo e mais o lombo truncado de tratar de arranxalo. Celi, padriños Manolo e Fina, Angela, Tita, Diego e Carmen, (Manolo e Paquita, descansade), Dolores, Ricardo, Diego e Marta, Mundy, Celia, Laura e Alberto! Moitos bicos a todos, pronto poderedes contar conmigo a full!

...Y mucha gente más me habrá ayudado, y quizás me los olvidé, pero vosotros sabéis quienes sois y lo que habéis hecho, a todos, GRACIAS y también a los que no me habéis ayudado, muchas gracias, puesto que con vuestra dejadez también me habré espabilado.

Hasta pronto Lleida-Pirineus

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Abbreviation List

Arachidonic Acid	AA	AminoAdipic SemiAldehyde	AASA
Acyl-CoAHydrolase	ACH	Acyl-CoASyntetase 2,4,6	ACS2, 4, 6
Alpha Linolenic Acid	ALA	Adenosin MonoPhosphate	AMP
Adenosin DiPhosphate	ADP	Adenosin TriPhosphate	ATP
AcetylCoA Acyltransferasa-1	ACAA1	Acyl-CoA Oxidase-1	ACOX1
Amyotrophic Lateral Sclerosis	ALS	Acyl-CoALysophospholipid	ACL
α -Amino-3-hydroxy-5-Methylisoxazole Proprionic Acid	AMPA	acyltransferase	
Blood-Brain Barrier	BBB	B-cell lymphoma 2	Bcl-2
Cardiolipins	CL	Coenzyme A	CoA
Cytochrome c	Cyt c	ClicloOXigenase 1 / 2	COX1, COX2
Cholesterol	CHO	CerebroSpinal Fluid	CSF
Central Nervous System	CNS	Calcium	Ca ⁺²
ClicloOXigenase 1 / 2	COX1, COX2	Cytochrome P450	CYP450
cytosolic Phospholipase A ₂	cPLA ₂	Carbohydrate-Response Element-Binding Protein	ChREBP
CarboxyMethyl Lysine	CML		
Cluster of Differentiation 36	CD36		
1,2-DiAcylGlycerol	DAG	DesoxiriboNucleid Acid	DNA
DocosoHexaenoic Acid	DHA	Double Bound Index	DBI
2,4 DiNitroPhenylhydrazine	DNP	8-oxo-desoxiGuanosine	8-oxo-dG
Double Strand Break	DSB	Dihomo- γ -Linolenic Acid	DGLA
DocosoPentaenoic Acid	DPA		
Elongases	ELOVL	Endoplasmic Reticulum	ER
EicosaPentaenoic Acids	EPA	Electron Transport Chain	ETC
Excitatory AminoAcid Transporter-2	EAAT2	Epoxy-EicosaTrienoic acids	ETT
Enzyme-Linked ImmunoSorbent Assay	ELISA	Extracellular-signal-Regulated Kinases	ERK1/2
Fatty Acid	FA	Fatty Acid Binding Protein	FABP
Δ 5 Fatty Acid Desaturase	FADS1	Fatty Acid Transport Protein	FATP
Δ 6 Fatty Acid Desaturase	FADS2	FrontoTemporal Dementia	FTP
FUsed in Sarcoma	FUS		
γ -AminoButiric Acid	GABA	Gas Chromatography	GC
GLutamete Transporter-1	GLT1	Glutamic SemiAldehyde	GSA
GlyceroPhosphoLipids	GPL	Glutamate	Glut
Glial Fibrillary Acidic Protein	GFAP		
Hepatic Nuclear Factor 4 α / γ	HNF-4 α / γ	High Density Lipoprotein	HDL
4-HydroxyNonEnal	4-HNE	4-Hydroxy-2-HexEnal	HHE
Histone γ 2AX	γ -2HAX	HydroxyEicosaTetraEnoic acid	HETE
Hepatocellular carcinoma G2	HepG2	Human dermal Microvascular Endothelial Cells-1	HMEC-1
IsoProstane	IsoP	Inositol 1,4-diPhosphate	IP ₂
InterLeukin	IL	Inositol 1,4,5-triPhosphate	IP ₃
independent Phospholipase A ₂	iPLA ₂	InmunoHistochemistry	IHQ
Linoleic Acid	LA	Low Density Lipoprotein	LDL
Long-Chain-PUFA	LCPUFA	LeucoTrienes	LT
LipoXines	LX	Lipoxigenase 1 / 2	LOX1,LOX2
Liver X Receptor α	LXR α	Liquid Chomatography Spectrometry	Mass LCMS

Neuro2A	N2A	Neuroblastoma×SpinalCord 34	NSC-34
N-Methyl-D-Aspartate	NMDA	NeuroProtectin D-1	NPD1
Nuclear Factor Kappa-light-chain-enhancer of activated B cells	NFκB	NonSteroidal Anti-Inflammatory Drug	NSIAD
Membrane Contact Sites	MCS	MalonDiAldehyde	MDA
MalonDiAldehyde Lysine	MDAL	Mitogen Activated Protein Kinase	MAPK
mamalia Target Of Rapamicyn	mTOR	Motor Neuron	MN
Mitochondria-Associated Membrane	MAM	Macrophage mediators in	Maresin
mitochondrial DNA	mtDNA	Resolving Inflammation	
Organotypic	OT		
Patale Activated Factor	PAF	Phosphatidil-Cholines	PC
PhosphoLipid	PL	Phosphatidil-Ethanolamines	PE
ProstaGlandines	PG	Prostacyclines	PGI
Phosphatidil-Iinositols	PI	PhosphoLipase B, C, D	PLB, PLC, PLD
Protein Kinase B	PKB, AKT	Phosphatidil-Serines	PS
PeRoxidability Index	PRI	Protein Kinase C	PKC
Phosphatidyl-Inositol-4,5-bisphosphate 3-Kinase	PI3K	PolyUnsaturated Fatty Acid	PUFA
Reactive Lipid Species	RLS	Reactive Nitrogen Species	RNS
Reactive Oxygen Species	ROS	RiboNucleid Acid	RNA
Resolvin D, E	RvD, RvE	Retinoid X Receptor α	RXR α
Copper Zinc SuperOxide Dismutase	SOD	Sterol Carrier Protein	SCP
Sterol Regulatory Element-Binding Protein	SREBP	Copper Zinc SuperOxide Dismutase Glynine93Alanine	SODG93A
SphyngoMyelin	SM	Syntaxin-3	STX3
secreted Phospholipase A ₂	sPLA ₂	Soluble N-ethylmaleimide-sensitive factor-Attachment protein	SNARE
S-(2-succinyl)cysteine	2SC	REceptor	
1,2,3-TriAcylGlycerol	TAG	Tumor Necrosis Factor - α	TNF-α
ThreoHydroxyAspartate	THA	Tumor Growth Factor-β	TGF-β
TransActive Response Binding Protein-43	TDP-43	ThromboXane	TX
Uncoupling Protein 3, 4	UCP3, 4	Unfolding Protein Response	UPR
VeryLongchainFA	VLFA	UBiQuilin-2	UBQN2
Western Blot	WB	Wild Type	WT

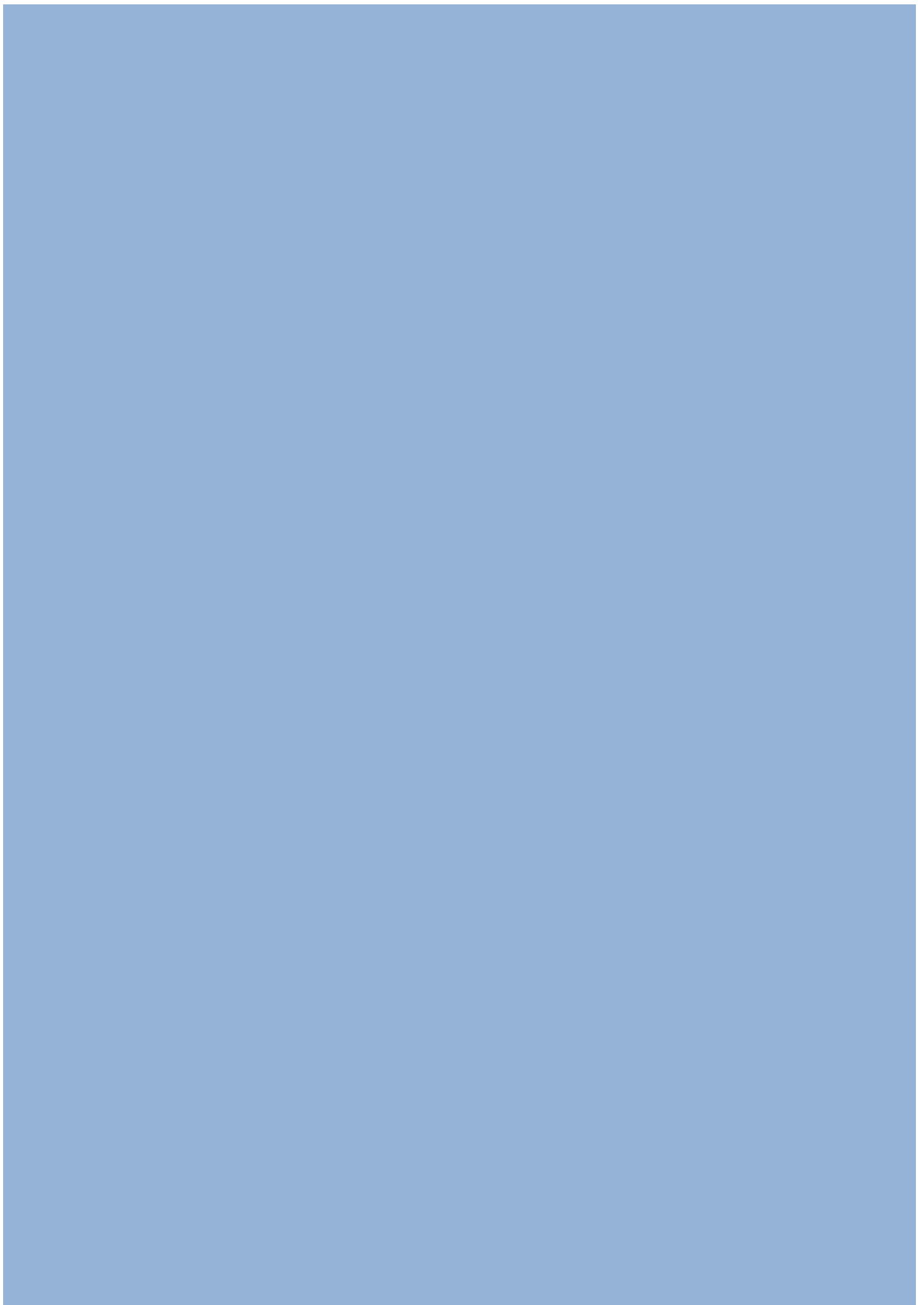
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1. Introduction



1.A PUFA Physiology

1.A1 PUFA structure and relevance in phospholipids

Polyunsaturated fatty acids (PUFA) belong to the lipid family. They are fatty acids (FA) having at least two or more carbon-carbon double bonds. But let's start from the beginning with a brief introduction of what a FA is, how many diverse forms there are and how this would have an influence in the different biological outcomes (for a review of the topic see (Tvrzicka et al. 2011)).

Structurally, FA are composed of a carboxylic (organic acid) group at one end and a variable length aliphatic carbon chain on the other, seeded with none (saturated), one (monounsaturated) or multiple (polyunsaturated) carbon-carbon double bonds. The carbon atom on the acid group is chemically an electrophilic centre (electron deficient area) and therefore susceptible of being attacked by nucleophilic species (electron rich area). Hence, this carbon is termed alpha and the last one on the chain is named omega (see Figure 1). This nomenclature is often used in biomedicine and nutrition being referred as omega-x or n-x, meaning a double bond located on the xth carbon-carbon bond, counting from the terminal methyl carbon (as said before, designated as n or ω) along the carbonyl chain towards the carboxylic region. For instance, linoleic acid (common nomenclature, LA) is a C18:2 fatty acid (meaning eighteen carbons and two carbon-carbon double bonds), belonging to the n-6 family (or omega-6, ω-6, specifying the position of the latest double bond). This point of view of the nomenclature is useful for nutritional purposes since the same family members, ω-6 or ω-3, share related biosynthetic pathways, and even similar outcomes.

Other classifications of FA are based on the length of the chain, being short (up to six carbons), medium (ranging between six and twelve), long (from thirteen to twenty-one) and very long (more than twenty two) FA, and/or the optical activity of those species (relying on the 3D structure). Stereospecifically, each particular double bond could be either *cis*, if the structural configuration on which adjacent hydrogen atoms are on the same side of the double bond (and therefore “bulky” sides are closeby) or *trans*, when the two hydrogen atoms are bound on opposite sides of the double bond.

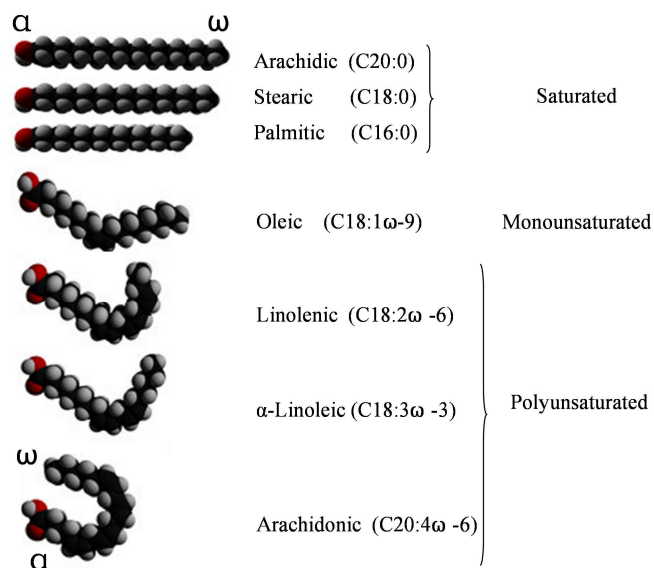


Figure 1. FA structure. 3D representation of different FA structures and its classification, according to the number of double bounds. It can be clearly seen that the number of unsaturations bend the aliphatic chain rendering each FA to specific steric impedances. Symbols α and ω represented the first and the last carbon atom of the aliphatic chain respectively.

These variable situations (e.g. chain length, number of double bonds and/or stereospecificity of those) physically affect to the properties of different FA. This variability of the sterical incapacitances and packing difficulties at low scale are reflected, at macromolecular level, in terms of melting point temperature, fluidity and/or viscosity variations, as other hemorheological parameters. For instance, longer chains (increased number of carbon) are related to lower melting temperature. Double bonds also favour lower melting points and increased fluidity. Finally, *cis* configuration is another factor that caused melting point decrease, compared with the same FA in *trans* configuration. This data is summarized and presented in Table 1 and Figure 2.

Fatty Acids Melting Points			
Saturated	T (°C)	Unsaturated (<i>cis</i>)	T (°C)
Butiric (C4:0)	-6	Myristoleic (C14:1 ω-5)	-4
Caproic (C6:0)	-3	Palmitoleic (C16:1n ω-7)	1
Caprilic (C8:0)	17	Oleic (C18:1 ω-9)	13
Capric (C10:0)	32	Gadoleic (C20:1 ω-11)	23
Lauric (C12:0)	44	Unsaturated (<i>trans</i>)	
Miristic (C14:0)	54	Elaidic (C18:1 ω-9)	46
Palmitic (C16:0)	63	Vaccenic (C18:1 ω-7)	40
Stearic (C18:0)	69	Linoelaidic (C18:2 ω-6)	28
Araquidic (C20:0)	77	Polyunsaturated	
Behenic (C22:0)	80	Linoleic (C18:2 ω-6)	-5
Lignoceric (C24:0)	84	α-Linolenic (C18:3 ω-3)	-11
Cerotic (C26:0)	88	Araquidonic (C20:4 ω-6)	-50
		Docosohexaenoic (C22:6 ω-3)	-44

Table 1. Melting point of different FA. Celsius degrees.

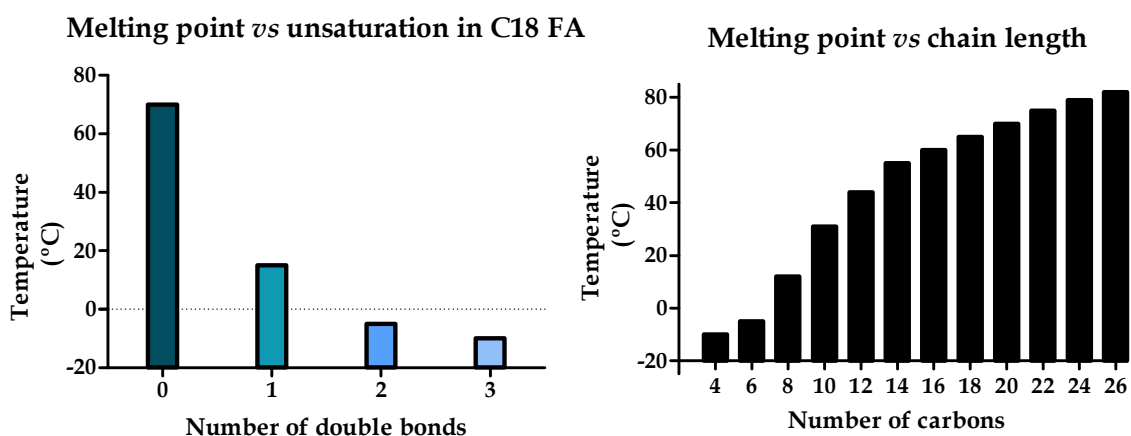


Figure 2. FA melting points. Graph representation of melting point temperatures of various FA in relation with the number of double bounds (left panel) or the number of carbon in the aliphatic chain (right panel). Data obtained from (Nelson DL, Cox 2005) and (Knothe and Dunn 2009).

As previously shown, structural differentiation confers a wide capacity for fine tuning modulation. This is biologically relevant since, within cells, free FA are often rapidly converted

into more complex forms, including phospholipids (PL), plasmalogens, triglycerides (TAG) and derivatives of those. We will later dig deeper into PL metabolism, biosynthesis and maintenance but just as an introduction for now, PL are major constituents of any membrane bilayer within a cell, also with sterols, sphingolipids and proteins. All these biomolecules are held together by coulombic, Van der Waals and hydrogen bonding forces. Regular composition of PL consists in diglyceride (two fatty acid chains covalently bonded to a glycerol molecule through ester linkages) and a phosphate group and a simple organic molecule (commonly choline) attached to it. This particular composition of glycerophospholipids (GPL), with one polar head (phosphate) and a non-polar (or low polar) chains allows an amphipathic behaviour in aqueous solution, since they possess one hydrophobic side (aliphatic chain tail) but also, a hydrophilic head on the molecule (phosphate group, represented as a red dot in Figure 3, next page). This organisation in aqueous solution is the key chemical PL property for being perfect candidates for, in general, cell organelle membrane scaffold.

Different GPL “families” are studied based on the structure of the polar group, finding phosphatidylcholines (PC), phosphatidylethanolamines (PE), phosphatidylinositols (PI), phosphatidylserines (PS) and cardiolipins (CL). Each family comprises numerous *molecular species* that keep the same head group but changed acyl chain; some relevant forms are showed in Figure 3. Synthesis location of those families differs, since CL and majority of PE are synthesized in mitochondria whereas other PL families are mostly generated in the endoplasmic reticulum (ER). This is also relevant for FA (discussed later in chapters 1.B2 and 1.C2) and plasmalogen synthesis, since many steps are started in peroxisomes to be finished at ER and/or mitochondria implying that a good communication between those organelles and a correct inner-cell trafficking is crucial for an optimal lipid balance.

Arousing from particular FA properties mention above, but also with increasing complexity by playing among combinations of different polar groups and/or residues, viscosity, curvature, permeability, elastic compressibility and fluidity of such membranes could therefore be successfully modified solely (but not only) by mixing specific amounts of particular FA incorporated to GPL.

1.A1.1.- Glycerophospholipids

Structurally, while the hydrocarbon chain at the *sn*-2 position is usually ester-linked to the glycerol moiety, the one in the *sn*-1 position can be linked via an ester, ether or a vinyl ether bond. Length of the alkyl chain typically varies from 14 to 24 carbons and, for the most relevant GPLs, the number of double bonds ranges from 0 to 6. Usually, alkyl chain in the *sn*-1 position is saturated or monounsaturated, while that in the *sn*-2 position is often polyunsaturated but again, the degree of unsaturation would change wedge form of the acyl chains making it more or less bulky. Even more, since membrane bilayers (outer leaflet cell membrane, Golgi, ER, peroxisomes and/or mitochondria) are sprinkled with numerous proteins, interaction with those in specific regions (eg lipid rafts) would affect its association (itself but whitening other proteins too) and obviously its functional outcome (reviewed in (Stillwell and Wassall 2003) and (Nelson DL, Cox 2005)).

Due to the large number of different alkyl chain combinations, each GPL “family” consist of numerous structurally different molecular species, thus eukaryotic cells can contain hundreds of

ordered) were more rigid and it is believed that oxygen diffusion events were reduced on those areas (Dumas et al. 1997; Subczynski, Hyde and Kusumi 1991). So, in general terms, at liquid ordered phases there was lower quantity of tocopherol and lower oxygen diffusion, hence, components were correctly localized, i.e. where more peroxidation events can occur. Altogether this data suggest that specific and controlled positioning of all membrane constituents, GPL, SM, CHO, proteins and antioxidants, is crucial for a correct membrane function.

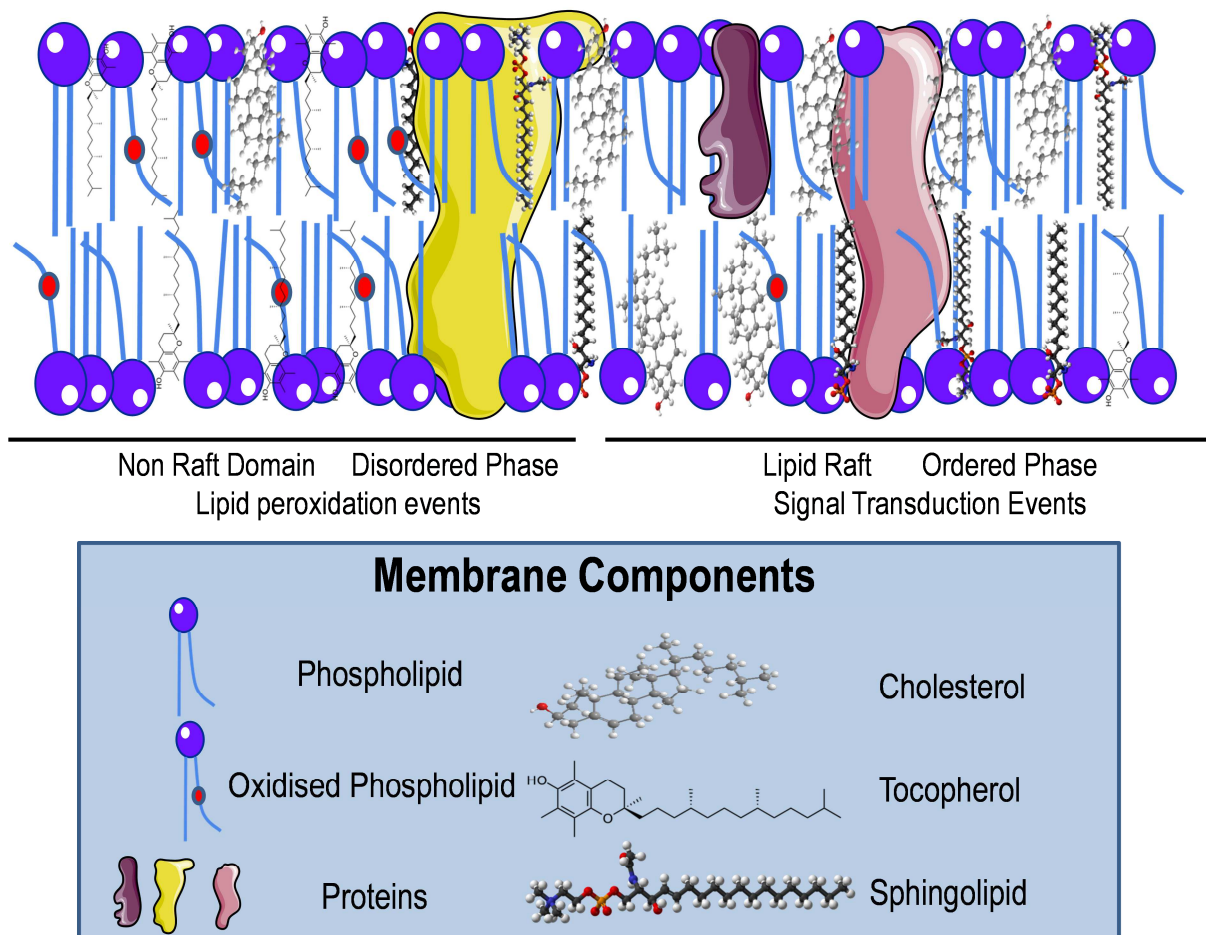


Figure 4. Membrane representation. Components of a membrane showing lipid raft domains and their characteristics (Higher CHO, SM and proteins enrichment), whereas non raft domains had higher levels of tocopherol (but also more oxidised PUFA). Not to scale.

In chapter 1.B3 we will dig deeper on membrane modification mechanisms by deacylation and reacylation processes and in the next section and 1.C2 we will say a few words about lipid signalling events. Just mention here that both are very active processes and thus FA biochemistry not only comprises the so cold “free” FA but also GPL, TAG and much more complex derivatives (i.e. lipoxins, eicosanoids, docosanoids or plasmalogens; discussed in section 1.C1.2) whose powerful functions are still under debate.

1.A2 PUFA major functions

PUFAs have been related to interfere and/or regulate a huge variety of functions in very different organisms (i.e. birds, worms, humans). In general, functions could be clustered in a number of physiological roles, as: i) energy substrates; ii) structural and functional components

of cell membranes and, finally, iii) signalling purposes, themselves, and/or as precursors for lipid mediators, components affecting signal transduction pathways and gene transcription. Therefore, among others pathophysiological events, PUFAs have been linked to:

PUFA -related Processes	
Process	References
Learning and memory	(Hashimoto et al. 2006)
Neurotransmitter release	(Aïd et al. 2003)
Autocrine and paracrine communication	(Nicolas G Bazan 2008; Kitson et al. 2013)
Physiquiathric and mood disorders	(Freeman et al. 2006; McNamara et al. 2013)
Immunity and inflammation	(Calder n.d.; Serhan et al. 2004)
Membrane ion channels, enzymes and receptors	(Eckert et al. 2011; Gawrisch et al., 2008.; Im 2012)
Adhesion molecules	(Yates et al. 2011)
Apoptosis	(Akbar et al. 2005)
Neurogenesis and neurite growth	(Calderon and Kim 2004; Innis 2007)
Pro/antioxidative potentiation	(Nicolas G Bazan 2005; J.-M. Lee and Johnson 2004; Yavin, Brand, and Green 2002)

Table2. PUFA-related processes. List of processes and references in which PUFAs had relevant functions.

1.A2.1.- Energy substrates

Dietary FAs, in the form of TAG, are the primary source of the body's energy representing (in a balanced diet) 25-35% of the total energy intake in humans. Compared with proteins and carbohydrates, FAs have about twice as much energy value and their storage in adipose tissue needs less amount of water. The estimated energy value of long and very long chain FAs is about 38 kJ/g, and for those medium chain FAs approximately 29 kJ/g. While short chain FAs represent a local energy source for enterocytes and colonocytes, the others must be delivered (discussed in section 1.B1.1), generally in esterified forms or albumin-complexed. Also important, FAs take part in the process of transferring and depositing crucial lipid soluble molecules (such as vitamins A, D, E and K) and are precursors of lipid mediators.

Unfortunately, as fat intake has increased within recent years in western-type environments (reviewed in (Simopoulos 2011)), the percentage of FA in the energy intake could represent nowadays up to 40-45% of the total, depending on food sources and habitual consumption. Hence, the evolutionary positive role of FA as a energy storage for further necessities, altogether with the sedentary lifestyle of western population and their increased fat consumption turned nowadays fat into the focus of non-communicable diseases. Especially since epidemiological studies pointed that visceral adiposity (possibly emerged from fat intake unbalance) was a risk factor to developed metabolic syndrome (Björntorp 1993). Therefore, to conceal this major threat of western civilization, nutritional recommendations have been established about total fat and particular fat types, including essential FA and ω -3 PUFA (discussed in chapter 1.B4).

1.A2.2.- Structural membrane actions

As stated in the previous chapter, FAs, in the form of GPL, are the structural components of all cell membranes. Their profile have a profound influence in the biophysical properties of those membranes and, thus, the activity of membrane associated proteins (i.e. enzymes, ion channels, receptors and transporters) (Nelson DL, Cox MM. 2005). As indicated above, the tuning capacity of specific molecules (CHO and/or specific proteins) or the degree of unsaturation of FA present in GPL to promote higher or lower membrane fluidity should be considered (Chapkin et al. 2008; Stulnig et al. 2001). Finally, a very remarkable function of fats as insulators is found in many living organism, especially relevant, for instance, in marine mammals.

1.A2.3.- Signalling purposes

A) FA itself as second messengers

From preliminary studies by Berridge in 1984 (Berridge 1984), the hydrophilic inositol 1,4,5-triphosphate (IP₃) and the lipophilic 1,2-diacylglycerol (DAG) are considered second messengers. Both are generated from the membrane lipid phosphatidylinositol 4,5-bisphosphate (IP₂) by the action of a phospholipase C (PLC, for a review on its regulation see (Bunney and Katan 2011)). Mechanistically, IP₃ interacts with an intracellular IP₃ receptor and leads to the mobilization of Ca⁺² from intracellular stores (ER and/or mitochondria), whereas DAG directly activates protein kinase C (PKC) and thereby initiates important down-stream signal transduction cascades (Nelson DL, Cox MM. 2005). Other phospholipases (discussed in section 1.B3.1) would also release some FA and derivatives, which had relevant signal transduction activities. For instance, phosphatidic acid (PA, excised by phospholipase D, PLD), is rapidly converted to DAG (with the aforementioned consequences). But, in parallel, this substance is necessary for appropriate mTOR (mamalian target of rapamycin, a key protein representing a relevant survival cascade) signalling too (Fang et al. 2001). Through phospholipase A (PLA) action, docosahexaenoic acid (DHA, C22:6 ω -3) or arachidonic acid (AA, C20:4 ω -6) could be also released from the membranes and interact with multiple nuclear transcription factors (discussed below) and/or could be non-enzymatically oxidised too and those new lipid species (e.g. HETE, NPD1, 8-iso-PGF_{2 α} , among others) may interact with specific cellular receptors for achieving another different outcome.

From the complex lipid signalling overview seen before, which is in fact much more coiled, it seems clear that there is not a single mechanism for FA regulation of gene transcription. The classical point of view implied a specific FA to enter the cell in order achieve its regulation, but nowadays is well accepted that this could be overcome through membrane receptors (e.g. G-proteins coupled, reviewed in (Kostenis 2004)) which not only turn active by non-esterified FA, but also very complex derivatives. It is therefore depending upon the cell-specific context, the target genes or the overall status of the cell, that FAs could take very different routes to alter transcription (Duplus and Forest 2002).

B) FAs as precursors of lipid mediators

Through the action of multiple enzymes, but through non-enzymatic oxidation too, FAs are converted into relevant signalling lipid species, such as eicosanoids (i.e. LT, PG, prostacyclines -PGI- and tromboxanes-TX), isoprostanes, endocannabinoids, docosanoids (maresins, docosatrienes, neuroprotectins, neuroprostanes), resolvins (D and E series) and sphingolipid derivatives (e.g. ceramide, sphingosine 1-phosphate, sphingosylphosphorylcholine). All those species compose an enormously wide family which exerts a myriad of different outcomes in multiple locations across the body, but which could be separated, in a very simplistic view, into pro or anti-inflammatory ones, and will be discussed in chapter 1.C.

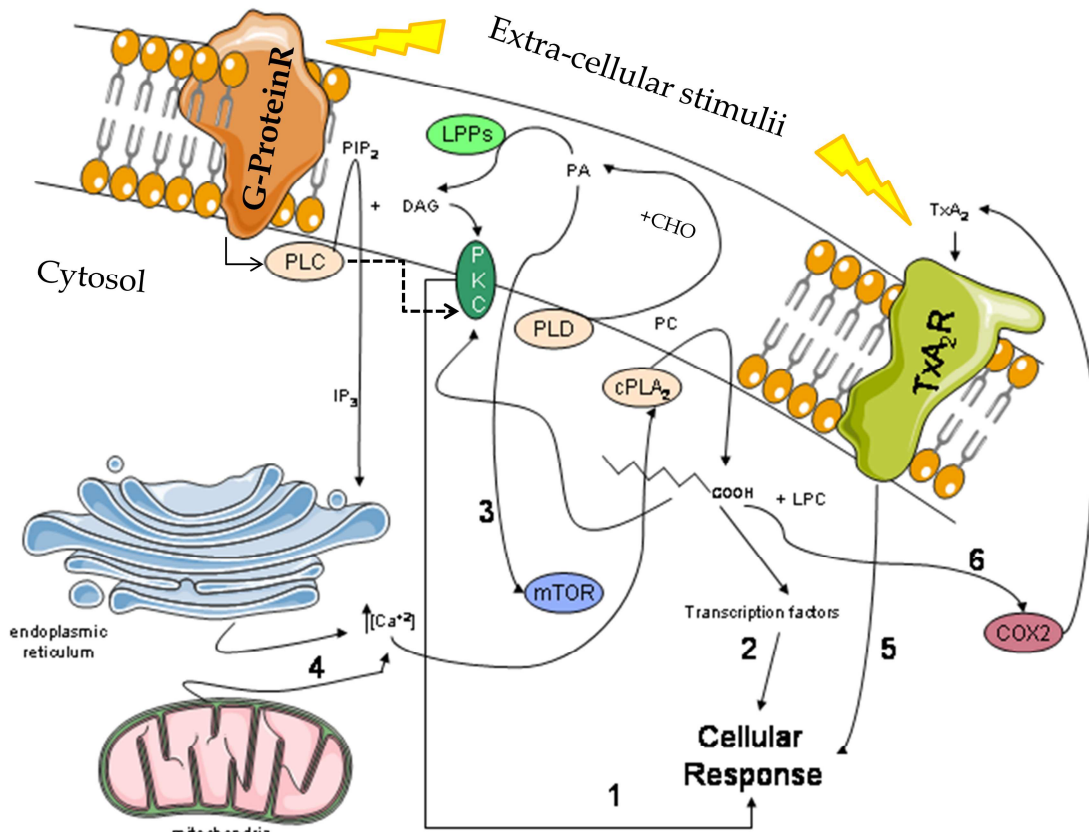


Figure 5. PUFAs cellular signalling. Cellular signalling response to FA and its derivatives could be achieved in multiple ways: (1) DAG direct action on protein kinase C (PKC) will trigger kinase pathways. (2) Free FA, cleaved from membrane by cPLA₂ (which is sensible to Ca⁺² concentrations), would interact with different transcription factors (discussed below) and translocate to nucleus where they activate specific pathways. (3) PA (which could be released by phospholipase D- PLD, action under extracellular receptor stimulation) is necessary for the correct mTOR signalling. (4) Ca⁺² release could be triggered by specific IP₃ (whose accretion could be PLC-dependent, through extracellular G-protein receptor stimulation) receptors present in ER and start signalling events. (5) Specific membrane receptors (e.g. TXA₂R and/or G-protein-coupled receptors, but also PG-dependent ones, among others) could themselves initiate an appropriate signalling cascade. Although, upon stimulation (e.g. PLC), they may influence PKC behaviour too, present in the surroundings, and ultimately affect cellular responses (e.g. nuclear factor kappa-light-chain-enhancer of activated B cells -NFkB- or mitogen-activated protein kinase -MAPK- cascades). (6) Finally, another possibility for free FA is to undergo further processing to achieve specific lipid products (through action of cyclooxygenases-COX-, lipoxygenases-LOX- and/or cytochrome P450-CYP450) which potentially enhance paracrine and/or autocrine signalling. (cPLA₂, Ca⁺²-dependent phospholipase A₂; LPC, lysophosphatidil-choline; PA, phosphatidic acid; PC, phosphatidil choline; TXA₂, tromboxane A₂; COX2, cyclooxygenase 2; CHO, Cholesterol; LPPs, lysophosphatidic acid phosphatase).

C) Palmitoylation

Recently, a new form of post-translational modification involving FA attachment was found, the palmitoylation. This modification consists in the introduction of the palmitate lipid in the cysteine residues of a specific protein (a recent revision on the topic could be found (Blaskovic et al. 2014)). Another cellular lipidations such as myristoylation and prenylation, can also occur, opening a new field in signalling regulation, but due to its chemical properties (specially its reversibility), palmitoylation seems the most relevant. Lots of proteins have been shown to be palmitoylated, therefore, multiple mechanisms of cellular metabolism are affected (e.g. signalling, ion transport across membranes, protein folding and degradation, synaptic plasticity, endocytosis, exit from the ER, transcription, bacterial and viral infection, among others; reviewed in (Nadolski and Linder 2007 and Planey and Zacharias 2009)). The obvious consequence of this modification is clear, to upgrade protein lipophilicity and help in any-membrane attachment, which ultimately results in a variation of its regular location. This was proposed to affect, for instance, synaptic plasticity (Conibear and Davis 2010) and Ras (proto-oncogene) regulation (Rocks et al. 2005). Among the identified 23 DHHC (core Asp-His-His-Cys motif which is essential for transferase activity, *in vitro* and *in vivo* (Huang et al. 2009)) mammalian palmitoyl-acyl-transferases, there was found several neuronal-specific, which exhibit a particularly marked substrate specificity, pointing that this post-translational modification is tightly regulated. However, due to the multiple mechanisms potentially affected, palmitoylation is still a wide open field for research.

D) FA direct interaction with transcription factors

Transcription factors are protein structures that bind to specific DNA sequences, usually close to the target genes, in order to control (commonly, by enhancement or repression at the promoter area) the flow of genetic information from DNA to messenger RNA. This specific DNA interaction is the defining feature of any transcription factor, that is, they must contain one or more DNA-binding domains. On the contrary, other molecular species, such as coactivators, chromatin remodelers, histone acetylases-deacetylases or methylases, which alter genetic flux too, lack those specific domains. FAs, specially long chain ones (C20-C22) but also medium and some lipid derivatives (e.g. epoxyeicosatrienoic acids, ETT (Liu et al. 2005)) could act as ligands of these cellular triggers. Hence, they could modulate gene transcription which, ultimately, influences cell signalling and fate (Chapkin et al. 2008). Two general mechanisms characterize FA control over transcription factors: one implies direct binding to the protein structure (see below) whereas the other refers to the greater stability and/or abundance of a specific transcription factor, but a direct binding is unlikely.

Therefore, among some others, non-esterified long chain unsaturated FA (C20-22) and some of their metabolites have been identified as effective ligands of nuclear receptors and/or transcription factors like:

PUFA Interactions Among Nuclear Receptors		
Nuclear Receptor / Transcription Factor		References
Direct Interaction	PPAR $-\alpha, -\beta/\delta, -\gamma 1$ and $-\gamma 2$	(Xu et al., 1999) reviewed in (Berger et al., 2002)
	LXR α	(Ou et al., 2001)
	RXR α	(Lengqvist et al. 2004; de Urquiza et al. 2000)
	HNF4 α and HNF4 γ	(Dhe-Paganon et al. 2002; Wisely et al. 2002)
Indirect	SREBP	(Xu et al. 1999)
	ChREBP	(Dentin et al. 2005)
	NF κ B	(Camandola et al. 1996)

Table 3. PUFAs interactions among nuclear receptors. List of references and interactions founded between nuclear receptors/transcription factors and PUFAs and their derivatives.

We will discuss now some details of the aforementioned transcription factors:

1.-Peroxisome-proliferator activator receptor (PPARs) are members of the steroid hormone nuclear receptor superfamily and play important roles in lipid metabolism and homeostasis, generally through an induction of FA degradation (increasing peroxisomal and mitochondrial oxidation, reviewed elsewhere). Three subtypes of PPARs have been characterized in humans, PPAR- α , $-\gamma$, and $-\delta$ (the latter also known as PPAR- β ; γ generates three isoforms) whose mechanism of action implies homo and/or heterodimerization (the latter, more frequently) with the 9-*cis*-retinoic acid receptor (RXR) and binding to PPAR-responsive elements in the promoter region of various target genes, ultimately regulating their transcription. Their DNA and protein sequences are highly conserved among them, especially upon the DNA binding domain, meanwhile the ligand binding pocket possess a wider variation to achieve their specific selectivity (Xu et al. 1999). There have been found homologous proteins in many different species, including all metazoan phyla, pointing out the relevance of their physiological functions across evolution (reviewed in (Escriva, Delaunay and Laudet 2000)).

In rodents, as well in humans, PPAR- α is highly expressed in the liver, skeletal muscle, heart, and kidney meanwhile PPAR- γ is predominantly found in white and brown adipose tissue, colon, endothelial and vascular smooth muscle cells and, to a lesser extent, in immune cells and liver. Finally, PPAR- δ is ubiquitously expressed, but its action is especially relevant in skeletal muscle. In the central nervous system (CNS), expression for all isoforms was found, but δ is the predominant (Basu-Modak et al. 1999). Thanks to knock out, inducible, deletion and silencing studies upon the family members performed in rodents over the past years, a complex time-dependent cell-specific distribution was found, in CNS too (reviewed in (Keller et al. 2000)). Whereas PPAR- α and γ are expressed at very low levels, predominantly in astrocytes and microglia respectively, PPAR δ has been found in neurons of numerous brain areas as well as in immature oligodendrocytes, revealing a key feature helping a correct axon myelination (Peters et al. 2000). Interestingly, recent studies (Ciana et al. 2007) had demonstrated a differential male-to-female induction of PPAR, at least for the liver, which could be on the basis of the different lipid handling by each of the two sexes.

Regarding its activation, several FA and natural occurring derivatives (e.g. eicosanoids, PG, HETES) interact with PPARs (Krey et al. 1997), besides lots of synthetic agonist had been

proved to do so (reviewed in (Fruchart 2013; Derosa and Maffioli 2012; Bernardo and Minghetti 2006 and Bhurruth-Alcor et al. 2010) with particular preferences between the different isoforms. Synthetic thiazolidinediones (e.g. pioglitazone and rosiglitazone, already approved treatments for type-II diabetes) are preferred substrates for PPAR- γ induction, whereas fibrates do so to PPAR- α or thia-fatty acids (synthetic sulphur-containing FA with plasma lipid lowering effects) could have an effect on all of them (Bhurruth-Alcor et al. 2010).

2.- Liver-X-Receptor (LXRs) are crucial nuclear receptors for lipid homeostasis (for a review in this topic see (Jakobsson et al. 2012; Repa and Mangelsdorf 2002)). *In vitro* LXR interaction with FA (serving as direct antagonists) has been proved for some of the PUFA family (Ou et al. 2001), but surprisingly not for the unsaturated stearic acid (C18:0). In response to oxysterols (derivatives of CHO), the two LXR isoforms (α and β , with a 77% amino acids homology) formed heterodimers with retinoid X receptor to be fully activated and induces the expression of genes required for the reverse CHO transport. This fact explains the extensive research aimed to develop synthetic agonist to help in dyslipidemia treatments, in general, and more specifically in metabolic syndrome and related cardiovascular disarrangements, being statins of special relevance (for a review on the statins and their relevance in CNS see (A Farooqui et al. 2007)). LXR activation induces genes for *de novo* lipogenesis in liver in two separate pathways: i) transcriptional induction of SREBP1c (Repa et al. 2000); ii) by up-regulation of ChREBP expression (Cha and Repa 2007). LXR-mediated increases in both ChREBP and SREBP-1c will raise expression of lipogenic enzymes to enhance fatty acid synthesis from glycolytic end-products, being therefore considered a master hepatic lipogenic factor.

3.-Sterol regulatory element-binding proteins (SREBPs) comprise another transcription factor family. Composed of three members (named 1a, 1c and 2 respectively), they are activated (by cleavage from ER-Golgi and nuclear membranes) when low levels of cellular CHO are present. In order to enhance CHO and FA biosynthesis, they bind specific DNA regions (10 bp length, named sterol regulatory element) located in promoter regions of various genes (for a review on the SREBP topic see (Xiao and Song 2013)). SREBP-2 is relatively selective for CHO biosynthesis enhancement, meanwhile SREBP-1c activates the FA pathway (e.g. promote expression of the fatty acid synthase) and SREBP-1a remains in between, with a mild activation of both. Two genes encode their protein sequences, besides the latter had different splicing to raise the two isoforms (Brown and Goldstein 1997). In relation with SREBP-1c, PUFA cause an activation, whereas, surprisingly, saturated or monounsaturated FA suppressed the induction of lipogenic genes by inhibiting its expression (reducing mRNA stability) and processing (Nakamura et al. 2004).

4.- Carbohydrate-response element-binding protein (ChREBP) heterodimerizes with Max-like protein X and bind to the carbohydrate response element regions of the DNA when a substantial decrease of AMP/ATP ratio is present. Recently, it has been reported that ChREBP has two isoforms, ChREBP- α and ChREBP- β , and that they are located mainly in the cytosol and nucleus, respectively (Herman et al. 2012). Moreover, ChREBP is susceptible of being phosphorylated by various stimuli (e.g. protein kinase A, adenosine-monophosphate kinase), and therefore blocked in the cytosol, inhibiting the control over genes related to glycolysis, lipogenesis, and gluconeogenesis (e.g. liver type pyruvate kinase, fatty acid synthase and glucose-6-phosphatase catalytic subunit, respectively). Thus, the main function of ChREBP is to

regulate metabolic gene expression to convert excess carbohydrate into triglyceride, rather than glycogen. But this protein could repress PPAR- α , hypoxia inducible factor-1b and sirtuin-1 (among other transcription factors, for a review see (Iizuka 2013)) activities too, having a greater gene expression interference.

5.-Nuclear factor kappa-light-chain-enhancer of activated B-cells (NF κ B) pathway represents a key factor in cell survival. It had been implicated in a myriad of diverse situations, from the immune response to infection (the origin of its discovery) to cancer, as well as inflammatory and autoimmune diseases or synaptic plasticity and memory events (for a review see (Gilmore 2006)). Early studies about PUFA action on the pathway, showed a differential role for ω -3 and ω -6 fatty acids (Camandola et al. 1996) and it has been proved that some of PUFA derivatives affect it too (Ho et al. 2008; Sánchez-Galán et al. 2009). Remarkably, apart from the direct influence of PUFA and its derivatives in the signalling cascade, NF κ B pathway is affected by PKC action. Hence, several members of the pathway are phosphorylated or helped to be stabilised (e.g. IKK $_{\alpha/\beta}$, RelA, among others) by most of the PKC isoforms studied (but with particular cell/tissue or pathology variations), providing another frame for PUFA's influence on cell fate.

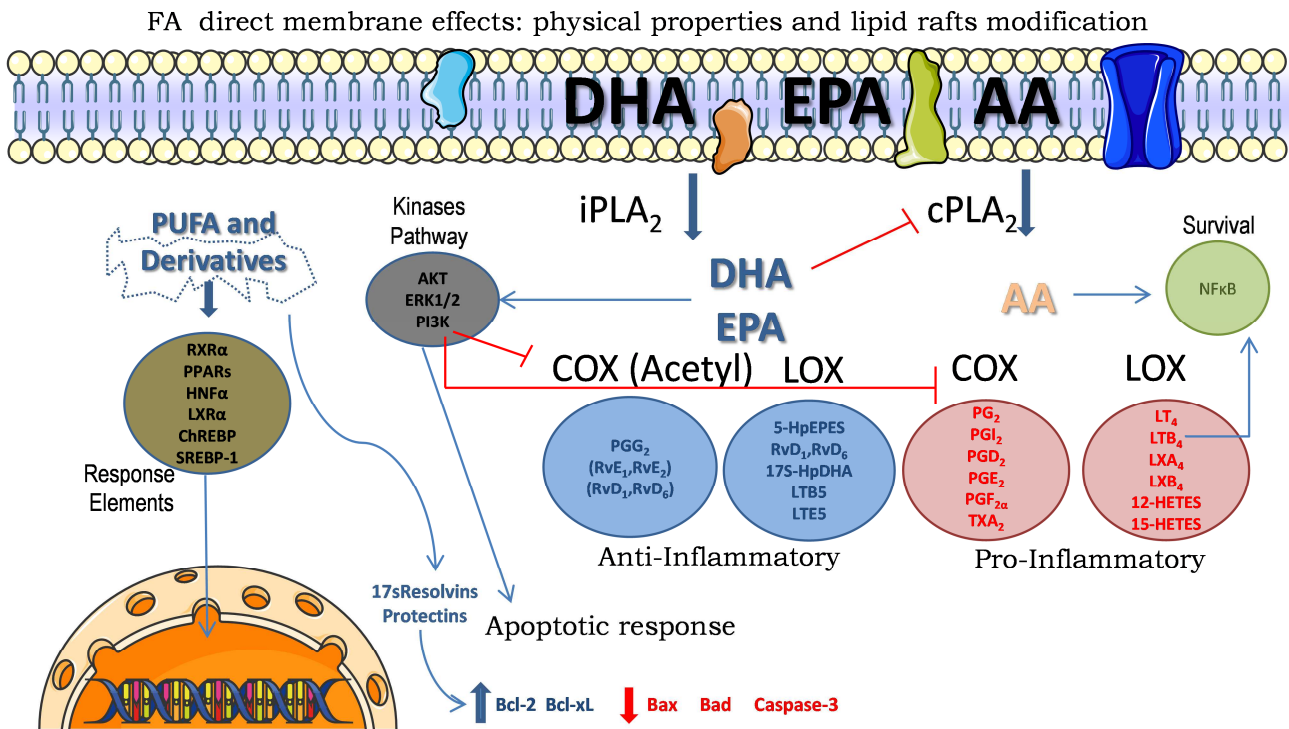


Figure 6. PUFAs actions. Apart from their specific membrane functions, under PLA₂ activity, PUFA are released from the membrane and could initiate various cascades and/or directly interact with response elements to enhance different cellular mechanisms. Importantly, PUFAs could also serve as substrates for the synthesis of multiple signalling molecules.

1A2.4.-Cell Survival

Akbar and co-workers (Akbar et al. 2005) linked DHA to crucial signalling cascades, PI3K-AKT/mTOR. As a consequence, it has been proved that cell survival is altered by various kinases pathways, susceptible to be PUFA and PUFA-derivative sensitive. For instance, the phosphoinositide 3-kinase (PI3K) and the MAPK pathways are activated in injured neurons

(Henshall et al. 2002) as well as in tumours (reviewed in (Bertucci and Mitchell 2013)). PUFA and their anti-inflammatory derivatives could alleviate PI3K mediated cell death, at least in yeast models (Couplan et al. 2009) or in lipopolysaccharide-induced microglial inflammatory response (Xu et al. 2013), but could also result in increased mortality in cancer cell-lines (Toit-Kohn, Louw and Engelbrecht 2009). Furthermore, in activated microglia, PI3K inhibition enhanced prostanoids production, and expression of COX-2 could be regulated by PI3K as a response to neuroinflammation (de Oliveira et al. 2012). Interestingly, a synthetic derivative of PGF_{2α}, latanoprost, is able to promote retinal ganglion cell survival and neurite outgrowth through a PGF receptor-mediated modulation of the PI3K pathway (Zheng et al. 2011). Therefore, MAPK pathways are involved in neuroinflammation in many ways, including the enhancement of IL-6 synthesis in sensory neurons (St-Jacques and Ma 2011) and the regulation of IL-1-mediated COX-2 expression (Moolwaney and Igwe 2005) and those pathways could be affected by different lipid derivatives in a feedback loop.

Concluding: DHA and AA, two different motorways.

DHA and AA are chosen as paradigmatic examples from the two main eukaryotic fatty acid families, ω -3 and ω -6 respectively. They are “endproducts” themselves since their unique characteristics confer them special functions. Besides, they are crucial because they represent main precursors of a broad range of paracrine substances acting in a wide type of schemes, with different outcomes. In terms of inflammation, it is generally well accepted that both families symbolize two different actions in response to an insult (with the exception of AA-derived lipoxins). This is, AA and ω -6 derivatives initially predisposes to inflammation whereas DHA, EPA and ω -3 derivatives alleviate and, up to an extent, try to solve the urgency.

For one simple molecule, DHA, to have an effect in so many presumably unrelated processes, it should function in a fundamental level, common to most cells. On the other hand, ω -3 docosapentaenoic acid (DPA) is a DHA precursor and membranes enriched in this FA posse very subtle membrane fluidity alterations respect to those with DHA. Furthermore, ω -3 DPA is only two protons diferent, requires less energy (and reduced complexity) to be synthesized and it is more resistant to peroxidation than DHA. Why this molecule is tenaciously conserved through evolution (especially concerning its visual and cognitive virtues) is discussed in an interesting publication (Crawford et al. 2013).

It is been proved that ω -3, as well as ω -6 FA, are involved in: i) hormone production; ii) formation of potent lipid peroxidation products (which could be detrimental, but signalling useful too, reviewed in section 1.C2.3) ; iii) direct effectors on specific enzyme activity or as indirect effectors through transcription events and/or iv) membrane structure and function alterations (reviewed in (Stillwell and Wassall 2003)). All those general modes of action are not mutually exclusive, rendering ω -3 and ω -6 FA pleiotropic effects.

1.B PUFA Maintenance

1.B1 PUFA systemic and cellular delivery

1.B1.1.- Systemic delivery

Along digestion, phospholipase A₂ (discussed later in section 1B3.1), inespecific esterases and lipases, and bile acids are secreted, initially at the stomach and through small intestine. Most of those enzymes are originated in the pancreas and emulsified fats breakdown into free FA, mono and diglycerides and cholesterol-esters to form mixed micellae. They are composed by bile acids, CHO (dietary, and bile-secreted too), the aforementioned break fats, PL and dietary liposoluble vitamins (A, D, E and K). This process takes place mostly in the upper part of the small intestine, and along it, increased amounts of lipolysis products enrich micellae composition. Those enzymes digregate lipids at neutral pH and the lipid enrichment of micellae renders then “soluble” and easily absorbed by enterocytes at microvessels, in a passive manner. But this uptake could be also helped by specific proteins, such as CHO capturing proteins (i.e. Niemann Pick C1 like 1), ATP-binding cassette transporters or microvessel membrane-FABP (fatty acid binding protein) (Berne and Levy 2000). ER of enterocytes reesterifies FA and monoglycerids to obtain triglycerids (major chylomicron component, up to 77%), PL (up to 9%) and Cholesterol-esters (3%) to form, combined with apolipoproteins (synthesized in the rough-ER and mainly composed by apolipoprotein B, ≈100 KDa, 1%), the chylomicrons. These substances, conformed by a lipid core but protein coated, could range from 0.08 to 0.6 micrometers and are secreted to lymphatic system, bypassing portal vein transportation and liver, to arrive wherever they are needed along the lymph and finally re-entering into the blood stream at the thorax. This is the common transportation for long FA, but it’s not the case for those short and medium chain lengths FA. Due to their higher aqueous solubility they avoid reacylation, chylomicron forming and secretion, being ready for use through blood stream from enterocyte, thus, entering directly to the liver by portal circulation.

Passing across adipose tissue and skeletal muscle capillaries, plasma chylomicrons are cleared. This could take around one to two hours after ingestion; meanwhile those substances could reach up to 2% of the plasma, conferring it turbidity and a yellow colour. Lipoprotein-lipase is responsible for this clearance, acting at capillar endothelium level. These enzymes hydrolysed triglycerids and PL at chylomicrons to form glycerol and free FA which immediately diffuses through membranes. Those FA are readily re-esterified to be stored for further requirements. Hence, the liver plays key roles: i) decomposing FA to obtain energy; ii) synthesising triglycerides from carbohydrates; iii) synthesising other lipid compounds from FA, specially CHO and PL. Meanwhile, adipose tissue: i) stores triglycerides forming fat; ii) is a major endocrine organ, synthesising or assisting in the synthesis of important hormones as adiponectin, TNF α , IL-6, leptin, resistin among many others; iii) regulates free FA levels; iv) the brown type one generates heat by uncoupling mitochondrial respiratory chain. Both tissues are therefore central organs controlling dietary fats and its further release when required.

Moreover, free FA transportation occurs, representing 5% of total lipids in plasma after chylomicron clearance. Nevertheless, it is not usually related with digestion processes, instead it is more commonly linked to energy expenditure recovery. There are at least two signals which cooperate to evoke FA delivery to form storage depots. One is the α -glicerophosphate decay in tissues with high energy demand and/or secondly, hormone-sensitive lipase activation.

However, free FA in plasma is scarce, regularly only 0.45 g in the whole circulatory system. Surprisingly, this low relative amount is enough, since its turnover is especially high. Half-life of a plasmatic FA is around 2-3 minutes, and when depleted, new FA is desorbed from storage depots. The flexible amounts of FA transported in plasma helped by albumin are also remarkable. Starvation or diseases such as type-I diabetes deplete carbohydrates and, under such conditions, FA/albumin ratio could peak to 30/1, when is normally around 3/1.

In fact, the majority of lipid delivery along the body is lipoprotein linked. Apart from chylomicrons, there are four types of lipoproteins, which could be classified attending its density after centrifugal distribution (expressing a ratio between triglycerides and proteins presented on them): i) very low density, containing high amounts of triglycerides, but moderate PL and CHO; ii) medium density, which are in fact very low density ones but half depleted of triglycerides (therefore raising its PL and CHO percentage); iii) low density, already triglycerides depleted, with very high amounts of CHO, but moderate PL quantity and iv) high density ones, where protein composition rises to 50%.

These are some important points related to lipid transport from dietary sources to the whole body through the circulatory system, but, what happens with lipids crossing cell membranes or the inner trafficking within the cell? These issues will be discussed below.

1.B1.2.- Regulation across cell membranes

The physical properties mentioned before claimed for very low FA solubility in aqueous solutions. For decades, there had been controversy on whether FA transportation across membranes occurs eventually by chance (by simple passive diffusion events) or facilitated by proteins. Nowadays the general idea is that both issues could happen, but for optimization, protein-mediated transport is more common.

Flip-flop and diffusion events take place naturally. Hamilton and co-workers (Kamp and Hamilton 2006; Kamp and Hamilton 1992; Hamilton 2007) demonstrate not only that proteins are not completely necessary for fatty acids to go across cytosolic membrane but also that they are not required for releasing those fatty acids into cytosol. Further, they demonstrated that extracellular membrane crossing could be much easier for fatty acids than for glucose, water or small non-electrolytes.

But driving forces for free diffusion are based on concentration and gradient generation, so it would be impossible to meet the requirements when high metabolic tissues demand it fast (e.g. muscle upon contraction). Thus, from a physiological point of view, it would be interesting to have a better control of FA trafficking to: i) ensure FA uptake when low levels are present inside cytosol; ii) avoid FA export when low levels are present outside the cell and uptake when inner quantities are sufficient (the latter may not take place because of gradient loss); iii) potentially select a particular FA type (specific enrichment) and finally iv) allow those rapid adjustments when metabolic fluctuations occurs. A scheme representing FA membrane trafficking is pictured next page in Figure 7.

So, in order to optimise transportation to and across biomembranes, FA and some of their derivatives, are helped by proteins. For instance, albumin levels in plasma and interstitial spaces

could range from 300 to 600 μ M and such an “unspecific” protein may help to “dissolve” 100 to 400 μ M (extreme cases up to 1,5mM) fatty acids (Richieri, Anel and Kleinfeld 1993). Finally, taking into account particularities found in the CNS (energetic demands, highly complex cell types, brain blood barrier intersection) its FA transportation and metabolism will be discussed later on section 1.B5.

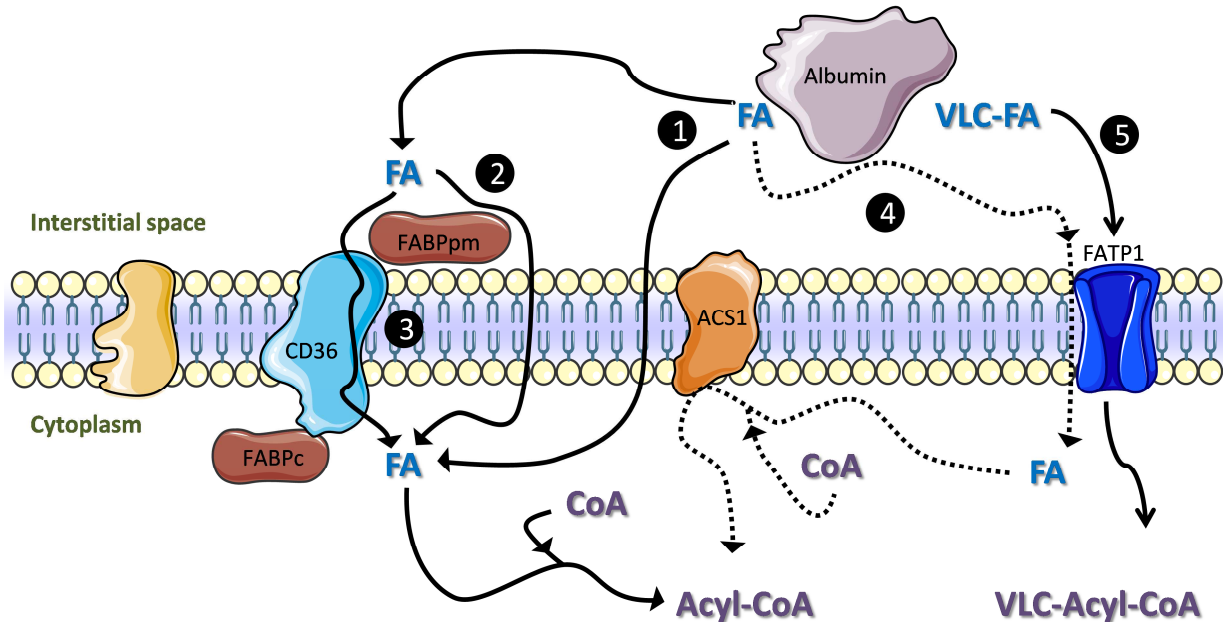


Figure 7. FA delivery across the membrane. Current scheme of FA transport mechanisms to intersect cell membranes. Since the exact mechanism of transmembrane translocation of FA is still unresolved, Figure 7 shows the most likely ones: (1) In view of their hydrophobic nature, Albumin-desorbed FA could cross the membrane by simple diffusion. (2) Alternatively, CD36 (88kDa; also referred as fatty acid translocase), alone or together with the peripheral membrane protein FABPpm (plasma membrane-associated fatty acid-binding protein; 43kDa) accepts FA at the cell surface to increase their local concentration and thus increase the number of FA diffusion events. (3) It is possible that FA membrane crossing is actively achieved through CD36 too. Once at the inner side of the membrane, FA are bound by cytoplasmic fatty acid binding protein (FABPc) before entering metabolic or signalling pathways and transformed into Acyl-CoAs. (4) Additionally, a minority of FA are thought to be transported by fatty acid transport proteins (FATP1) and rapidly activated by plasma membrane acyl-CoA synthetase (ACS1) to form acyl-CoA esters. (5) Very-long- chain fatty acids are preferentially transported by FATPs and, by action of their synthetase activity, directly converted into very-long-chain acyl-CoA esters.

1.B1.3.- FA inner trafficking

Different membranes in a single cell had clearly shown different lipid distribution. For instance, plasmatic membrane exhibits a transverse lipid composition asymmetry with high amounts of sterol and sphingolipids, whereas ER displays symmetrical distribution and contains low level of both species (Voelker 1991). Migration into and between organelles could be a difficult task because most lipid species lack any intrinsic motif that mediates their intracellular distribution like proteins do. However, some sort of connectivity between ER, Golgi, mitochondria and peroxisomes has to operate to interconnect FA fate. As commented previously, interplay between those organelles is necessary to achieve specific amounts of a required lipid for metabolic purposes or, if is not delivered, need to be synthesized. This internal connectivity could be, essentially, vesicular or non-vesicular mediated. It has been demonstrated that both systems occur but the latter is more likely to be restricted to membrane contact sites (MCS,

discussed in next section), where ER and virtually all the organelles “touch” each other (reviewed in (Holthuis and Levine 2005)).

Non vesicular spontaneous interconnection in between one of the mentioned areas and/or with the cytoplasmatic membrane could exist as i) total free desorption, stochastically diffusion across the cytosol and absorption to the target membrane or, on the contrary, ii) being helped by specific proteins (lipid transport proteins, LTP). Both processes have no net energy expenditure, but proteins can greatly facilitate (desorption and diffusion across aqueous cytoplasm are believed to be the more difficult steps) and more likely regulate final destination (reviewed in (Helmkamp 1986) and (Lev 2010; Lev 2012)). Finally, other possibility for FA exchange in between membranes includes collision, which could be “activated” when a substantial part of the lipid extends from the bilayer surface.

LTP are nowadays being extensively studied. From this research became clear that monomeric exchange (a single lipid specie intermembrane interchanged) proceeds even when vesicular pathways are blocked due to genetic manipulation or chemicals. For instance, a well-studied case is the delivery of ceramides (synthesized in the ER) to the *trans*-Golgi (Hanada et al. 2003) or the PI delivery form the ER to both the Golgi and the plasma membrane (Whatmore et al. 1999). Both routes are highly conserved throughout evolution and are both LTP mediated. Thanks to crystallographyseveral LTPs structures were elucidated (with and without their natural ligands). In general, their tunnel-shape determined lipid selectivity and more surprisingly, some of the elucidated structures had a “lid” to close the tunnel which, in turn, is opened through a conformation change when LTP is bound to a membrane. LTP targeting for a specific membrane is not clear yet, but studies in the past years pointed that Trp residues present at membrane binding sites helped in the correct positioning, but in a non-specific manner (Phillips et al. 2006).

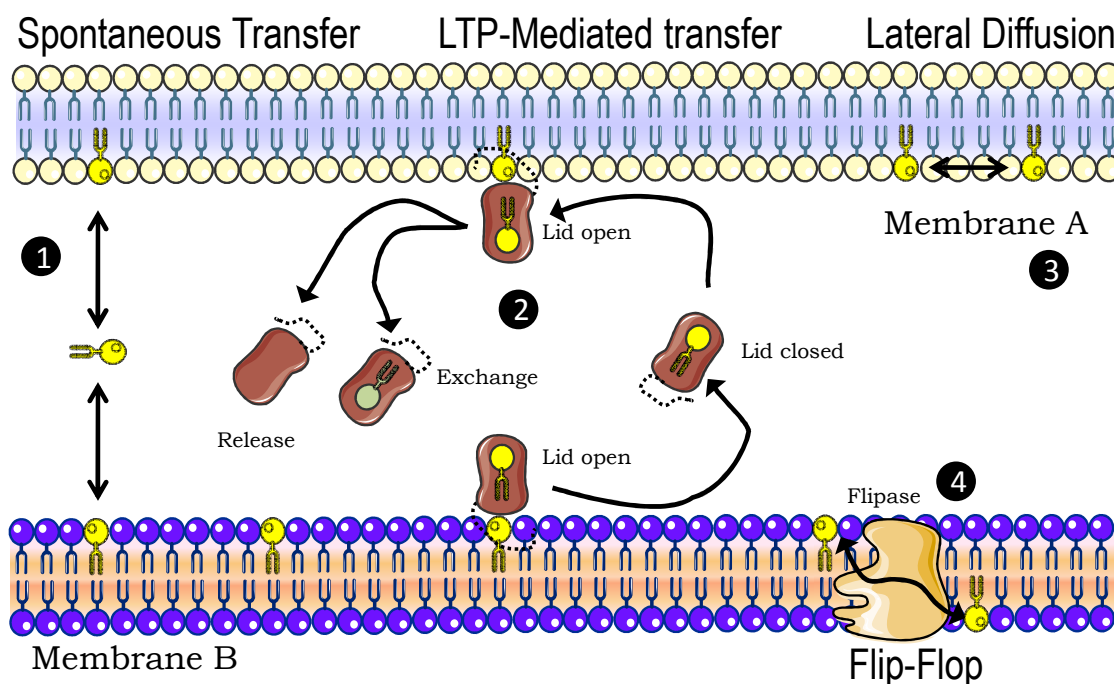


Figure 8. FA intermembrane transportation. There are four main mechanisms for non-vesicular lipid transport: (1) spontaneous transfer; (2) transbilayer LTP-mediated; (3) lateral diffusion and (4) flip-flop (which could be spontaneous or protein-helped, by flippases). The last two are not commonly involved on lipid layer exchange (only when membranes are connected through bridges), but also occurs naturally and remodelate lipid bilayers.

All in all LTP non vesicular transport represents a precisely, non-energy wasting and elegant way to translocate lipid species between two membranes probably much more efficiently than spontaneous processes, but further research is needed to clarify different aspects like membrane target specificity, its regulatory mechanism and cytoskeleton relationships, among others.

1.B1.4.- Lipid transport at membrane contact sites

Membrane contact sites (MCS) are defined as regions where two membranes are closely apposed but the membranes do not fuse and thus each organelle maintain its identity. MCS have been described for ER with mitochondria, Golgi, peroxisomes, endosomes, lysosomes and lipid droplets, as well as the plasma membrane (for a review see (Elbaz and Schuldiner 2011 and Rowland and Voeltz 2012)). The most studied ones are those between the ER and mitochondria. In fact, there is a fraction of the ER which can be isolated, that is attached to mitochondria (named the mitochondria-associated membrane, MAM) and this fraction is enriched in enzymes that are involved in lipid synthesis. Hence, for some lipid species (e.g. PC, PE or DHA, discussed later), synthesis started in the ER but mitochondria is required for several steps of the process.

ER-mitochondria MCS can have different structural features. Some contact sites are discrete, whereas others are more extensive, circumscribing almost completely around the mitochondrial membrane. Contact sites appear to be stable structures because the two organelles stay tethered to each other even as they move along the cytoskeleton, pointing out the relevance of this linkage. Spectacular live cell imaging videos show that the two organelles can traffic in a coordinated fashion without any noticeable disruption in their contact (Friedman et al. 2010). Lipid transport at the MCS could also occur as protein mediated or spontaneously. Again, when transport is LTP mediated, is more likely to be better regulated, hence more efficient. An example of this process is, for instance, the production of PE from PS in mammalian cells. PS is scarce in the mitochondria (2-3% of total membrane PL), but among other diverse functions, is required for the mitochondrial resident enzyme PS-decarboxylase. PS formation is ATP consuming and occurs through the exchange of a serine residue with either the choline moiety of PC or the ethanolamine moiety of PE. This process is catalysed by two enzymes, PS-synthase 1 (for both substrates) and 2 (specific for PE) which are mainly resident in the ER (specially at MAM, remarkable in hepatocytes) but could be found in the Golgi too (Daum and Vance 1997). Furthermore, most of the PE synthesized in mammalian cells comes from the decarboxylation of PS at the inner mitochondrial space (although two alternative mechanism of synthesis exists). Hence, the transport of PS from the ER to the mitochondria and PE back from the mitochondria to the ER is a remarkable example of bidirectional non-vesicular lipid transport mechanism at the MCS and how those regulate lipid biosynthesis and distribution.

1.B2 PUFA biosynthetic pathways: desaturase and elongase

De novo FA biosynthesis involved different enzymes (i.e. desaturases, elongases) distributed in various organelles across the cell (i.e. microsomes, ER, mitochondria, peroxisomes). For its obtention a coordinated cascade of processes (i.e. elongation, desaturation and β -oxidation) takes place in those precise locations. Because we lack the $\Delta 12$ and $\Delta 15$ desaturases present in

plants, mammals cannot synthesize all sort of PUFAs we need from the ω -3 and the ω -6 series. Hence, some FA must be dietary provided and consequently named “essential FA”. We will focus in the two most relevant PUFAs as examples from both series, DHA (ω -3) and AA (ω -6), here we will discuss how these FA are formed arising from their dietary sources, that is, the C18:2 ω -3 (alpha-linolenic acid, ALA) and the C18:3 ω -6 (LA).

1.B2.1.-DHA synthesis

Stated long time ago by Dr Sprecher (Sprecher 1981), DHA synthesis has been recently revisited in non-mammalian species, for which certain Δ 4 desaturase activity was proposed (Qiu 2003). Nevertheless, the canonical eukaryotic route for DHA synthesis, starting from its main precursor, ALA, involves a Δ 6 desaturation step, performed by specific FADS2 (52KDa), followed by an elongation step, executed by a PUFA selective elongase, ELOVL5, to form C20:4 ω -3. This reaction, in which malonyl-CoA is the two carbon donor and NADPH the reducing agent, takes place at the microsomes (ER) and involves four separate reactions: condensation (β -ketoacyl CoA synthase), reduction (β -ketoacyl CoA reductase), dehydration (β -hydroxyacyl CoA dehydrase) and reduction once again (*trans*-2, 3-enoyl-CoA reductase).

The initial condensation step is the rate limiting factor and takes place at the cytosolic surface of the ER membrane. Chain length of the end-product is determined by a serine residue of the elongase at the luminal surface (Denic and Weissman 2007). It is therefore believed that end-product specificity is driven by a distinct chain length rather than by a number of repeated two-carbon additions.

After these two steps, another desaturation phase is required (Δ 5, FADS1) followed by to consecutive elongation steps (ELOVL2 and 5) to form C22:5 ω -3 and another ELOVL2 elongase cycle to achieve C24:5 ω -3. Δ 5 and Δ 6 desaturases share up to a 75% sequence similarity in humans (for a review on those enzymes and their relation to FA abundance see (Lattka et al. 2010)). They introduce a double bound at position 5 (being substrates C20:3 and 20:4 for the in the ω -3 and ω -6 series respectively) or 6 (being substrates C18:3 and C18:2 for the in the ω -3 and ω -6 series respectively) of the acyl chain. Finally, FADS2 action desaturates once more to produce C24:6 ω -3. The last step takes place in the peroxisomes and includes a β -oxidation to successfully synthesize DHA. A scheme of the described mechanism is pictured in Figure 9 in the next page.

FADS2 mRNA expression occurs principally in adrenal glands, but high amounts were found in the liver, brain and cerebellum too (Leonard et al. 2000). Interestingly, the level in foetal liver and brain was 6-fold greater than that found in the adult pointing to an early synthetic necessity. The same pattern of expression was observed for human FADS1, but with lower general levels, and again, the level in foetal tissues was several times higher than in adults. This may be related to their chromosomal location, since they share close positions in chromosome 11q12. Also remarkable, human Δ 5 shares approximately 60% of their proteic sequence with mouse and rat Δ 6. Nevertheless it is not clear whether these genes evolved through duplication, but since both desaturases were found to have been developed from a single protein in zebrafish, it seems clear that both had a common origin (Hastings et al. 2001). However, recently polymorphism findings showed an important role for these variations on the regulation of FA metabolism (reviewed in (Glaser, Heinrich and Koletzko 2010)). Similarities in the protein sequence are

reflected at structural levels, since both desaturases contain a cytochrome b₅-like domain, as well as three conserved histidine-rich domains (HXXHH histidine-box motif) (Cho et al. 1999a) as other membrane-bound desaturases usually do. A schematic representation of the structural and actual membrane attachment is shown in the next page, Figure 10. Finally, as soon as FADS1 and FADS2 were cloned (Cho et al. 1999b), researches could verify that dietary PUFAs downregulated their expression (at least in the liver). Besides, enzyme expression is influenced if essential FA is present on the diet. Therefore, increased expression is achieved upon consumption of FA rich on essential FA (e.g. corn oil). On the contrary, ingestion of food poor in those (e.g. butter), decreases their levels. Furthermore, hepatic activity of both desaturases was suppressed by fasting and induced by re-feeding carbohydrate and when agonist of PPAR (fenofibrate) is used, its expression also increases. However, this seems restricted to the liver. CNS played in “another league” and dietary changes have to be sustained across time to achieve a substantial change on their lipid profile or expression pattern of lipid-regulatory genes (Igarashi et al. 2007a; Hofacer et al. 2011 and Kitson et al. 2012).

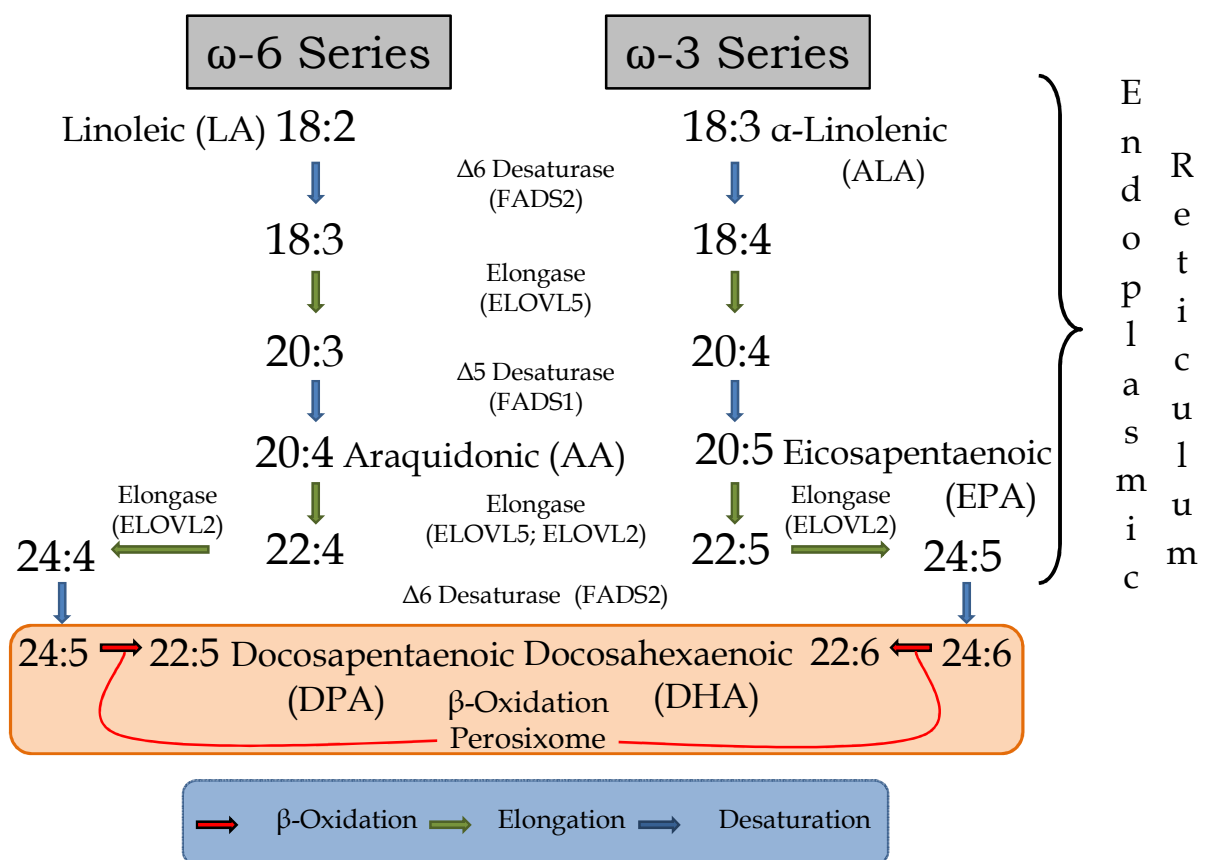


Figure 9. FA de novo synthesis. The scheme here represented the most common mechanism for representative PUFAs synthesis from their essential FA precursors, separated into the two *vias* (ω-3 and ω-6). Note that necessary enzymes are shared for both *vias*. Most of the synthesis is achieved in the ER, but for final steps mitochondrial translocation is required.

In mammals, seven ELOVL have been found, being 1, 3, 6 and 7 specific for saturated or monounsaturated FA and 2, 4 and 5 for PUFA ones. The expression pattern along the body differs, since 1, 5 and 6 are ubiquously expressed (with high levels in liver, testis, adrenal glands and white adipose tissue) meanwhile 2, 3, 4 and 7 has a tissue specific distribution. Although the physiological consequences of such specificity are not clear yet, it is believed to respond to tissue-specific demand of long-chain-PUFA (LCPUFA). Therefore, whereas ELOVL 1, 4 and 7 may act as enzymes controlling the synthesis of LCPUFA as membrane components for optimal

membrane function, the ELOVL 3 and 6 are believed to take part in a more complex system controlling cellular and whole body lipid homeostasis (Guillou et al. 2010). For instance, ELOVL3 expression is under control of glucorticoids, norepinephine and the three isoforms of PPAR. In contrast, ELOVL1 (often named “housekeeping” elongase) liver expression is not regulated by PPAR α , liver X receptor or SREBP-1c (sterol response element binding protein-1c) and not even subjected to nutritionally induced changes (Wang et al. 2006) meanwhile ELOVL7 is highly expressed in the kidney, pancreas, adrenal gland and prostate, where was found to be linked to cancer development in the latter (Tamura et al. 2009).

Finally, EPA and DHA have been proposed to have a complete different biosynthetic pathway for some marine eukaryotic and prokaryote microbes (Metz et al. 2001). Those species take advantage of a specialised poliketide synthase enzyme to form them and are very interesting as biotechnology tools for massive, cheap and clean FA production.

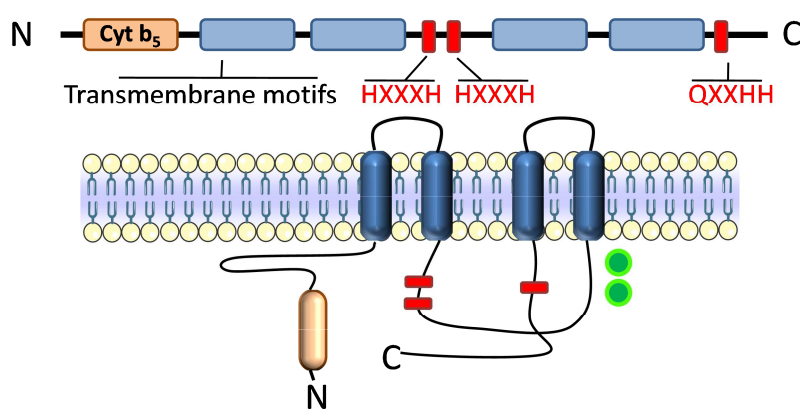


Figure 10. Desaturases structure.

Schematic amino acid sequences of membrane-bound fatty acid desaturases from plants, animals and other organisms. All of them had three strongly conserved histidine-rich sequences (blue boxes) with the general motifs HXXXH, HXXHH and HXXHH. These boxes are required

for enzyme activity and are separated by membrane-spanning domains that must provide the correct orientation for the active sequences. Many enzymes, including the mammalian FADS1 and FADS2, contain a cytochrome b_5 -like N-terminal extension (brown box). Electrons acquired from NADH cytochrome b_5 reductase are transferred to cytochrome b_5 and then to the active site of the desaturase where the redox reaction proceeds through two iron atoms (green circles) that are stabilized by conserved histidine boxes interaction.

1.B2.2.- AA synthesis

Similarly, AA *de novo* synthesis was established long time ago (Sprecher 1981). It shares with DHA most of its enzymes, pathways and locations, being therefore “competitors”. But, since AA only possess 2 more carbon atoms and 2 more double bond than its precursor, LA, elongation and desaturation steps comprises one and two steps, respectively. Thus, it starts with a $\Delta 6$ desaturation followed by elongation (ELOVL5) and finally a $\Delta 5$ desaturation again to form AA. All of these steps take place at the microsomes, in the ER. Nevertheless, AA synthesis is part of a longer process which leads to achieve 22:5 ω -6 DPA, in a very similar way than it is done for DHA, hence including delivery to mitochondria to perform a β -oxidation step. This FA, DPA, is interesting since its accumulation in tissues (especially CNS) takes place when insufficient amounts of DHA and its ω -3 precursors are present in the diet, serving therefore as a marker for inadequate ω -3 intake.

Although it is now clear that FADS1, FADS2, ELOVL2 and ELOVL5 are involved in the metabolism of essential ω -3 and ω -6 FA, it is uncertain whether they play key roles (if any) in the synthesis of “non-essential” PUFAS (those of the ω -7 or ω -9), even when early works

(Mead 1958) pointed out the possibility of sharing the same pathways and enzymes. Further research is required to shed some light on this minority FA since, for instance, mead acid (C20:3 ω -9) is known to be synthesized in animals fed with a PUFA deficient diet and is in fact used as a relevant indicator of such deficiency when accumulated.

Finally, it is important to remark the complex machinery involved in *de novo* synthesis of FA. As explained in this and previous chapter, not only specific enzymes and substrates are required for precise biosynthesis of the desired lipid specie, but also optimal interconnection with different organelles and their orchestrated timing.

1.B3 PUFA Reacylase and phospholipase systems

Delivery after ingestion, maintenance inside a specific PL, inner trafficking and *de novo* synthesis are part of a general mechanism for FA balance. Membrane structure modification by reacylase and phospholipase systems are both crucial to regulate and help to maintain correct levels of specific lipid species and to face both, physiological and pathophysiological conditions.

1.B3.1.- Phospholipase system

A phospholipase is an enzyme that hydrolyzes PLs into FAs and other lipidic substances. There are four major classes, termed A, B, C and D, distinguished by the cleavage reaction location which they catalyze and therefore, the products obtained. Phospholipase A (PLA) comprises a superfamily of enzymes whose members cleave the *sn*-1 acyl chain (PLA₁) or the *sn*-2 acyl chain (PLA₂), releasing a FA. Phospholipase B cleaves both *sn*-1 and *sn*-2 acyl chains and is also known as a lysophospholipase. Phospholipase C cleaves before the phosphate, releasing DAG and a phosphate-containing head group (commonly, IP₃) which results in intracellular Ca⁺² increase. Therefore, this enzyme plays a central role in signal transduction, releasing secondary messengers such as those aforementioned in chapter 1.A2 (Figure 5), which are related to multiple events directly, but to even many more indirectly (for an excellent review in PLC see (Kadamur and Ross 2013)). Finally, phospholipase D cleaves after the phosphate, releasing phosphatidic acid and an alcohol. Both types C and D are considered phosphodiesterases.

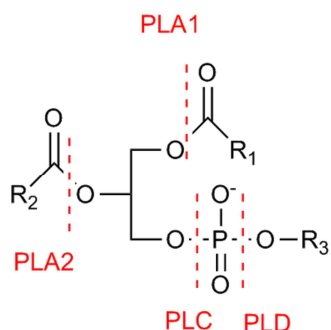


Figure 11. Phospholipases cleavage sites. Cleavage sites for each phospholipase family. Note that an enzyme that displays both PLA₁ and PLA₂ activities is called Phospholipase B.

PLA₂ is the more extensively studied family of phospholipases since both products, FA (specially AA, DHA and EPA) and lysophospholipid, represent first steps in generating important second messengers (whose formation is discussed in section 1.C1.2). It is especially relevant in inflammation and immune responses, besides sleep regulation, pain perception or

GPL-hydroperoxides detoxification and clearance associations. In fact, like other phospholipases (due to space limitation we will only focus on PLA₂), functions and implications related to them raised from the particular products that they generate on upon its activity and which serve as substrates for further synthesis of multiple bioactive lipidic compounds. PLA₂ superfamily is composed by several unrelated protein families with common enzymatic activity (for a review related to CNS, see (Sun et al. 2004)). In the classification based upon the Ca⁺² requirement for their activity, they can be divided into three categories: i) secretory PLA₂ (sPLA₂) that require millimolar concentrations of Ca⁺²; ii) the cytosolic PLA₂ (cPLA₂) that require micromolar concentrations of Ca⁺²; and iii) the Ca⁺² independent PLA₂ (iPLA₂). Regarding its location, sPLA₂ are stored in cytosolic granules or synthesized upon stimulation and then secreted extracellularly whereas cPLA₂ and iPLA₂ are intracellular enzymes. cPLA₂ are located in the cytosol and translocated into the membrane, while iPLA₂ are located both in the cytosolic and in the membrane fractions. Other members of the PLA₂ family are the lipoprotein-associated PLA₂ (lp-PLA₂), also known as platelet activating phospholipase and the recently discovered lysosomal phospholipase.

sPLA₂ are structurally characterised by their (relative) low molecular weight (14kDa average), histidine and Ca⁺² requirements in the active site and six conserved disulfide bonds along the sequence. Their functions are diverse, since more than ten subfamilies have been found in different species (Burke and Dennis 2009) but some of the more remarkable are involved in the pathophysiology of inflammatory diseases, and have long been considered “inflammatory enzymes” (Yedgar, Lichtenberg and Schnitzer 2000). Nevertheless, some sPLA₂ isoforms have been reported to have a protective, anti-inflammatory potential too (Murakami et al. 2011) and an unambiguous role in antimicrobial function and PLs digestion in the stomach (Eerola et al. 2006). For a more extensive study of sPLA₂ see (Lambeau and Gelb 2008 and Murakami and Lambeau 2013). Mammalian sPLA₂s do not show a distinct preference for particular fatty acids, whereas there is some specificity for certain head groups of the PL substrate: generally sPLA₂s show a high activity with anionic PL but some PLA₂ subfamilies also hydrolyze phosphatidylcholine (PC) vesicles (Singer et al. 2002). To date, the direct relevance of sPLA₂ in the eicosanoid production remains unclear, but it is true that those enzymes mediated AA release (which can be in an auto or paracrine manner) and accumulation would activate a variety of prostaglandin synthases, lipoxygenases and cytochrome P450 proteins which ultimately raise eicosanoids production.

Lysophospholipids (the other subproduct) can be converted into lyso-phosphatidic acid or acetylated to form platelet activated factor (PAF), a well-known specie that plays key roles in different pathophysiological events (Murakami and Lambeau 2013) and which mediates a feedback loop by the activation of another PLA family member, lp-PLA₂.

On the other hand, cPLA₂ (which are classified in six sub families) had longer protein sequences (reflected by 65 to 105 kDa ranging weight; for a general classification on the PLA family see (Schaloske and Dennis 2006)) and Ca⁺² loading is required for a complete functionality (not in the case of γ isoform). Surprisingly, this load is not required for catalysis, but rather for intracellular membrane translocation of the enzyme. Those enzymes have remarkable different specificity for the FA present in the PL *sn*-2 position. Therefore, cPLA₂ α has specificity for the AA in this position, whereas cPLA₂ δ is specific for LA-containing PL. In contrast, β and γ isoforms have very little FA discrimination and ϵ and ζ isoforms hydrolyze both, AA and LA (for a profound review on cPLA topic see (Ghosh et al. 2006 and Schaloske et al. 2006)).

The iPLA₂s are Ca²⁺-independent enzymes and, like the cPLA₂s, utilize a serine residue for catalysis. The group consist of six enzymes and the most extensively studied one is the iPLA₂β which includes several splice variants which may exert an inhibitory response (Larsson, Claesson and Kennedy 1998). A structural feature of iPLA₂ is the presence of several ankyrin (structural anchors) repetitions which may be responsible for protein–protein interaction between monomers. Functionally, these enzymes are not specific with regard to the fatty acid being released but it seems that ATP helps to stabilize the protein (Lio and Dennis 1998). Main functions of this family are related with membrane homeostasis maintenance through its remodelling (reviewed in (Akiba and Sato 2004)). In addition, they play a role in processes connected with the metabolism of reactive oxygen species, at least in macrophages (Martínez and Moreno 2001) and astrocytes (Jianfeng Xu et al. 2003). They have been implicated in membrane transformation during apoptosis (Wissing et al. 1997) resulting in AA release and increasing caspase 3 activation, which could end up with the enzyme cleavage itself (Atsumi et al. 1998). Later on in we will discuss about the susceptibility of PUFAs to be oxidized if they are not effectively protected, so together with observations mentioned before, suggest that ROS could serve as a factor for regulating iPLA₂ activity, although the exact mechanism remains to be elucidated.

1.B3.2.- Reacylase system

The deacylation-reacylation cycle maintains a balance between free and esterified FA, resulting in normal membrane integrity and function, including optimal activity of membrane-bound enzymes, receptors and ion channels involved in normal signal-transduction processes. Using acyl-CoAs as donors, GPLs are formed by *de novo* pathway (Kennedy pathway (Kennedy and Weiss 1956)) and modified by a remodelling pathway (Lands' cycle (Lands 1958)) to generate membrane asymmetry and multiple lipid species (for an excellent review on GPL homeostasis see (Hermansson, Hokynar and Somerharju 2011)).

In neuronal tissues, four major enzyme families are responsible for membrane deacylation-reacylation cycle: acyl-CoAsynthetase (ACS), acyl-CoAhydrolase (ACH), acyl-CoAlysophospholipid acyltransferase (ACL) and phospholipaseA₂. The picture below shows a representation of the overall process.

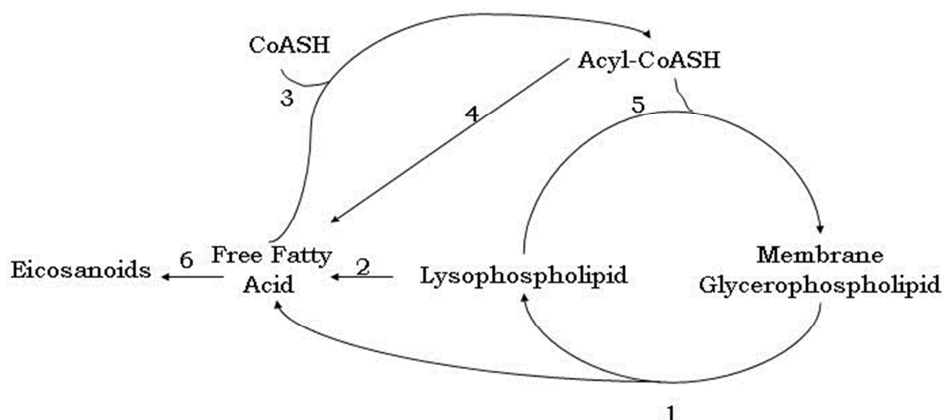


Figure 12. Deacylation-reacylation cycle. (1) PLA₂; (2) Lysophospholipase; (3) Acyl-CoA synthetase; (4) Acyl-CoA hydrolase; (5) Acyl-CoA lysophospholipid acyltransferase; (6) Cyclooxygenases, lipoxygenases. CoASH is a cofactor required for the activation of a determined acyl group.

A) ACS

ACS converts free FA into acyl-CoA esters. Essentially, all cellular metabolic pathways in which FAs participate firstly require their activation into CoA derivatives (for a profound review see (Watkins 1997)), with a notable exception, pathways for conversion of PUFAs, AA and DHA to bioactive eicosanoids and docosanoids, respectively. Nowadays, 26 ACSs are encoded by the human and mouse genomes, and could be classified according to its FA specificity, being short (2 to 4 carbons), medium (4 to 12), long (12 to 20; the more studied ones, reviewed in (Watkins 2008)), bubblegum (14 to 24, whose name aroused from *Drosophila* mutant "bubblegum") and very long-chain, (18 to 26) synthetases. Another classification take into account its location within a cell, being therefore, cytosolic, microsomal (ER-resident), mitochondrial or peroxisomal (Watkins and Ellis 2012). The ACS reaction is ATP-dependent (Groot, Scholte and Hülsmann 1976), and in some cases Mg^{2+} is also required for a complete activation (Farooqui, Horrocks and Farooqui 2000). These enzymes are regularly membrane-bound and act on non-polar hydrophobic substrates. Their products (acyl-CoAs) are water-soluble and very powerful detergents. ACS function is especially relevant for the synthesis of unsaturated long chain acyl-CoA, since long term presence of free FA could result on its oxidation, with generation of potentially toxic (but also signalling) peroxides and hydroperoxides.

B) ACH

ACHs represent a group of enzymes that cleave acyl-CoAs into fatty acids and coenzyme A (CoA-SH). ACH relevance is therefore related to control levels of those species, because they participate in a large number of reactions, including lipid synthesis and oxidation, energy metabolism and potential regulation of a variety of signalling pathways (for a review see (Kirkby et al. 2010)). Although those enzymes have been less investigated than ACS, ACHs were localised in the cytosol, mitochondria, peroxisomes and ER. Within these compartments, they are distributed in a wide range of mammalian tissues, being detected in brain, liver, kidney, heart, lung, steroidogenic and brown adipose tissues, where they exert important functions, especially in the brain where its hydrolyzing activity is much higher than in any other organ in the body. Thirteen mammalian ACH genes are divided into two types, which differ according to the structural organization of the catalytic domains: type I enzymes contain an α/β -hydrolase domain and type II enzymes comprise one or two "hot dog-like" thioesterase domains (Han and Cohen 2012). Human orthologs are located within a very narrow region of chromosome 14 as a gene cluster (Hunt et al. 1999). Their activity is regulated by substrate for some of the family members, causing an inhibition, but they seem not to be affected by of non-esterified FA accumulation. Some of the family members have been shown to be under PPARs (Hunt et al. 1999), SREBP (especially long-chain, brain resident ACH (Takagi et al. 2005)) or HNF4 α (Dongol et al. 2007) control. Finally, also noteworthy, a knock out animal model of ACOT7 (Ellis, Wong and Wolfgang 2013) was found to exert hyperactive neural response when fasting and some kind of neurodegeneration, reflected by locomotor defects and increased GFAP immunoreactivity in older animals, pointing its relevance in neuroprotection.

C) ACL

ACLs acylates (insertion of an acyl group) the *sn*-1 and/or the *sn*-2 positions of a given lysophospholipid. Because there are many species of GPL differing in the phosphoryl head groups, the fatty acids in chain lengths and degrees of saturation, many ACLs should exist and participate in both, *de novo* synthesis and remodelling. High selectivity for the activated FA (therefore, acyl-CoAs) desaturation degree and length is present in a particular enzyme. In general, there is higher prevalence for saturated (or monounsaturated) acyl-CoAs insertion in the *sn*-1 position of a given GPL, meanwhile, in the *sn*-2 position acyl-CoAs is more likely polyunsaturated. Combined actions of that enzyme family and the PLA₂ family would finally produce the great variety of GPL. ACL activities are widely distributed in various cells and tissues, and are tightly bound to microsomal and plasma membranes (for a review on ACL topic see (Shindou et al. 2009)).

All in all, membrane remodelling is a tightly regulated mechanism. In “resting” cells, one can assume that reacylation dominates, and hence, the bulk of cellular FA is found in the esterified form. But, upon stimulation (which could be caused by a myriad of factors), transient dominant reaction is the PLA₂-mediated deacylation, which results in dramatic releases of free FA (specially signalling relevant AA and DHA) that is now available for exerting its particular function (e.g. eicosanoid or docosanoid synthesis). However, activation conditions only last for a while (basics of any signalling event) and reacylation dominates again until replenishment of the intracellular pools of a particular FA is achieved.

1.B4 Essential FA dietary requirements

Essential FAs are required for a normal cell function and serve as a substrate/scaffold for further FA synthesis, if a specific need or depletion occurs. So, international organizations, nutritionists and medical doctors published some dietary recommendations for general healthy subjects (in different status; i.e. pregnancy, development, aging), but also for disease and to prevent them.

In a typical western society, adult intake ranges 1-2 g/day of ALA, meanwhile LCPUFAs is somewhere around 150-300mg/day (Lauritzen et al. 2001). In Spain, ω -3 FA consumption is approximately 380 mg/day (340 and 40 mg/day of DHA and EPA respectively (data obtained from Ministry of Agriculture, 2005)), the majority (67%) due to blue fish (tuna, sardine or salmon) consumption. Spanish dietary essential FA (ALA and LA) intake range between 0.4 and 3.4 g/day for ALA and 4 to 29 g/day for LA (with average values of 1,2 and 12 g/day for ALA and LA respectively (Sala-Vila et al. 2011)).

Omega 3 index (sum of DHA and EPA FA percentage in erythrocytes, extensively used in cardiovascular research) is remarkably high in Spanish population in comparison with other western countries (e.g. 7,1% in Spain vs 4,9% in USA-excluded Alaska Inuit population for whom reaches up to 20%). However, is lower than what is estimated for the highest marine product consumers worldwide (e.g. Iceland, Norway, Korea or Japan). Tables in the next page represent average values for FA daily intake recommended for healthy subjects (USA Institute of Medicine in 2002 (Trumbo et al. 2002)).

Omega 3 and 6 Essential FA Daily Dietary Requirements					
Vital Stage	Age(years)	Ω-6 (LA)		Ω-3 (ALA)	
		Male	Female	Male	Female
Babies	0-12 months	4,4*	4,4*	0,5*	0,5*
Childs	1-3	7	7	0,7	0,7
Childs	4-8	10	10	0,9	0,9
Childs	9-13	12	10	1,2	1
Teenagers	14-18	16	11	1,6	1,1
Adults	19-50	17	12	1,6	1,1
Elderly	≥ 51	14	11	1,6	1,1
Pregnancy	Any age	-	13	-	1,4
Breastfeeding	Any age	-	13	-	1,3

* Breast milk from a healthy woman (at least following above mentioned recommendations) provides enough ω-6 and ω-3 PUFAs. Data represented daily consumption in grams.

Table 4. Omega 3 and 6 essential FA dietary requirements.

More recently, WHO (World Health Organisation) has established a daily ingestion for healthy adults (included non-pregnant or non-breast feeding females) of around 0,250 g/ of EPA+DHA summation. This recommendation does not specify individual dosage for those FA, due to the lack of scientific relevant evidence. However, they suggest a maximum value (2 g/day), possibly due to lipid peroxidation and cytokine production affectance (“Fats and Fatty Acids in Human Nutrition. Report of an Expert Consultation.” 2010). In this line, Mozaffarian and collaborators (Mozaffarian and Rimm 2006) showed, thanks to a risk-benefit study, that more than 500 mg/day of DHA+EPA intake has no net effect in diminishing cardiovascular risk. On the other hand, in 2009 EFSA (European Food Safety Authority, (European Food Safety Authority 2009)) proposed the same quantity for long ω-3 PUFAs as the labelling reference intake, but they suggest ALA (2g/day) and 10g/day for the ω-6 PUFA LA consumption too. Even so, differences in dietary recommendations reflect different nutritional purposes, since some advices are proposed to correct clinically evident deficiency in a given population, meanwhile other are based on cardiovascular and/or neurodevelopment health.

However, controversy arises, since some international organizations suggest avoiding intensive fish intake (especially bigger ones like tuna, emperor or big sharks) during pregnancy, breastfeeding and early childhood due to high risk of contaminants potentially present on them (toxic heavy metals and related species, particularly methyl mercury) (Mozaffarian and Rimm 2006). Anyway, this could be avoided by tiny blue fish ingestion (e.g. sardine or mackerel, since large and long-lived animals could accumulate those toxins) or by biotechnology-produced algae. The picture below is just to have an idea how nutritional status, regarding FA, vitamins E and C has evolved along humanity.

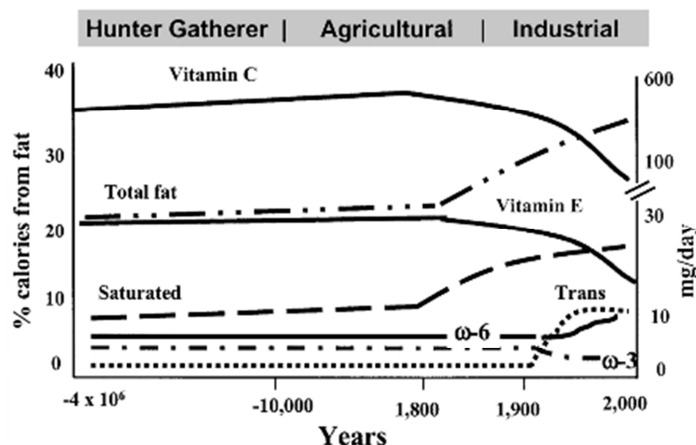


Figure 13. FA and antioxidants intake along human evolution. Hypothetical scheme of fat and fatty acid (ω -3, ω -6, *trans* and total) intakes (as % of calories from fat) and intake of vitamins E and C (mg/day) along human evolution Copied from (Simopoulos, Leaf and Salem 1999).

1.B4.1.- ω -3 deficiency

Taking into account western society ω -3 FA consumption plus limited endogenous synthesis (currently under debate for CNS tissues), deficiency could arise both, on disease or by nutritional unbalance. However, this is hard to prove because i) there are no clear specific recognized symptoms for such deficiency; ii) ω -3 and ω -6 interdependency and interconnectivity could, up to an extent, mask such unbalance. However, impaired growth, reproductive disturbances and skin lesion are mostly related to ω -6 deficiency (Kremmyda et al. 2011). On the other hand, dysopsia and abnormal electroretinogram could point a specific ω -3 unbalance. Even so, the most noticeable marker for ω -3 deficiency is the accumulation of ω -6 long chain PUFAs, particularly ω -6 DPA (22:5 ω -6) (Neuringer et al. 1986) and ω -6 adrenic acid (22:4 ω -6). The opposite (ω -6 deficiency), is not normally reflected by a PUFA ω -3 accretion. Finally, a concomitant deficiency (ω -3 and ω -6) would raise mead acid (C20:3 ω -9). In general, even if ω -3 deficiency is hard to find, based on their potential positive outcome, some dietary recommendations regarding optimal ω -3 status are offered in different conditions.

Finally but also remarkable, it is the fact that an unbalance in the ω -3/ ω -6 dietary intake could enhance different signalling pathways, and therefore modulate responses to various stimuli, as recently demonstrated in terms of learning and memory processes (Hajjar et al. 2012) or inflammation (Liu et al. 2013).

1.B4.2.-Pregnancy and development

Since Lamptey and co-workers showed in 1976 that ω -3 deficient rats had decreased learning abilities (Lamptey and Walker 1976), lots of different test had also pointed out behavioural, olfactory or visual disarrangements in rats, mice or rhesus monkeys under such deficiency. Anyway, it is difficult to extrapolate those results to human infants and, in fact, some authors suggest that several of the differences encountered in early development stages are faded out along lifetime (Agostoni et al. 1997). In any case, most (80%) of the brain DHA accrues in the human foetus from week 26 until term (Sabel et al. 2009). The presence of LCPUFA-specific placental FABP (Fatty acid binding protein) as well as increased accretion of intrauterine DHA could determine why maternal DHA depots seem depleted after pregnancy (Lauritzen et al. 2001). Therefore, it is strongly recommended for preterm infants to be fed with DHA

supplements to improve their cognitive (Agostoni et al. 1997) and visual (Carlson et al. 1996) conditions, whether healthy termed ones should do, is still controversial.

1.B4.3.-Cardiovascular diseases

From long time ago (1965 by Sir Austin Bradford), outstanding evidences showed lower cardiovascular risk when high ω -3 index exist *in vivo*. Potential mechanisms for this reduced risk included anti-inflammatory, anti-thrombotic, antihypertensive, hypo-triglyceridemic and antiarrhythmic properties found in ω -3 FA rich diets, particularly in long chain ones. However, some recent meta-analyses studies of randomized trials pointed out low significance related to prevention (Rizos et al. 2012, Chowdhury et al. 2012 and Chowdhury et al. 2014), seeming that when damage is done, ω -3 PUFAs are beneficial to reduce its outcome but it fails preventing it when a balance diet is already present in a healthy individual. In any case, government health institutions still recommend two fish pieces per week in a balanced diet aimed to increase cardiovascular protection.

1.B4.4.- Neurodegenerative diseases

Studies on ω -3 function and levels in neurodegenerative diseases have been extensively performed, particularly in Alzheimer, Parkinson and some dementias (for reviews see, (Calon 2011; Sydenham, Dangour and Lim 2012; Saugstad 2006). In contrast to cardiovascular disarrangements, ω -3 supplementation seems to offer a preventive neuroprotection, especially in Alzheimer and mood disorders where adequate ω -3 correlates with a better cognitive function retention and better behaviour (Calon 2011).

Regarding amyotrophic lateral sclerosis (ALS), there is a recent paper that shows a deleterious effect in EPA supplementation diet in a wide used model of disease, copper zinc superoxide dismutase (with a glycine/alanine substitution in the 93 amino acid, SODG93A) overexpansion (Yip et al. 2013). Authors related this diminished survival to increased oxidative stress and accretion of 4-hydroxy-2-hexenal (HHE) in activated microglia. Other studies with valproic acid (a FA acting as histone deacetylase inhibitor that showed antioxidative and antiapoptotic properties and reduced glutamate (Glut) toxicity in preclinical studies) failed to prolong lifespan in both, animal model (Crochemore et al. 2009) and patients (Piepers et al. 2009). Interestingly, the combination of a high intake of PUFAs and vitamin E has been related with a 50–60% decreased risk of developing ALS, and these nutrients appear to act synergistically (Veldink et al. 2007). Similarly, a very recent publication (Fitzgerald et al. 2014) epidemiologist focused also in the possible relation of dietary consumption of ω -3 FA and the risk of ALS development or a better outcome after diagnosis and, for both issues, higher levels of dietary ω -3 correlated with reduced ALS development probability, and also importantly, once diagnosed those patients had better progression. All in all, those researches suggest a possible prevention and better outcome after ω -3 PUFAs consumption for various neurodegenerative diseases, and may even be better if those levels are increased concomitant with substantial autoxidative protection.

1.B4.5.- Sex dimorphism

Data in Table 4 showed different FA necessities along a lifetime for male and female individuals. This is completely reasonable, and is believed to be linked to differential

peroxisomal β -oxidation rate and/or hormone synthesis and processing for both sexes. In fact, this could rely on the very different adipose tissue organization (reviewed in (White and Tchoukalova 2014 and Stevens et al. 2010)). Studies from professor Burdge group (Bakewell, Burdge and Calder 2006 and Childs et al. 2008) pointed that, in general, female have greater DHA synthesis from its precursors (possibly by stimulation at the transcriptional level) and circulatory (plasma) levels than male. From works studying women using oral contraceptives (Magnusardottir et al. 2009) or hormone-replacement therapy (Giltay et al. 2004b) and a study of sex-hormone treatment in trans-sexual subjects (Giltay et al. 2004a) was clear that hormone function had very relevant consequences in PUFA handling.

Also important, in response to dietary manipulation, ω -3 metabolism seems to be affected by gender, since desaturases $\Delta 5$ and $\Delta 6$ changed its activity and expression (Extier et al. 2010) (upregulated in female liver in response to ω -3 replenishment diet) as well as PUFA-related synthetic machinery, having increased $\Delta 4$ desaturation index (DHA/ ω -3DPA ratio) for females too (Alessandri et al. 2012). Importantly, again CNS PUFA-synthetic enzymatic machinery was more difficult to be affected, and no differences were found regarding sexual dimorphism (Extier et al. 2010). Furthermore, the opposite occurs; FA synthesis is dependent on the hormone production, at least in neuroblastoma cell line (Alessandri et al. 2008) or an elegant animal model of ovariectomized females treated with different dosage of 17- β estradiol (Alessandri et al. 2011) unveiling sex as a relevant factor regarding PUFA metabolism.

1.B5 PUFA and Central Nervous System

1.B5.1.- Delivery across brain blood barrier

As stated before, FA are important substrates for energy supply but also relevant as building blocks for membrane synthesis and signalling mediators (discussed in the next section). This is especially relevant in such a complex “orchestrator” apparatus as the CNS, which is the second lipid accretion tissue (after adipose) whose PUFAs accounts up to 20% of dry weight (Owada 2008). In fact, there is an entire evolutionary theory which points out the relevance of shore based diets, particularly rich in DHA, trying to explain hominid encephalization burst (Cunnane et al. 2007). So, taking into account that particular insulation issues that apply for CNS and *in situ* synthesis which may not be sufficient (DeMar et al. 2006), we will discuss here how FA are transported to and passed through brain-blood barrier to overcome PUFA needs at CNS.

Blood-brain barrier (BBB) is the cellular structure that keeps CNS sectioned from the rest of the whole body and maintains cerebrospinal fluid (CSF) and blood separated. It occurs along all capillaries adjacent to CNS and could represent up to 12 m² surface in an adult human (Abbott et al. 2010). It consists of tight junctions (zipper-like) and high-density cells restricting passage around the capillaries and do not exist in regular circulatory system. Those endothelial cells, pericytes and astrocytes restrict the diffusion of microscopic particulae and large or hydrophilic molecules into the CSF, while allow diffusion of small hydrophobic molecules (O₂, CO₂, hormones, etc). Therefore, for crossing BBB, different epithelial walls and even cell types must be intersected. A schematic representation of BBB is shown below.

After a postprandial peak, plasma levels of triglycerides in healthy subjects are maintained stable. They are mainly distributed as sterified lipids complexed with lipoproteins but there is a controversy on whether unesterified PUFAs are sufficient or not to maintain CNS lipid levels, in order to achieve their well-known neuroplasticity capacities (Purdon, Arai and Rapoport 1997). More than twenty years ago it was demonstrated that lipoprotein receptors are expressed at brain capillaries (Mérésse et al. 1989) and that they show modulator capabilities related to PLs transfer, at least in those isolated brain capillaries. Nowadays it is believed that only unesterified forms are selectively incorporated (Rapoport, Chang and Spector 2001). Thus, it is demonstrated that dietary intake of PUFAs influence plasma derived levels, and that those indirectly influence brain PUFA metabolism, so BBB is unambiguously overcome by dietary fatty acids.

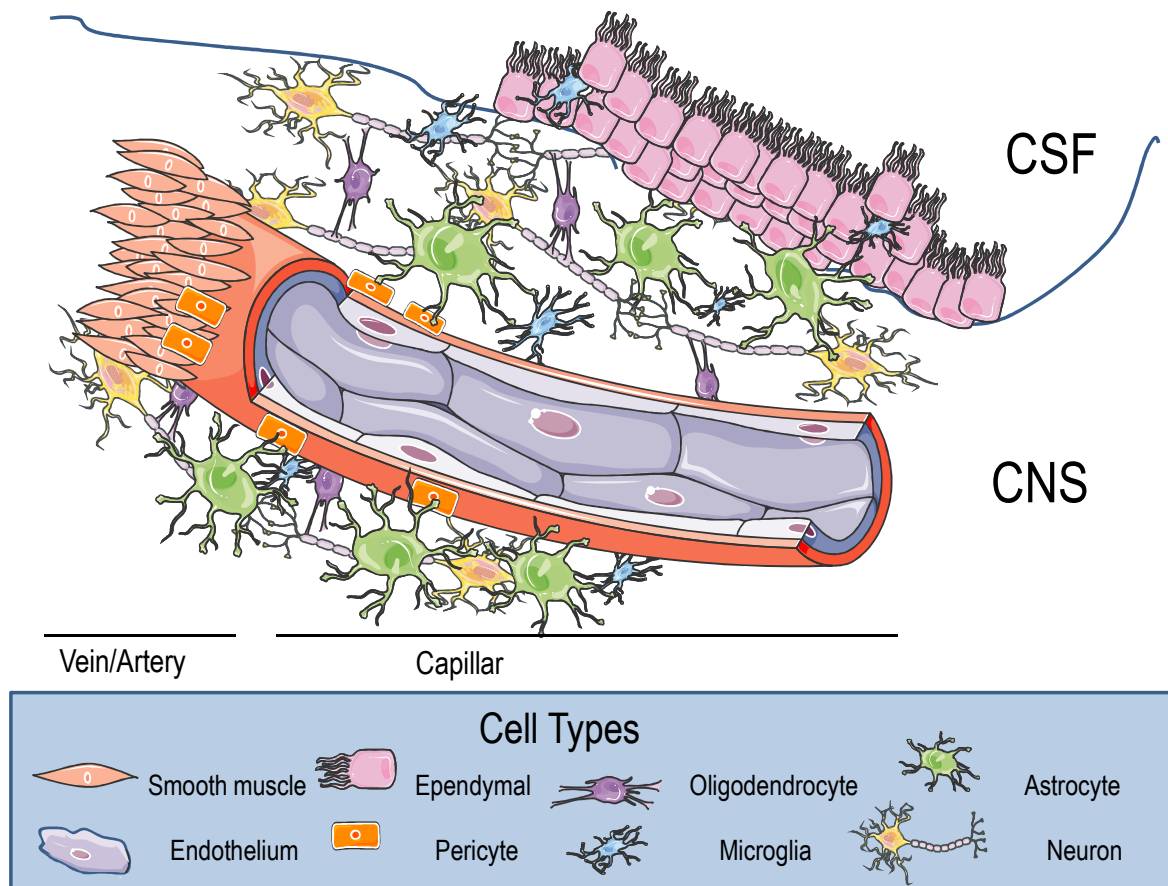


Figure 14. Blood-brain barrier scheme. Cell types encountered in the BBB and their relationships (CSF, cerebro-spinal fluid). Not to scale

It is believed that up to 3-5% of AA and 2-8% of DHA is daily replaced from rat brain GPL by the unesterified PUFAs presented in plasma (Rapoport, Chang and Spector 2001). The actual quantity in humans is estimated to be 0,3% for AA, but higher amounts are believed to be achieved by *de novo* synthesis through elongation and desaturation processes of their precursors or by deacylation and reacylation processes (see chapter 1.B2 and 1.B3, respectively). Dietary supplementation of human subjects with DHA (but also for AA) undoubtedly boost plasma levels of non esterified DHA, remarkably with no net increase of serum lipoproteins, (Conquer and Holub 1998) but how this increase is affecting brain levels (whether its synthesis from ALA is significant) or which forms (stereoisomers specificity, preferential bioavailability, etc) are more prone to be uptake by the brain remains unclear.

Using DHA as a paradigmatic PUFA example, current models for delivering FA into the brain via plasma include passive diffusion of non-esterified DHA through the BBB (Spector 2001) and/or uptake by HDL or LDL containing DHA lipids via specific lipoprotein receptors on the luminal membrane of endothelial cells (Balazs et al. 2004). The first possibility, is supported by the of endothelial lipase that was found in brain capillary endothelial cells (Sovic et al. 2005) which was regulated (negatively, both protein and mRNA levels) when PPAR α and γ agonists were applied. Surprisingly, those lipases possess a remarkable specificity for DHA positioning within the PL (Chen and Subbaiah 2007). Also remarkable is the preferential cleavage of ALA over LA by $\Delta 6$ desaturase present in endothelium (Cunnane et al. 1994) and how its evolution over a lifetime changed opposed to liver resident ones, Endothelium type FADS2 activity is enhanced during development and scarce in adults, contributing to brain-development-related DHA necessities.

Another possibility is that a sophisticated selective carrier mechanism exists for the transportation of ω -3 FA into the brain (Beisiegel and Spector 2001), including a BBB transport system that is highly selective for PUFAs esterified into PL such as DHA lysoPC (Bernoud et al. 1999). In fact, a recent study has demonstrated that lipoprotein particles can cross the BBB, at least in *Drosophila* (Brankatschk and Eaton 2010), suggesting that the lipoproteins could act as transporters of therapeutic lipid molecules across the BBB for the treatment of brain disorders.

Finally, in a recent published paper (Chen and Subbaiah 2013), Chen and collaborators proposed that DHA stereospecificity in a given PL (being at *sn*-1 or *sn*-2 positions) may determine its destination. They claim for the DHA in *sn*-1 position at the PC to be more “protected” against the reacylase/deacylase cycle and therefore have more possibilities to be released at the BBB and, ultimately, uptake.

1.B5.2.- In situ synthesis

For a long time, neurons were believed to lack the ability to synthesize DHA from its ω -3 FA precursors (Igarashi DeMar et al. 2007b). In fact it wasn't until recent studies (Kaduce et al. 2008) that PUFAs *in situ* synthesis was solely attributed to astrocyte action (Kaduce et al. 2008; Moore et al. 1991) rather than to a neuronal origin. In any case, this synthesis is believed to be scarce, so dietary DHA supplements in the forms of PL or/and TAG were (and still are) usually recommended in order to promote brain health across lifetime, but specially during early development (Guesnet and Alessandri 2011) and elderly.

For optimal *in situ* synthesis, adequate amounts of precursors are needed, but also large batteries of different enzymes are required (commented in chapter 1.B2). Nevertheless, studies from Dr Rapoport's group (DeMar et al. 2005; DeMar et al. 2006) reveals that the contribution of *in situ* synthesis for both AA and DHA to brain PL is indeed very little. In those works, both with a non-deficient diet for the FA family studied, they estimated *de novo* synthesis represent less than 1% for both AA and DHA. The majority of unesterified precursors that cross the BBB undergo through β -oxidation (59% LA and 67% ALA, respectively) or acylation processes

(11% of LA, 12% ALA, respectively) rendering *de novo* synthesis residual and pointing out that delivery of final products (the required FA itself on its multiple forms; e.g. PC, PS, lysoPL, etc) but not its precursors must be the mechanism that avoids PUFAs depletion in the brain. In fact, a recently published review (Rapoport, Ramadan and Basselin 2011) using *in vivo* radiolabeled [$1\text{-}^{14}\text{C}$]DHA intravenously perfusion (for both rats and humans) they pointed out that the incorporation rate of DHA to brain equals its rate of metabolic consumption suggesting that if an increase need is required, *in situ* synthesis could be insufficient.

All in all, those data pointed out how complex regulatory machinery operate for FA delivery at the BBB and that FA destination after crossing differs enormously between them, further research is needed to clarify whether in physiological conditions, lipoproteins or phospholipases at the BBB are key factors to meet CNS FA delivery and requirements (it seems so) or, in the contrary, *in situ* synthesis (regardless neuronal or astrocytic origins) is sufficient. How this weak equilibrium is disrupted in disease and potential therapeutics regarding delivery and upgrading local synthesis are also major points to be elucidated.

1.B5.3.- Neurotransmitting

Vesicle formation, delivery to synapsis, exocytosis and substrate clearance represented essential compulsory processes for a correct neurotransmission. Synaptic proteins could be enhanced in order to optimize neuronal dialog, the basic tenet of the CNS. However, numerous events could interfere these chemical information interchange (e.g. oxidative stress, cytoskeleton deregulation, membrane deareagments, among others) causing detrimental or misunderstanding connectivity and could even lead to denervation and ultimately, neuron death. In this sense endocannabinoid system demonstrated (Berghuis et al. 2007) to be very relevant for axon guidance and synaptogenesis. Further, astrocytic support function (commented in the next chapter) is also crucial in this delicate system. ω -3, but also ω -6 PUFA could enhance synaptic membrane expansion (Darios and Davletov 2006) with an increased expression of syntaxin 3 (STX3, a protein involved in vesicle formation and exocytosis in synapsis) and seems clear the PUFA influence in the SNARE (soluble N-ethylmaleimide-sensitive factor-attachment protein receptor) protein complex formation and stability (García-Martínez et al. 2013 and Lang, Halemani and Rammner 2008; for an excellent revision on the FA-SNARE regulation see (Davletov, Connell and Darios 2007)). In fact, the SNARE proteins complex are believed to provide the required specificity for vesicle docking and sorting as well as they represent the minimal basic machinery required for membrane fusion (Weber et al. 1998). Finally, since membranes must adopt different curvatures during fusion, the commented membrane structural actions of PUFA are also crucial to complete exocytosis, as showed by cone-shaped lipids when they may favour the appropriate membrane geometry (reviewed in (Chernomordik and Kozlov 2003)).

In this sense, deacylation-reacylation machinery was relevant, since, in cultured neurons (Marszalek et al. 2005), overexpression of ACS6 promoted an increased DHA-CoA accumulation (respect to oleic acid or AA) and, ultimately, neurite outgrowth (previously found for ACS2 too (Marszalek et al. 2004)). Interestingly, silencing its expression (by RNA interference) resulted in a decreased neurite outgrowth of various neuronal cell lines (Kim et al.

2009) and further, *dAcs1* (ACS4 orthologue in drosophila) was found essential for correct axonal targeting and normal synaptic vesicle formation (Liu et al. 2011).

Also importantly, expression and function of Glut receptors (e.g. the glial excitatory amino-acid transporter 2, EAAT2, which is specially relevant since its excitotoxicity involvement in the ALS pathogenesis and will be commented in section 1.D2.3), could be influenced by AA (Zerangue et al. 1995), causing a reduced Glut recovery. This mechanism seems to be triggered by AA itself, but whether PLAs play a role by influencing local membrane release is still controversial in this model. However, this opened the door for a more coiled synaptic-membrane-structural PUFA action. Therefore, all in all, PUFA action and regulation on the continuous synaptic remodeling represents important points for a correct neurotransmission and, possibly more important, promising therapeutic intervention in various diseases.

1.C PUFA Pathophysiology

1.C1 Inflammation induction and resolving phase

1.C1.1.- Inflammation partners

Since inflammation could play a key role in neurodegeneration, and particularly in ALS (reviewed in (Evans et al. 2013)), the importance of this phenomena should be discussed. Neuroinflammation refers to the rapid reaction on the CNS, through activation of the resident immune cells, in response to infections, trauma, toxins and ischemia, among others (Frank-Cannon et al. 2009). It is a complex combinatory mechanism of acute and chronic responses in which all CNS population (neurons, astrocytes and microglia) and infiltrating leukocytes take part. Innate immune response in CNS is responsible for microglia activation resulting in release of pro-inflammatory cytokines (Interleukins-IL-1 β , -IL-6- and TNF α - among other), chemokynes (e.g. prostaglandin E₂, PGE₂) and nitric oxide (and other oxidative derived species such as superoxide and peroxynitrite), but also rescue anti-inflammatory signals (IL-4, IL-10, nerve growth factor-NGF-, BDNF, insulin-like growth factor-1, glia derived neurotrophic factor-GDNF-, leukemia inhibitory factor-LIF-, ciliary neurotrophic factor-CNF-, among others); for a review see (David and Kroner 2011). (Consilvio Vincent and Feldman, 2004)

Autoinflammation is a relative new concept (McDermott et al. 1999). It was proposed as an emerging family of clinical disorders which were characterized by seemingly unprovoked inflammation episodes without high number of neither autoantibodies nor T-lymphocytes activation. From this point, various diseases were related to developed the “autoinflammatory” imprint (recently reviewed in (Standing, Omoyinmi and Brogan, 2013)), like in the case of some granulomatous diseases, as chronic granulomatous synovitis with uveitis and cranial neuropathy (Blau syndrome) and Crohn’s disease, among others. Interestingly, both diseases have shown a dysregulation in the NF- κ B activation, but, as other autoinflammatory diseases, aetiology seemed more complex than initially (genetically) though. Also importantly, some multiple sclerosis patients showed complications compatible with autoinflammation episodes (Kümpfel et al. 2007) and, more recently, a significant host predisposition (Kastner, Aksentijevich and Goldbach-Mansky 2010) is proposed to open the “classical” definition to a broader one.

Focusing in neuroinflammation-related cell types, astrocytes play crucial roles supporting neuron activity, both under physiological conditions and disease. This cell type, with an ectodermal origin, could grow, in specific brain regions, up to ten times more numerous than neurons in the CNS, although in the whole brain, neuronal (counted as NeuN positive cells) and nonneuronal cells have almost equal number (Azevedo et al. 2009). Since they envelop synaptic terminals, astrocytes clear most of the synaptic neurotransmitters (Glut, γ -Aminobutyric acid - GABA- and glycine, among many others). They provide trophic factors (e.g. brain derived neurotrophic factor, BDNF, and tumor necrosis factor- α -TNF α), energy (lactate and FA among others) and precursors (e.g. adenosine, purines) for neuron optimal function. Astrocytes are not immune cells per se, but can, in specific conditions, contribute to the immune response (reviewed in (Philips and Robberecht 2011)). Evidences of astrocyte regulated intracellular Ca⁺² concentration rise/fall accompanied firing synapses support the idea that astrocyte excitability is important not only for astrocyte-astrocyte crosstalk but also for astrocyte-neuron ones. Altogether, those findings gave rise to the “tripartite synapse theory” (Araque et al. 1999), in which not only pre and post-synaptic neurons are important for optimal synaptic function, but

also astrocyte population surrounding them. Ca^{+2} balance is also noteworthy related to ALS, since it is known to be deregulated and plays a key role on pathophysiology of the disease linking ER and mitochondria (recently reviewed in (Prell et al. 2013)). Finally, astrocytes are also responsible for glucose and FA uptake from the blood across BBB and therefore they regulate CNS energy flow (which is an important issue in ALS (Dupuis and Oudart 2004)).

Microglia are the resident macrophages of the CNS and have two main distinct roles: first, they help astrocyte population to support neurons in a concerted mechanism and the second is related to its immunological role, which could be cytotoxic-linked. They derive from primitive myeloid progenitors and, resembling to them, recent studies classify microglia according to its role as neuroprotective or detrimental for CNS (Henkel and Beers 2009) being M1 related to the latter and M2 to the former. Hence, their inflammatory outcome is believed to be based in both, by intrinsic factors and by microglia-neuron-astrocyte cross-talk. When activated, microglia undergoes morphological changes to an amoeboid shape and proliferates. They also migrate toward injured areas; release various powerful soluble factors and phagocyte foreign substances or unwanted self debris.

Like microglia, astrocytes also exhibit double edge sword behaviour. However, under neuroinflammation, shift from proinflammatory towards anti-inflammatory processes is poorly understood until date. When activated, they result in astrogliosis, usually identified by glial fibrillary acidic protein (GFAP) and aldehyde dehydrogenase-1 family-member-1 expression, concomitant with cell body hypertrophy, and which could lead to pro-inflammatory cytokines release (mostly like microglia ones, but also producing neurotransmitters like Glut) and/or anti-inflammatory ones (transforming growth factor- β , IL-6, Interferon- γ , among others) (a complete review in astrocyte function could be found at (Sofroniew and Vinters 2010)). Finally, other players in the inflammatory game are T cells, which could infiltrate CNS and modulate its outcome (regarding ALS those are a relevant papers (Chiu et al. 2008; Beers et al. 2008)) and oligodendrocyte and pericyte population, whose action regarding neuroinflammation is poorly understood yet.

It is important here to bear in mind that inflammation is a physiological response to an insult and, in general, acute neuroinflammation is a protective mechanism trying to “fix the problem” up to a extent, whereas chronic inflammatory status produces long-lasting and self-perpetuating mediators that remain after the insult, hence being more often related with the detrimental outcome (Glass et al. 2010). This is a plausible explanation why those cell populations could both, help to diminish or to exacerbate inflammatory damage, depending on how profound the aggression is.

Also noteworthy is the difference between anti-inflammatory and resolving actions of a specific molecule. Resolution is a relatively recent term (Serhan et al. 2007) and is defined, in contrast to anti-inflammatory species, by its action not only serving as agonist for inflammation responses (e.g. lowering lymphocyte infiltration and/or diminishing adhesion-molecule synthesis) but also by promoting active processes to achieve homeostasis/*catabasis*-return from disease (e.g. promoting uptake and clearance of apoptotic cells, stimulating expression of antimicrobial defense mechanism). Anyway, in general terms for all cases, first steps after an insult involved generation of proinflammatory mediators (classically, leukotrienes-LT- and prostaglandins-PG, mostly AA-derived) to be substituted afterwards by PGE_2 and PGD_2 which gradually induced anti-inflammatory and pro-resolution key enzymes (by LOX upregulation) which, in turn,

generate lipoxins, resolvins and protectins (Levy et al. 2001) for helping resolution. This new lipid profile is termed “lipid mediator switch” and is crucial for inflammation resolution. In fact recent studies (Schwab et al. 2007) have shown that COX-2 inhibition (classically pro-inflammatory, but signalling helpful) results in a delayed cleaning, and, therefore, slower recovery.

Broadly speaking in CNS, the mechanism could start by TNF α and IL β release by microglia and astrocyte followed by its binding to their specific receptors and upregulation of gene transcription via NF κ B pathway (Blais and Rivest 2001). Among them, AA signalling cascade genes. Hence cPLA $_2$ and sPLA $_2$ in one side, and cyclooxygenases, lipoxygenases and thromboxane synthases (COX, LOX and TXS respectively, discussed below) release and modify AA to form powerful lipid species (generally termed eicosanoids for its 20 carbon content: LT, PG, prostacyclines -PGI- and tromboxanes -TX- in general). And, on the other hand, phospholipases (specially plasmalogen-selective phospholipase A $_2$ -PLsEtn-PLA $_2$) could also release DHA (and/or EPA) activating docosanoid synthesis which could, in turn, counteract those outcomes, since most of their derivatives (maresins, neuroprotectins, neuroprostanes) and closely related EPA-derived eicosanoids and dihomo-gamma-linolenic acid (DGLA) derived ones (less prominent) exert anti-inflammatory properties. Below, there is a scheme of the aforementioned process and the cell types involved, and in the next chapter we will say some words about the synthesis of those derivatives, generally termed oxolipids.

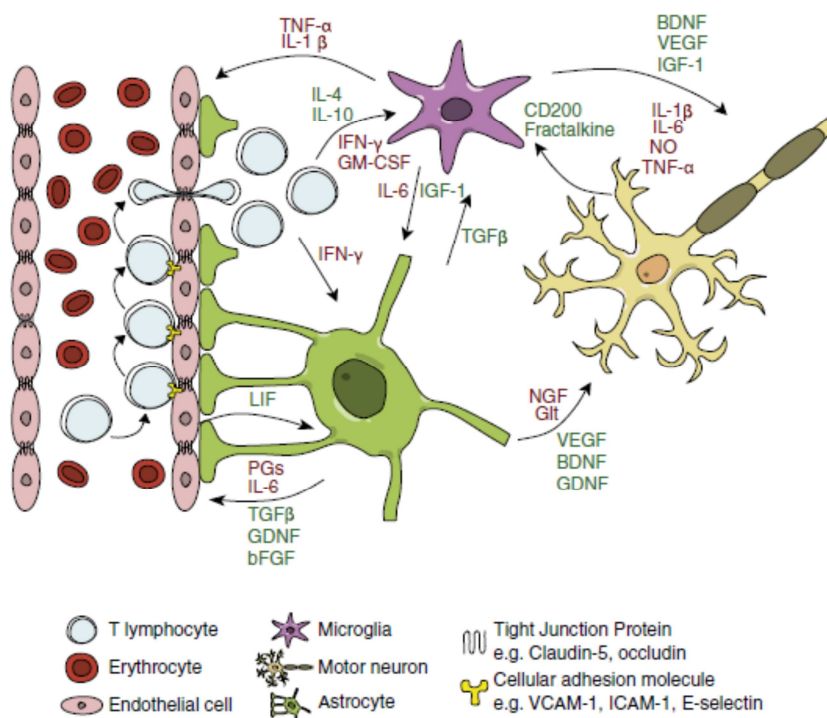


Figure 15. Inflammation partners in CNS.

Inflammatory-derived and neurovascular changes in amyotrophic lateral sclerosis. VCAM-1 Vascular Cell Adhesion protein 1; ICAM-1 InterCellular Adhesion Molecule-1; GM-CSF Granulocyte-Macrophage Colony Stimulating Factor; BDNF Brain-Derived Neurotrophic Factor; CD200 Cluster of Differentiation 200; VEGF Vascular Endothelial Growth Factor; IGF-1 Insulin Growth Factor-1, IFN- γ Interferon- γ ; bFGF basic Fibroblast Growth Factor. Copied from (Evans et al. 2013).

1.C1.2.- Oxidative-derived inflammatory-relevant lipid species

In common with other lipid mediators, all these lipid species are not stored in any cellular compartment, meaning they are quickly synthesized upon demand and therefore rely on the abundance of its precursors as well as the enzymes responsible for their synthesis (for an excellent review on oxolipids synthesis in CSN see (Phillis, Horrocks and Farooqui 2006).

Therefore, for some of them, the limiting factor is their relative abundance of the precursor, since they share, and therefore compete for the same enzymatic machinery with many other mediators.

A) Cyclooxygenases

COX-1 and COX-2, confined chromosomes nine and one respectively, catalysed the limitant step in the synthesis of PG, PGI and TX (collectively termed prostanoids). Those heme-containing bifunctional enzymes possess two catalytic centers. They are 65% homologous and, among FA, their preferred substrate is AA (other substrates include cannabinoids (Kozak, et al. 2001) and lipo-amino acids (Prusakiewicz et al. 2002)). However, their activities differ, since COX-1 is constitutively expressed in most tissues and produces derivatives that generally serve a housekeeping function, whereas COX-2 (constitutively expressed in the kidney, stomach, and CNS) was initially characterized as an inducible enzyme whose expression is enhanced in response to inflammatory stimuli, cytokines and transcription factors (e.g. IL-1 β , TNF α , LPS, PAF, TGF- β , NF- κ B) (O'Banion 1999). Under pathological conditions COX-2 expression was observed increased (respect to COX-1) in neurons and astrocyte, whereas in microglia, the latter is more often expressed (Consilvio, Vincent and Feldman 2004), although this cell type "selectivity" is not well understood. Nevertheless, COX-2 action was also reported to increase under excitotoxic (kainic acid) conditions in neurons (Adams et al. 1996) as well as in astrocytes (Sandhya and Farooqui 1998) and can be suppressed by Glut antagonists (e.g. MK-801, dexamethasone) implying that COX-2 regulation is dependent on synapse activity. Importantly, astrocyte and neuronal activation are sometimes non-simultaneous. Thus, neurons are more often rapidly induced and silenced, whereas astrocytes could sustained its induction for a longer period (Sandhya et al. 1998). These timing differences are crucial since it is known that the same PG could operate different responses (even opposed) depending upon the target cells and, of course, different PG could evoke opposed responses on the same cell.

Nomenclature of prostanoids aroused due to their structure, which is nowadays extremely wide, but originally resembled that of prostanoic acid. Subindex numbering of those molecules refers to the number of unsaturation along the aliphatic chains residues and the letter is related to the type, unsaturation degree and substituent present in the ring (Herrera E. 1993). During the conversion of substrates (we use AA as a representative) to oxolipids, there are two sequential steps. First, a pure cyclooxygenase phase operates where an O₂ molecule is added to form PGG₂; secondly, peroxidase action of the enzyme converts it to PGH₂, involving free radical release. This PG is subsequently metabolised by tissue-specific synthases to yield a variety of products (e.g. PGE₂, PGD₂, PGF_{2a}, PGI₂, TXA₂, 15d-PGJ₂) which could be modified to generate a greater array of specific PG, with very different outcomes.

Finally, regarding COX substrate preferences, some differences have been reported. Although AA is the preferred substrate for COX-1 and COX-2, other fatty acids can be oxygenated by both isoforms with varying efficiencies (Wada et al. 2007), having COX-2 more extensive array of substrates compared with COX-1, presumably because of a \approx 20% larger active site (Kurumbail et al. 1996). However, oxygenated products are scarce when DHA is the substrate (12%, versus 30% of EPA, respect to AA) and in fact, until recently DHA was not considered a valid substrate

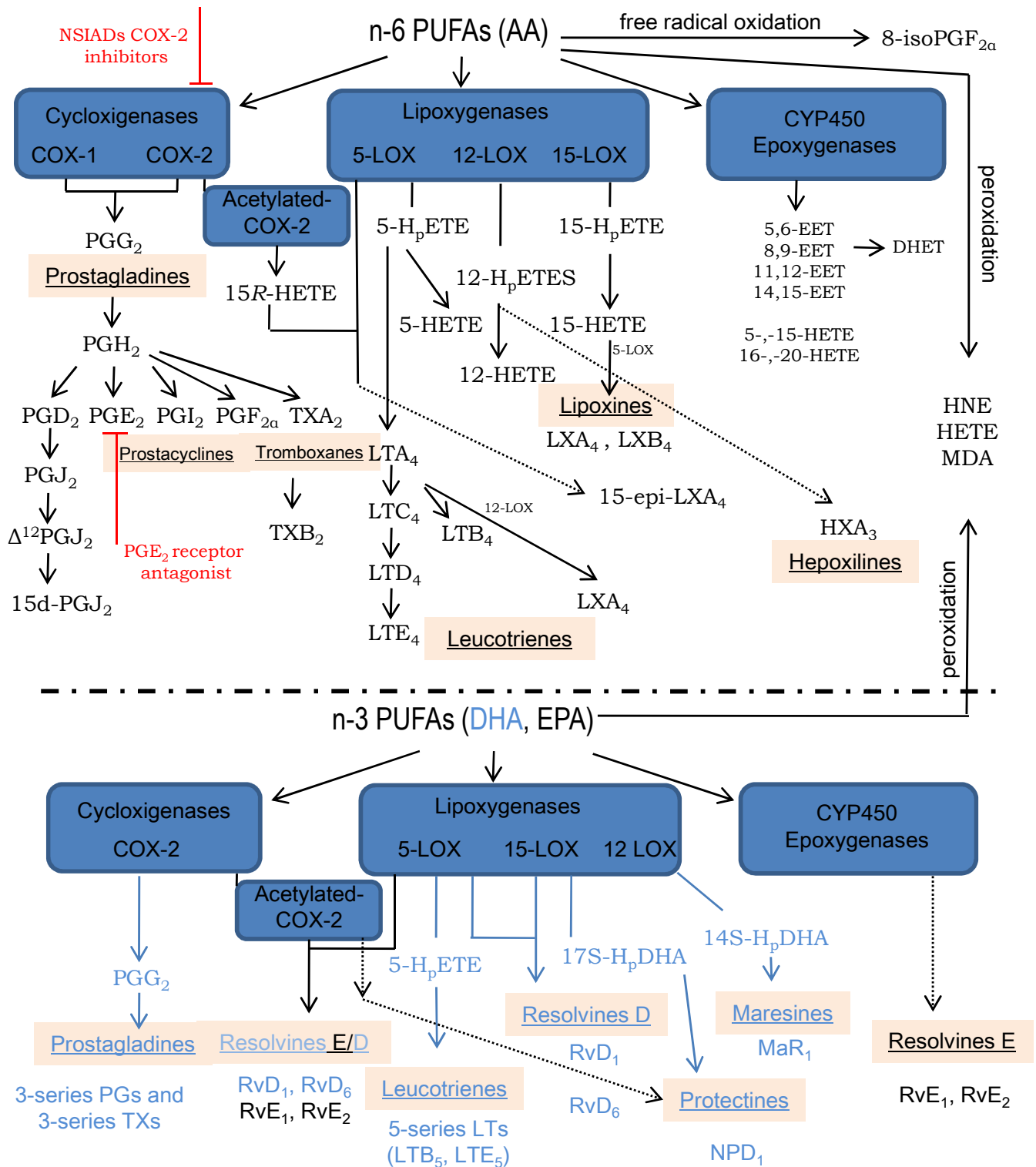


Figure 16. Inflammatory-stimulated PUFAs derivatives. Schematic representation of relevant lipid derivatives raised in inflammatory processes, depicted by FA family (ω -3 vs. ω -6) and responsible enzymes. In red, inhibitors, in blue, DHA derived and in black AA and EPA derived substances. NSIAD, Non-steroidal anti-inflammatory drug.

B) Lipoxygenases

Lipoxygenases (LOXs) constitute a heterogeneous family of lipid peroxidizing enzymes capable of oxygenating PUFAs containing *cis*, *cis* 1-4 pentadiene structures to their corresponding hydroperoxy derivatives. Lipoxygenase proteins have a single polypeptide chain (molecular mass \approx 75–80 kDa) with an N-terminal β -barrel domain and a larger catalytic domain containing a single atom of non-heme iron critical for its optimal function (Brash 1999). Since 1974 (Hamberg and Samuelsson 1974), when the formation of 12-hydroxyeicosa-5,8,10,14-tetraenoic acid (12-HETE) was described as being formed by exogenous AA addition to trombocytes, it was proved that those enzymes families were found in both, superior animals and plants. In mammals, LOXs could be classified according to their positional specificity of AA oxygenation into 5-, 8-, 12-, and 15-LOXs or attending its positional specificity of arachidonate oxygenation into *S* and *R* isoforms (Meruvu et al. 2005). In recent years, LOX biochemistry and its regulation had gained increasing attention due to its intimate relation with inflammation-resolution processes and, especially in allergic responses. Hence, intensive research has been done, mainly in 5, 12 and 15-LOX

The 5-LOX is a Ca^{+2} -dependent membrane-binding which is translocated to the nuclear membrane and whose fully activation also requires a helper protein, known as 5-LOX-activating protein (FLAP) (Peters-Golden and Brock 2003). This location close to the nucleus, and the high probability of ROS leak on their catalysis could influence redox tone and thereby modulate, for example, the activity of oxidant-sensitive transcription factors such as NF- κ B (Bonizzi et al., 1999). the Ca^{+2} dependence of this enzyme is also noteworthy, since this ion is largely known to be deregulated in various neurodegenerative processes (reviewed in (Calì, Ottolini and Brini 2013 and Prell et al. 2013)). 5-LOX is the key enzyme for the LT (the name comes from its discovery being generated from “leuko”cytes and conserved 3 carbon-carbon double-bond, “trienes”) synthesis (Funk et al. 2002) and catalyzes the oxygenation of AA to form 5-HEPETE, and finally the epoxide intermediate LTA_4 . This LT can be later hydrolyzed by LTA_4 hydrolase to leukotriene B₄ (LTB_4). Another possibility renders LTA_4 to be conjugated with glutathione by leukotriene C₄ synthase to yield LTC_4 (other possibility of LTA_4 is to serve as substrate of 12-LOX to form LXA_4). Then, LTC_4 can be converted by γ -glutamyl transpeptidase to LTD_4 . In turn, LTD_4 could be also converted to LTE_4 by dipeptidases. Those derivatives (LTC_4 , LTD_4 , LTE_4), are termed cysteinyl LT and are mainly produced by eosinophils, basophils, and macrophages cells. LTD_4 and LTE_4 are secreted (not having an intracellular function to date) and the three of them are relevant in allergic responses as slow-reacting substances of anaphylaxis (Austen et al. 2009).

Finally, using a DHA derivative, 17-hydroperoxy-docosahexaenoic (17-(R,S)-HPDA) acid, 5-LOX also catalyzes its conversion into resolvines one and two (RvD1, RvD2, discussed below). Interestingly, this synthesis could be also aspirin triggered, and when is under such conditions, predominant lipid specie posses *R* configuration (Hong et al. 2003). These potent species have been proved to reduce neutrophil recruitment and infiltration as well as functioning as pain reduction agents in mice (Hong et al. 2003; Spite et al. 2009) possibly serving as new “antiinflammatory therapy”.

Two types of 15-LOX have been characterized in humans: reticulocyte-type (15-LOX-1) and epidermal-type (15-LOX-2). This enzymes displayed differential substrate specificity, LA is the preferred substrate for 15-LOX-1 whereas AA is the preferential election for 15-LOX-2. Thus,

LA is metabolized to 13S-hydroperoxyoctadeca- (9Z, 11E)-dienoic acid, which is later reduced to 13S-hydroxyoctadeca-(9Z,11E)-dienoic acid (13-HODE). On the other hand, 15-LOX-2 oxygenates AA to form 15(S)-HPETE, which is reduced to 15(S)-HETE (Mahipal et al., 2007). One important action of 15-LOX-1 is related with the synthesis of Neuroprotectin D1 (NPD1) (Calandria et al. 2009) since its action upon DHA generates 17-(S)-HPDHA as an intermediate, which after epoxidation and hydrolysis reaction generated NPD1. It was demonstrated that this lipid specie protects against oxidative stress-induced cell death and to exert pro-resolution signals, in retinal pigment epithelial cells. In the brain, NPD1 was related to attenuated protein misfolding responses (Calandria et al. 2012) which are specially relevant in Alzheimer disease (Lim et al. 2005; Zhao et al. 2011) but also in ALS (Ilieva et al. 2007; Walker and Atkin 2011) since it is largely known an alteration in unfolding protein response (UPR) of the ER involved in its pathogenesis (recently reviewed in (Matus et al. 2013; Prell et al. 2013)).

Three types of 12-LOX have been described and they catalyze the stereo-specific oxygenation of AA to yield 12(S)- hydroperoxyeicosatetraenoic acid (HPETE, a well known thromboxane suppressor by inhibition of platelet cyclooxygenase (Brüne and Ullrich 1991)) and 12(S)-hydroxyeicosatetraenoic acid (HETE). Both 12 and 15-HETE have been linked with hypertension (González-Núñez et al. 2001), endothelial pathology (Anning et al. 2005) and even renal function (reviewed in (Hao and Breyer 2007)). 12-HPETE is also a substrate for the synthesis of HXA₃ mediated by hepoxilin synthases (even when this could also be obtained by the CYP450-mediated catalysis, reviewed in (Nigam and Zafiriou 2005)). Lots of functions have been related to be hepoxilin modulated, most of the research has been done in neutrophils (Nigam and Zafiriou 2005) but they were also related to hyperpolarization in rat hippocampal slices (Carlen et al. 1994).

C) Acetyl-salicylic acid-stimulated ω -6 anti-inflammatory mediators: Lipoxins

Lipoxins are generated in humans from AA via LOX enzymes and comprise 2 distinct regioisomers, lipoxin (LX)A₄ and LXB₄. They were among the first lipid mediators recognized to have both antiinflammatory and proresolving actions (Serhan et al. 2008) by stimulating monocytes and macrophages to perform phagocytosis without releasing cytokines or chemokines. Classically, their biosynthesis proceeds via 15-LOX and 5-LOX mediated conversion of AA during cell-cell interactions (e.g. epithelial-leukocyte, leukocyte-leukocyte) or, in the contrary, 12-LOX mediated in the vasculature during platelet-leukocyte interactions and their actions proceed via activation of specific receptors (found in murine and human CNS brain atlas; <http://human.brain-map.org>; <http://mousespinal.brain-map.org/imageseries/detail/100028215.html>). However, an intriguing novel lipoxin route involving COX-2 and 5-LOX under the presence of aspirin was discovered, the 15-epi-LXA₄ (Clària and Serhan 1995). Its biosynthesis was recently proposed to be alternatively initiated by CYP450 enzymes and this pathway may underlie its generation in the absence of aspirin. For a review on lipoxin synthesis and resolving functions see (Ryan and Godson 2010). Since in one hand, aspirin was proved to acetylate both COXs (Loll, Picot and Garavito 1995) (more recently CYP450 too) causing its inhibition by active site alteration and, on the other, DHA and EPA are known to be substrates for acetylated COX, this opened a new route for more aspirin triggered lipoxins, which, in fact have been found (EPA derived resolvines, RvE1 and DHA-derived 17R-

hydroxydocosahexaenoic acid, among others, discussed below) with novel powerful resolution properties.

D) ω -3 Pro-resolution mediators: Resolvins, Protectins and Maresins

Resolvins represent a novel potent lipid mediator family *in vivo* arising from ω -3 FA at final stages of acute inflammation. Those local, short-lived lipids species exerted their function, together with protectins and the previously described lipoxins, on recently discovered membrane receptors (Krishnamoorthy et al., 2010) but, interestingly, do not activate PPAR (all isoforms) or RXR factors (at least in HEK-293 cells). As pointed before, resolution is an active process and resolvins are termed so since, i) they are produced during cell-cell interactions occurring in the resolution phase of acute inflammatory response; ii) they “stop” further neutrophil entry to sites of inflammation, and iii) reduce proinflammatory exudates (Bannenberg et al. 2005). All those lipid mediators, generally termed docosatrienes (twenty-two carbons, 3x C-C double bounds), were found thanks to a complex bioinformatics approach and its *in vivo* relevance was confirmed by LC-MS/MS. Depending on the ω -3 source (EPA or DHA), Resolvins are classified as E and D series. On the other hand, Protectins and Maresins were described as DHA hydroxyl derivates (for a review (Ariel and Serhan 2007; Spite and Serhan 2010)); the latter discovered in macrophages (Macrophage mediators in resolving inflammation (Serhan et al. 2009) and the former found in immune cells and/or neural tissues (Mukherjee et al. 2004). In the past years (for a recent review see (Serhan, Dalli and Colas 2014)) research was focused in structural and biosynthesis elucidation of those potent mediators, trying to clarify whether these substances could be responsible for the “inflammatory switch”.

E) Isoprostanes

Isoprostanes are lipid species emerging from nonenzymatic free-radical oxidation of PUFAs, sometimes (but not always) when they are esterified in biomembranes. Those compounds are named prostanes since, when firstly described (70's decade (Porter and Funk 1975)), its structure had a cyclopentane (prostane) ring. However, nowadays compound family has grown a lot and many different structures could be found (for profound review on isoprostanes generation and function see (Milne et al. 2011)). In fact, there is controversy just on its nomenclature (Mueller 2010), in simple, IUPAC proposed C20 derivatives (mainly AA source, but also EPA ones) are termed isoprostanes (IsoP), C22 derived ones (often DHA derived) neuroprostanes (NeuroP, firstly described by Roberts in 1989 (Roberts et al. 1998)) and C18 (could arise from α and/or γ linolenic acids) Phytprostanes -found in plants too. A sub classification of those species was needed and F₂, E₂, D₂, A₂, J₂-IsoP (AA derived with a closed cyclopentane ring but also open structures like E₂- and D₂-IsoK; EPA derived, F₃-IsoP; DHA derived, F₄-IsoP) and NeuroP were subdivided according to where oxygenation takes place, arising 5, 8, 11, 12 and 15 series (this is the case for the simplest AA-derived IsoP; the more double bonds the more possibilities). The myriad of different structures arises since initial stochastically-radical-oxidation takes place close to a high number of double bounds (along those FA) and those reactions could terminate in a great variety of options. However, there are some C-C double bounds more likely prone (based on their hydrogen pK) and/or exposed (depending on structural configuration or their degree of concealment) to oxidation, and, also importantly, some of those “unspecific” products were in fact substrates for further synthetic processes. For instance, in the AA-derived IsoP generation, series 5 and 15 are predominant, but

the 12 and 8 series (minority) could serve for dioxolanes (another IsoP type, with two 5-vertexing) synthesis and therefore, reduced its accretion (Yin, Morrow and Porter 2004). For a more detailed study of EPA derived IsoP see (Yin, Brooks, Gao and Porter 2007).

IsoP, and some of the related family members, are considered a new class of biomarkers for oxidative stress measurements (Roberts and Morrow 2000) and are especially relevant among lipid peroxidation ones. Besides the major lipid oxidation products (HNE and MDA (Spickett 2013), IsoP fullfills the requirements to be a good marker: They are (i) frequently accumulated up to detectable quantities in biological fluids and tissues, allowing the definition of a normal range; (ii) stable compounds; (iii) their formation increases dramatically *in vivo*, in a number of models of oxidant injury; (v) their formation is modulated by antioxidant status.

Nevertheless, IsoP family have been proved to affect very different aspects of cell fate, from actions on vascular system (where F₂-IsoP are specially relevant (Hou et al. 2004)), muscle contraction, nociception or cell proliferation. Those actions, are believed to take place through “specific” membrane receptors, since some have been shown to bind to classical prostanoid (for PG) membrane receptors (for instance TX receptor is known to bind F₂-IsoP), although most IsoP are “orphan” receptors to date.

1.C2 Lipid peroxidation: Friend or foe?

1.C2.1.-Chemistry of oxidative stress

Oxidative stress is a term used to explain a situation when, an unbalance in between physiological oxidative production and antioxidant defence counteract (enzymatic and non enzymatic too) and/or reparatory systems is present. In principle, this situation could be therefore achieved when antioxidant defence and/or repairing systems fail to detoxify physiological noxious by-products or, on the other hand, when regular occurring oxidation is no longer under strict control, hence, promoting damage to cell molecules constituents (proteins, sugars, lipids and nucleic acids). This, among others, is the basic tenet of several pathophysiological states, such as neurodegeneration (reviewed in (Barber and Shaw 2010)), cancer or aging (Harman 1956). Although any biomolucule is susceptible to receive this modification, proteins, due to its high overall abundance, are more probably affected by oxidative processes and are therefore believed to account (as final acceptors) for the majority reactive species generated (50%–75%) (Davies, Fu and Wang 1999). However, damage to DNA, often measured by the accretion of 8-oxo-deoxiguanosine (8-oxo-dG) as well as proteic systems designed to detect (double strand break -DSB-, e.g. phosphorylation of histone γ H2AX (Rogakou et al. 1998)) and respond to DNA-oxidative damage are relevant mechanisms, especially in the “germ” cells, since any DNA mutation could be therefore inherited.

From an evolutionary point of view, oxidative biochemistry (phosphorylation), which in superior eukaryotes is mainly taken part in mitochondria or chloroplasts, turned out to be a very satisfactory mechanism. Ancient archeas, bacteria and cyanobacteria started oxygen production, as an undesirable metabolic by-product, around 3400 million year ago. Approximately 1000 million years later, Earth atmosphere reflected the “work” done. This event was known as “the

oxygen burst”, which ultimately caused one of the first massive extinctions (almost complete) of obligated anaerobic organisms, but on the other side helped to promote a massive biodiversity. In any case, from this oxygenated atmosphere, and helped by aforementioned organelles (whose eukaryotic evolution was elegantly explained by the Russian biologist Konstantin Mereschkowsky in the endosymbiotic theory (Mereschkowsky 1910), organisms evolved to live in an oxygenated ambient, taking enormous benefits, specially, in terms of energy production.

However, there are hundreds (possibly thousands, since extremophiles research is an enormously growing field) of organisms which obtain energy without oxygen being the final electron acceptor, through multiple ways, from methane or acetate to sulphur or even halogens or uranium (*Methanothermothrophila*, *Sulfolobus* genus, *Geobacteraceae*, *Geobactermetallireducens* respectively, reviewed in (Schäfer, Engelhard and Müller 1999)). In any case, those organisms also grapple with side effects of oxidative reactions and represent an interesting research field, because those different options to optimize energy sources give rise to various approaches in terms of antioxidant capacity design. Either way, eukaryotic anaerobic cell respiration, consisting in glycolysis, produces 2 ATP per unit of glucose consumed. On the contrary, aerobic respiration (composed by glycolysis, plus Krebs cycle and oxidative phosphorylation) could produce up to 36 ATP per glucose. All in all, aerobic respiration in eukaryotes is roughly 18 times more efficient than anaerobic. Furthermore, efficiency of the process for energy extraction from nutrients is believed to be about 40%. The remaining 60% is converted in heat, which is useful for poikylothermic organisms, but could become an issue to deal with for homeothermic ones.

Nevertheless those energetic benefits pay a bill, which is the production of undesired oxidative species. But let's start from the beginning, what is an oxidant? What is a free radical? Or where do they come from? Chemically, redox reactions represent a group of natural occurring reactions which involve electron transference between two species. So oxidant processes have to be understood as a pair of coupled reactions, reduction of one counterpart with the oxidation of the other. Under this situation, oxidant is the specie which “receives” those electrons, being itself therefore reduced on its oxidation state. On the contrary, a reducing agent will decrease its oxidation state (because it is electron donor) causing the oxidation of the pair. Hence, is important to bear in mind that any specie is oxidant or reducing depending on the counterpart which is confronted. Nonetheless, in biological systems, those conditions are in an homeostatic range, so the oxidant behaviour of a given substance is normally “permanent”.

Among oxidants, free radicals are one of the most powerful agents. In a simple definition, a free radical is any atom (e.g. oxygen, nitrogen, sulphur) or group of atoms (e.g. $\cdot\text{O}_2^-$ superoxide anion, $\text{HO}\cdot$ hydroxyl radical) or molecular species (e.g. ascorbate radical, lipid radical, $\text{LO}\cdot$ or $\text{LO}_2\cdot$) capable of independent existence (commonly extremely short due to its high instability) that contains at least one or more unpaired valence electrons (the ones in the more exterior atom shell) or a open outer shell configuration (Halliwell B, Gutteridge JMC 2000). In biology, due to its relevance, free radicals are also known as reactive oxygen species (ROS), reactive nitrogen species (RNS) (Halliwell B, Gutteridge JMC 2000). and more recently, reactive lipid species (RLS), although, in nature, all sort of radicals can be found.

In eukaryotic biota, those radical species are mainly generated along the electron transport chain (ETC) in mitochondria and chloroplasts. Mitochondrial ETC comprises very sophisticated and

complicated proteic systems which could be “divided” in five complexes (each composed by multiple subunits, but interestingly not all encoded in the mitochondrial DNA, mtDNA) and electron donors-transporters (e.g. Ubiquinone, Coenzyme Q). All of them are cristae resident, thus, embedded in the inner mitochondrial membrane. ETC bioenergetics, composition and physiology will be discussed below, just say here that they orchestrate a controlled transfer of energy from the substrate (e.g. pyruvate, malate, succinate) to molecular oxygen (the final acceptor) forming, along this process, the corresponding reduced equivalents (e.g. NADPH⁺, FADH₂) and generating an intermembrane electrochemical gradient ($\Delta\Psi$) which ultimately results in ATP production (through ATP synthase) and/or heat (uncoupling proteins, UCP).

Hence, mitochondrial ETC complex I and III have been blamed for main ROS production long time ago (Turrens and Boveris 1980). However, there is still controversy on which of them are “the more responsible”. Nowadays, it is believed that CI ROS production could be counteracted more efficiently by mitochondrial antioxidant defence, but due to its location and functionality, affects mtDNA more significantly (reviewed in (Stefanatos and Sanz 2011)). On the other hand CIII ROS are more prone to affect extra-mitochondrial molecules (Chen et al. 2003), and possibly related with signalling events to control this excess.

However, during millions of years, those processes were refined to avoid undesired leaks in the system, which could generate the mentioned radicals and/or oxidant species with those harmful consequences. Pointed long time ago (Richter 1997), taking into account this evolutionary process and its statistically-stochastically-linked physiological leak, organisms evolved to understand and react when situations turned dangerous. There are sensitive mechanisms which detect the unbalance and operate towards solving it. This fact changed the classical harmful focus into, up to an extent, benign signalling. So nowadays, ROS, RNS and RLS are known to have double edge-sword behaviour. Nobody is saying that general indiscriminate damage to neither nucleotides nor proteins is beneficial, but, along million of years, is reasonable to think that organisms developed a wide array of mechanisms in order to ascertain their status and therefore orchestrate a reasonable response, among them oxidative signalling (for a review see (Martindale and Holbrook 2002)). In fact antioxidant supplementation, aimed to minimize radical production, is nowadays controversial (Bjelakovic et al. 2013 and Dolara et al. 2012). Some studies have shown that antioxidant supplementation could have no effect in health subjects with a balanced diet and a reasonable active lifestyle (Taghiyar et al. 2013) or even, in turn, exacerbate oxidative damage (Schnorr et al. 2011 and Bjelakovic and Gluud 2007). This may be explained, since if dietary intake is exceeded, local synthesis and detoxifying mechanisms would render “unnecessary” and the body would reach another homeostatic situation, potentially harmful if this dietary supplements failed to be at the right time and location.

This relates to a relative new concept, mitohormonesis (Tapia 2006), which, in brief, refers to the already mentioned minimal oxidative damage needed to achieve a balanced status of the organism's natural response to the oxidant compounds. This was partially validated by finding an increased life expectancy in *C elegans* (Schulz et al. 2007). However, it seems pretty clear that those antioxidant-dietary supplements are beneficial when an altered diet or pathology is present (Kim, Kim and Choue 2013 and Miyamae et al. 2013) and there is no discussion on the positive role of radical production for pathogen control, like physiologically produced oxidant derivatives by myeloperoxidase action in neutrophils, Nitric Oxide signalling or NRF2 translocation, among other beneficial properties.

1.C2.2.- Mitochondrial physiology

We will present here a brief description of mitochondrial bioenergetics and components trying to shed some light on its physiology. As stated before, ETC could be subdivided into five complexes (complex I, CI; II, CII; III, CIII; IV, CIV or cytochrome-c oxidase and V, CV, or ATP synthase) each one composed of multiple subunits and mobile electron shuttles - ubiquinone (Coenzyme Q, CoQ), a lipidic quinone and cytochrome c (Cyt c), a heme-containing peptide -. A representation is shown in page 74, Figure 17.

mtDNA encodes several, but not all, subunits of the ETC. Apart from 2 ribosomal and 22 transfer RNAs, mammalian mtDNA encodes only 13 proteins (7 from CI, 1 from CIII, 3 from CIV, and 2 from CV) (Mitochondrial Oxidative Phosphorylation 2012). Also remarkable, for a correct mitochondrial functionality, this organelle needs from, approximately, 1000 (Elstner et al. 2009) nuclear-coded cytosol-synthesized proteins, delivered through two classical “pathways”, but with increasing novel partners (both issues recently reviewed in (Schmidt, Pfanner and Meisinger 2010)). The vast majority of mitochondrial proteins (taking into account mtDNA encoded and nuclear encoded ones) shows a prokaryotic origin, as reflected by the findings of orthologous phylogenetically related ones. However, a large number of proteins were incorporated during the evolution of eukaryotic cells, with increased complexity, probably for optimising regulation since those cells had also higher networking and their functioning proceed more specifically. Thus, actual eukaryotic mitochondrial proteome represents a mosaic of ancestral components and components emerged though evolution to adapt their new functionality, for which no orthologous are found in prokaryotes.

In mammalian mitochondria, CI catalyzes the oxidation of reduced NADH by CoQ. This complex is the largest in the ETC system, consisting of ≈ 45 subunits in mammals. Ultrastructural studies of purified CI revealed an “L” shaped object, consisting of two arms, a hydrophilic “peripheral arm” protruding into the matrix, and a hydrophobic “membrane” arm, embedded in the mitochondrial inner membrane (Efremov, Baradaran and Sazanov 2010). This two arms harbour the three functional modules: i) the dehydrogenase site, responsible for the oxidation of NADH to NAD⁺; ii) the Q module, in the hinge region between the two arms, contains the CoQ reduction site; ii) the P module, which is responsible for proton translocation. Various human diseases have been linked to mutated or malfunction of CI (reviewed in (Fassone and Rahman 2012)), most of them with an early clinical manifestation. Interestingly in a recent paper (Ghiasi et al. 2012) researchers find a reduced complex I activity concomitant to an increase in ADP content, in ALS patients’ circulating lymphocytes. Finally another SOD1 mutation linked to ALS was found to alter C I activity and ATP production (in animal model (Coussee et al. 2011) suggesting a CI involvement in the ALS pathogenic mechanism.

CII is a succinate dehydrogenase which represented the only membrane-bound member of the tricarboxylic acid (TCA) cycle. This enzyme catalyzes the oxidation and dehydration of succinate to fumarate coupling this reaction to the reduction of ubiquinone to ubiquinol. CII is the smallest among the ETC complexes, consisting of four subunits and three Fe–S centers and having a FAD (Flavin-adenin-dinucleotide)-binding domain. The crystal structure consists of a hydrophilic head protruding into the matrix, a hydrophobic tail embedded in the inner

membrane and a short segment projecting into the intermembrane space (Sun et al. 2005). Interestingly, mRNA expression levels of both, FAD and succinate dehydrogenase complex subunits were found decreased in ALS patients (Lin et al. 2009).

Finally, CIV (which is believed to represent a rate limiting step of the ETC (Pacelli et al. 2011)) is the unique responsible of final electron acceptor of oxygen, but unlikely responsible of ROS production (Yu et al. 2011), and represents the only mitochondrial complex that has been found to have different isoforms on 5 of the 10 nuclear-encoded proteins. The existence of tissue and developmental specific forms is believed to occur to provide a platform for tissue-specific cell signalling and for a better adaptation to tissue/age demands too (Hüttemann et al 2008). In line with this, this complex was found to undergone accelerated evolution in primates (Uddin et al. 2008 and Grossman et al. 2004) respect to the other complexes. CIV is the only complex to be ATP/ADP-binding-regulated, also probably due to an increased adaptation of its activity to the particular energy demand. This complex also developed a special Ca^{+2} sensitivity. Apart from a direct effect (mammalian Cyt c have a Ca^{+2} binding site (Kirichenko et al. 2005), high extra-mitochondrial Ca^{+2} levels promote CIV dephosphorylation (Hopper et al. 2006) and this could lead to a mitochondrial hyperpolarization and increased ROS production.

Also remarkable, very relevant due to its function in transduction events leading to apoptosis, is the role of Cyt c (recently reviewed in (Wu and Bratton 2013)). This intrinsic pathway for self-controlled cellular death is conserved from worms to humans and represents one of the most likely forms of suicide in a specific cell when deleterious effect of various stimuli can no longer be confronted. Interestingly a significant Cyt c deletion was found in CNS of SOD1G93A mouse at endpoint (120 days but not in early stages (Kirkinezos et al. 2005)), linked to an increased MDA accretion suggesting an involvement of this ETC element in ALS development too.

For evaluation of relative contributions of mitochondrial complexes to oxygen consumption, several mitochondrial specific inhibitors and substrates could be added sequentially in an experiment, as routinely performed in our laboratory (López-Erauskin et al. 2013). Therefore, one can depict each-complex oxygen consumption in permeabilized samples, as well as the overall contribution in intact tissue or isolated mitochondria. This is a valuable and helpful tool for specific detection of the question, when the overall process (respiration) is believed to be altered.

1.C2.3.- Lipid peroxidation events

Let's focus now on lipids, particularly PUFAs, and their potentially harmful oxidative amplification. Particular composition of mitochondrial membrane lipids was extensively studied along the 90's at the laboratory of Dr Shalme and Dr Kligenberg (Schlame et al. 1991) and more recently revisited thanks to lipidomic analyses (Kiebish, Han and Seyfried 2009). Both studies showed big local differences from mitochondria of different sources. There are adaptive variations depending on the tissue, which is up to an extent reasonable, but even for the same tissue differences were found (e.g. fast or slow stretch muscle (Stefanyk et al. 2010)), or the synaptic location (e.g. pre or postsynaptic (Kiebish, Han and Seyfried 2009)) and of course, pointed long time ago, related to temperature where the specie is adapted to (Dey et al. 1993).

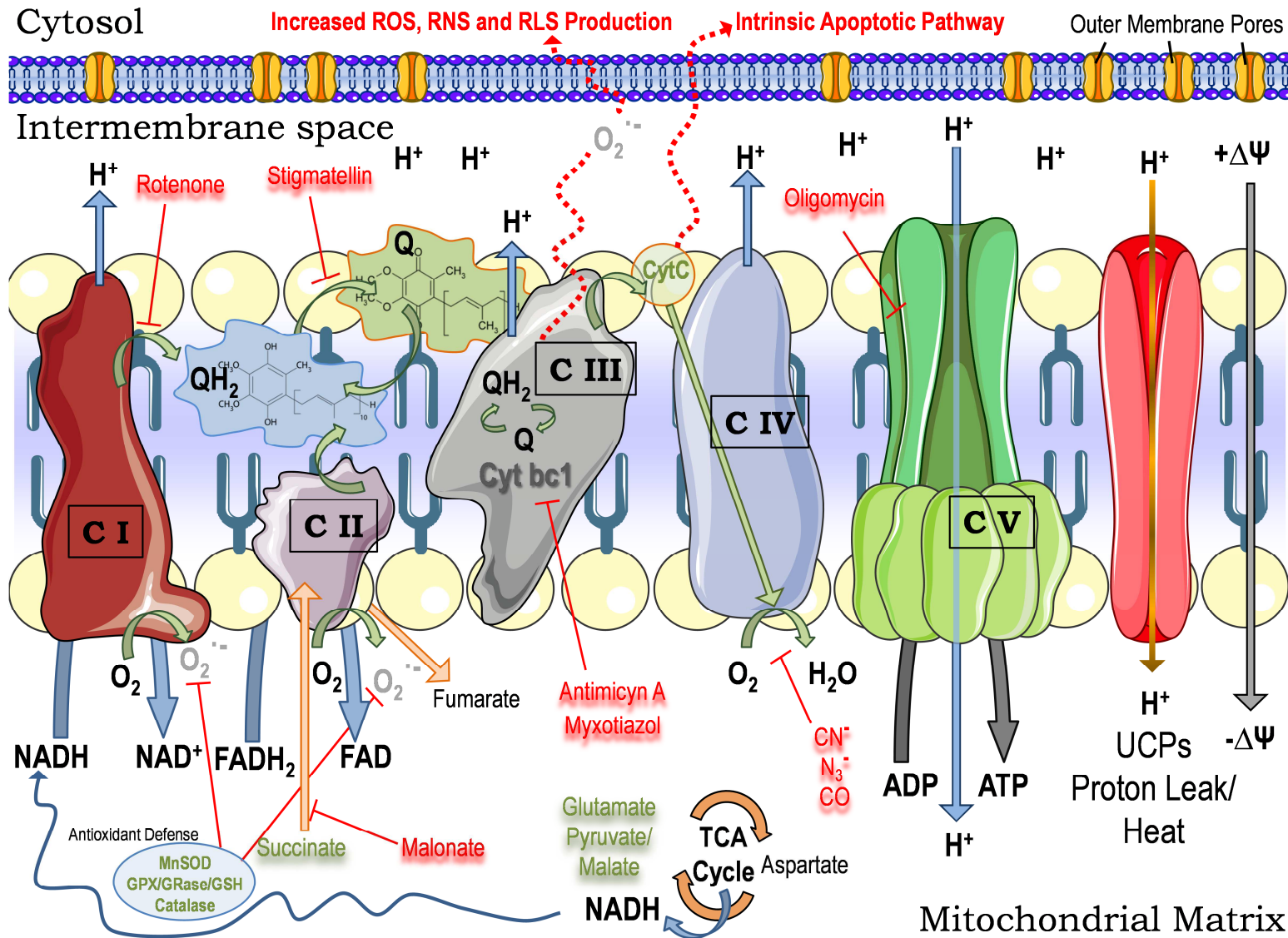


Figure 17. ETC depiction and physiology. From left to right CI (NADH dehydrogenase) generates reduced equivalents of Ubiquinone (QH₂) and pumps protons from the NADH generated in the TCA cycle (tri carboxylic acid) into the intermembrane space. The CII (succinate dehydrogenase activity) also generates Ubiquinone, while consuming FADH₂. CIII complete the Ubiquinol (Q) cycle (helped by the cytochrome bc1) as well as transmit electrons to CytC (cytochrome c) and releases protons to the intermembrane. All those complexes generate free radicals as by products which, for CI and CII, are in part counteracted by the mitochondrial antioxidant defence machinery (catalase, manganese superoxide dismutase, glutathione, glutathione peroxidase, and glutathione reductase; MnSOD, GSH, GPX, and GRase respectively). Complex IV (cytochrome c oxidase) reduced oxygen to water and sends protons to the intermembrane space. The electrochemical gradient ($\Delta\Psi$) generated by the pumped protons is used by CV to couple its entrance (protons) back to the mitochondrial matrix to ATP generation. Other possibility, helped by the uncoupling proteins (UCPs), is to “waste” the electrochemical gradient formed along the ETC to generate heat. Radical generated in CIII affects more easily extramitochondrial species and, under specific harmful conditions, Cyt c could be launched out from the mitochondria triggering

the intrinsic apoptotic pathway. Inhibitors are shown in red, substrates in green and products in black. Electron flux is represented by green arrows and proton flux by blue arrows. Not to scale.

Surprisingly, temperature could in fact regulate the rate of incorporation of FA into those mitochondrial PLs, at least in *in vitro* astrocyte cultures (Tocher and Sargent 1990). However, broadly speaking, one can assume that mitochondrial membranes are principally enriched in PE, PC, CHO and CL, representing, approximately 26%, 27%, 21% and 7% of lipids, respectively.

Among them, mitochondrial CHO levels are found the lowest in any membrane (probably to minimize sterical impedances and reduce cholesteryl oxidation) and CL is the only mitochondrial-specific one. Remarkable, CL displayed an extremely precise acyl composition for a given particular specie and/or tissue and its accretion could rise to represent up to 25% of total GPL in the inner mitochondrial membrane. CL contains normally only one or two types of sterified FA (i.e. LA and 18:1 are the most frequently found in humans, raising up to 80% of the CL FA (Schlame et al. 2005)). Although CL composition has a strong difficulty to be dietary modified, could be changed up to an extent specially in highly metabolic tissues (e.g. liver, heart (Stavrovskaya et al. 2013)). This strong uniformity in the FA pattern, also reflected by the identical tetraenoyls found in majority of CL, had stereochemical implications (e.g. symmetry) that very likely affect the physico-chemical molecular properties: i) symmetry will increase molecular entropy since increases the freedom of rotational and vibrational motion and thus may affect interactions between CL and other components of the mitochondrial membrane as well as the physical state of the membrane itself; ii) symmetric CL may freely adopt the optimal binding conformation with respect to the central carbon atom (in contrast to the asymmetric one which could be more sterically constrained); iii) chiral properties of the central carbon atom may affect the capacity of CL to act as a local proton buffer (Kates, Syz, Gosser, & Haines, 1993), which is believed to represent a key factor on its biological function.

Also noteworthy is the incorporation of different FA into other GPL. As a component of them, DHA mainly takes the *sn-2* position, especially in PS, PE and PC; while AA is also incorporated into the *sn-2* position, but the majority in PI and PC. Different from DHA and AA ALA, LA and EPA have lower incorporation rate into the membrane GPL and lower reesterification rates when consumed (Zhang et al. 2011).

From the previously commented location of the mitochondrial ETC complexes and carriers, embedded in the membrane, and their composition, it seems clear that those lipid species are potentially targets of the mitochondrial ROS and RNS, thus converting themselves in RLS. Particularly, unsaturated FAs, due to their double bounds (bis-allylic hydrogen are much more prone to be abstracted by radicals), are more susceptible to be oxidised. Importantly, if this oxidation occurs *via* radical chemistry, consequences are potentially more harmful, since breakdown of those double bounds would generate higher amounts on new radicals, and therefore amplify damage. However, two interesting issues emerged here since, as stated before, i) a minimal damage is believed to be necessary to establish a balance point where a drastic increase could be sensed and up to an extent, orchestrate an ordered response, and ii) multiple signalling events raised related to coordinated (e.g. LOX and COX mediated) oxidation of PUFAs. Also noteworthy, in the already discussed mechanism, in case of increased peroxidation, esterified FA exchange from the GPL membranes could be performed by PLA and acyltransferase and possibly account for sufficient turnover.

Furthermore, it is plausible to speculate with a potential antioxidant role of PUFAs, understanding it as previously commented prevalence to be a preferred oxidation substrate, in order to “protect” other biological species. From this point of view, the high vulnerability to

peroxidation of free PUFAs in CNS (where there is a lack of intense antioxidant defences) and its close-to-damage mitochondrial location, coupled with their relative abundance in those CNS tissues could point that PUFAs might play a passive protective role of nucleotides, hence limiting their oxidation, fact already demonstrated, at least in vitro (Kim et al. 2010).

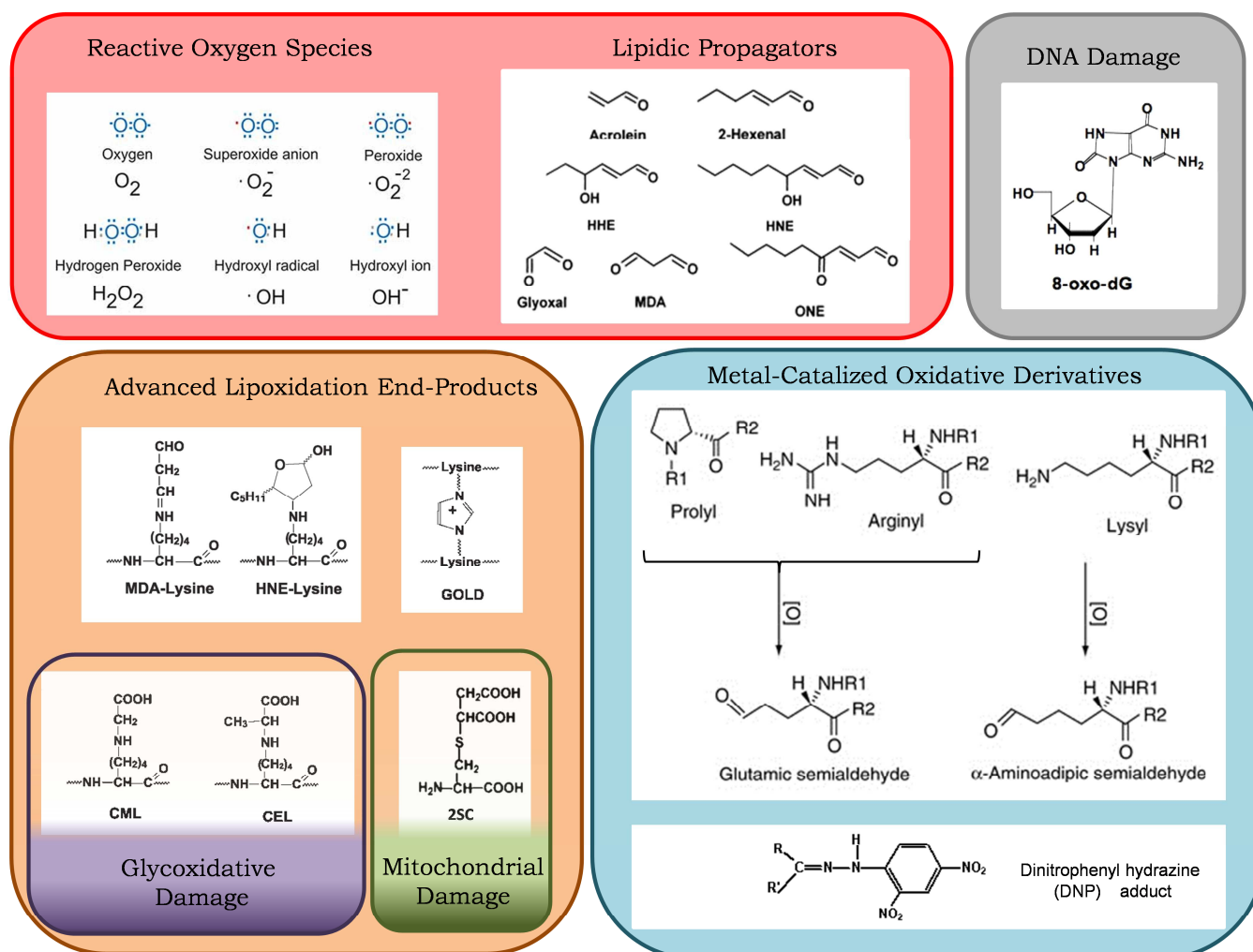


Figure 18. Representative oxidative products structure scheme. ROS formed in the mitochondria could interact with different lipid structures to form multiple lipidic propagators. These species are characterized by the presence of highly reactive carbonyl groups (remarkable for those α/β unsaturated), hence potentially increasing and spreading the oxidative damage. Those propagators could form stable adducts with different biological substances, especially with protein residues and those substances could be used to ascertain the oxidative status of a given sample as they fulfil the previously commented requirements to be a successful oxidative damage marker. Further, according to the source of the oxidative damage, we could account for lipoxidation (MDA-Lys, HNE-Lys), glycoxidation (CML, CEL), DNA (8-oxo-dG) or mitochondrial (2SC) damage or metal catalysed carbonylation (GSA, AASA or DNP adducts) as oxidative-affected pathways.

Finally, for a better support of this concept, the formation of some lipoxidation (and also nitrosilated FA) products were demonstrated to be reversible (Bathyany et al. 2006), specially through GSH function. Also relevant, some enzymatically-synthesized lipid species could be also generated through a non-enzymatically pathway (Morrow et al. 1990). Hence, those facts open the possibility for higher regulation of enzymatic functioning and/or signalling in relation to oxidised PUFAs and their derivatives.

In any case, lipid oxidation (GPL, but also free FA and PUFAs) occurs physiologically and specific products are usually found. Furthermore, from lipidic intermediates, highly reactive aldehydes could be generated, and also relevant, some PG could undergo dehydration and oxidative modifications which would also interact with other cellular components. All those species could be sometimes crosslinked (the most frequently are covalently bounded) with virtually all sort of protein residues (but especially to cysteine, histidine and lysine groups *via* Michael addition (Requena et al. 1997; Uchida and Stadtman 1992)). Since they form stable adducts with them, these substances could be very useful as biomarkers of oxidative status/stress (for a profound review on the lipoxidation adducts formation see (Domingues et al. 2013) and regarding PL oxidation see (Reis and Spickett 2012). 4-hydroxy-alkenals (especially nonenal, 4-HNE, and hexenal, HHE), malondialdehyde (MDA) and 2-propenal (acrolein) protein adducts are the most commonly studied oxidative-produced lipidic derivatives (and also more often accumulated in biological samples) and meet the commented features to be considered valuable oxidative stress markers. Furthermore, unspecific carbonylated products (insertion of C=O double bond) are often accumulated and commonly detected through 2,4 dinitrophenylhydrazine (DNP) incubation and WB. Anyway, multiple methodological approaches (e.g. WB, ELISA, HPLC, GC/MS, LC/MS/MS) compose a more or less accurate and reliable state-of-art in a specific situation. However, origin of the damage (e.g. glucidic, purely lipidic or metal catalysed protein-protein), even when is sometimes difficult to interpret (e.g. MDA is generated as by-product of TX and PG synthesis too) gives relevant information helping to better represent the whole situation and possibly pointing to a metabolic pathway which could be more affected or susceptible. In addition, as commented before, when a specific accretion of those molecules occurs, could be either due to i) failure of the detoxification system; ii) for an increased indiscriminate damage and/or iii) an specific signalling purpose.

All in all, those data reinforce the complex machinery operating in the physiology of lipids related to the oxidative status in a specific situation. Moreover, when pathology overcomes, this tightly cross linked net had multiple ways to try to resolve the situation. Finally, in order to reduce damage to the minimum, this homeostatic mechanism could lead to a lipid profile adjustment. How dietary lipid could influence this outcome is an interesting question and is one the focus of this work.

1.D Amyotrophic Lateral Sclerosis

1.D1 ALS Introduction

The amyotrophic lateral sclerosis (OMIM #105400) is an adult onset neurodegenerative disease, characterised by selective loss of both upper (comprising the cortex and the corticospinal tract) and lower motor neurons (MN) arising from the brainstem nuclei and ventral roots of the spinal cord. This devastating disease was initially described by Charcot in 1869 and represented the most common MN disorder with a prevalence of 2-3 per 100,000 people. ALS is, in reality, a member of heterogeneous disorders covering different forms of heritance, age and location for initial onset and different markers and proteins are involved to be deregulated. Initially, this illness was classified to be sporadic (when a familial linked heritage is missing or etiopathogenesis remains unclear) or familial (genetically linked, representing up to 15%), but whereas is generally acknowledged that the clinical presentations of sporadic and familial ALS are indistinguishable, there are subtle differences in pathology (Ajroud-Driss and Siddique 2014).

The first relevant research finding was established more than 20 years ago when Rosen and colleagues demonstrated (Rosen 1993) that mutations in copper/zinc superoxide dismutase (SOD) were a primary cause for ALS, which led to development of mouse models (Gurney et al. 1994) of the familial form. Since then, more than 100 different heterozygous mutations in SOD have been found (reviewed in (Gaudette, Hirano and Siddique 2000)) in patients with ALS (representing approximately 15-20% of the familial forms), and, for many of them, an animal model was developed. Also noteworthy, along the past years, multiple enzymes were demonstrated to be mutated and/or deregulated up to an extent, showing a more broad spectra than was initially thought (an excellent review on the genetics behind the pathophysiology of ELA could be found in (Al-Chalabi et al. 2012 and Ajroud-Driss and Siddique 2014)). In figure 20 there is a picture of the yearly progression of genetic/protein involvement in the pathology.

Another breakthrough point was recently found thanks to geneticists, when an intronic expansion of a hexanucleotide (GGGGCC) repeats in the chromosome 9 open reading frame 72 (C9ORF72) gene was demonstrated (DeJesus-Hernandez et al. 2011 and Renton et al. 2011) to represent the major cause (35%) of familial form of ALS, and very importantly, frontotemporal dementia (FTD) too. Although, surprisingly, the ALS penetrance in people carrying this repetition varies enormously along lifetime (Majounie et al. 2012), raising from almost zero (for young individuals, below 34 years) to 50% at 58 years and finally almost complete for those individuals who reached 80 years old. This suggests that this characteristic predisposition to suffer the disease required extra unknown-yet events to be finally developed. In between these two discoveries, more than 19 different proteins were related to participate in ALS development, with different particular features. Hence, mutated and/or misslocalized or phosphorylated forms of TDP-43 (TransActive Response DNA Binding Protein-43 kDa, TARDBP), FUS (FUsed in Sacroma protein) and UBQLN2 (Ubiquilin-2, Ubiquitin-like protein) were described for various phenotypes, from purely “typical” ALS to FTD. Further, disease-associated gene variants (e.g. encoding *elongator protein-3* (Simpson et al. 2009), *inositol 1,4,5-trisphosphate receptor 2* (van Es et al. 2007), *dipeptidyl-peptidase 6* (van Es et al. 2009)) were also described suggesting that ALS is not a simple disease implying only one or two groups of related proteins, monogenic mutations or so. Instead, it comprises several distinct hallmarks, which make more difficult to establish a precise coiling the data interpretation of those treatments when they fail.

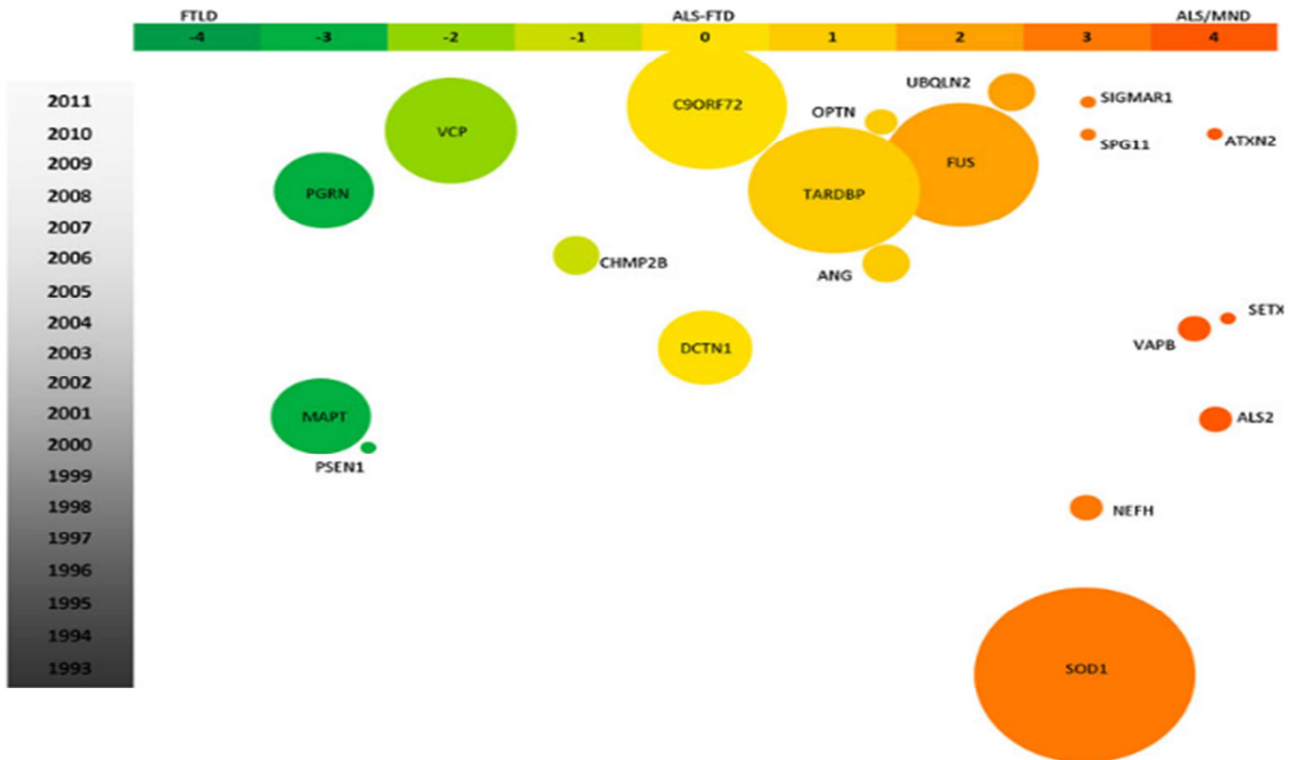


Figure 19. Genes founded implied in ALS/FTD development. Copied from (Al-Chalabi et al. 2012). NEFH, NEuroFilament Heavy polypeptide; ATX2, ATaXin-2; SIGMAR1 SIGMAR1 gene variant; DCTN1, DynaCTiN heavy subunit-1; PSEN1, PreSENIlin-1; PGRN ProGRaNulin; VCP, Valosin Containing Protein.

Epidemiological studies showed a little increased disease prevalence in European ancestry (Cronin, Hardiman and Traynor 2007; Zaldívar et al. 2009), in contrast, for instance, to Latin American, native American or ethnically mixed populations. Dealing with gender dimorphism, a higher incidence in men, respect to women (even this difference is faded out in the elderly, reviewed in (McCombe and Henderson 2010)) is known. This sexual dimorphism was relevant since some specific differences in disease progression are also found. Some of them were reproduced in murine models of the disease (Suzuki et al. 2007) and were modified by estrogens therapy (Choi et al. 2008). From those epidemiologic studies, many different situations had been shown to affect illness development. Environmental risk factors (recently reviewed in (Trojsi, Monsurrò and Tedeschi 2013)), veterans of the Army (Gulf war (Cox et al. 2009)), grass-field sportsman players (Beghi 2013), western-Asian populations (Kaji et al. 2012; Lee 2011), exposure to pesticides (Furby et al. 2010) and some occupancies (McGuire et al. 1997; Park et al. 2005) were among many other cited that play a role in the incidence or development of this disease.

1.D2 Mechanism involved

As pointed previously, many different tissular and cellular events are related to ALS development. These can be clustered as: i) mitochondrial- Ca^{+2} -ER deregulation; ii) energetic unbalance; iii) non-cell-autonomous inflammation/excitotoxicity; iv) proteinopathy; v) heavy metals and toxic/ environmental agents exposure; etc. Here, we will discuss briefly about them.

1.D2.1.-Mitochondrial-Calcium-ER dysfunction

Regarding ALS and mitochondria, relevant amount of research has been done (nice reviews were recently published (Cozzolino et al. 2013; Tan, Pasinelli and Trotti 2014)). Very closely-related to mitochondrial function, decreased Ca^{+2} buffer capacity was extensively described both in patients and animal models (Guatteo et al. 2007; Siklós et al. 1996). Miss-localization of mutated SOD (usually found in the cytosol, but also in nucleus, ER and intermembrane space in disease models) have been also described in animal models, linked to anti-apoptotic Bcl-2 in the mitochondria (Pasinelli et al. 2004) as well as aberrant mitochondrial swollen and vacuolization, both in animals and human patients (Bendotti et al. 2001; Mattiazzi et al. 2002; Siklós et al. 1996). Using the SODG93A murine model, decreased mitochondrial respiration was also found (Mattiazzi et al. 2002) in animals under clinical stages, but whether preclinical ones are affected is still under debate. Further, regarding oxidative damage, an impairment of Cyt c was found and reduced respiration complexes linked to an increased MDA accretion (also in preclinical animals) in isolated forebrain mitochondria of this mouse model (Kirkinetzos et al. 2005). Of note, it should be reminded that mitochondrial respiration is very sensitive to lipid peroxidation (Echtay et al. 2003) and links with the “energetic unbalance theory”, which will be discussed later in this section.

Anyway, in these early works, increased carbonylation and lipid hydroperoxides were also found for brain and spinal cords of older animals, however, the methodology used could be criticised. This increased oxidative damage, even whether to be cause or consequence is controversial yet, was initially found as augmented carbonylation in spinal cord (Shaw et al. 1995) and motor cortex (Ferrante et al. 1997) of patients. Higher glyco- and lipoxidative products (Shibata et al. 2001) were found in all CNS population in the spinal cord, as well as damage to DNA was verified, as pointed the accretion of 8-oxodG (as previously commented, extensively-studied as oxidative biomarker of DNA damage) (Ferrante et al. 1997). The latter was also found increased in CSF of patients (Ihara et al. 2005), concomitant with an increased 4-HNE too (Smith et al. 1998). Regarding oxidative-derived IsoP, increased 15-F₂t-IsoP levels were found in CSF from patients suffering Alzheimer, but not in those ALS patients, respect to the control ones (Montine et al. 1999). However, in a later study (Mitsumoto et al. 2008), significant accretion of urinary 8-oxodG and 15-F₂t-IsoP, (both ELISA measured) was demonstrated, but interestingly none of those levels were correlated with an increased plasma carbonyl content (DNP measured) nor a better clinical outcome. However, one should take into account that increased excreted levels of IsoP or 8-oxodG could have two sides. One can assume that there is a raised production of those species, but is also reasonable to think in a better clearance of those substances in these individuals. So, whenever is possible, a more reliable measure of such species, aimed to express an increased oxidative damage, should be done in situ. In any case, collectively, all those outstanding findings pointed towards oxidative stress as a relevant factor in the ALS pathogeny.

Some of those human hallmarks were recapitulated in the wide variety of transgenic animal models (e.g. TDP-43, SODG93A, FUS, in mouse, rat, drosophila and zebrafish species, among others), tissular (lumbar slice organotypic culture) and cellular models developed. Taking into account their limitations, organotypic (OT) culture model stands out, since it conserves cell to cell interactions. This is relevant since not only one cell type but a concert of them (e.g. MNs, astrocytes, microglia, interneurons and muscular junctions) are involved in the degeneration. Also interesting, but just for the opposite, MN primary cultures may clarify what specific MN

signature would help to better confront different stimuli, aimed to reproduce the different ALS features.

As pointed before, in ALS there is an unbalance in the Ca^{+2} homeostasis (reviewed in (Grosskreutz, Van Den Bosch and Keller 2010)). MNs are known to be vulnerable to membrane depolarization and increased intracellular calcium concentration (Arakawa et al., 2002). Hence, higher levels of such ion increased their susceptibility to undergo cell death (Gou-Fabregas et al. 2009; Kaiser et al. 2006), but, even when some specific responsible enzymes (e.g. protein phosphatases, endonucleases, or proteases) are known, the exact mechanism is not fully understood yet. We (Ilieva et al. 2007) and many others (recently reviewed in (Prell et al. 2013 and Roussel et al. 2013) had pointed to deregulated ER, UPR stress and Ca^{+2} unbalance as key partners on pathophysiology of ALS, linking ER and mitochondria. These two cellular locations are the main ones responsible for Ca^{+2} regulation and a combined reduction of calcium buffering capacity and a high number of Ca^{+2} -permeable α -amino-3-hydroxy-5-methylisoxazole propionic acid (AMPA) receptors in several animals models and in patients was demonstrated (reviewed in (Kwak et al. 2010)).

The relative importance of vesicular transport in cellular and sub-cellular lipid homeostasis and sorting remains unclear. As previously commented, it is a key mechanism required for a correct neurotransmission. But it is also believed to be an important connexion route from trans-Golgi and plasma membrane, helping to maintain especially high levels of SM and PS on that membrane. However no direct evidence of such transportation has been proved for mitochondrial or peroxisomes-ER connection even when for mitochondrial and peroxisomes exists (Schumann and Subramani 2008). Furthermore, fragmented Golgi apparatus was already described for preclinical classical mouse model (Gonatas, Stieber and Gonatas 2006) and patients (Stieber et al. 1998). Vesicular transport requires intact cytoskeleton organization and functionality. It is also energy dependent (opposed to LTP mechanism) and comprises a very complex mechanism involved in different processes, ranging from lipid droplet formation (Jacquier et al. 2011) to autophagy (reviewed in (Knævelsrud and Simonsen 2012)), which has been linked to various neurodegenerative diseases (Salminen et al. 2013; Shen et al. 2013), including ALS (Zhang et al. 2013; Zhang et al. 2014). In fact, the finding of a relatively new familial form (named ALS8) of this disease related with mutations (P56S and T46I) in the gene encoding an ER-resident vesicle-associated membrane protein (Nishimura et al. 2004 and Kanekura et al. 2006) opened a new possible therapeutic route. This protein is related to regulation of vesicle trafficking (Rocha et al. 2009) but also plays a critical role in the UPR and, its malfunction, results in increased MN vulnerability to ER stress (Prosser et al. 2008). Interestingly, defects in this protein does not lead to morphological defects at the neuromuscular junction nor to muscle denervation in mice (and zebrafish, Kabashi et al. 2013), and only leads to a mild, late-onset motor impairments. However, in flies, this mutation caused a marked ER stress, with an accumulation of ubiquitinated proteins in brain neurons (Moustaqim-Barrette et al. 2014) and, furthermore, a misslocalization of oxysterol and ceramide binding proteins, suggesting an integral mechanism of sterol and SM metabolism malfunction.

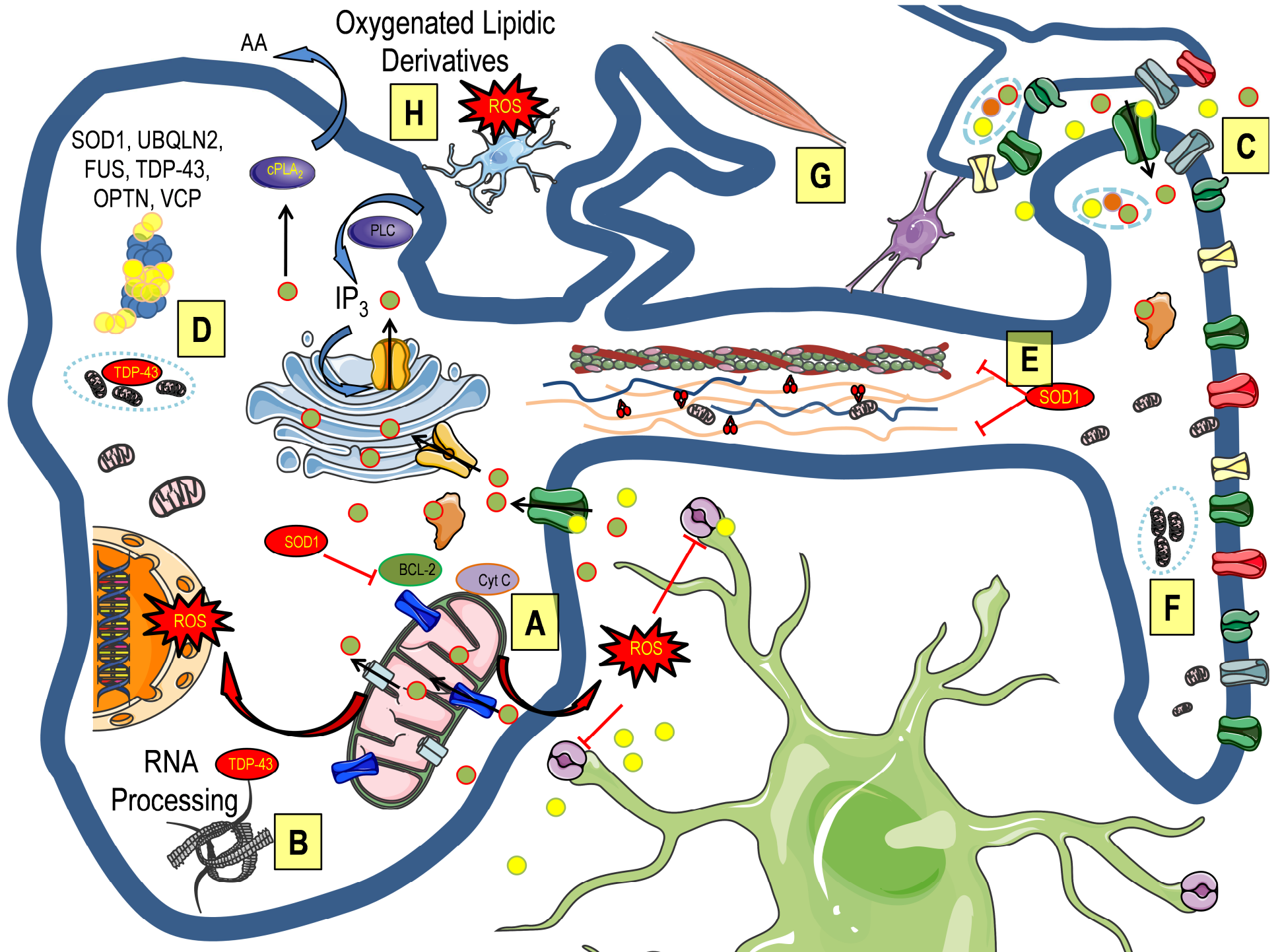
Finally, we discuss some issues regarding pro-survival signalling. Some years ago it was demonstrated that NF κ B inhibition leads to neuron protection from the Glut-mediated injury (at least in cultured cells (Pizzi et al. 2005)), a mechanism already involved in pathophysiology of ALS. In the SODG93A mouse model, it was demonstrated (Prell et al. 2014) that microglial activation of the NF- κ B pathway accounts for the MN loss, both *in vitro* and *in vivo*.

Furthermore, Julien and collaborators (Swarup et al. 2011) shown that synthetic inhibition of NF- κ B in another mouse model of ALS (TDP-43) reduced denervation in the neuromuscular junction and TDP-43 silencing (by siRNA transfection in microglial cells) increased neuron survival whereas, the contrary, TDP-43 up-regulation, resulted in increased microglia-mediated neurotoxicity in primary cultures. Also importantly, a relation between inflammatory signalling, TNF- α mediated, and NF κ B was shown in other model of ALS, the threo-hydroxyaspartate (THA) excitotoxicity (developed by Rothstein (Rothstein et al. 1993) and commented in the next section) on OT spinal cord slice cultures (Tolosa et al. 2011). In this work, researches showed increasing production of COX-2 concomitant with MN loss along the culture as well as drastic decay of them when co cultures were performed with TNF- α . Furthermore they demonstrate down-regulation of the main astrocytic Glut transporter (GLT-1, ortologous to EAAT2) in the combined excitotoxic and TNF- α treatment. Altogether, this data reinforces the link of various prominent pathogenic mechanisms of ALS, excitotoxicity, neuroinflammation and pro-survival signalling, at least for some models.

Also noteworthy, results from our group refer to an altered phospho-ERK1/2 signalling upon TDP-43-mediated toxicity in cell lines under different stress stimuli, spinal cord OT culture as well as human patients (Ayala et al. 2011). This is relevant since implication of PI3K pathway was demonstrated some years ago (Wagey et al. 1998) and more recently confirmed for humans and animal models (Dewil et al. 2007). Patients were reported to have increased spinal cords protein levels and activity of PI3K respect to controls, but no changes in activity nor expression in ERK1/2 was found in this early work. Interestingly, those two pro-survival pathways (PI3K-AKT and ERK1/2) were recently proved to be enhanced by palmitic acid (in muscle cell line, but surprisingly, both pathways at the same time (Pu et al. 2011)) and DHA (in neuron cell line, activates AKT but not upstream PI3K (Akbar et al. 2005)). In another recent paper (Peviani et al. 2014) researchers showed that activation of AKT3 (one of the three isomers of protein kinase B/AKT pathway) increased survival of MNs both in *in vitro* co-cultured (astrocyte and MNs) and *in vivo* “fast” SODG93A model although in previous paper, the same group found no substantial changes in AKT pathway in this murine model of ALS (Peviani et al. 2007). Unfortunately, this MN preservation does not ameliorate disease progression of the animals (although only females were studied in both papers). On the other hand, DHA pretreatment was observed to significantly increase neuronal survival by promoting ERK-related survival pathways, at least in Alzheimer disease models (Florent-Bécharde and Koziel 2007). However, further research is needed and, to our knowledge, no deep examination have been developed regarding PUFA’s action alleviating excitotoxicity, reducing oxidative spread and/or counteracting inflammatory ALS components even when compiling evidences pointed an specific altered lipid status in patients tissues (Ilieva et al. 2007).

1.D2.2.- Energetic unbalance: ALS hypermetabolism

Once a patient is diagnosed, their body mass index, better than dyslipidemia (Paganoni et al. 2011), is predictor of its outcome, with worst prognosis for lower body mass individuals (Greenwood 2013). Hence, dietary interventions focusing in a correct energetic status have been shown to be beneficial in animal models (e.g. high fat diet (Dupuis et al. 2004), L-carnitine (Kira et al. 2006) and caprylic-TAG (Zhao et al. 2012), among others) as well in humans (Dorst, Cypionka and Ludolph 2013; Wills et al. 2014 and Beghi et al. 2013) (for a review on this topic see (Dupuis et al. 2011)). Not surprisingly, on the contrary, caloric restriction in SODG93A



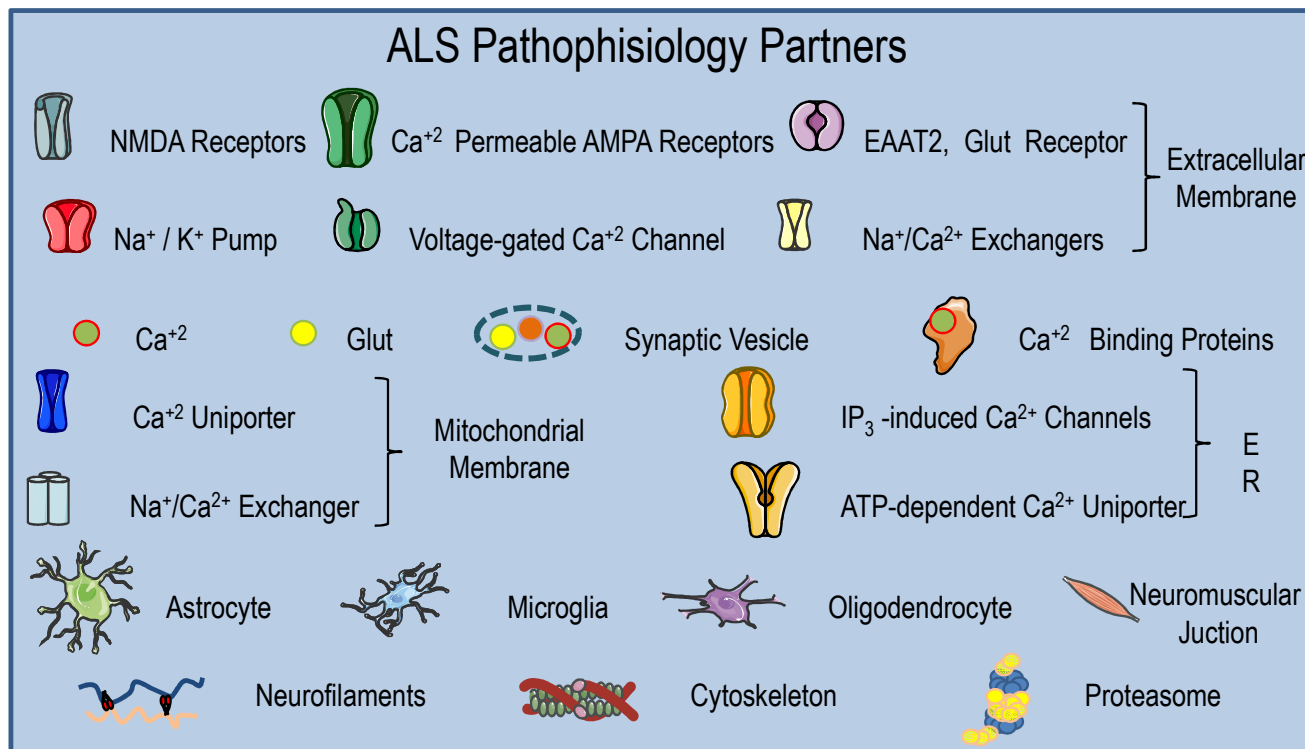


Figure 20.-ALS pathophysiology partners scheme.(A) Mitochondrial dysfunction increased ROS production, which could reduce astrocyte EAAT2 Glut buffering capacity, leading to excitotoxicity, as well as damage to DNA. Further, CytC could be launched from mitochondria, altogether with mutated SOD1 blocking Bcl-2 prosurvival signalling would seriously compromise cell viability. (B) Altered RNA processing was demonstrated in patients. TDP-43 aggregates and mislocalized could be found (with degenerated mitochondria too) vacuolized and/or inside proteasome (D) when the UPR is exhausted. Those facts altered normal ER function. Other proteins were found accumulated inside proteasome (i.e. valosin-containing protein (VCP), optineurin (OPTN)). (C) Ca²⁺ metabolism in MN is different than in regular neurons. They possess high number of membrane Ca²⁺ permeable AMPA receptors concomitant with lower cytoplasmic Ca²⁺ binding proteins,

rendering them to be very sensitive to Ca²⁺ overload. Furthermore, Glut binding to AMPA receptors, promote increased Ca²⁺ entrances. Those situations, together with IP₃ signaling (which could be triggered by PLC activation), could result in Ca²⁺ desorption from ER depots and, ultimately, its uptake by mitochondria, comprising this organelle too. Mitochondrial (i.e. entrance through the Ca²⁺ uniporter; release through the Na⁺/Ca²⁺ exchanger) and ER (Ca²⁺ intake is mediated by the sarco-endoplasmic reticulum calcium ATPases -i.e. through ER Ca²⁺ uniporter- Ca²⁺ depletion could occur through IP₃ dependent channels) Ca²⁺ trafficking is represented. Ca²⁺ is required for cPLA₂ activity. High plasmatic Ca²⁺ content could result in higher plasma membrane FA desorption, potentially causing enhanced lipoxidative products formation. Altogether, this claimed for a key role for this ion along ALS pathophysiology. (E) Mutated SOD1 altered cytoskeleton structure (some neurofilaments) and blunted axonal transport too. This would alter neurotransmission (less number of synaptic vesicles or altered configuration). (F) Fewer, smaller and sometimes vacuolated mitochondria were found in patients synapses. (G) Muscle denervation (whether a cause or a consequence) leads to neuron degeneration and apoptosis. (H) ROS generated by mitochondrial malfunction could also activate microglia and initiate a pro-inflammatory lipid derivatives cascade, possibly resulting in a feedback loop by astroglial activation (with less pro-surviving factor release, e.g. BDNF, IGF, VEGF and enhancing inflammatory intermediates). A similar mechanisms may operate in non MN cells. Not to scale

animal model have been shown detrimental (Patel et al. 2010) but some interesting issues also aroused. Oxidative carbonylation of proteins in skeletal muscle (measured by WB) was reduced in caloric restricted animals compared with *ad libitum* ones (both sexes), but lipoxydation (MDA, spectrophotometrically measured) was increased, showing complex crosslinked oxidative responses to diet. Furthermore, both types of superoxide dismutase (mitochondrial and cytoplasmic) and TNF- α were drastically raised as a result of caloric restriction, again in both sexes, but only restricted females raised their uncoupling protein 3 levels, possibly trying to reduce de oxidative production. However, the same group had previously reported (Hamadeh and Tarnopolsky 2006) that only females were protected against detrimental effects of short-term mild caloric restriction (60%, from postnatal days 40 to 55) in the same mice strain.

The previously commented preclinical outcomes in animal's models (e.g. increased oxidative damage, lower mitochondrial capacity, reduced Ca⁺² buffering) as well as premature weight loss (seven days after birth, unpublished observations), altogether with some clues for hypermetabolic status (probably due to skeletal muscle origin), both in animal models (Capitanio et al. 2012) and patients (Vaisman et al. 2009 and Funalot et al. 2009) suggest that early events are very relevant in the pathogenesis, which, ultimately, reflect the MN loss, and finally leading to motion and behavioural consequences. Those features could also point to a mitochondrial deregulation possibly linking those two pathogenic mechanisms. In any case, the pharmacological studies focused in hypermetabolism "reduction" through thyroid hormone regulation failed to improve survival, with no gender differences found (Li et al. 2012). Research focussed in dietary optimization for energetic balance could be beneficial in terms of a better handling of disease, once diagnosed. In this sense, transplantation with adipose-tissue derived human stem cell to a SODG93A mouse model showed alleviation (Kim et al. 2013) of clinical onset and prolonged life span concomitant with increased levels of neurotrophic factors.

Since the anti-inflammatory implication of PPAR γ agonists, and the well documented participation of inflammatory processes underlying the pathogenesis of ALS, promising research has shown an alleviated response, not only in survival, but also disease progression (better MN and muscular preservation) in the SODG93A murine model under pioglitazone supplementation (Schütz et al. 2005). Unfortunately, translation to humans revealed no effect on survival (Dupuis et al. 2012). Anyway, despite this disappointing result, research on this field, aimed to a better lipid status control and signalling is still promising, and more efforts should be done since PPAR expression and regulation have been recently studied regarding its influence upon natural occurring neuronal stem cells (reviewed in (Cimini and Cerù 2008)). Thus, even when physiological localization of those neuronal stems cell seems is far from mainly affected disease location, they represented another potential therapeutic field of action. In fact, another recent publication (Benedusi et al. 2012), demonstrates, in females of the SODG93A mouse model, that there is an activation of PPAR γ (nuclear localization) in MNs concomitant with clinical symptoms and this activation is produced (at least *in vitro*) by lipid peroxidative subproduct 4-HNE, as mentioned, present in CSF of ALS patients too.

Of note, statin treatment, aimed to control CHO status by reducing LXR action, had shown contradictory results, increasing confusion to clinicians. General statin function is the mevalonate synthesis blockade, therefore resulting in reduced CHO and their derivatives. (24(S)-hydroxycholesterol) concentration. But interestingly, the later is produced in large amounts in CNS and is the principal endogenous LXR agonist therein. Furthermore, side effects of statins have been proved in some individuals, including muscle toxicity, such as myopathy

(Sathasivam and Lecky 2008). Initially, no harmful effects had been published (diminished survival) linking ALS and statins usage (Edwards, Star and Kiuru 2007; Drory et al. 2008; Colman et al. 2008). However later studies suggest a gender specific variation (Nefussy et al. 2011) and a recent review (Beltowski 2010) also revealed that statins may increase the risk of ALS by inducing LXR-dependent perturbations of cholesterol/phytosterol metabolism in the CNS.

Regarding FA delivery, in a very recent paper developed with a TDP-43 knock-in mouse model (Stribl et al. 2014) researchers showed impaired lipid metabolism as reflected by downregulation of the CD36 protein expression in old animal brains. Also remarkable, the transcriptome analysis of those mice (brain and muscle tissues) showed a dysregulation of many mitochondrial-related genes and electron microscopy images confirmed impaired morphology in motor cortex and hippocampus, although this cristae morphology disruption was not observed in spinal cords. In this line, lipid-raft domains in ALS, were recently described in the SODG93A mouse model (Zhai et al. 2009) comparing the specific lipid-raft-resident protein changes. This study identified 154 proteins. Among them, 41 had quantitative statistical differences. Also important, they found proteins uniquely expressed in SODG93A (17; 29% related to cytoskeletal regulation, 24% microglia/inflammation, 17% vesicular transport, respectively), and, on the contrary, only few expressed in the WT animals (9 proteins). Importantly, a majority of the identified proteins were found downregulated in the SODG93A animals. Hence, among them vesicular transport, neurotransmitter synthesis and release represented approximately 20%, but also metabolism (19%), cytoskeletal regulation (15%) and microglial activation/inflammation (9%) were represented, all of them major threats in pathophysiology of this devastating disease.

Finally, a link between fat storage location and functional and survival alleviation in patients was recently observed (Lindauer et al. 2013) suggesting that not only having enough energy depots is relevant but also where those are located. All in all, is therefore believed that optimal energetic equilibrium along lifetime could help to maintain a better status, with upgraded responses, hopefully ultimately alleviating pathology and extending survival.

1.D2.3.-Non cell autonomous inflammation/excitotoxicity

Non-cell-autonomous toxicity, meaning, MN damage derived from other cell types (e.g. astrocytes, microglia, muscle cells, among others) than MN solely was elegantly demonstrated by Clement and colleagues (Clement et al. 2003) by creating a chimeric mice. It had been anyway speculated before, since protein mutations, already recognized to evoke a fALS-like disease, were ubiquitously expressed along the body and among different cell types. Experiments developed by Lino and collaborators (Lino, Schneider and Caroni 2002) and Pramatrova (Pramatrova et al. 2001), where mutant SOD expression was restricted to motoneuron or astrocytes (Gong et al. 2000) failed to cause specific neuron degeneration nor death. Therefore, from those early works, deleterious mutations were shown to act in a non-cell autonomous specificity. Subsequent molecular biology developments, such as Cre/Lox cassettes to selectively turn on and off specific genes in interested locations and for a limited time, confirmed that MN neighbourhood really matters. Hence, all CNS population, microglia (Corcia et al. 2012), astrocyte (Rothstein et al. 1995), oligodendroglia (Kang et al. 2013) and

even pericyte (Winkler et al. 2013) as well as neuromuscular junctions (Shindo et al. 1995) of patients were shown to be affected, up to an extent, along disease progression.

Therefore, shortly after the discovery of SOD1 mutations, a defective Glut transporter protein EAAT2 (Rothstein et al. 1995) was found in spinal cord and cortex glia from sALS patients. Thus, this provided one of the first lines of evidence that indicate a possible role of Glut-mediated excitotoxicity in this disease (recently reviewed in (Philips and Rothstein 2014)). Further, the same group rapidly established the previously commented excitotoxicity tissular model (Rothstein et al. 1993), useful thanks to its preservation of cell-to-cell interactions. In this model of explanted lumbar region spinal cords, the addition of THA blockades Glut reuptake, leading to MNs loss in 30 days. In this widely used model, as previously commented, we demonstrated a relation between TDP-43 phosphorylation and ERK1/2 signalling and, up to our knowledge, we were among the first to show a decreased O₂ consumption under THA treatment, which, up to an extent, could be rescued by antioxidant treatment (the second paper of this thesis).

Anyway, Glut neurotransmission also involves other receptors. Furthermore, Riluzole®, the unique approved drug for ALS treatment, directly interacts with GABA and glycine receptors (Mantz et al. 1994 and Umemiya and Berger 1995, respectively) in addition to its antiglutamatergic action. Of note, both substrates (GABA and glycine) represented the major ionotropic inhibitory neurotransmitters in MNs. In any case, and leaving apart all metabotropic Glut receptors (for further immersion see (Caraci et al. 2012)), MNs express all three types of ionotropic Glut receptors too, AMPA, N-methyl-D-aspartate (NMDA) and kainate receptors, with different expression patterns and interactions among them (for a profound review see (Rekling et al. 2000)). Other excitatory molecules may play a role and, from the tripartite synapse theory, not only MNs but astrocyte and surrounding cells support a correct neurotransmission (Araque et al. 1999). Altogether with differential expression of some of synaptic enzymes found in patients, and sometimes recapitulated in models, there are compelling evidences conforming a wider picture of neurotransmission malfunction and excitotoxic involvement in ALS.

We previously commented the powerful machinery acting in membrane remodelling (e.g. PLAs, ACS and SNARE actions, among others), thus it is worthy describing how these weak equilibriums could be modified by PUFAs' actions in the synaptic cleft. Extensive research has been done in Alzheimer disease and PLAs (for a review see (Schaeffer et al. 2010)) and in Parkinson too, where a mutation in PLA₂ (group VI) was recently found to produce an early-onset rare form (Shi et al. 2011). However, ALS research in this field is still poor, even when higher expression and activation (phosphorylated) of cPLA₂ (110kDa) was found in motor neurons, astrocytes and activated microglia of patients (Noriyuki Shibata et al. 2010) as well as lumbar sections of the SODG93A and the SODG85R mouse models (Kiaei et al. 2005). In a model of spinal cord injury, (Liu et al. 2006) downregulation of cPLA₂, already described to be present in all along spinal cord motor neurons (Ong, Horrocks and Farooqui 1999) was demonstrated to be beneficial in terms of reduced inflammatory cytokine production, lower lipoxidative damage and neuronal loss. Moreover, PLA₂ injection after injury induced a massive demyelination, a fact that is counteracted by administration of an inhibitor. Altogether, this could open a potentially interesting therapeutic point of action, but precaution should be taken, since chronically inactivation of both PLAs (cPLA₂ and iPLA₂) was demonstrated to be detrimental, at least in cultured hippocampal neurons (Forlenza et al. 2007). Definite proof for this membrane remodelling therapeutic potential comes from a recent work (Staats et al. 2013).

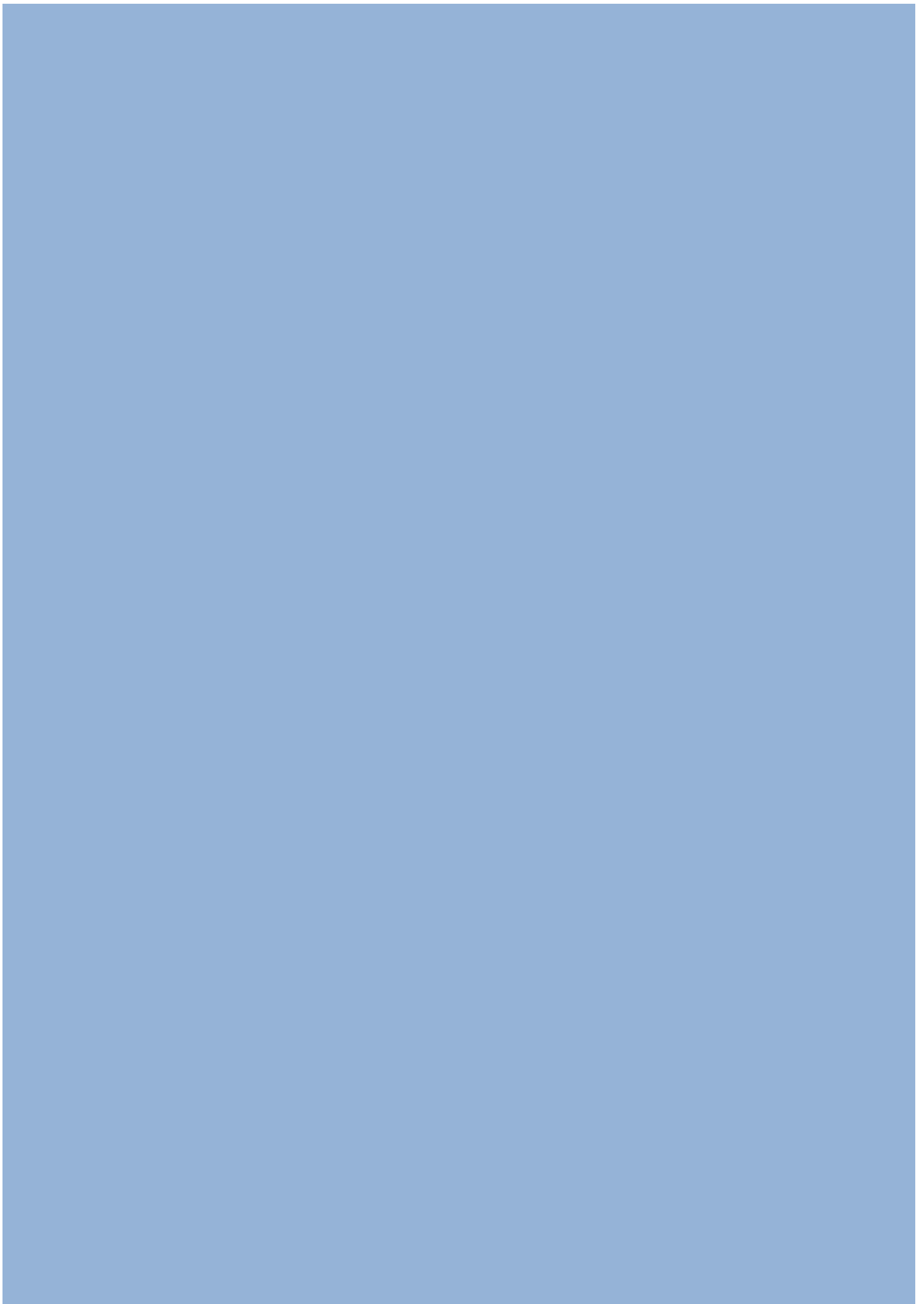
They firstly found a microsatellite polymorphism marker for association with sALS, which was related to phospholipase C delta 1 (PLC δ 1). Hence they focus the study in the SODG93A mouse model, finding increased gene expression of *plcd1* in spinal cords and further confirmed by WB in end-stage animal. Crossing PLC δ 1^{-/-} animal and mutated SOD significantly increased survival, with alleviated nuclear shrinkage, without changes in glial activation, nor aggregation or MNs number at end stage, compared to ALS mice expressing PLC δ 1. Possible mechanism behind those findings imply the commented function in second messenger action of PLC, this is, the hydrolysis of IP₂ to form DAG and IP₃, which may create a feedback loop by the increased Ca⁺² release through IP₃ specific receptors in ER, resulting in increased excitotoxicity.

Finally, as pointed before, inflammation's implication is clear, since early involvement and release of various cytokines and chemokines was found in patients (for a list in CSF see (Tateishi et al. 2010)). Hence, the modulation of its duration and intensity represent a potential beneficial treatment. In this sense, the influence of potent lipid mediators have been found to be relevant in Alzheimer's disease (recently reviewed (Bazan 2013)) and, interestingly, also in ALS (Liu et al. 2012) although to date this is the unique paper we found regarding those mentioned potent lipid intermediates and ALS. In this work, ResolvinD1 minimizes macrophage phagocytosis in ALS patients *in vitro* as well as promotes a reduced transcription of inflammatory cytokines and chemokines, revealing an interesting therapeutic approach to be applied in early detection.

Furthermore, recent studies (Abraki et al. 2013) demonstrate an important cross-talk in response to different stimuli for achieving an orchestrate pro/anti-inflammatory response, since both PPAR- γ stimulation via 15d-PGJ₂, product of COX-2 action (found increased in spinal cord of ALS patients (Kondo et al. 2002)), and the inhibition of the latter enzyme could lead to similar standards of neuroprotection through the activation of nuclear factor E2-related factor 2 signalling pathway, decreasing NF- κ B and reducing pro-apoptotic Bax/Bcl-2 ratio. And, for instance, PGE₂ suppression was demonstrated to increase motor function and lifespan in SOD1 mutant mice in mechanism implying a ROS reduction (Shin et al. 2012). Other example of inter-cellular dialogue in response to inflammation using stem cells to generate motor neurons and cocultured them with mutated (SODG93A) glia, demonstrate its sensitization towards PGD₂, since its inhibition partially rescues motor neuron loss (Di Giorgio et al. 2008). Finally, other examples to stress the relevance of this interconnectivity emerged from the finding of NF- κ B immunoreactivity depletion from neuronal nucleus in spinal cord of patients, concomitant to an increased accretion in microglia (Sako et al. 2012). This might render neurons more vulnerable as well as prone microglia to inflammation-related processes.

Globally, all this multiple factors interfering between each other render ALS to have many faces. This may be among the most difficult point to be confronted. Hence, like most biological systems, unravel the complexity and interconnectivity of processes involved to finally rise ALS-like phenotype, challenge us and gives encourage force to keep researching. In any case, due to intrinsic ramification, a definite cure would probably emerge from cutting off several of different aspects rather than focusing in a single frame of the scene. In this sense, based on the multifactorial functions in FA metabolism, there are plenty of possibilities to be explored trying to alleviate disease sintomatology.

2. Hypothesis



2. Hypothesis

As commented in the introductory section, PUFA physiology is very important for global homeostasis. Numerous biologically relevant processes have been shown to be dependent on PUFA or its derivatives, and/or their actions are fundamental for a healthy condition.

On the other hand, CNS is particularly exquisite in terms of FA handling, further, special requirements of this tissue (e.g. high energetic demands, low antioxidant capacity, particular vascular and immune systems, extremely high cellular specificity, among others) points to a critical regulation of lipid metabolism for optimal functioning.

Finally, both ALS patients and models have shown mitochondrial, ER and Ca²⁺ malfunction in numerous cell types in the CNS linked to a hypermetabolism status, also in the muscular tissue. Furthermore, relevant inflammatory parameters as well as oxidative status (closely impinged by PUFA status) are raised along the disease progression in multiple locations.

Knowing the potential role of PUFA in all those processes and the sexual differences found in both, ALS and PUFA metabolism, altogether, we therefore hypothesized that *PUFA and/or their derivatives could alter oxidative status and responses to it in biological samples. Therefore they might play a role in the modulation and spread of oxidative damage and inflammation in various models of ALS disease and, further, those outcomes could be dietary modified in animal models.*

3. Objectives

3. Objectives

In order to validate the above mentioned hypothesis, we propose the following objectives:

GOAL 1.- To determine the potential of phenolic antioxidants as modulators of oxidative stress in a wide variety of biomolecules and their biological significance.

- **AIM 1.1-**To establish, by using immunological methods, a suitable methodology to ascertain the degree of protection which different phenolic antioxidants could offer to representative biomolecules (LDL, BSA, Human plasma) against various oxidative stress conditions.
- **AIM 1.2-**To describe the effects of different phenolic antioxidants in the oxidative modification of proteins and lipids in human LDL under the Cu^{+2} oxidative system.
- **AIM 1.3-**To establish the biological relevance (measured by cell viability test in two different cell lines-HMEC-1 and HepG2) of the antioxidant potential of various phenolic antioxidants against the noxious effect of *in vitro* oxidized LDL or oxidative stress inducers in human plasma.
- **AIM 1.4-**To evaluate the biological relevance of an *ex vivo* oxidative system operated in both, a diet-induced hypercholesterolemic hamsters feed with a polyphenol extract and human plasma oxidized with Fe-Asc and protected with luteolin.

GOAL 2.- To describe the relevance of DHA and TDP-43 related processes in sALS and different ALS models.

- **AIM 2.1-**To describe DHA related enzymatic machinery (FADS1/2, ACAA1/2, ACOX1, SCP2) in sALS samples and different ALS models.
- **AIM 2.2-**To characterize DHA-related proteins (drebrin and syntaxin-3), its synthesis and the responsible enzymatic machinery in sALS samples and its *in vivo* and *in vitro* relation under stress conditions (TDP-43 and oxidative stress).
- **AIM 2.3-**To establish the relevance of FA precursors in OT model of ALS in terms of cell survival, fatty acid and lipidomic signatures and mitochondrial functionality (O_2 consumption) and lipid-phase antioxidants influence.

GOAL 3.- To define and describe the possible beneficial outcome of a nutritional intervention, regarding lipid unsaturation degree, in a mouse model of ALS.

- **AIM 3.1-**To determine the effects of a dietary intervention (consisting in different lipid unsaturation degrees) on behavior, clinical phenotype and survival in a mouse model of ALS.

- **AIM 3.2.**-To test the biochemical effectiveness of the above-mentioned dietary intervention by measuring lipid profiles in different tissues, as well as surrogates of PUFA abundance (sintaxyn) and unfolding protein response elements (Ubiquitin).
- **AIM 3.3.**-To measure dietary interference in terms of protein oxidative modifications and its possible relationship with tissular lipid profile changes in above mentioned model.
- **AIM 3.4.**-To establish the potential relationship of nuclear damage response and protein damage crosstalk in such dietary intervention.

GOAL 4.- To clarify, in the same mouse model, the relationship between oxidative damage and mitochondrial dysfunction along the disease, with particular relevance on sexual dimorphism found.

- **AIM 4.1.**-To define a novel method for evaluation of mitochondrial function, based on O₂ consumption, in fresh slices of mice's spinal cord.
- **AIM 4.2.**-To evaluate, through the aforementioned methodology, the effect on the O₂ consumption of the SODG93A overexpression mouse model, dissected into the different mitochondrial complexes.
- **AIM 4.3.**-To determine the relationship between general vs. mitochondrial-specific protein oxidative damage measurements and the mitochondrial dysfunction in both genders of commented mouse model, in various points along disease progression.
- **AIM 4.4.**-To investigate whether estrogens treatment may recapitulate the modulated mitochondrial functionality in an *in vitro* cell line (N2A) model of ALS.

In order to answer all those questions, the main objectives were depicted into different research works, and fortunately were successfully written (but not all of them already published) to compose the Thesis core:

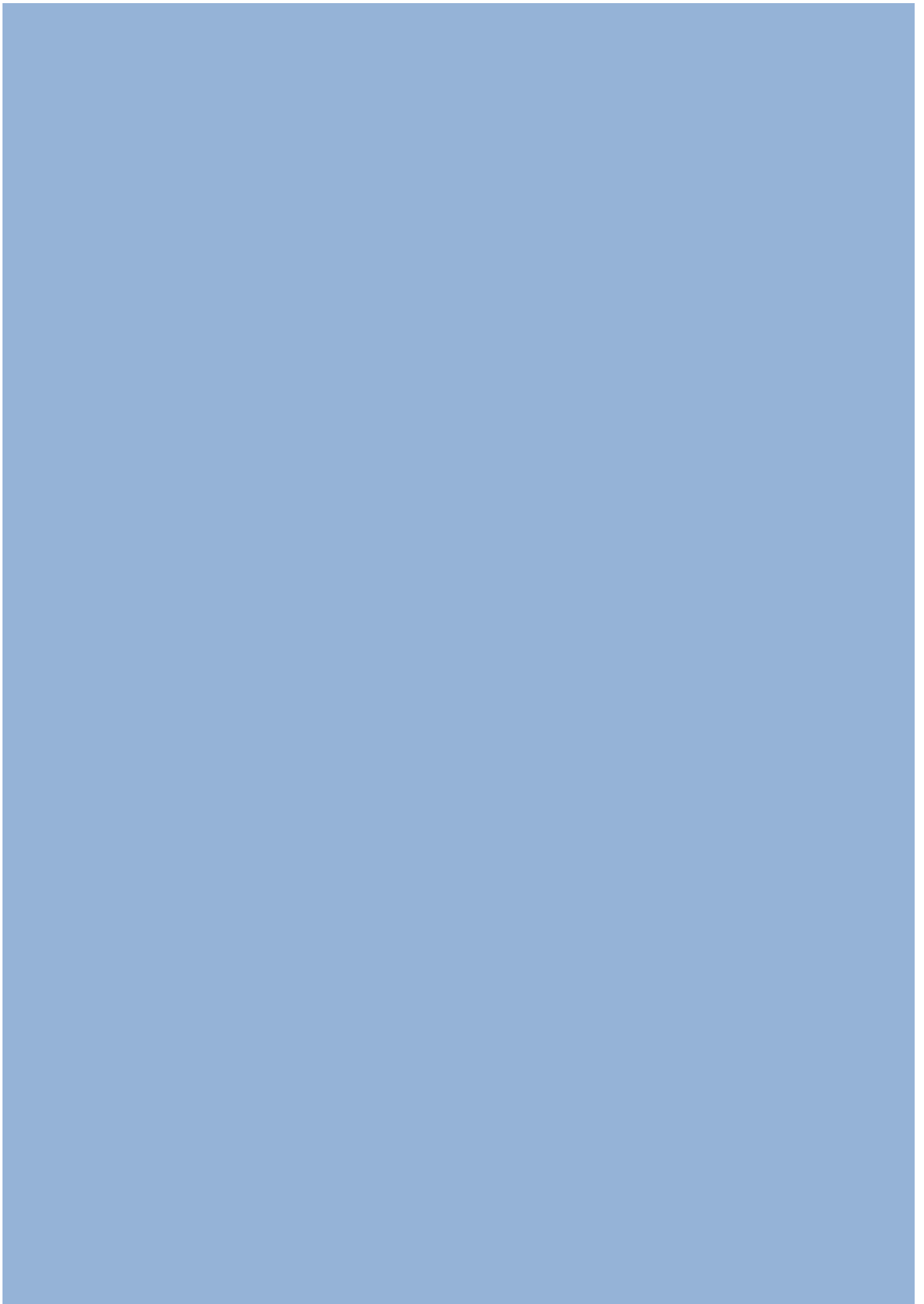
Paper one. Title: "Plant-derived Phenolics Inhibit the Accrual of Structurally Characterised Protein and Lipid Oxidative Modifications".

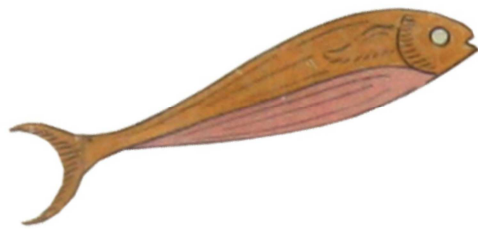
Paper two. Title: "Interplay between TDP-43 and docosohexaenoic acid-related processes in amyotrophic lateral sclerosis".

Paper three. Title: "Dietary Lipid Unsaturation Influences Survival and Oxidative Modifications of an Amyotrophic Lateral Sclerosis Model in a Gender-Specific Manner".

Paper four. Title: "Gender specific differences in spinal cord mitochondrial function and oxidative damage markers in a mouse model of ALS in early stages of disease".

4. Articles





4.1 Article 1

Title: “Plant-derived Phenolics Inhibit the Accrual of Structurally Characterised Protein and Lipid Oxidative Modifications”.

Authors: Soler-Cantero A, Jové M, Cacabelos D, Boada J, Naudí A, Romero MP, Cassanyé A, Serrano JC, Arola L, Valls J, Bellmunt MJ, Prat J, Pamplona R, Portero-Otin M, Motilva MJ.

Journal: Public Library of Science, PLoS ONE 7(8): e43308

Received: April 5th 2012 / Accepted: July 23rd 2012. Published: August 29th 2012.

DOI:10.1371/journal.pone.0043308

Plant-Derived Phenolics Inhibit the Accrual of Structurally Characterised Protein and Lipid Oxidative Modifications

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Abstract

Epidemiological data suggest that plant-derived phenolics beneficial effects include an inhibition of LDL oxidation. After applying a screening method based on 2,4-dinitrophenyl hydrazine- protein carbonyl reaction to 21 different plant-derived phenolic acids, we selected the most antioxidant ones. Their effect was assessed in 5 different oxidation systems, as well as in other model proteins. Mass-spectrometry was then used, evidencing a heterogeneous effect on the accumulation of the structurally characterized protein carbonyl glutamic and amino adipic semialdehydes as well as for malondialdehyde-lysine in LDL apoprotein. After TOF based lipidomics, we identified the most abundant differential lipids in Cu⁺⁺-incubated LDL as 1-palmitoyllysophosphatidylcholine and 1-stearoyl-sn-glycerol-3-phosphocholine. Most of selected phenolic compounds prevented the accumulation of those phospholipids and the cellular impairment induced by oxidized LDL. Finally, to validate these effects *in vivo*, we evaluated the effect of the intake of a phenolic-enriched extract in plasma protein and lipid modifications in a well-established model of atherosclerosis (diet-induced hypercholesterolemia in hamsters). This showed that a dietary supplement with a phenolic-enriched extract diminished plasma protein oxidative and lipid damage. Globally, these data show structural basis of antioxidant properties of plant-derived phenolic acids in protein oxidation that may be relevant for the health-promoting effects of its dietary intake.

Citation: Soler-Cantero A, Jové M, Cacabelos D, Boada J, Naudí A, et al. (2012) Plant-Derived Phenolics Inhibit the Accrual of Structurally Characterised Protein and Lipid Oxidative Modifications. PLoS ONE 7(8): e43308. doi:10.1371/journal.pone.0043308

Editor: Jose Vina, University of Valencia, Spain

Received: April 5, 2012; **Accepted:** July 23, 2012; **Published:** August 29, 2012

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Funding: This study was supported in part by Research and Development grants from the Spanish Ministry of Education and Science (BFU2006-14495/BFI) and the Generalitat of Catalunya (2005SGR00101) to RP; the Spanish Ministry of Health (FIS 04-0355, 05-2214 and 05-2241) to MPO, Spanish Ministry of Education and Science (AGL2005-07881-C02-01 and AGL2006-12433) to MJM and MPO. Supported partially by the COST B-35 Action. The present work was supported by the CENIT program from the Spanish Minister of Industry and by a consortium of companies led by La Morella Nuts S. A. (Reus, Catalonia, Spain) with the following companies: Shirota Functional Foods, S. L.; KRAFT; BTSa, Biotecnologías Aplicadas, S. L.; Selección Batallé, S. A.; Industrial Técnica Pecuaria, S. A.; Neuron BioPharma, S. A.; Grupo Leche Pascual, S. A. U.; Innaves, S. A. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Competing Interests: This study was partly funded by a consortium of companies led by La Morella Nuts S. A. (Reus, Catalonia, Spain) with the following companies: Shirota Functional Foods, S. L.; KRAFT; BTSa, Biotecnologías Aplicadas, S. L.; Selección Batallé, S. A.; Industrial Técnica Pecuaria, S. A.; Neuron BioPharma, S. A.; Grupo Leche Pascual, S. A. U.; Innaves, S. A. JV is employed by Shirota Functional Foods. There are no patents, products in development or marketed products to declare. This does not alter the authors' adherence to all the PLoS ONE policies on sharing data and materials, as detailed online in the guide for authors.

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Introduction

The oxidative stress hypothesis of atherosclerosis is based on the fact that free radical-derived damage participates in atherogenesis pathophysiology by means of LDL modification, among other mechanisms [1–3]. Supporting this hypothesis, LDL modified by oxidation (oxLDL) has been detected in atherosclerotic lesions [4–6] and oxLDL exhibits various proatherogenic activities *in vitro* [3,7].

It is important to emphasize that oxLDL represents a heterogeneous population of modified forms of LDL that differ greatly in their chemical composition and biological properties. The conversion of native LDL into highly modified LDL via

oxidative processes can occur by two major mechanisms: In the first case, the events start with the complete loss of LDL's endogenous antioxidants (i.e., α -tocopherol, ubiquinol-10), followed by the conversion of a majority of the polyunsaturated fatty acids (PUFA) into their corresponding hydroperoxides. Then, these primary lipid oxidation products are fragmented into secondary lipid oxidation products, such as malonyldialdehyde or 4-hydroxynonenal, which can react with the N \sum -amino group of lysine residues from LDL apoprotein (Apo B-100). Consequently, the particle's electrophoretic mobility increases and the lipoprotein becomes "high uptake" [8]. Additionally, in the subendothelial space, oxLDL may exert a "Trojan horse effect", e.g. allowing the diffusion of those lipid mediators modifying

endothelial and vascular smooth muscle cells. The second case is characterized by the immediate and preferential oxidation of amino acid residues from Apo B-100 in the absence of substantial consumption of lipid soluble antioxidants and/or occurrence of lipid peroxidation [9]. Nevertheless, apoprotein oxidative modifications have been not studied as extensively as lipid-phase ones.

The beneficial effects of Mediterranean diet concerning cardiovascular diseases are well known. Most of them are associated with olive oil and wine consumption [10,11], nutrients with a high content of phenolic acids. With regard to the influence of diet on atherosclerosis, the ingestion of fruits and vegetables (phenolic-rich vegetal sources) is related to a lesser development of atheroma plaque [12,13]. This effect is mainly attributed with their protective effects against LDL oxidation [14–17]. Despite a great deal of research having been devoted to the prevention of lipid peroxidation in LDL by antioxidants, including phenolic acids [18–21], few studies have reported the prevention of protein oxidation in LDL by exogenous antioxidants. Apo B-100 modifications, e.g., the binding of lipid peroxidation products or direct oxidation of amino acid side-chain residues, are thought to finally result in the formation of new epitopes that are specifically recognized by scavenger receptors [22–25], but the potential preventive effect of nutritional compounds on apoprotein oxidative modifications have not been studied so extensively.

To fill those gaps, the antioxidant effect of 21 different vegetal-derived phenolic compounds (mainly founded in olive oil and grape-derived products) in the oxidation of apolipoprotein of human LDL was assessed in this study. For that purpose, the quantification of carbonyl groups (detected by Western-Blot) was carried out in LDL-model systems. The antioxidant behaviour of the more active phenols was then further characterized by measuring the protection of the lipidome changes induced by Cu^{++} , the accumulation of specific oxidation and lipid peroxidation markers in LDL apoproteins. The preventive role on the loss of cell viability induced by Cu^{++} -treated LDL was tested using these phenolic compounds. Finally, in order to test whether those or related phenolic compounds would have similar effects *in vivo* in an atherosclerosis model, carbonyl content of plasma proteins and lipid oxidation markers were analysed in hypercholesterolemic hamsters fed with a phenolic-enriched diet.

Methods

Reference Compounds

α -Tocopherol was purchased from Sigma-Aldrich Chemical Co (St. Louis, MA, USA). Phenolic standards from the following sources were used without further purification: 2-(3,4-dihydroxyphenyl)-4,5-dihydroxy-3-[3,4,5-trihydroxy-6-[(3,4,5-trihydroxy-6-methyl-oxan-2-yl)oxymethyl]oxan-2-yl]oxy-chromen-7-one (rutin), 4',5,7-trihydroxyflavone (apigenin), apigenin 7-*O*-glucoside, 3',4',5,7-tetrahydroxyflavone (luteolin), luteolin 7-*O*-glucoside, *trans*-4-hydroxycinnamic acid (*p*-coumaric acid), 2-(3,4-dihydroxyphenyl) ethyl alcohol (OH-tyrosol) (3,4-DHPEA), 2-(4-hydroxyphenyl) ethyl alcohol (tyrosol) (*p*-HPEA), oleuropein, verbascoside and vanillin from Extrasynthese (Genay, France); 3,4-dihydroxycinnamic acid (caffeic acid), ferulic acid, and 3,4,5-trihydroxybenzoic acid (gallic acid) from Fluka Co. (Buchs, Switzerland); Pinoreosinol from Arbonova Sales (Turku, Finland). Phenolic enriched grape seed extract was obtained as previously described [26].

Isolation of Phenolic Compounds by Semipreparative HPLC

Secoiridoid derivatives 4-(acetoxyethyl)-1,2-dihydroxybenzene (3,4-DHPEA-AC), 4-hexenoic acid, 4-formyl-3-(2-oxoethyl)-2-(3,4-dihydroxyphenyl) ethyl ester (3,4-DHPEA-EDA), methylated form of the oleuropein aglycone (ME 3,4-DHPEA-EA) and 4-hexenoic acid, 4-formyl-3-(2-oxoethyl) 2-(4-hydroxyphenyl) ethyl ester (*p*-HPEA-EDA) were isolated from virgin olive oil phenolic extract by semi-preparative HPLC method according to the method of Artajo et al. [27]. Stock solutions of commercial standards and phenolic compounds isolated from virgin olive oil were dissolved in methanol/ H_2O (80:20 v/v) and stored at -40°C before the evaluation of their antioxidant activity. The chemical structures of the phenols included in the study are shown in Figure S1.

Hypercholesterolemic hamsters and human plasma

Twelve male Gold Syrian hamster weighing 127.55 ± 6.75 g were randomly assigned to two groups ($n = 6$ for each group) with approximately equal mean group body weights. They were caged and maintained in a 12:12 (light:dark) cycle at $22 \pm 2^\circ\text{C}$ and $50 \pm 10\%$ relative humidity with free access to both food and water. Food intake and body weight were controlled every week.

The control group ate an atherogenic diet [28] in which the cholesterol content had been set at 5% and which was supplemented with 15% of lard, and the experimental group ate this atherogenic diet supplemented with a 0.2% of phenolic-enriched vegetal extract (Table 1). The diets were maintained during 12 weeks and the animals were deprived of food for 15 h. Hamsters were anesthetized and then sacrificed by heart puncture and plasma and serum were collected and stored at -20°C until analysis. For metabolomic analyses, the method of Wikoff et al was used [29]. The plasma triglycerides, cholesterol, HDL, LDL, and alkaline phosphatase content were quantified by enzymatic

Table 1. Control and supplemented diet composition.

Component	Control (g)	Supplemented (g)
Casein	200	200
L-Cysteine	3	3
Corn starch	362	362
Sugar	140	140
Corn oil	0	0
Cellulose	50	48
Minerals	35	35
Lard	150	150
Vitamins	10	10
Cholesterol	50	50
Polyphenol extract	0	2
Total weight	1000	1000
Energy (Kcal/g diet)	4.62	4.62
Carbohydrates (g/Kg)	502	502
% Energy	43.5	43.5
Proteins (g/Kg)	203	203
% Energy	17.6	17.6
Lipids	200	200
% Energy	39	39

The control diet is an atherogenic diet.
doi:10.1371/journal.pone.0043308.t001

colorimetric reactions using commercial kits (Spinreact, Girona, Spain).

Human plasma was obtained from 6 different, healthy male donors after an overnight fast (mean age: 25 ± 3) by standard venepuncture and centrifugation using EDTA coated Vacutainer tubes. Both plasma obtention and animal experiments were supervised and approved by the Experimental and Ethics Committee of the University of Lleida.

Protein oxidation screening method: Protein oxidation and Western blot analysis

Aliquots of phenolic acid compounds dissolved in methanol were transferred to Eppendorf tubes and desiccated under a nitrogen current at room temperature. The dried phenols were redissolved to a final concentration of 5 μM with PBS (except when indicated) containing dissolved protein. Then, protein (700 $\mu\text{g}/\text{ml}$) was oxidized by exposure to different prooxidants. We used i) CuSO_4 (5 $\mu\text{mol}/\text{l}$ free Cu^{++}); ii) Hemin: H_2O_2 (30 $\mu\text{mol}/\text{l}$: 5 $\mu\text{mol}/\text{l}$); iii) H_2O_2 (5 $\mu\text{mol}/\text{l}$); iv) Ascorbate: Fe^{3+} (1.5 mmol/l : 8 $\mu\text{mol}/\text{l}$); v) ultraviolet radiation (λ 254 nm) and v) myeloperoxidase (MPO) (0.77 U/mL and H_2O_2 100 $\mu\text{mol}/\text{l}$) in phosphate buffered media at 37°C for 3 hours, according published procedures [30]. All samples were used immediately or stored at -80°C for further analysis.

To assess the extent of protein oxidation, 2,4-dinitrophenylhydrazine (DNP)-reactive carbonyls were measured by Western Blot as previously described [31] (See Methods S1 to further information).

Measurement of glutamic (GSA) and amino adipic (AASA) semialdehydes and malondialdehyde lysine (MDAL)

The concentration of chemically characterized markers of protein oxidative modification GSA, AASA, and MDAL, in LDL apoproteins was evaluated by gas chromatography/mass spectrometry (GC/MS) as previously described [31] (See Methods S1 to further information).

Lipidome analyses

Lipid composition was assessed by both fatty acid analysis (see Methods S1 to further information) and time of flight mass spectrometry (TOF)-based lipid molecular species analyses. In both cases the total lipids from LDL were extracted with chloroform:methanol (2:1, v/v) in the presence of 0.01% butylated hydroxytoluene as previously described [31].

For TOF-based lipid molecular species analyses, lipid extracts (from LDL) or methanolic extracts (from hamster's plasma) were submitted to mass-spectrometry using a LC ESI-QTOF MS/MS 6520 (Agilent Technologies, Barcelona, Spain), coupled to a capillary LC module using an untargeted approach as described [29] (see Methods S1 to further information). In order to offer a relative quantification of 1-palmitoyl-2-(5-oxovaleryl)-sn-glycero-3-phosphocholine (POVPC) and 1-palmitoyl-2-glutaryl-sn-glycero-3-phosphocholine (PGPC), bioactive lipids present in oxLDL mass profiles [32] were integrated for an m/z of 594.3 for POVPC and 610.2 for PGPC with a Δ of 0.01 Da.

FRAP assay

The ferric reducing antioxidant power of the samples was estimated according to the procedure previously described [33,34]. Briefly, FRAP reagent, was mixed with distilled water and either of sample or appropriate reagent blank. The readings at 30 min were selected for calculation of FRAP values. Reduction power activities were as μmol of Trolox equivalents, per gram of dry matter.

Cell viability

Both HMEC (kindly provided by Anne Negre-Salvayre, INSERM, Toulouse [35] and HepG2 viability were measured with the MTT-based Cell Toxicity Colorimetric Assay Kit (Sigma-Aldrich, St.Louis, MA, USA) according to the manufacturer's instructions after oxLDL tert-butylhydroperoxide (t-BOOH) as described [36,37]. The results were expressed as the percentage of viability versus cells exposed to non-oxidized LDL or untreated with t-BOOH. Further details are described in the Methods S1 section.

Statistical analyses

All statistics were analysed using the SPSS software (SPSS Inc., Chicago, IL, USA). Differences between the groups were analysed by the Student's T tests or ANOVA (with post-hoc analyses for detecting differences between specific pairs), after assessment of normal distribution of variables by the Kolmogorov-Smirnov test. Correlations between variables were evaluated by the Pearson statistic and plotted with the Metaboanalyst software [38] The 0.05 level was selected as the point of minimal statistical significance in every comparison.

Results

Effect of individual phenolic compounds on LDL oxidation. LDL oxidation by different methods induces accumulation of carbonyl in LDL apoproteins: differential inhibitory potential of phenolic compounds

The antioxidant capacity was quantified after Western Blot of DNP reactive carbonyls in LDL apoproteins (Figure 1A) being the value corresponding to oxLDL considered 0% of antioxidant capacity. The anti-DNP immunoreactivities which are lower than that found in oxLDL were interpreted as anti-oxidant activity and that which are higher as prooxidant activities. The different phenols were tested at three concentrations (5, 50 and 100 μM) (Figure 1B), using α -tocopherol as a reference. Apoprotein oxidation was significantly inhibited by the majority of the phenols tested. The OH-tyrosol showed the maximal efficiency even at 5 μM , higher than the efficiency of α -tocopherol. Luteolin (flavonoid), pinoresinol (lignan), gallic and caffeic acids showed a good efficiency which was concentration-dependent. These phenols reduced the Cu^{++} induced oxidation by between 60 and 80%. The secoiridoid derivatives (3,4-DHPEA-EDA and *p*-HPEA-EDA) showed a slight activity, similarly to α -tocopherol. Other phenols, such as verbascoside, vanillin, 3,4-DHPEA-AC and the methylated form of the oleuropein aglycone (ME 3,4-DHPEA-EA) showed lower antioxidant activity with oxidation inhibition values below 20%. The prooxidant effect shown by some phenols, such as oleuropein, tyrosol and apigenin in its aglycone and glucosidic forms should also be noted.

As Figure 1B shows, different phenolic compounds exhibit differential effects in a dose dependent fashion, in the apoprotein moiety of human LDL. According to this first screening, the more active phenols selected were: OH-tyrosol (OH-tyrosol), 3,4-DHPEA-EDA (3,4-DHPEA) as secoiridoid derivative; pinoresinol (Pin) as a lignane; luteolin (Lut) as a flavonoid; and gallic (Gallic) acids as a phenolic acid.

In order to extend those findings from Cu^{++} to other oxidation systems, we measured the effects of phenolics in different systems ranging from ultraviolet radiation to enzymatic paradigm (Figure 1C, D, E, F and G). Of those, only UVA, Fe^{+3} -Asc and H_2O_2 increased carbonyl content more than 50% in LDL (Figure 1D, E and F). In those systems, all phenols analysed had

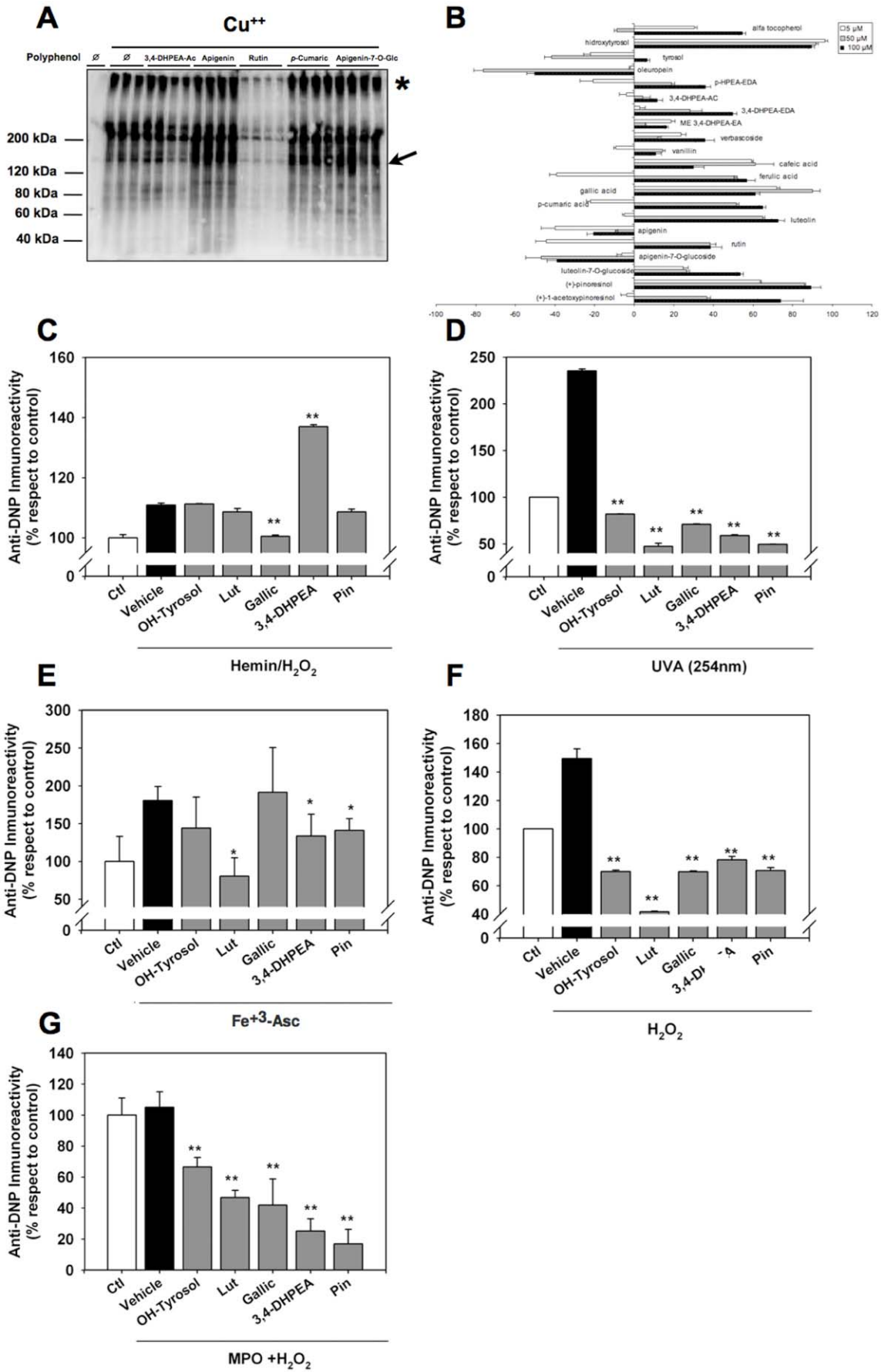


Figure 1. Plant-derived phenolic acids inhibit protein oxidation in isolated human LDL to varying degrees. **A:** Representative Western Blot of the screening phase for LDL apoprotein protection in oxLDL. Data are presented for 3,4-DHPEA-AC, apigenin, rutin, *p*-cumaric acid and apigenin-7-O-glucoside at 100 μ M. Veh:Vehicle, * indicates Apo B-100 molecular weight and arrow indicates protein fragmentation induced by oxidation. **B:** Effect of plant-derived phenolic acids in protein carbonylation in Cu^{++} -incubated LDL. All phenols were tested at three concentrations (5 μ M, 50 μ M and 100 μ M). LDL and Cu^{++} incubated LDL were used as control of native and oxidized LDL. The antioxidant capacity of each phenol at different concentrations is expressed as percentual values, considering that the immunoreactivity of Cu^{++} -incubated LDL is considered 0% of antioxidant capacity - positive values reveal decreased carbonyl formation and negative values reveal increased protein carbonylation-. LDL Apoprotein oxidation was also prevented to various extents in oxidation induced with Hemin: H_2O_2 (**C**), Ultraviolet radiation (254 nm) (**D**), Fe^{3+} :Ascorbate (**E**), H_2O_2 (**F**) and MPO: H_2O_2 (**G**) as indicated in the *Methods and Materials* section. In the case of C-G, phenols were tested at 5 μ M. In these, carbonyl contents are expressed as percentual values, considering that the immunoreactivity of LDL incubated without oxidant (Ctl) as 100% of carbonyl content. * $p < 0,05$ and ** $p < 0,01$ by ANOVA respect to oxidant-incubated LDL. Data shown are mean \pm S.D., (n=4 for each data point). doi:10.1371/journal.pone.0043308.g001

a strong antioxidant action, with the exception of Fe^{+3} -Asc, where only luteolin (and 3,4-DHPEA and pinorresinol to a minor extent) had a significant effect. Of note, pathogenically relevant systems such as MPO+ H_2O_2 do not offer a significant increase in carbonyl staining (Figure 1G). Most importantly, all selected phenolic compounds are able to significantly inhibit the accrual of carbonyl modification after MPO+ H_2O_2 incubation, being pinorresinol the most active.

In order to extent those results to other proteic systems, BSA and human plasma were oxidized using Hemin- H_2O_2 , UVA and Fe^{3+} -Asc. These results (Figure S2) do not allow to distinguish any individual phenol as a general antioxidant, i.e. its effect being independent of the protein and oxidation-system used. Generally, BSA is less oxidizable than LDL in same conditions, and only pinorresinol and luteolin diminish significantly protein oxidation in specific systems (Figure S2B and S2C). In contrast, human plasma is more oxidizable than BSA (under UVA and Fe^{+3} -Asc). Under Fe^{3+} -Asc, again pinorresinol and luteolin stand out as significant inhibitors of protein oxidation in plasma (Figure S2E and S2F). Of note, several polyphenols (notably gallic acid) exhibited prooxidant actions under these conditions (Figure S2B and S2D).

Cu^{++} incubation induces accumulation of metal-catalyzed oxidation (MCO), lipoxidation markers in LDL apoproteins and changes in LDL lipidome: differential inhibitory potential of phenolic acid compounds

Taking into account that DNP reactive carbonyls could arise from either lipid peroxidative damage or the direct modification of aminoacid residues by MCO [39] specific probes for each of those oxidative modifications were measured by using GC/MS. The results show that Cu^{++} incubation led to significant increases in the MCO markers GSA, AASA and an even greater increase in the lipoxidation marker MDAL (Figure 2A, B and C). OH-tyrosol and the lignane were the most effective compounds for inhibiting GSA accumulation. Luteolin also prevented its accumulation in Cu^{++} -treated LDL. Neither gallic acid, nor 3,4-DHPEA-EDA were effective (Figure 2A). A similar pattern was observed for AASA accumulation, but in this case, gallic acid was significant inhibitors of its formation (Figure 2B). Finally, OH-tyrosol and pinorresinol were potent antioxidants in considering MDAL accumulation, while 3,4-DHPEA-EDA, and specially luteolin (with no significant effect), were among the lowest in this sense (Figure 2C). To reinforce the importance of the lipid composition in relation with the lipoxidative modifications of proteins, a significant correlation was observed ($r^2 = 0.91$; $p < 0.0001$) between PI and MDAL formation (Figure 2D).

Carbonyl modification of apoproteins can arise from lipid peroxidation. In such a case, the LDL fatty acid composition exhibits PUFA consumption. To test this, the fatty acid composition of LDL was analysed after Cu^{++} -induced oxidation, demonstrating significant losses in PI and PUFA content (Table 2). For this reason we examined the potential for prevention of this

phenomenon. OH-tyrosol, and the lignane were among the most potent compounds, almost preventing the effect of Cu^{++} . Gallic acid was less potent, and luteolin and 3,4-DHPEA-EDA had almost no effect on the oxidative modification of LDL.

After TOF-based analyses of oxLDL, palmitoyllysophosphatidylcholine (PLPC), 1-stearoyl-sn-glycero-3-phosphocholine (SGPC) and 1-oleoylglycerophosphocholine (OGPC) comprised more than 90% of the differentially present lipids in Cu^{++} -treated LDL (Figure 2E). Similarly to the fatty acid analyses, luteolin and gallic acid exhibit the lowest capacity for preventing the build-up of PLPC, while the other compounds prevented the accumulation of this compound almost completely. Luteolin was the only compound unable to inhibit the formation of SGPC (Figure 2F and 2G).

Taking into account that 1-palmitoyl-2-(5-oxovaleryl)-sn-glycero-3-phosphocholine (POVPC) and 1-palmitoyl-2-glutaryl-sn-glycero-3-phosphocholine (PGPC) have been identified as biological effectors of oxLDL [32], the presence of those compounds was ensured. As expected, their level increased in Cu^{++} -treated samples (12 and 4-fold over untreated samples, respectively). Luteolin and gallic acid prevented the accumulation PLPC to a lower extent when compared with the other compounds (Figure 2F).

Biological relevance of plant-derived phenolics antioxidant effects: Loss of cell viability induced by Cu^{++} -treated LDL and in vivo evidences of protein and lipid antioxidant activity

To further reinforce the biological relevance of the antioxidant potential of those compounds and the methodology described here for its identification, we examined the cytotoxic potential of Cu^{++} incubated LDL in an endothelial cell culture model. For this purpose, the endothelial cell line HMEC-1 was treated with Cu^{++} -treated LDL and 18 h later, the viability of the cultures was assessed with the MTT assay. The results demonstrate that oxLDL led to a loss of 60% of viability and OH-tyrosol prevented partially those effects (Figure 3A), inducing only a 10% of viability loss. Unexpectedly, luteolin, a compound with a low antioxidant potential, based on lipidome changes, showed a significant preventive effect on the oxLDL induced loss of viability.

To ascertain whether this was due to a specific cellular effect (e.g. by modulation of antioxidant cellular responses in endothelial cells), we examined the potential influence of those compounds in *tert*-BOOH-mediated cell death in a HepG2 cell line, an unrelated cell line. Those analyses demonstrate that luteolin, OH-tyrosol and 3,4-DHPEA-EDA were the only compounds able to prevent significantly the loss of viability secondary to treatment with *tert*-BOOH (Figure 3B).

The correlation of cell viability with antioxidant capacity reinforced the pathogenic importance of LDL apoprotein oxidative modification, as that GSA amount showed the most significant correlation with the loss of viability induced by oxLDL (Figure 3C).

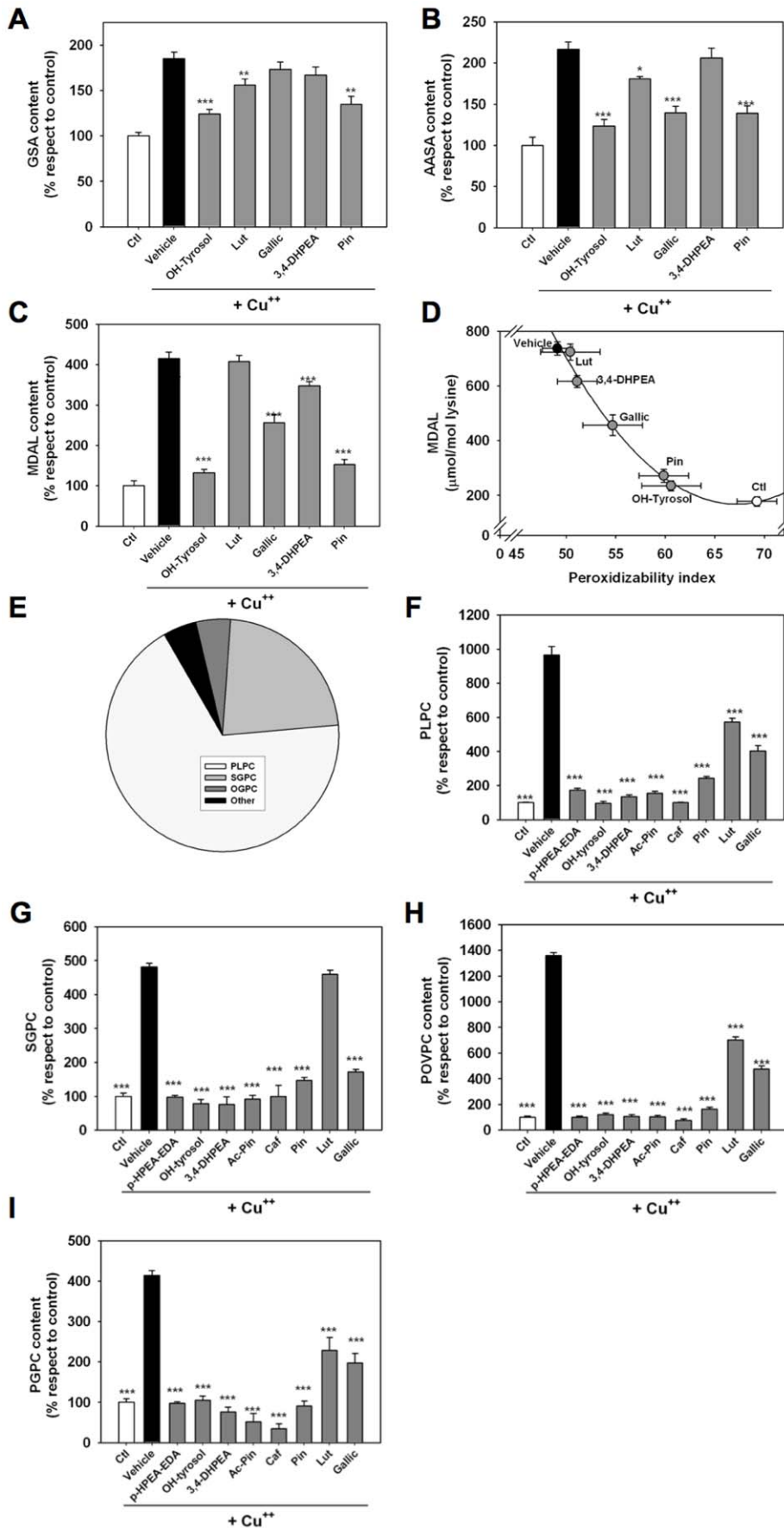


Figure 2. Cu⁺⁺-incubated LDL show significant increases in the amounts of mass-spectrometry characterized protein and lipid oxidation markers, whose formation is inhibited by selected plant-derived phenolic acids. A–C show GC/MS analyses of GSA and AASA (markers of metal-catalyzed oxidation), and MDAL, originated from lipoxidation. Values shown are % changes of mean \pm S.E.M. over values from non-oxidized LDL (GSA: 5945 \pm 61 μ mol/mol lysine; AASA: 1128 \pm 20 μ mol/mol lysine); *p<0,05; ** p<0,01 and *** p<0,001 respect to Cu⁺⁺ incubated LDL. D: protein lipoxidative damage shows a quadratic relationship with peroxidizability index (PI) ($r^2=0,911$; p<0,0001; model:[MDAL]=1,03*[PI]²-151,26*[PI]+5698) E: Pie plot showing distribution of differential (Student's T test p<0.001) lipid species between control and Cu⁺⁺-incubated LDL, after TOF-based lipidome analyses. F: Effect of plant-derived phenolic acids in the accumulation of PLPC induced by Cu⁺⁺-incubation. G: Effect of plant-derived phenolic acids in the accumulation of SGPC induced by Cu⁺⁺-incubation. H: Effect of plant-derived phenolic acids in the accumulation of POVPC induced by Cu⁺⁺-incubation. I: Effect of plant-derived phenolic acids in the accumulation of PGPC induced by Cu⁺⁺-incubation. Values shown are mean \pm S.E.M. over values from Cu⁺⁺-incubated LDL, *** p<0,001 (n = 4 for each data point). doi:10.1371/journal.pone.0043308.g002

Protein antioxidant activity of phenolic acids should be bioavailable. For this reason we analysed the plasma proteins from a hypercholesterolemic model (Golden Syrian Hamsters under hypercholesterolemic diet, showing an increase around 125% in cholesterol levels respect animals under standard chow) under a diet enriched in vegetable-derived phenols. The polyphenol supplementation did not induce any signs of toxicity nor changes in alkaline phosphatase, indicating that it was well tolerated. Despite an effect in LDL cholesterolemia was noted, no significant differences were evidenced in other values analysed (Table S1). Nevertheless, the results (Figure 3D) demonstrate that phenolic-enriched diet significantly diminishes steady state levels of circulating protein carbonyls. Furthermore, their intake reduces oxidability of proteins *ex vivo* under Fe³⁺-Asc system, both in hypercholesterolemic hamsters (Figure 3E) and in human plasma with exogenously added luteolin at 5 μ M (Figure 3F). Noteworthy, compounds with masses compatible with oxidized phospholipids as PLPC, OGPC and PGPC were detected in the methanolic extract of hamster plasma (Figure S3, S4, S5). The levels of those metabolites were diminished in animals under phenolic-enriched diet (Figure 3G, H and I). Reinforcing the importance of specificity of oxidative damage measurements, FRAP assay of plasma demonstrated that polyphenol-enriched diet did not change antioxidant capacity (Figure 3J), although it changed significantly

profiles of metabolic parameters by hierarchical clustering (Figure 3K).

Discussion

The present work demonstrates the antioxidant properties of selected plant-derived phenols (mainly found in olive oil and grape-derived products) in protein oxidation both *in vivo* and *in vitro*, and the existence of some heterogeneity in the mechanisms. We offer a novel approach for analysing and screening the antioxidant properties of natural products over LDL modification, especially in its protein components. After a screening phase, five different compounds were selected for further analysis. We have demonstrated for the first time, the effect of those nutritional compounds on the accrual of structurally characterized markers of both protein (GSA, AASA and MDAL) and lipid peroxidation (POVPC, PGPC) in oxLDL. The pathogenic importance of LDL protein oxidation is shown by the fact that it was the only factor that correlated with oxLDL-induced cell death. To extend the validity to an *in vivo* setting, we have shown that phenolic intake in a hypercholesterolemic context diminishes protein carbonyl content in plasma as well as the concentration of lipid peroxidation markers.

Table 2. Effect of Cu⁺⁺ and phenolic acids in LDL fatty acid composition.

	Ctl	Cu ⁺⁺	OH-Tyrosol	Lut	Gall	3,4-DHPEA	Pin
16:0	21,11 \pm 0,59*	24,78 \pm 0,78	23,39 \pm 0,84	26,55 \pm 0,91	24,25 \pm 0,65	24,77 \pm 0,8	23,32 \pm 0,10
16:1n-7	3,06 \pm 0,28*	3,27 \pm 0,55	3,00 \pm 0,66*	3,33 \pm 0,26	3,25 \pm 0,87	3,10 \pm 0,7	3,26 \pm 0,15
18:0	11,55 \pm 0,16	11,08 \pm 0,93	8,90 \pm 0,30*	11,63 \pm 0,35	10,08 \pm 0,41	11,41 \pm 0,0	9,36 \pm 0,46*
18:1n-9	22,77 \pm 0,97**	26,38 \pm 0,26	24,91 \pm 0,27	25,37 \pm 0,06	25,24 \pm 0,93	25,74 \pm 0,0	24,61 \pm 0,69
18:2n-6	28,84 \pm 0,50**	24,97 \pm 0,21	30,39 \pm 0,33**	23,11 \pm 0,81	28,02 \pm 0,8**	26,09 \pm 0,9*	29,78 \pm 0,13**
20:3n-6	1,59 \pm 0,47*	0,98 \pm 0,07	1,39 \pm 0,85*	0,88 \pm 0,02	1,18 \pm 0,14*	1,01 \pm 0,1	1,24 \pm 0,22*
20:4n-6	6,05 \pm 0,96**	3,08 \pm 0,70	4,62 \pm 0,19*	2,67 \pm 0,25	3,77 \pm 0,14*	3,32 \pm 0,6	4,29 \pm 0,65*
ACL	17,74 \pm 0,9	17,5 \pm 0,7	17,6 \pm 0,2	17,5 \pm 0,1	17,5 \pm 0,8	17,5 \pm 0,7	17,6 \pm 0,1
SFA	34,41 \pm 1,2*	38,1 \pm 0,3	33,8 \pm 0,0*	40,2 \pm 0,6*	36,1 \pm 0,4	37,9 \pm 0,8	34,6 \pm 0,3*
UFA	65,59 \pm 2,2*	61,8 \pm 1,7	66,2 \pm 1,0*	59,7 \pm 0,4	63,8 \pm 0,6	62,0 \pm 2,2	65,4 \pm 1,2*
MUFA	26,07 \pm 0,7*	30,3 \pm 0,5	28,0 \pm 0,2*	28,8 \pm 0,8	28,7 \pm 0,1	29,0 \pm 0,2	28,0 \pm 0,2*
PUFA	39,52 \pm 0,8**	31,5 \pm 0,2	38,2 \pm 0,1**	30,8 \pm 0,6	35,1 \pm 0,6*	33,0 \pm 0,0	37,4 \pm 0,2*
PUFAn-3	1,67 \pm 0,02*	0,9 \pm 0,08	1,2 \pm 0,1	0,8 \pm 0,1	1,0 \pm 0,5	1,0 \pm 0,7	1,3 \pm 0,1
PUFAn-6	37,85 \pm 1,2*	30,5 \pm 0,4	36,9 \pm 0,9*	30,05 \pm 0,1	34,1 \pm 0,1*	31,9 \pm 0,3	36,1 \pm 0,1*
DBI	124,58 \pm 3,2**	104,6 \pm 0,6	119,0 \pm 0,6**	103,2 \pm 0,0	111,6 \pm 0,8*	106,6 \pm 0,5	117,3 \pm 0,7**
PI	69,26 \pm 2,3**	49,1 \pm 0,1	60,6 \pm 0,1**	50,4 \pm 0,2	54,6 \pm 0,9*	51,1 \pm 0,1	59,8 \pm 0,6*

Values: mean \pm S.E. ACL, average chain length; SFA, saturated fatty acids; UFA, unsaturated fatty acids; PUFA n-6/n-3, polyunsaturated fatty acids n-6 or n-3 series; MUFA, monounsaturated fatty acids; DBI, double bond index; PI, peroxidizability index,

*p<0,05 and ** p<0,01 respect to values in Cu⁺⁺ incubated LDL by ANOVA post-hoc analyses (n = 4 for each data point).

doi:10.1371/journal.pone.0043308.t002

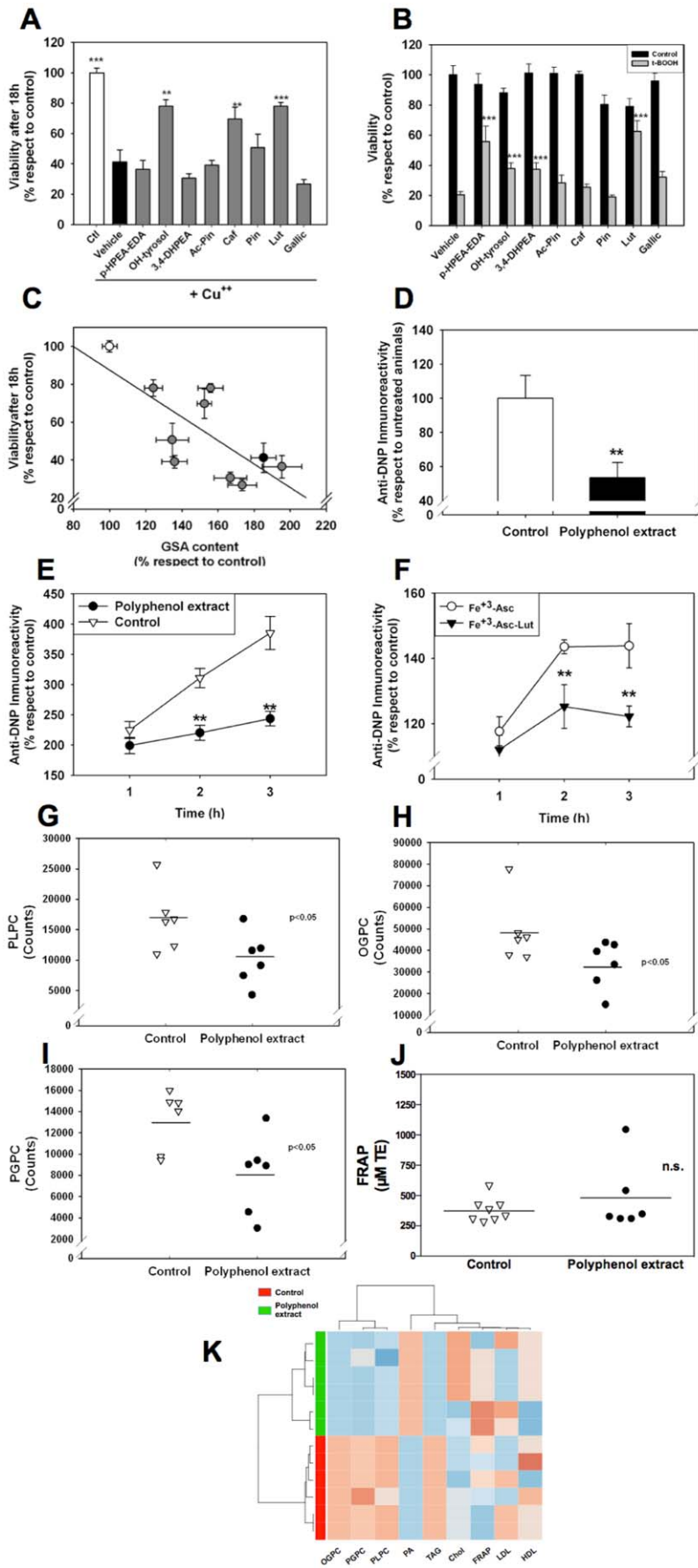


Figure 3. Plant-derived phenolic acids inhibit both the effects of oxidative stress in endothelial and HepG2 cell culture and protein oxidation in diet-induced hypercholesterolemia in vivo. **A:** Effect of plant-derived phenolic acids in cell death in HMEC (endothelial cell line) induced by Cu^{++} -incubated LDL; ** $p < 0,01$ and *** $p < 0,001$ respect to cell death induced by Cu^{++} incubated LDL ($n = 6$ for each data point). Values shown are mean \pm S.E.M. over values from samples treated with control LDL. **B:** Effect of plant-derived phenolic acids in HepG2 capacity to withstand t-BOOH induced cell death; *** $p < 0,001$ respect to cell death induced by t-BOOH ($n = 6$ for each data point). Values shown are % changes of mean \pm S.E. over values from control samples. **C:** Endothelial cell death induced by Cu^{++} -incubated LDL is strongly correlated with GSA content ($r = -0.734$; $p < 0,016$ by the Pearson correlation test). To validate this in vivo, proteins from hypercholesterolemic hamsters were analyzed for carbonyl content with OGPC in plasma from hypercholesterolemic hamsters with a dietary supplement of phenolic acid-enriched vegetal extract (**E**) and pooled human plasma (**F**) were oxidized with Fe^{3+} -Asc as indicated in the *Methods and Material* section. Aliquots were taken at indicated time points and processed for determination of carbonyl content. **G:** Effect of phenolic acids-enriched diet intake in the steady state levels of a compound compatible with PLPC in plasma from hypercholesterolemic hamsters. **H:** Effect of phenolic acids-enriched diet intake in the steady state levels of a compound compatible with OGPC in plasma from hypercholesterolemic hamsters. **I:** Effect of phenolic acids-enriched diet intake in the steady state levels of a compound compatible with PGPC in plasma from hypercholesterolemic hamsters. **J:** Effect of phenolic acids-enriched diet intake in FRAP activity of plasma. **K:** Heat-map showing that phenolic acids-enriched diet induces a significant hierarchical clustering of measured parameters, including both oxidative damage and metabolic (cholesterol, HDL and LDL-cholesterol, triacylglyceride and alkaline phosphatase activities), revealing an important biological effect. The carbonyl content is expressed as a percentual value, considering that the immunoreactivity of plasma from hypercholesterolemic hamsters individuals (Controls in **D**) or protein incubated without oxidant (Ctl) (in **E**) as 100% of carbonyl content. ** $p < 0,01$ by Student's T test respect to untreated animals (**E,G,H,I,J**) or oxidant-incubated human plasma (**F**). Data shown are mean \pm S.E.M., ($n = 4$ for each data point). For clustering analyses, values of samples were log transformed and hierarchical clustering was performed using Pearson correlation coefficient as distance measure and the Ward's clustering algorithm. Colors in K express intensity/abundance with red colors showing high levels and blue colors lower levels. doi:10.1371/journal.pone.0043308.g003

In order to establish whether structural features determine the effect on the resistance of LDL to Cu^{++} -induced oxidation, the chemical structures of the phenolic compounds should be considered (Figure S1). Important differences in the protection of the apoprotein oxidation were observed in this study, similar to those observed by other authors using the lag time of LDL as marker oxidation [40,41]. The differences between those phenols are attributable to their chemical structure, e.g. OH-tyrosol possesses a 3,4-dihydroxy structure linked to an aromatic ring that confers the moiety with a higher proton dislocation, facilitating a higher scavenging activity than observed with tyrosol, which only has a hydroxyl group linked to an aromatic ring (Figure S1). The protective effect of the OH-tyrosol structure has biological relevance as OH-tyrosol and tyrosol are the more simple phenols detected in plasma and LDL after the ingestion of virgin olive oil and red wine [42,43]. It should be noted that OH-tyrosol, with the highest potential for inhibition of MDAL, has been previously described as a potent inducer of cellular antioxidant responses, both in oxLDL-induced and in tert-BOOH-induced cell stress [36,44].

The antioxidant capacity shown by oleuropein and its secoiridoid derivatives was quite different. The aglicon derivative of oleuropein (3,4-DHPEA-EDA) and the ligstroside derivative (*p*-HPEA-EDA) showed a positive result as antioxidants, mainly at the maximum concentration tested. These compounds exhibit a high selectivity for lipid-related changes since they mainly prevented Cu^{++} induced changes in lipidome and MDAL in LDL. Although no previous results were available on lipid or protein antioxidant properties, 3,4-DHPEA-EDA is a compound of special interest because of its presence as one of the major phenolic antioxidant compounds in virgin olive oil. Moreover, it is an important source of OH-tyrosol in plasma. In contrast with these data, a similar phenolic structure, the 3,4-DHPEA-AC showed no significant antioxidant activity in this system. This may be attributed to the potential proton dislocation due to double bonds in the elenolic structure in 3,4-DHPEA-EDA. Reinforcing the importance of conjugation, oleuropein, or glucose-conjugated elenolic acid, showed the more remarkable prooxidant activity of all phenols included in the study in agreement with its previous reported pro-oxidant activities [45,46]. Most interestingly, as oleuropein is considered a proapoptotic agent with potential use as an anti-tumoral agent [47,48], it may be suggested that those protein prooxidant properties could be involved in the beneficial effects of oleuropein.

Flavonoids such as rutin, flavones (apigenin and luteolin), and their glucosides (apigenin-7-*O*-glucoside and luteolin-7-*O*-glucoside) can scavenge reactive oxygen radicals, by donating a hydrogen atom or electron [49,50]. Their radical scavenging activity seems to be substantially dependent on three structural groups: (i) the *ortho*-dihydroxyl structure (catechol structure) in the B ring, which is the obvious radical target site, (ii) the 2,3 double bond in conjunction with 4-oxo function, which is responsible for electron delocalization, and (iii) the additional presence of both the 3- and the 5-OH groups for maximal radical scavenging potential and the strongest radical absorption. Our data suggest the importance of the *ortho*-dihydroxyl structure in the prevention of protein modification, as luteolin and rutin -both containing this structure- act as more effective antioxidants than apigenin, a very similar molecule. Comparing the antioxidant activity in the copper-induced LDL oxidation of the luteolin and luteolin-7-*O*-glucoside, the antioxidant capacity of both structures was similar. Despite the described preventive effects of those flavonoids in the diminution of the lag-phase of LDL induced by Cu^{++} and other oxidants [51,52] no data were available on their role as inhibitors of protein oxidation markers. In fact, luteolin can be classified as an agent with more potential for preventing direct oxidation (i.e. GSA and AASA accumulation) than for preventing lipid peroxidation, as it shows a lower power for protecting against Cu^{++} -induced lipidome changes in LDL, in agreement with previous data showing a modest inhibition in the formation of thiobarbituric acid-reactive substances driven by Cu^{++} [53]. In contrast with this relative low *in vitro* potential, it shows a high efficiency in both cell systems as it is able to completely block tert-BOOH-induced changes in cell viability and it shows a high potential against oxLDL-induced cell death, in agreement with the reported inhibitory effect of luteolin in oxidized LDL-induced endothelial monocyte adhesion and/or oxidised LDL uptake [53].

Other major phenols quantified in virgin olive oils and grape-derived products are lignans, with a 2,3-dibenzylbutane skeleton, whose concentration is related to the olive cultivar of origin [54]. Although they are important as sources of lignans enterodiol and enterolactone by colonic flora metabolism, our data reveal that acetoxypinoresinol and pinoresinol possess antioxidant activity, in agreement with previous reports, where it was shown that some vegetable extracts, rich in pinoresinol, were able to inhibit LDL oxidation [55,56]. Their antioxidant activity could be more closely related to their chelating properties than scavenging activity, as they only exhibit a hydroxyl group linked to an aromatic ring.

Globally, acetoxypinoresinol and pinoresinol exhibit similar potencies in the inhibition of direct protein oxidation and lipid peroxidative damage, as well as in the prevention of lipidome changes induced by Cu^{++} .

With regard to the phenolic acid group (ferulic, cumaric, caffeic and gallic acids) (Figure S1), all the phenols showed antioxidant capacity at 50 and 100 μM . Ferulic and *p*-cumaric acids showed a slight prooxidant activity at 5 μM , that may be attributed to H_2O_2 *in vitro* production from phenolic compounds [57,58]. According to their mechanism of action, the phenolic acids may be classified as free radical terminators interfering with lipid oxidation by rapid donation of a hydrogen atom to peroxy radicals. Their antioxidant activity is related to the molecule containing at least two neighbouring phenolic hydroxyl groups; three such groups are even more desirable facilitating the interference. Results of the present study showed that the caffeic (with two neighbouring phenolic hydroxyl groups) and gallic acids (three hydroxyl groups) shown to have the highest antioxidant capacity. Previous results have demonstrated the antioxidant capacity of gallic and caffeic acids on lipid peroxidation [59–61], but only one reported the effect of gallic acids on protein modification, and that was related to nitrosative stress [62]. Concerning their cellular effects, gallic and caffeic acid differed in their effects: while gallic acid was unable to prevent oxLDL-induced or tBOOH-induced loss of viability, caffeic acid inhibited the toxic effects of oxLDL (data not shown). This agrees with the known effect of gallic acid as a proapoptotic agent [63–65] and the reported protective effect of caffeic acid in endothelial cell survival after oxLDL treatment [66].

All the phenols studied showed antioxidant capacity in the LDL model, the OH-tyrosol being the more effective. In general, all the phenols showed higher antioxidant activity than α -tocopherol, which could be attributed to the hydrophilic nature of the phenolic structures. In the biphasic microenvironment constituting core lipids and water phase, such as biomembranes and plasma lipoproteins, the location of phenols should be taken into account for understanding their antioxidant activity. Vitamin E (α -tocopherol) seems to be located within the membrane lipids or lipoprotein particles because of its high lipophilicity. However, it is demonstrated that flavonoid aglycones interact in the polar surface region of the phospholipids bilayers in membranes [67], offering a higher protection. This is specially relevant assuming that the antioxidant profile is completely dependent on the system. As shown by experiments with BSA and human plasma, phenolic interaction in protein oxidation is a very complex phenomenon, which depends on not only of the system used for oxidation, but also on the protein, the presence of lipids and the several mechanisms between protein-phenol and free radical source.

In summary, these data show novel antioxidant properties of plant-derived phenolic acid compounds in LDL oxidation and demonstrates phenolic activity in protein oxidation *in vivo*. It is also demonstrated that *in vitro* antioxidant measurements could only partially predict biologic responses to oxidized LDL, thus reinforcing the importance of a multidisciplinary approach for the description of oxidative phenomena in atherosclerosis pathogenesis and its dietary modulation.

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Supporting Information

Figure S1 Structures of plant-derived phenolics used in the present study.

(DOCX)

Figure S2 Representative phenolic acids inhibit protein carbonylation in different oxidative systems up to various extents.

All phenols were tested at 5 μM . Oxidation of BSA (**A,B,C**) or a human plasma pool (**D,E,F**) was induced with Hemin: H_2O_2 (**A, D**), Ultraviolet radiation (λ 254 nm) (**B,E**), and Fe^{3+} :Ascorbate (**C,F**) as indicated in the *Methods and Materials* section. Carbonyl contents are expressed as percentual values, considering that the immunoreactivity of protein incubated without oxidant (Ctl) as 100% of carbonyl content. ** $p < 0,01$ by ANOVA respect to oxidant-incubated protein. Data shown are mean \pm S.D., (n = 4 for each data point).

(DOCX)

Figure S3 Chromatographic and mass-spectra evidence for the presence of PLPC in methanolic extracts of plasma from hypercholesterolemic hamsters.

A: Extracted ion chromatogram of m/z 496.3398 (magnified in **B**) showing the peak quantified as PLPC (arrow in **A**). **C:** Mass spectra of the peak quantified as PLPC (arrowhead showing m/z peak with $\Delta < 0.05$ Da in comparison to a theoretical mass of $\text{C}_{24}\text{H}_{50}\text{NO}_7\text{P}$) (DOCX)

Figure S4 Chromatographic and mass-spectra evidence for the presence of OGPC in methanolic extracts of plasma from hypercholesterolemic hamsters.

A: Extracted ion chromatogram of m/z 522.3554 (magnified in **B**) showing the peak quantified as OGPC (arrow in **A**). **C:** Mass spectra of the peak quantified as OGPC (arrowhead showing m/z peak with $\Delta < 0.02$ Da in comparison to a theoretical mass of $\text{C}_{26}\text{H}_{52}\text{NO}_7\text{P}$) (DOCX)

Figure S5 Chromatographic and mass-spectra evidence for the presence of PGPC in methanolic extracts of plasma from hypercholesterolemic hamsters.

A: Extracted ion chromatogram of m/z 610.3715 (magnified in **B**) showing the peak quantified as PGPC (arrow in **A**). **C:** Mass spectra of the peak quantified as PGPC (arrowhead showing m/z peak with $\Delta < 0.01$ Da in comparison to theoretical mass of $\text{C}_{29}\text{H}_{56}\text{NO}_{10}\text{P}$) (DOCX)

Methods S1 Supplementary methods.

(DOCX)

Table S1

(DOCX)

Author Contributions

Conceived and designed the experiments: RP MPR MJM MPO. Performed the experiments: ASC MJ DC AN JB JCES AC. Analyzed the data: MPO ASC JP MJB. Contributed reagents/materials/analysis tools: MJM MPR LLA JV. Wrote the paper: MJ MPO.

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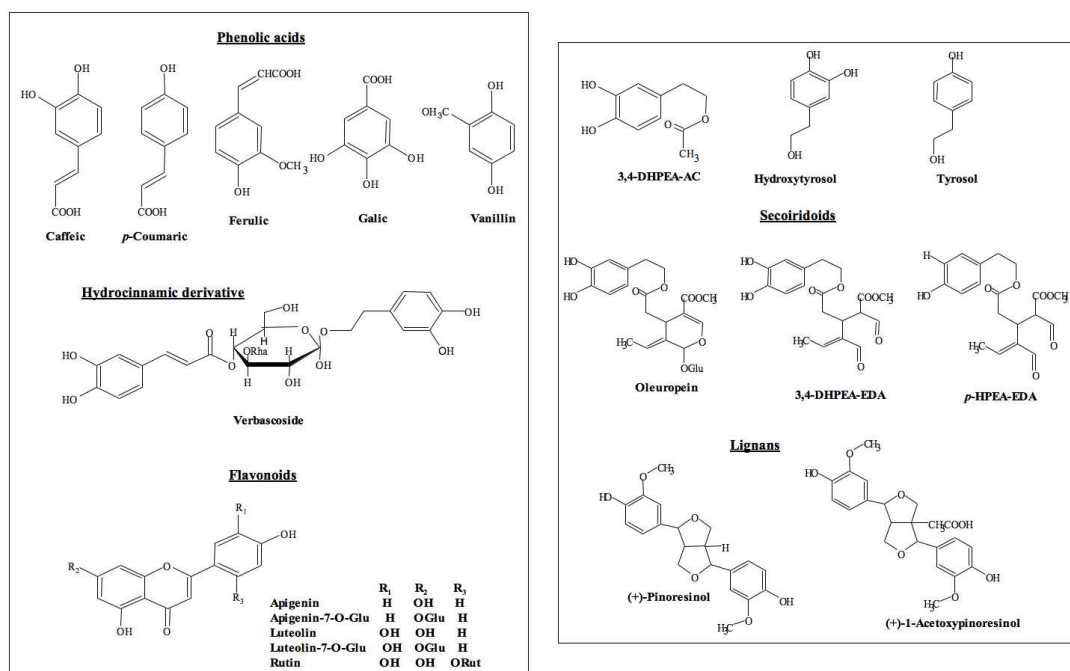
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Supplemental Table 1

	Control	Polyphenol extract	P (By Student's T test)
Final weight (g)	118.12±7.6	114.18±8.6	0.062
Total cholesterol (mg/dL)	455,0 ± 36,39	421,9 ± 12,07	0.108
LDL-Cholesterol (mg/dL)	403,8 ± 50,57	345,9 ± 44,09	0.4
HDL-Cholesterol (mg/dL)	327,7 ± 17,63	305,4 ± 10,03	0.27
Triacilglyceride (mg/dL)	225,0 ± 35,95	142,6 ± 9,492	0.051
Alkaline phosphatase (U/L)	54.07±18.3	47.63±6.6	0.56

Shown is mean±S.E.M (n=6)

Figure S1

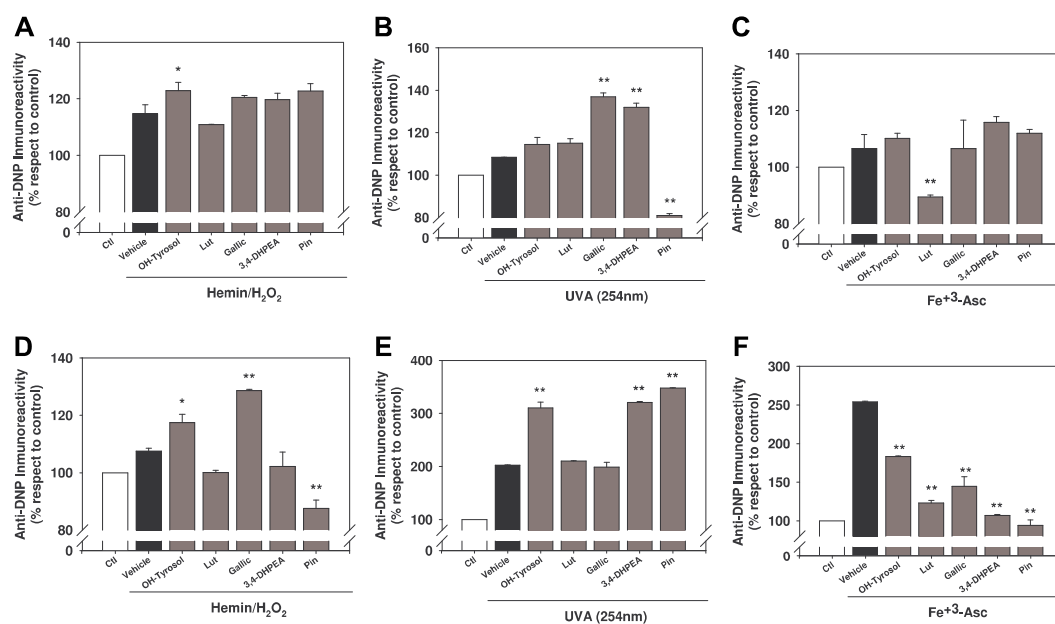


Structures of plant-derived phenolics used in the present study.

doi:10.1371/journal.pone.0043308.s001

(DOCX)

Figure S2

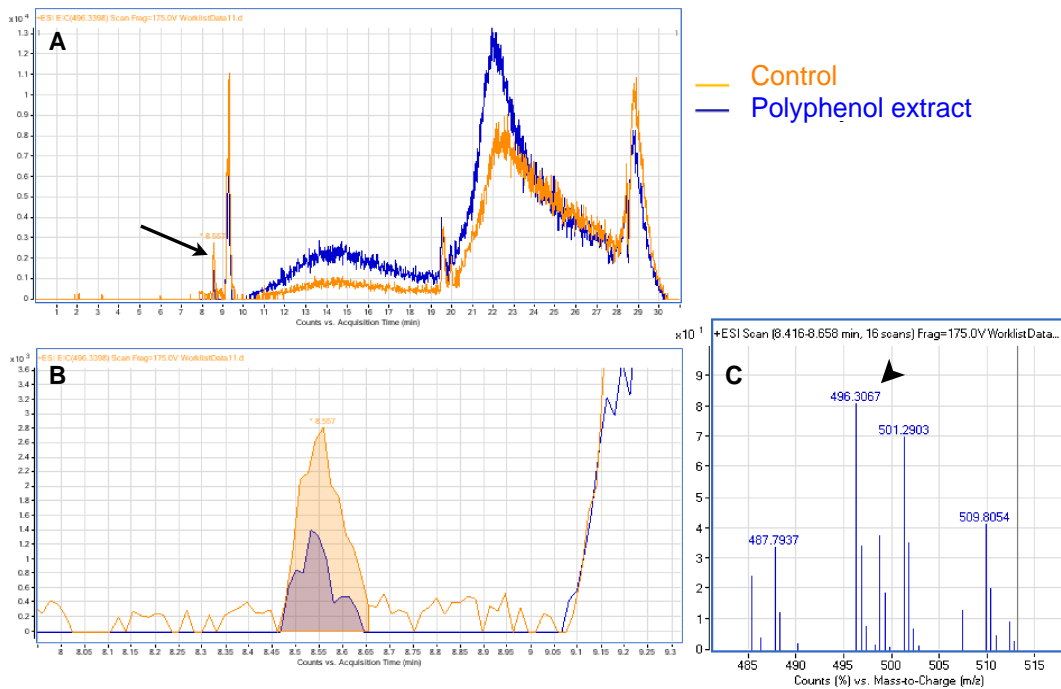


Representative phenolic acids inhibit protein carbonylation in different oxidative systems up to various extents. All phenols were tested at 5 μ M. Oxidation of BSA (A,B,C) or a human plasma pool (D,E,F) was induced with Hemin:H₂O₂ (A, D), Ultraviolet radiation (λ 254 nm) (B,E), and Fe³⁺:Ascorbate (C,F) as indicated in the *Methods and Materials* section. Carbonyl contents are expressed as percentual values, considering that the immunoreactivity of protein incubated without oxidant (Ctl) as 100% of carbonyl content. ** p<0,01 by ANOVA respect to oxidant-incubated protein. Data shown are mean \pm S.D., (n = 4 for each data point).

doi:10.1371/journal.pone.0043308.s002

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Figure S3

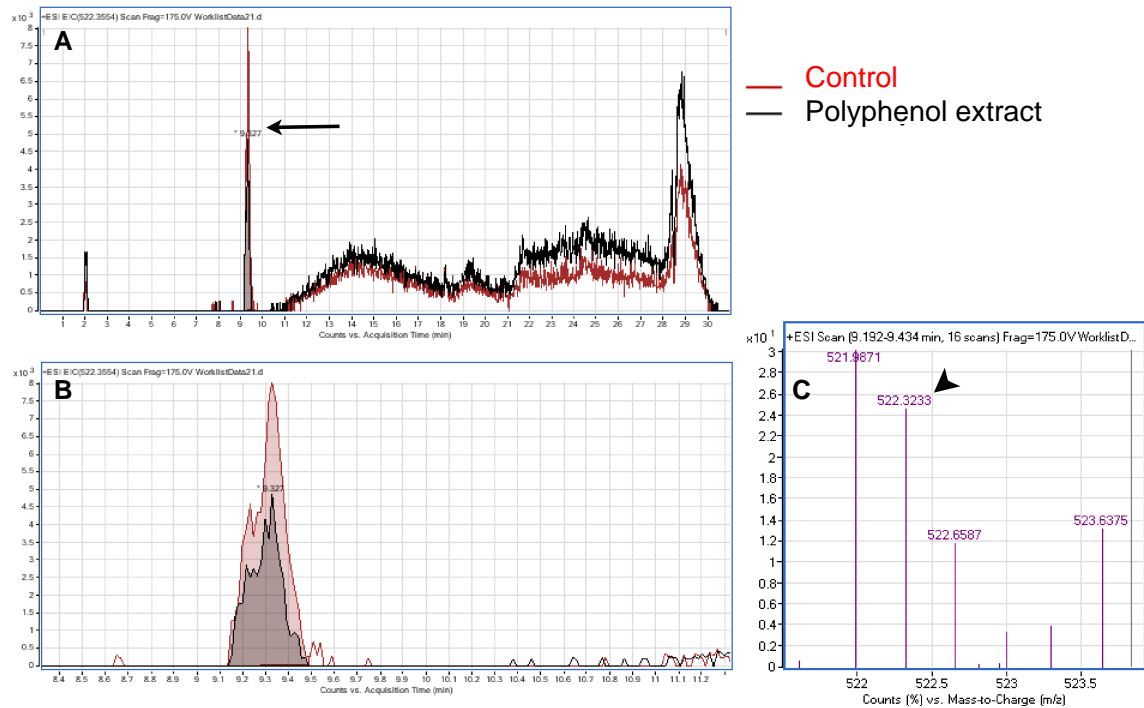


Chromatographic and mass-spectra evidence for the presence of PLPC in methanolic extracts of plasma from hypercholesterolemic hamsters. A: Extracted ion chromatogram of m/z 496.3398 (magnified in **B**) showing the peak quantified as PLPC (arrow in **A**). **C:** Mass spectra of the peak quantified as PLPC (arrowhead showing m/z peak with $\Delta < 0.05$ Da in comparison to a theoretical mass of $C_{24}H_{50}NO_7P$)

doi:10.1371/journal.pone.0043308.s003

(DOCX)

Figure S4

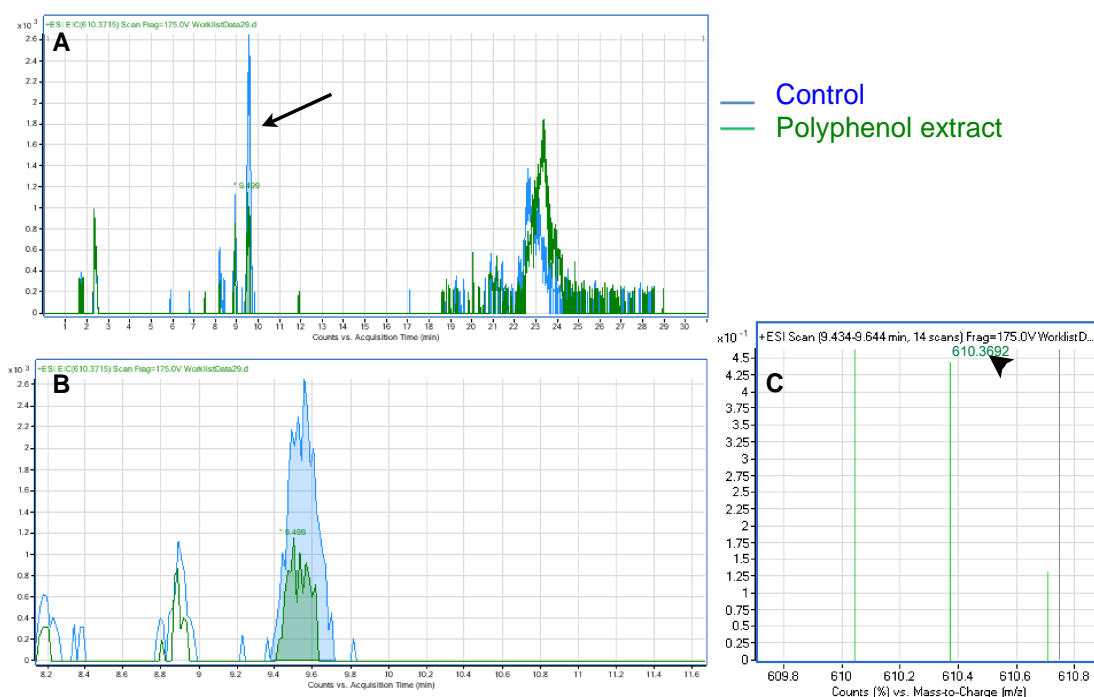


Chromatographic and mass-spectra evidence for the presence of OGPC in methanolic extracts of plasma from hypercholesterolemic hamsters. A: Extracted ion chromatogram of m/z 522.3554 (magnified in **B**) showing the peak quantified as OGPC (arrow in **A**). **C:** Mass spectra of the peak quantified as OGPC (arrowhead showing m/z peak with $\Delta < 0.02$ Da in comparison to a theoretical mass of $C_{26}H_{52}NO_7P$)

doi:10.1371/journal.pone.0043308.s004

(DOCX)

Figure S5



Chromatographic and mass-spectra evidence for the presence of PGPC in methanolic extracts of plasma from hypercholesterolemic hamsters. A: Extracted ion chromatogram of m/z 610.3715 (magnified in **B**) showing the peak quantified as PGPC (arrow in **A**). **C:** Mass spectra of the peak quantified as PGPC (arrowhead showing m/z peak with $\Delta < 0.01$ Da in comparison to theoretical mass of $C_{29}H_{56}NO_{10}P$)

doi:10.1371/journal.pone.0043308.s005

(DOCX)

SUPPLEMENTAL ONLINE MATERIAL

Supplemental Methods

Protein oxidation screening method: Protein oxidation and Western blot analysis.

Briefly, to 15 μ l of sample SDS was added to a final concentration of 6%, and, after boiling for 3 min, 20 μ l of 10 mM DNP in 10% trifluoroacetic acid were added. After 7 min at room temperature, 20 μ l of a solution containing 2M Tris base, 30% glycerol and 15% β -mercaptoethanol was added for neutralization and sample preparation for loading onto 4-20% gradient pre-made SDS-PAGE gels (Invitrogen, Barcelona, Spain). For immunodetection after SDS-PAGE, proteins were transferred using a Mini Trans-Blot Transfer Cell (BioRad Laboratories, Barcelona, Spain) to PVDF membranes (Immobilon-P Millipore, Bedford, MA, USA). Immunodetection was performed using a rabbit anti-DNP antiserum as the primary antibody (1:4000, Dako, Carpinteria, CA, USA). Peroxidase-coupled secondary antibodies were used from the Tropixchemiluminescence kit (TropixInc, Bedford, MA, USA). Luminiscence was recorded and quantified in Chemidoc equipment (BioRad, Barcelona, Spain), using the Quantity-one analysis software (Biorad). The average mode of background subtraction was chosen to quantify. Control experiments showed that omission of derivatization step, primary or secondary antibody addition produced blots with no detectable signal (data not shown). After developing, the blots were silver-stained as described to check the protein load (1).

Measurement of glutamic (GSA) and amino adipic (AASA) semialdehydes and malondialdehyde lysine (MDAL).

Samples containing 0.4 mg of protein were extensively delipidated using chloroform:methanol extraction (2:1 v/v, 3x) in the presence of 0.01% butylatedhydroxytoluene, and the proteins were precipitated by adding 10% of trichloroacetic acid (final concentration) and subsequent centrifugation. The protein samples were reduced overnight with 500 mM NaBH₄ (final concentration) in 0.2M borate buffer, pH 9.2, containing 1 drop of hexanol as an anti-foam reagent. The proteins were then reprecipitated by adding 1 ml of 20% trichloroacetic acid and then centrifuging this. The following isotopicallylabelled internal standards were then added: [2H8]Lysine (d8-Lys; CDN Isotopes); and [2H8]MDAL (d8-MDAL), [2H5] 5-hydroxy-2-aminovaleric acid (for GSA quantization) and [2H4]6-hydroxy-2-aminocaproic acid (for AASA quantization) as described(1). The samples were hydrolysed at 155° C for 30 min in 1ml of 6N HCl, and then vacuum dried. The N,O-trifluoroacetyl methyl ester derivatives of the protein hydrolysate were prepared as previously described(1). The GC/MS analyses were carried out on a Hewlett-Packard model 6890 gas chromatograph equipped with a 30m HP-5MS capillary column (30m x 0.25mm x 0.25 μ m) coupled to a Hewlett-Packard model 5973A mass selective detector (Agilent Technologies, Barcelona, Spain). The injection port was maintained at 275° C; the temperature program was 5 min at 110° C, then rising by 2° C/min to 150° C, then by 5° C/min to 240° C, then 25° C/min to 300° C, and finally hold at 300° C for 5 min. Quantification was performed by external standardization using standard curves constructed from mixtures of deuterated and non-deuterated standards. The analytes were detected by selected ion-monitoring GC/MS. The ions used were: lysine and d8-lysine, m/z 180 and 187, respectively; 5-hydroxy-2-aminovaleric acid and d5-5-hydroxy-2-aminovaleric acid (stable derivatives of GSA), m/z 280 and 285, respectively; 6-hydroxy-2-aminocaproic acid and d4-6-hydroxy-2-aminocaproic acid (stable derivatives of AASA), m/z 294 and 298, respectively; and MDAL and d8-MDAL, m/z 474 and 482, respectively. The amounts of products were expressed as the ratio μ mol GSA, AASA, or MDAL/mol lysine.

Lipidome analyses.

Fatty acid profiles

For fatty acid analyses, the chloroform phase was evaporated under nitrogen, and the fatty acids were transesterified by incubation in 2.5 ml of 5% methanolicHCl for 90 min at 75° C. The resulting fatty acid methyl esters were extracted by adding 2.5 ml of n-pentane and 1 ml of saturated NaCl solution. The n-pentane phase was separated, evaporated under nitrogen, redissolved in 75 μ l of hexane and 1 μ l was used for the GC/MS analysis. Separation was performed in a SP2330 capillary column (30m x 0.25mm x 0.20 μ m) in a Hewlett Packard 6890 Series II gas chromatograph (Agilent Technologies, Barcelona, Spain). A Hewlett Packard 5973A mass spectrometer (Agilent Technologies, Barcelona, Spain) was used as the detector in the electron-impact mode. The injection port was maintained at 220° C, and the detector at 250° C; the temperature program was 2 min at 100° C, then rising by 10° C/min to 200° C, then 5° C/min to 240° C, and finally held at 240° C for 10 min. Identification of fatty acid methyl esters was done

by comparison with authentic standards and based on mass spectra. Results are expressed as mol %. The following indexes were calculated from the fatty acid composition: Saturated Fatty Acids (SFA)= Σ % of saturated fatty acids; Unsaturated Fatty Acids (UFA)= Σ % unsaturated fatty acids; Monounsaturated Fatty Acids (MUFA)= Σ % of monoenoic fatty acids; Polyunsaturated n-3 Fatty Acids (PUFAn-3)= Σ % of polyunsaturated fatty acids n-3 serie; Polyunsaturated n-6 Fatty Acids (PUFAn-6)= Σ % of polyunsaturated fatty acids n-6 serie; Average Chain Length (ACL)= $[(\Sigma \text{ \%Total}14 \times 14) + \dots + (\Sigma \text{ \%Total } n \times n)]/100$ (n= carbon atom number); Peroxidizability index (PI) = $[(\Sigma \text{ mol\% Monoenoic } \times 0.025) + (\Sigma \text{ mol\% Dienoic } \times 1) + (\Sigma \text{ mol\% Trienoic } \times 2) + (\Sigma \text{ mol\% Tetraenoic } \times 4) + (\Sigma \text{ mol\% Pentaenoic } \times 6) + (\Sigma \text{ mol\% Hexaenoic } \times 8)]$.

LC-TOF based lipidome analyses

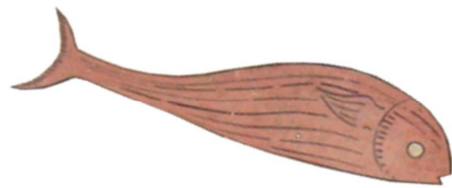
Briefly, lipid samples, extracted as above, after drying and reconstitution with mobile phase (see below) were injected into a reversed-phase chromatography system, using a Zorbax C18 column (150 x 0.5 mm x 5 μ m) at a flow rate of 8 μ l/min in a LC system consisting of a capillary pump (Agilent 1200). Buffer A was water with 0.1% formic acid, and buffer B was acetonitrile with 0.1% formic acid. The column was equilibrated in 5% B and the gradient was 5%--95%B over 50 min. The eluant was directed to an ESI source, with a nebulizer gas flow of 15 l/min at 300° C with a capillary voltage of 3500 V operating in positive mode, with a dual spray for reference mass (m/z 121.05087 and m/z 922.0098). The instrument was calibrated immediately prior to the test. For the data analysis with the Agilent MassHunter Profiling software, five repeated injections of each extract sample were measured by the same LC/MS method. The acquired MS data were extracted by the Molecular Feature Extractor in the Agilent MassHunter Qualitative software. In this process, the identified ions were clustered to "Molecular features" comprising different isotopic distribution and adducts from the same molecule. The obtained files were grouped according to the samples into two respective groups (control samples vs Cu⁺⁺ treated samples or control hypercholesterolemic hamsters vs hypercholesterolemic phenolic-enriched vegetal extract supplemented hamsters) and loaded into the Agilent MassHunter Profiling software. For the differential analysis of both groups the features of each group were compared using Student's T Test. The resulting masses were searched for in the Lipid Maps Databases (<http://www.lipidmaps.org/tools/index.html>), and among 73 differential molecular features found, 17 were significantly increased (p<0.01) over values found in control incubations of LDL (being the remaining 56 diminished). Among those, the three most abundant had masses compatible with 1-palmitoyllysophosphatidylcholine –PLPC- (measured mass: 495.3328, theoretical mass: 495.3325), 1-stearoyl-sn-glycero-3-phosphocholine –SGPC- (measured mass: 523.364, theoretical mass: 523.3638) and 1-oleoylglycerophosphocholine –OGPC- (measured mass: 521.3476, theoretical mass: 521.3481).

Cell viability

HMEC cell line (endothelial cell), kindly donated by Dr. A. Negre-Salvayre (INSERM, Toulouse, France) were cultured in 100mm plates with high glucose DMEM containing 10% FBS until they were 70-80% confluent. Afterwards, the cells were harvested, counted and seeded in 96-well microplates (25,000 cells/well) with the same culture medium, leaving a strip of wells free of cells to be used as a blank. The cells were immediately centrifuged at 1000 rpm for 4 min, without stop brake, in order to obtain a fast and homogeneous attachment to the bottom of the wells. After 6 h, the cell culture medium was removed and serum-free DMEM was added to the cells. One hour later, the culture medium was removed again and 100 μ l of serum-free DMEM containing non-oxidized LDL, oxLDL, oxLDL in the presence of phenolic acids or the vehicles alone, was added to each well. The final concentration of LDL in all conditions was 200 μ g/ml. Eighteen hours later, the culture medium was removed and 100 μ l of PBS was added to each well in order to avoid possible interferences, immediately before determining viability. The effect of phenolic compounds on the cellular capacity to withstand tert-butylhydroperoxide (t-BOOH) challenge was measured. The HepG2 cells were serum starved (0.5% FCS) in the presence of selected phenolics (5 μ M) for 8 h. The cells were then challenged with 200 μ M t-BOOH as peroxide donor, and 2 h later, cell viability was estimated with the 3-(4,5-Dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) test, according manufacturer instructions.

Supplemental Literature Cited

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4.2 Article 2

Title: “Interplay Between TDP-43 and Docosohexaenoic Acid-Related Processes in Amyotrophic Lateral Sclerosis”.

Authors: Cacabelos D, Ayala V, Granado-Serrano AB, Jove M, Boada J, Cabre R, Ramírez-Nuñez O, Gonzalo H, Torres P, Soler Cantero A, Serrano JC, Bellmunt MJ, Romero MP, Motilva MJ, Nonaka T, Hasegawa M, Ferrer I, Pamplona R, Portero-Otín M.

Journal: Proceedings of the National Academy of Sciences, PNAS
Submitted 28th August.

Interplay between TDP-43 and docosahexaenoic acid-related processes in amyotrophic lateral sclerosis

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Submitted to Proceedings of the National Academy of Sciences of the United States of America

Docosahexaenoic acid (DHA), a key fatty acid in nervous system homeostasis, is depleted in spinal cord of sporadic amyotrophic lateral sclerosis (sALS) patients. In this work we show that sALS leads to changes in spinal cord distribution of DHA synthesis enzymatic machinery. This is closely related to pathological deposits of Tar-DNA binding protein 43 (TDP-43), since transfection of neurons with aggregation prone C-terminal fragments of TDP-43 recapitulates diminished levels of these enzymes in motor neurons with TDP-43 aggregates in vivo. Further, drebrin, a DHA dependent synaptic protein, is depleted in sALS samples and it is associated to TDP-43 aggregation in vitro. However, chronic excitotoxicity, preceding motor neuron disease, increases DHA amount, with both enhanced concentrations of neuroprotective DHA-derived resolvin D, and higher lipid peroxidation-derived moecules such as 8-iso-prostaglandin-F₂-α (8-iso-PGF₂α) levels. Since α-tocopherol improved mitochondrial respiratory function and motor neuron survival in these conditions, it is suggested that oxidative stress could boost motor neuron loss. Cell culture experiments, showing enhanced expression of desaturases (FADS2) and β-oxidation enzymes after H₂O₂ challenge shows that DHA production can be an initial response to oxidative stress, driven by TDP-43 aggregation and drebrin loss. The finding of altered levels of desaturases and peroxisomal and mitochondrial β-oxidation enzymes in human sALS suggest that in early stages of the disease increased DHA could act as a response over chronic excitotoxicity in spinal cord, involving several DHA synthetic enzymes, but later on this could contribute, by lipid peroxidation, to motor neuron loss.

lipid peroxidation | lipidomics | drebrin | desaturases

Introduction

Polyunsaturated fatty acids (PUFA) are essential for neuronal function. Neuronal membranes host the highest amount of highly unsaturated PUFA, whose function is multiphaceted: modulation of biomembrane physical characteristics, precursors of bioactive paracrine regulators, control of neurotransmitter and synapses physiology, among other (1). As an example, docosahexaenoic acid (DHA), a member of the PUFA family, is involved in synaptic transmission, as its depletion by nutritional deficiencies leads to downregulation of the synaptic components drebrin and syntaxin-3(2, 3). DHA can be produced from n-3 precursors by a series of different elongation and desaturation steps, finally comprising a peroxisomal beta-oxidation step(4). On the other hand, PUFAs, and particularly DHA –due to the high number of unsaturations in its aliphatic chain- are also preferential targets of oxidative modifications (5). Thus, a trade-off between PUFA function and its sensitivity to lipid peroxidation has been achieved

through hominid evolution(6–8). In this equilibrium, an adequate tissular status of lipophilic antioxidants plays a key role in the protection of those PUFA. In this line it should be reminded that DHA supplementation, described as neuroprotective, may be more beneficial with α-tocopherol addition(9, 10). Besides α-tocopherol, several reports have hypothesized the neuroprotective role of other antioxidant micronutrients, such as those present in virgin olive oil in conditions such as ageing, hypoxia-reperfusion, Alzheimer's disease, and other neurodegenerative conditions(11, 12)

Recent data demonstrates that the intake of foods high in n-3 PUFAs could help to prevent or delay the onset of ALS (13). In line with this, prior data showed decreased levels of DHA in spinal cord from sporadic ALS (sALS) patients (14), a fatal neurodegenerative disease. However, the potential changes in DHA synthesis machinery behind those alterations were unknown. Further, no information was available about the potential protective role of PUFA and antioxidants in chronic excitotoxicity, a pathogenic mechanism in sALS and other neurodegenerative diseases. Acute excitotoxicity shows that there are relevant interactions between PUFA and lipophilic or hydrophilic antioxidants(15, 16) .

Significance

Dietary polyunsaturated fatty acids of the n-3 family, such as docosahexaenoic acid or linolenic acid, could play a role in prevention of amyotrophic lateral sclerosis, a motor neuron degenerative disease. This may be due to its essential role in maintenance of synaptic machinery. We demonstrate that in ALS patients enzymes for the synthesis of this fatty acid are altered, with closely resembling TDP-43 aggregates, a pathologic hallmark of the disease. Further, we show that TDP-43 aggregates diminish the levels of these enzymes, uncovering a novel pathway potentially therapeutic target for the study of ALS pathogenesis. of ALS pathogenesis.

Reserved for Publication Footnotes

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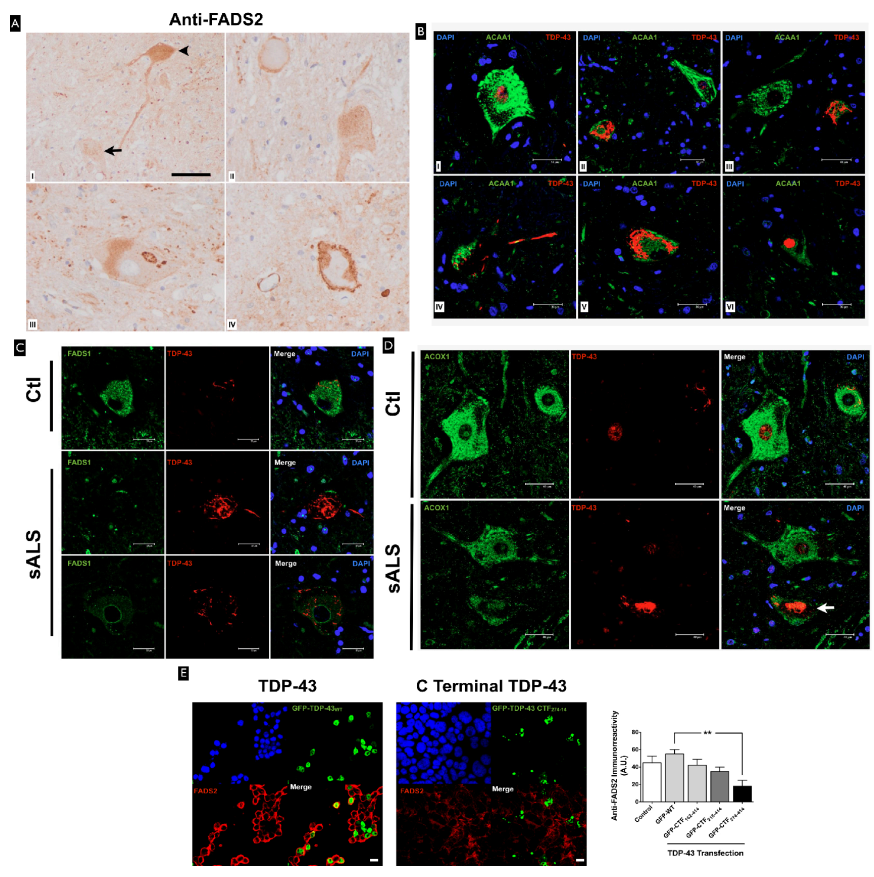


Fig. 1. Enzymes for DHA synthetic pathways are influenced by sALS in a close relationship with TDP-43 aggregation. FADS2 immunoreactivity is distorted in motor neurons from sALS samples, as shown by (A), with reduced FADS2 immunoreactivity in certain cells (arrowhead) while preserved in others (arrow) (I, magnification x200). This is accompanied by abnormal aggregation of FADS2 in a few motorneurons with reduced FADS2 immunoreactivity (II-IV, magnification x400). Confocal imaging in B shows that, in comparison with motor neurons from healthy individuals (I) motor neurons in sALS with TDP-43 aggregates show reduced ACAA1 content (II-VI). The same phenomena is present for FADS1 (C) and ACOX1 (D), showing reduced ACOX expression in sALS motor neurons with TDP-43 inclusions (arrow in D). As indicated by transfection experiments, CTF fragments of TDP-43 are able to reproduce the loss of FADS2 (E). Right panel in E shows the immunoreactivity quantification, with bars representing the means±S.E.M. of immunofluorescence values for different transfections (n=3-4 different experiments). ** Indicates p<0,001 with reference to values of GFP-WT-TDP-43 after one way ANOVA test. Paraffin sections slightly counterstained with haematoxylin. Bar in A = 25 µm.

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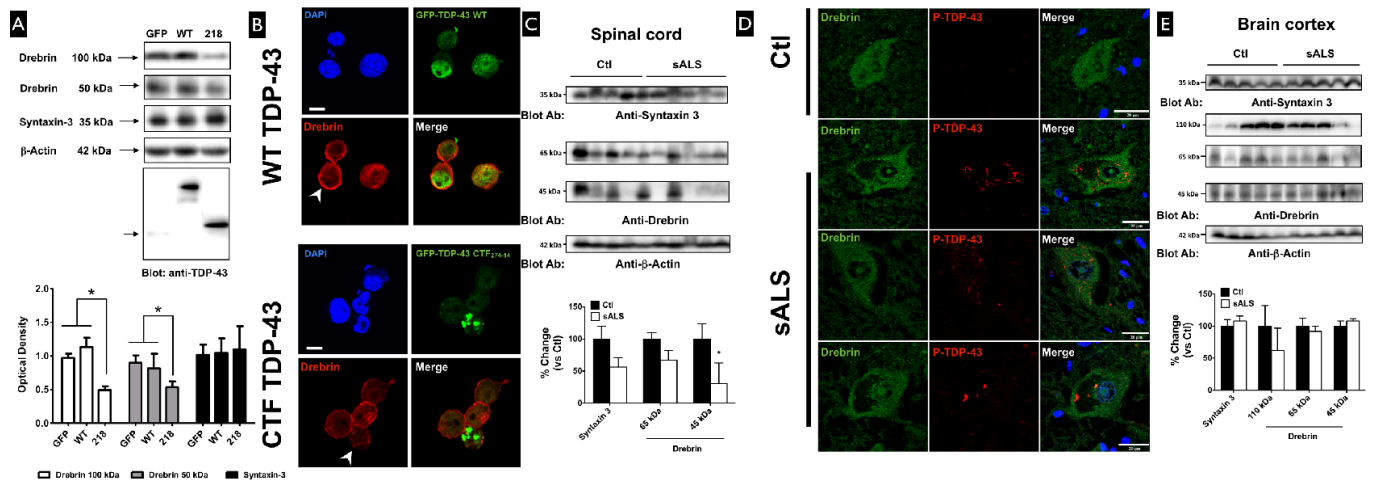


Fig. 2. TDP-43 aggregation and sALS are related to decreased content of the DHA-dependent protein drebrin in neurons. (A) shows that transfection with aggregation prone TDP-43 CTF leads to decreased amounts of the DHA dependent protein drebrin, but not syntaxin. This is cell-specific, as shown by coexistence of TDP-43 aggregates and drebrin depletion in confocal microscopy (B). Note the different abundance of drebrin in cells transfected with WT-TDP-43 (arrowhead in upper panel) and that in a cell showing CTF-TDP-43 aggregates (arrowhead in lower panel). This could explain changes present in samples from human spinal cord and brain cortex, revealing that sALS is associated to specific changes in the content the DHA dependent synaptic proteins drebrin in spinal cord (C), though immunofluorescence analyses show that motor neurons in sALS samples conserve drebrin levels (D), even with P-TDP-43 aggregates. In line with maintained DHA levels, brain cortex lysates do not show changes in drebrin nor in syntaxin levels. Lower panels in A, C and E show the densitometric analyses of the above western-blot. Numbers in the left of blots show the approximate molecular weight. Bars in A, C and E represent the means±S.E.M. being *p<0,05 with reference to values of GFP-WT-TDP-43 (A) spinal cord (C) or brain cortex (E) from control individuals after ANOVA (A) or Student's t test (C,E).

Besides excitotoxicity, it shall be reminded that most sALS patients exhibit Tar-DNA binding protein (TDP-43) aggregates. Gene deletion of *tardbp*, encoding TDP-43, leads to a phenotype consisting with altered lipid homeostasis (e.g. distorted fat storage and membrane trafficking mechanisms)(17). This suggest that,

perhaps, DHA synthetic machinery can be influenced by TDP-43 pathogenic events.

To fill these gaps, we have studied the enzymes responsible for DHA-synthesis as well as the potential loss of drebrin and syntaxin 3 associated to the ALS-linked DHA loss. We correlated

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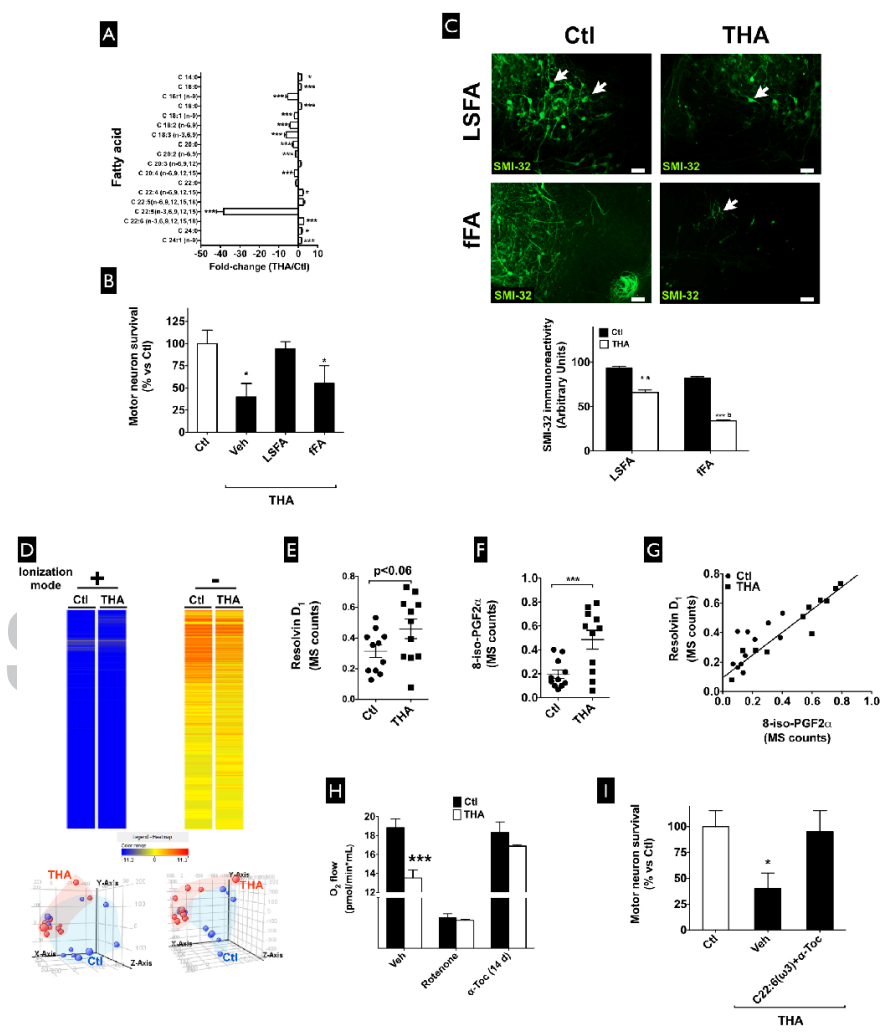


Fig. 3. Chronic excitotoxicity increases the concentration of DHA and biologically related compounds impinging selective changes in the lipidome with depletion of ω 3 precursors and mitochondria-derived oxidative stress. A) Variations in fatty acid composition (shown by fold-change) induced by chronic excitotoxicity in spinal cord reveal that the concentrations of the DHA precursor docosapentaenoic acid (C22:5(n-3,6,9,12,15)) and LNA (C18:3(n-3,6,9)) are severely decreased under these conditions. ω 3 depletion is pathogenically relevant, as shown by the fact that loss in motor neuron number induced by chronic excitotoxicity is prevented by linseed fatty acids (LSFA) incubation (B). C shows representative micrographs with the effect of LSFAs and fish fatty acids (fFA) in the number of neurofilament positive (SMI-32 immunoreactive) cells in ventral horns of spinal cord organotypic cultures, identified as motor neurons (arrows). D) Lipidome analyses after chronic excitotoxicity reveal relatively minor changes as shown by heatmap of lipids in positive (left) and negative (right) ionization modes. Lower panels show tridimensional Principal Component Analyses of these ionized lipids (blue spheres are control specimens, while red spheres are THA-treated cultures). E) Consistent with increased DHA availability, one of its enzymatic products, resolvin D1, shows a tendency for increased concentrations in cultures under excitotoxicity. F) Levels of the lipid peroxidation marker isoprostane 8-iso-PGF2 α are increased by chronic excitotoxicity, and directly correlated (G) to the resolvin D1 amount ($y = -0.2 + 0.75x$, $p < 0.0001$, $Rsq = 0.79$). H) In line with this, high-resolution respirometry suggests the potential implication of lipid peroxidation affecting mitochondrial function in the motor neuron loss induced by chronic excitotoxicity, as α -tocopherol treatment during 14 days (α -toc, 100 μ M) is able to prevent this function loss, which can be attributed to complex I activity. Further, I) indicates that oxidative stress can be pathophysiologically relevant, as loss of motor neuron induced by excitotoxicity is prevented by addition of DHA (combined with α -tocopherol (α -toc+DHA, 100 μ M both)) –but not DHA alone (data not shown)– is able to prevent motor neuron loss associated with chronic excitotoxicity. Bars in A, B, C, H and I represent the means \pm S.E.M. ($n = 11-15$ slices/condition) being * $p < 0,05$; ** $p < 0,001$ and *** $p < 0,0001$ with reference to Ctl values by Student's t test (A, E, F, I), one-way ANOVA (B, I) and two-way ANOVA (C). In C ^a and ^b superindexes indicate significant differences between the fatty acids used ($p < 0,0001$). Bars in C are 50 μ m long.

these findings with TDP-43 aggregates in spinal cord samples from sALS patients (i.e. where motor neuron death is almost complete). We have also used the chronic excitotoxicity model, at a stage preceding motor neuron death. In this system we studied the changes of lipidomic profile and the fatty acid composition to evaluate changes in DHA availability. In this line, we established that oxidative stress is able to modulate DHA synthesis and DHA-linked proteins. Finally, to shed light upon a potential novel therapeutic pathway, we have studied if the addition of α -linolenic acid (ALA), and/or DHA combined with several antioxidants is able to interact with diverse fatty acids rescuing motor neuron-

like cells from oxidative stress induced cell death and motor neurons from cell death in chronic excitotoxicity.

Results

sALS is associated with spinal cord specific changes in enzymes for DHA synthesis, associated in a cell-specific fashion to TDP-43 aggregates.

In a previous work, we have shown that sALS is associated with changes in fatty acid composition (14): we detected decreased DHA content in spinal cord and increased levels in brain cortex. DHA synthesis is dependent on the so called Sprecher's

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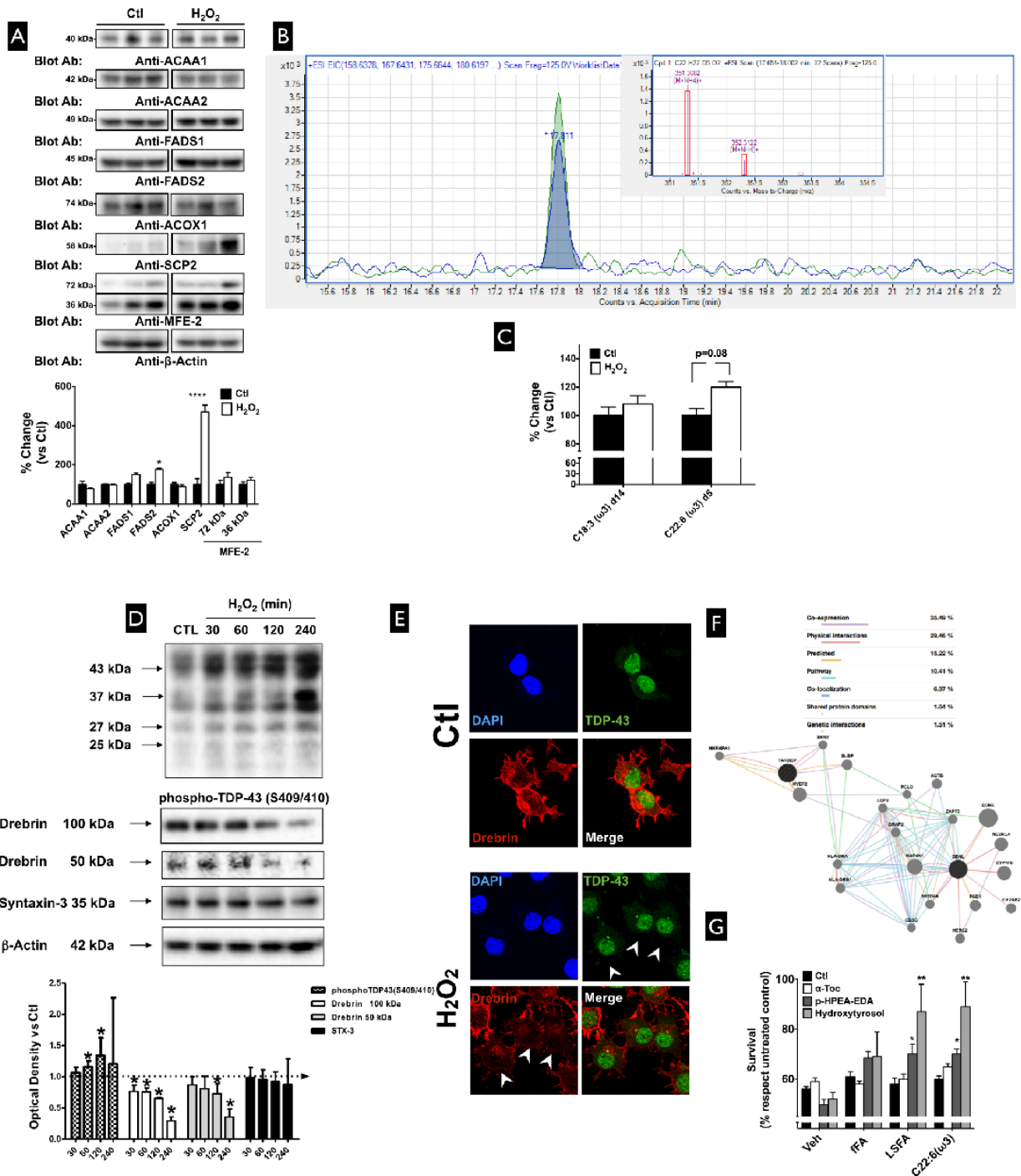


Fig. 4. Oxidative stress enhances DHA synthesis, associated to TDP-43 pathological events and drebrin loss, and its neuroprotective role is enhanced by exogenous antioxidants. A) Representative western-blot showing that H₂O₂ incubation of N2A cells, also changes the expression of FADS2 and SCP2. B) Representative chromatogram for d₅ labelled DHA (as evidenced by compatible mass spectra of the NH₄⁺ adduct in the inset), showing that levels are higher in H₂O₂ treated cells (green trace) in comparison with control cells (blue trace). Omission of d₁₄ labelled ALA resulted in undetectable signal of d₅ labelled DHA C) In line with these changes, capacity for conversion of d₁₄ labelled ALA to d₅DHA is slightly increased. This increased DHA synthesis can be a response to an H₂O₂-driven TDP-43 phosphorylation and aggregation, which precedes drebrin loss as shown by western blot (D) and immunocytochemical analyses (E), demonstrating loss of drebrin in those cells with TDP-43 aggregates (arrowheads in E). Interactomic analyses demonstrate that drebrin is mainly linked to TDP-43 by co-expression, with HLA-DRA, HLA-DRB1 and XRN2 as linking nodes. E) In contrast to organotypic spinal cord cultures H₂O₂-induced loss of NSC-34 viability is not prevented by α -tocopherol (α -toc, 200 μ M), but by the phenolic compounds derived from virgin olive oil p-HPEA-EDA (5 μ M) and hydroxytyrosol (25 μ M), in a fatty-acid specific fashion. Lower panels in A and D show the densitometric analyses of the above western-blots. Numbers in the left of blots show the approximate molecular weight. Bars in A, C, D and F are the means \pm S.E.M (3-4 experiments) being *p<0,05; **p<0,01; *** p<0,001 and **** p<0.0001 by Student's t test (A,C) or one-way ANOVA (D and F) with reference to Ctl.

shunt which coordinates a series of elongation and desaturation steps including a coordinated action of endoplasmic reticulum

and peroxisomal functions (4). Interestingly, FADS2 expression in tissue was affected by sALS, with some cells showing preserved

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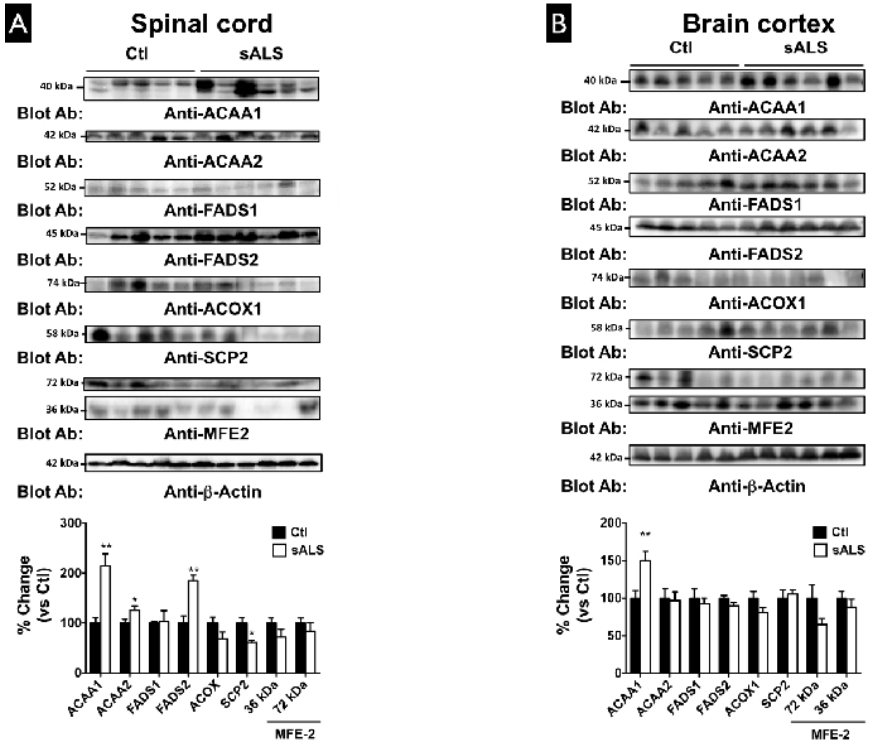


Fig. 5. DHA-synthetic enzymes are altered in brain cortex and spinal cord from sALS patients. In line with DHA synthesis being reactive as a response to stress, representative western blot analyses of enzymes for PUFA synthesis in human spinal cord (A) and brain cortex (B) lysates demonstrate specific increases in ACAA1 (both for spinal cord and brain cortex), ACAA2 and FADS2 that could explain compositional changes in fatty acids previously reported in sALS. Lower panels in A and B show the densitometric analyses of the above western-blot. Numbers in the left of blots show the approximate molecular weight. Bars in A and B represent the means±S.E.M. being *p<0,05 or **p<0,001 with reference to values of spinal cord (A) or brain cortex (B) from control individuals after Student's t test.

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immunoreactivity and others with marked depletion of this enzyme (Figure 1A). Phospho-TDP-43 aggregation is a hallmark for motor neuron demise in sALS. We found that cytosolic TDP-43 aggregates are associated with changes (generally decreased expression) of DHA synthetic enzymes such as ACAA1 (Figure 1B), FADS1 (Figure 1C) and ACOX1 (Figure 1D). Furthermore, *in vitro* experiments showed that the expression of the aggregation prone TDP-43 carboxy-terminal fragments(CTF)(18) leads to a significantly diminished expression of FADS2 (p<0,008 ANOVA between groups, Figure 1E), specially evident in those fragments with higher tendency to aggregate, such as CTF 274-414, thought it was also present in the other CTF (data not shown).

TDP-43 aggregation decreases the expression of the DHA-dependent synaptic protein drebrin, whose levels are low in spinal cord from sALS patients.

DHA is functionally linked to synaptic proteins, such as drebrin and syntaxin-3, as the expression of those proteins is directly related to DHA concentration (2, 3). In line with TDP-43 aggregation potentially interfering with DHA availability, overexpression of aggregation prone TDP-43 CTF (shown for CTF 218-414) induces a significant decrease in drebrin expression (p<0.05), but not in syntaxin-3 (Figure 2A and 2B). Reinforcing the validity of these *in vitro* approaches, western-blot analyses confirmed decreased contents of drebrin in spinal cord from sALS patients, while brain cortex did not show these changes (Figure 2C and 2E), in line with higher DHA content in this later location. Interestingly, this is not linked to direct loss of drebrin in motor neurons, since those showing TDP-43 aggregates do not appear to have decreased drebrin expression (Figure 2D). This would agree with other cells (non motor neurons) having decreased drebrin levels. Thus, while single cell type cell culture demonstrated that TDP-43 aggregation is linked to drebrin depletion, *in vivo* measurements suggest that other cells could help motor neurons to maintain homeostatic drebrin amounts, stressing the importance of intercellular relationships in spinal cord.

Chronic excitotoxicity leads to changes in whole lipidome and fatty acid profiles in lumbar spinal cord, compatible with increased DHA synthesis, associated to mitochondrial dysfunction and lipid peroxidation.

Chronic excitotoxicity in lumbar spinal cord slices is considered a model of slow neurotoxicity with similar features as sALS pathogenesis (19). Since we wanted to evaluate in a tissue paradigm (i.e. with capacity to reproduce intercellular relationships) the potential involvement of DHA changes in motor neuron demise, we evaluated some of the above mentioned parameters. Drebrin distribution, but not global content –in contrast with sALS-, was significantly altered in chronic excitotoxicity (Supplemental Figure 1). Furthermore, increased syntaxin-3 levels suggested increased DHA levels, a fact that was confirmed by fatty acid compositional analyses (Figure 3A), with a selective decrease of the DHA precursor DPA from ω3 family (without variations in the equivalent of the ω6 family). Estimation of desaturase activities showed that DHA synthesis is the most sensitive pathway of fatty acid synthesis under this chronic excitotoxicity model (Supplemental Figure 1). Therefore, chronic excitotoxicity could lead to a depletion of DHA ω3 precursors. To evaluate whether chronic excitotoxicity could lead to a depletion of DHA ω3 precursors we examined whether exogenously ω3 precursors (linseed fatty acids, LSFA) could enhance motor neuron survival in this model in comparison with final products (added as fish fatty acids, fFA). The results show that the presence of LSFA enhanced motor neuron survival and expression of motor neuron neurofilament markers in ventral horn of the spinal cord organotypic cultures, in comparison with fFA (Figure 3B and 3C).

To ascertain if these changes affected a particular lipid specie, the effects of chronic excitotoxicity on the lipidomic profile of lumbar spinal cord organotypic culture were studied. The detected changes (Figure 3D) mainly included decreased contents of specific lipids belonging to phosphatidyl-ethanolamine and phosphatidyl-serine families (Supplemental Table 1). Levels of specific ceramides and other quantitatively minor lipids were

681 also down-regulated. Nevertheless, the global profile did not
682 show a high number of differentiating molecules (144 differential
683 molecules between control and THA-treated samples, in a total
684 of 17832 molecular features, e.g. less than 1% of total lipids).

685 Since DHA is a precursor of the resolvin family of neuropro-
686 tective molecules we evaluated whether increased DHA would
687 sustain increased resolvin concentration. The results show that
688 levels of a lipid specie with mass compatible with the neuro-
689 protective DHA-derived resolvin D1 were increased in chronic
690 excitotoxicity treatment with THA (Figure 3E). This could suggest
691 that increased DHA synthesis in chronic excitotoxicity could be
692 part of a neuroprotector adaptive mechanism. However, in this
693 model PUFA content increased could also increase lipid perox-
694 idizability because double bonds in aliphatic chain confers high
695 susceptibility to peroxidation. Confirming this, the concentration
696 of the lipid peroxidation intermediate isoprostane 8-iso-PGF2 α
697 was increased in chronic excitotoxic conditions (Figure 3F), and
698 it correlated significantly with resolvin D1 levels (Figure 3G).
699 Other lipid peroxidation products -indicated in the Experimental
700 Methods section- did not increase or were detected (data not
701 shown), suggesting specificity of those oxidative changes.

702 Given this increased lipid peroxidation, we searched for po-
703 tential causes of it. The results (Figure 3H) demonstrate that
704 chronic excitotoxicity leads to a significant loss of oxygen con-
705 sumption (*ca* 30%). This is caused by a selective loss in mito-
706 chondrial complex I activity (Figure 3H), as they were completely
707 abrogated by rotenone. Thus, potential protective effects of DHA
708 could be limited by potentially enhanced free radical production,
709 compromising the availability of lipophilic antioxidants. There-
710 fore, we tested if a lipophilic antioxidant-DHA combination could
711 prevent motor neuron loss induced by chronic excitotoxicity. The
712 results demonstrated that a DHA- α -tocopherol combination (but
713 not DHA alone -data not shown-) prevents chronic excitotoxicity-
714 induced loss of motor neurons (Figure 3I).

715 All in all, these results suggest that spinal cord responses
716 to chronic excitotoxicity comprise increased DHA content, sus-
717 tained by an enhanced desaturase expression leading to increases
718 in DHA derived neuroprotective factors, linked to loss of drebrin
719 amount and distribution as well as to specific increases in lipox-
720 idation likely fuelled by a complex I related mitochondrial dys-
721 function.

722 *DHA synthesis at a cellular level is upregulated by oxidative stress*
723 *and its neuroprotective role is enhanced by exogenous antioxidants.*

724 The above mentioned results are compatible with DHA syn-
725 thesis being upregulated as a response to oxidative stress induced
726 by a chronic excitotoxicity-derived mitochondrial decay. To test
727 this, we evaluated whether DHA synthesis and drebrin expres-
728 sion were influenced by H₂O₂, a signal derived from complex I
729 dysfunction (20). H₂O₂ incubation increased significantly levels of
730 FADS2 (in accordance to the above described changes in spinal
731 cord ALS samples) and SCP2 (Figure 4A). Synthesis of DHA
732 was evaluated by metabolic flux experiments by measuring the
733 conversion from exogenously added *d*₁₄ALA to *d*₅DHA (Figure
734 4B). The results suggest that there is an almost significant ten-
735 dency for increased DHA synthesis (Figure 4C). This enhanced
736 DHA production could be a response to compromised DHA
737 availability.

738 To demonstrate this, we evidenced an early TDP-43 phospho-
739 rylation after H₂O₂ challenge, preceding drebrin loss in N2A
740 cells (Figure 4D and 4E). Globally, after interactomic analyses,
741 few nodes separate TDP-43 from drebrin, confirming the feasi-
742 bility of the proposed hypothesis (Figure 4F).

743 To extend these findings to other cellular systems, we stud-
744 ied the effects of exogenously added DHA or other fatty acids
745 in the loss of viability in the motor neuron like line NSC-34.
746 Cell death induced by H₂O₂ was prevented significantly by the
747 use of p-HPEA-EDA and hydroxytyrosol (natural hydrophilic

749 antioxidants of hydrophilic nature present in virgin olive oil) in
750 the presence of DHA and LSFAs, in contrast with α -tocopherol
751 (Figure 4G).

752 *ALS leads to significant changes in the levels of enzymes for*
753 *DHA synthesis in spinal cord and brain cortex.*

754 These results pointed out that increased expression of several
755 enzymes for DHA synthesis can be a response to oxidative stress.
756 Based on previous findings of oxidative damage in ALS samples,
757 we analyzed the tissular concentration of enzymes responsible for
758 DHA synthesis. The results (Figure 5A) showed that in spinal
759 cord the enzymes related to β -oxidation acetyl CoA acyltrans-
760 ferase 1 and 2 (ACAA1 and ACAA2) as well as those related to
761 early steps of desaturation -FADS2- were all increased in spinal
762 cords from sALS samples, perhaps as a compensation for motor-
763 neuron dysfunction of FADS2 (Figure 1A). In contrast, SCP2
764 levels were decreased. In brain cortex, significant increases were
765 only seen for ACAA1 (Figure 5B). This increase could provide
766 the biochemical basis for increased amounts of DHA present in
767 brain cortex (14).

768 Globally, these results suggest that in sALS, neuronal re-
769 sponses to oxidative challenge comprise increased expression of
770 DHA synthesis enzymes, preceded by TDP-43 dysfunction and
771 drebrin loss. Furthermore, they also show that motor neuron
772 survival is dependent on the interaction of both motor neuron and
773 surrounding cells with fatty acid sources, with preference of DHA
774 and its precursors, and that phenolic antioxidants could enhance
775 these beneficial properties.

776 Discussion

777 The results presented here evidence an important role of the
778 interaction between PUFA synthesis, TDP-43, antioxidants and
779 motor neuron disease. Thus, despite increased machinery for
780 DHA synthesis in spinal cord, apparently it is not able to fully
781 supply increasing needs of this important PUFA (based on data in
782 drebrin) in sALS samples. The resulting increased PUFA amount
783 (non-DHA) could serve as a substrate to lipid peroxidation (un-
784 der stress conditions). In this sense, data from our own group
785 and others show increased lipid peroxidation in several neurode-
786 generative diseases, including Alzheimer's disease, Parkinson's
787 disease, Creutzfeldt-Jacobs disease, Pick's disease and ALS (21).
788 In this work it is demonstrated that the organotypic spinal cord
789 culture, when affected by chronic excitotoxicity induced by the
790 glutamate uptake inhibitor THA, shows increased DHA concen-
791 trations and reduced arachidonic acid levels concurrent to motor
792 neuron loss. Further, we show that neuronal cell lines respond
793 to oxidative stress by increasing DHA synthesis, a fact that will
794 be focus of future studies. This result may be interpreted as a
795 general response to neuron insult, as DHA is precursor of the
796 potent resolvins and neuroprotectins implicated in the defence
797 towards inflammation and oxidative damage (22). Present data
798 show that TDP-43 phosphorylation, a consequence of oxidative
799 stress, precedes drebrin loss and overexpression of DHA syn-
800 thetic enzymes. It is known that drebrin shows an inverse rela-
801 tionship with oxidative damage (23). Further, drebrin interacting
802 proteins, such as Homer, are altered by oxidative stress, thereby
803 potentially compromising drebrin function (24). Other data show
804 that drebrin is phosphorylated by Cdk5 (25). Though other ki-
805 nases may be quantitatively more important in TDP-43 phospho-
806 rylation (26), Cdk5 colocalizes with TDP-43 in granulovacuolar
807 degeneration (27), suggesting that perhaps oxidative-stress driven
808 Cdk5 activation (28) could impact both in drebrin and TDP-43
809 functions. In fact, the most sensitive enzyme to oxidative stress
810 in N2A cells, SCP2, is the one that shows significant decreases
811 in spinal cord. This suggests that peroxisomal function may be
812 impaired in sALS, as previously indicated in transgenic models
813 (29). The peroxisome-ALS connection is also suggested by the
814 positive effects of some drugs in the peroxisomal proliferator
815

agonist receptor family (30, 31) in these models, though these are challenged by negative results in clinical trials (32).

In mammals, the synthesis of DHA is a complex pathway, depending, among other, on the levels of the ω 3 linolenic acid precursor, its conversion to eicosapentaenoic acid (EPA) (ω 3), through elongases and desaturases. Later on, EPA(ω 3) is elongated twice, leading to the ω 3 24:5 and, via peroxisomal β -oxidation, to DHA(4). The evaluation of elongase and desaturase ratios -even accounting them only as estimative indexes- suggests that earlier steps from ALA to EPA (ω 3) are diminished in the excitotoxic model. The best hypothesis explaining the low levels of linolenic acid and EPA (ω 3) are the marked increase of enzymes of the later steps (those involving elongation and beta oxidation), which coincide with increased FADS2 and ACAA1,2 expression in ALS samples. This phenomenon may explain the protective role of L-carnitine (33) in ALS models. Thus, besides mitochondrial β -oxidation, L-carnitine is a cofactor needed for peroxisomal β -oxidation (34). All in all, our results demonstrating that both enzymes in peroxisomal and mitochondrial β -oxidation (ACAA1 and ACAA2) are increased in samples from ALS patients disclose a novel pathogenic pathway. Furthermore, the fact that mitochondrial (ACAA2) form is affected is in line of previously reported (14) and present findings showing mitochondrial impairment in ALS. Noteworthy, the fact that several steps of PUFA synthesis depend on enzymes located in endoplasmic reticulum and mitochondria, and the findings reported (present work and(14)) showing that those organelles are affected in ALS are not casual findings. These data support the hypothesis that endoplasmic reticulum and mitochondrial disturbances present in ALS could also impinge PUFA syntheses in nervous tissue.

In this sense, it has been suggested that, in neurons, Δ 6 desaturation (mainly performed by *fads2*) may be the rate-limiting step for conversion from ALA to DHA(35). Despite it has been implicated in the pathogenesis of several psychiatric diseases(36, 37), no previous link between FADS2 and motor neuron disease was present. Interestingly, *in vitro* treatment of hippocampal cells with brain derived growth factor (a protective agent in several ALS models, reviewed in(38)) is able to increase *fads2* expression (39). Most importantly, data presented here suggest a hitherto unreported relationship between PUFA synthesis and ALS, again pointing to *fads2* as a novel player in the pathogenesis. Our data demonstrating specific increases in this desaturation key enzyme (both *in vitro* and *in vivo*) disclose a novel target of this disease validating the usefulness of organotypic spinal cord culture as a tool for pathogenic exploration of ALS molecular mechanisms.

Decreased indexes of ω 6 family may be explained by a limit in common desaturase cofactors or a selective balance towards ω 3 synthesis. It is known that in spinal cord injury models, while ω 3 fatty acids (ALA and DHA) have protecting roles, through antioxidant and anti-inflammatory activities, ω 6 AA acts in reverse way, worsening the outcome(40). Further, AA downregulate glutamate transporters *in vitro*(41), so decreased ω 6 family synthesis may be a compensative response. Concerning the source of increased DHA in organotypic culture, despite it has been recently shown that hippocampal neurons *in vitro* could produce DHA from ALA(42), it may be a minor source when compared to circulating DHA produced by liver or the transference from glial cells. In this sense, *in vitro* data showed that astrocytes have a larger capacity for producing DHA and AA from their precursors (43, 44) than neurons. Data shown here evidence that isolated motor neuron-like cells behave slight different compared with whole organotypic slices, suggest that glial-neuron interaction in fatty acid metabolism could play a significant role in ALS lipid dearrangements.

The increased survival of motor neurons in spinal cord slices offered by LSFA, in front of pure DHA and fFA suggest that the introduction of precursors, rather than the final form of

PUFA, could be an interesting therapeutic tool. In this line, recent data stresses the important neurophysiological differences between DHA and ALA(45). Our data, showing that drebrin was a common target in sALS and in chronic excitotoxicity, reinforce the importance of DHA-dependent processes in the pathogenesis of sALS. In this sense, it has been described that the lack of function of TDP-43, implicated in sALS, induces changes in a specific microRNA (*let-7b*), leading to impaired syntaxin-3 expression(46). Present findings, reporting cells with TDP-43 aggregations show also abnormal FADS2 immunostaining, support the notion of a pathogenically relevant interplay between TDP-43 and DHA-related processes, reinforced by findings with neuronal cell lines where TDP-43 pathological events (increased phosphorylation and cytosolic aggregation induced by H_2O_2) precede changes in PUFA synthesis and drebrin depletion. Previous data have shown that lipid peroxidation derived 15-deoxy- δ (12,14)-prostaglandin J(2) is able to reproduce TDP-43 pathological findings(47), but no relationship between TDP-43 and fatty acid synthesis has been previously reported. On the other hand, ALA shares biological targets with riluzole, one of the few accepted treatments for excitotoxicity (reviewed in (48)). It is known that ALA and riluzole act on the 2P domain of the K channel family TREK/TRAAK(49), and that this common action could explain reduction of cytopathological treats of neuronal demise in focal ischemia models. It is also known that ALA is able to prevent neuronal cell death, Bax expression and, interestingly, increased chaperone protection exclusively in motor neurons in an ischemia model of the spinal cord, preventing necrosis and apoptosis, adding evidence to the previously described neuroprotective action of ALA(50, 51).

It can not be neglected that perhaps DHA -in contrast to LSFA- is oxidized in chronic excitotoxicity conditions, contributing to loss of viability. The protective role of α -tocopherol, and its influence in mitochondrial function, supports this hypothesis. It has been previously demonstrated that DHA prevents neuronal cell death by decreasing responses to reactive oxygen species, increasing antiapoptotic protein expression and maintaining mitochondrial integrity and function(52). These results go in line with our data about increased expression of AIF in our samples (data not shown). On the other hand, DHA has been used with promising outcomes in models of spinal cord injury, where the inflammatory component is a clear mechanism of pathogenesis(53).

Despite mitochondrial (dys)-function has been previously invoked in ALS and ALS models, this is among the first direct evidences of loss of O_2 consumption by chronic excitotoxicity in lumbar spinal cords. Previous data ref? showing increased lipid peroxidation in this model, together with the preventive role of α -tocopherol, fully supports the hypothesis that chronic excitotoxicity leads, through loss of mitochondrial respiration, to motor neuron demise. Of note, it should be reminded that mitochondrial respiration is very sensitive to lipid peroxidation(54). The presented results are in line with previous data, suggesting that supplementation of DHA with α -tocopherol may be needed to conserve cellular bioenergetics into homeostasis(55) specially in neuronal tissues. Nevertheless, the lack of protective function of α -tocopherol towards oxidative stress induced demise in the motor-neuron like cells demonstrate the complexity of chronic excitotoxicity. Obviously, it may be argued whether H_2O_2 reproduces features of chronic excitotoxicity that may be prevented by antioxidant functions (e.g. mitochondrial anti-apoptotic (56)) of α -tocopherol in the organotypic culture. Similarly, α -tocopherol antioxidant potential is lower than that of other, structurally related, lipophilic antioxidants, such as γ -tocopherol or the tocotrienolic compounds (57). A straightforward interpretation may be that the interplay between glia and motor neurons plays a key role in the protection of α -tocopherol. In this line, it has been previously demonstrated that both α -tocopherol and γ -

953 tocopherol inhibit oxidative and inflammatory responses in excitotoxicity, leading to diminished oxidative damage in the model
954 of intracerebroventricular injection of kainate *in vivo*, with a clear
955 interaction of glial cells (58). Interestingly, it has been described
956 that preservation of mitochondrial function by α -tocopherol may
957 enhance glutamate transport in an experimental stroke model
958 (59).

960 It should be remarked that, in contrast to α -tocopherol, other
961 antioxidants, such as hydroxytyrosol and p-HPEA-EDA act, in a
962 fatty acid dependent fashion, as protective factors in the H_2O_2
963 induced loss of viability in NSC-34. These phenols, present in
964 virgin olive oil phenolic fraction, have pleiotropic functions. They
965 act as anti-inflammatory, antioxidants, anti-proliferative agents,
966 through their interaction with still poorly unknown receptors.
967 Interestingly, it has been recently shown that hydroxytyrosol acts
968 *in vivo*, preventing lipid peroxidation and glutathione depletion
969 in brain induced by the neurotoxic drug 3-nitropropionate (60).
970 Previous data revealed that, in different neuronal cell lines, hydroxytyrosol confers cytoprotection in a mechanism related to fatty acid uptake (61).

973 Globally, these results show that upregulation of DHA levels,
974 initially a compensatory response, could contribute to increased
975 peroxidizability and consequently to damage spreading. It is also
976 shown that DHA and other PUFA, when adequately protected
977 from lipid peroxidation by other dietary available compounds (α -
978 tocopherol or hydrophilic antioxidant polyphenols), could offer
979 neuroprotection in chronic excitotoxicity. Further work is needed
980 to evaluate its potential effect *in vivo*, but the present results may
981 help to define the potential of neuroprotective diets based on adequate combinations of PUFA and selected phenolic antioxidants.

982 Materials and methods

983 Patient samples

984 Samples were from ten ALS cases and eight controls (see supplemental Table 2 for demographic characteristics). The post-mortem delay was between 2 and 16 h 30 min and did not differ between the groups. The brain and spinal cord were rapidly removed. Half of the brain and alternate sections of the brain stem and spinal cord were immersed in 4% buffered formalin for four weeks and then selected samples from 40 different areas embedded and paraffin and processed for current diagnostic neuropathological studies or stored until use. Selected samples of the other half of the brain, alternate sections of the brain stem and spinal cord were rapidly frozen on dry ice, kept on individual tag plastic bags and stored at -80°C until use. All samples were obtained from the Institute of Neuropathology brain bank, a branch of the HUB-ICO-IDIBELL biobank, following the guidelines of the local ethics committees. Extensive pathological studies were done for ALS diagnosis as previously described (14, 62). Sample obtention and experiments have been carried out in accordance with The Code of Ethics of the World Medical Association (Declaration of Helsinki).

988 Reagents

989 All reagents, unless stated otherwise, were purchased from Sigma-Aldrich Chemical Co. 2-(3,4-dihydroxyphenyl) ethyl alcohol (hydroxytyrosol) from Extrasynthese (Genay, France) and 4-formyl-3-(2-oxoethyl) 2-(4-hydroxyphenyl) ethyl ester (p-HPEA-EDA) was isolated from virgin olive oil phenolic extract by semi-preparative HPLC method according to the method of Artajo et al. (63). Stock solutions of commercial standards and phenolic compounds isolated from virgin olive oil were dissolved in MeOH/ H_2O (80:20 v/v) and stored at -40°C before the incubation. Commercially available, fatty acid extracts Ecoflax Omega 3^r from linseed (LSFA), and Biomegatech fish^r, from fish (fFA) were obtained from BTSa (Madrid, Spain). Both DHA or fatty acid extracts were used at a final concentration of 100 μM in culture media (either organotypic or cell culture media). Fatty acid composition from LSFA was α -linolenic acid 60%, oleic acid 23%, linoleic acid 12%, stearic acid 2% and palmitic acid 2%, and from fFA was eicosapentaenoic 60% and docosahexaenoic 40%. Peroxide index values of these products were below detectable limits.

1002 Immunohistochemistry and western-blot

1003 Immunohistochemistry (IF) and western blot (IB) analyses were performed and quantified as previously described (14, 62). Antibodies used for evaluation of enzymatic system for DHA synthesis by IB were: peroxisomal acyl-coenzyme A oxidase 1 (ACOX1, Abcam ab599964, 1:300), Acetyl CoA acyltransferase 1 (ACAA1, Abcam ab84635, 1:1000); Acetyl CoA acyltransferase 2 (ACAA2, Abcam ab58278, 1:1000); Fatty acid desaturase 1 (FADS1, Abcam ab124363, 1:300), Fatty acid desaturase 2 (FADS2, Abcam ab72189, IB 1:1000); Sterol carrier protein 2 (SCP2, Abcam ab 93175, 1:200), Peroxisomal multifunctional enzyme 2 (MFE2, Abcam ab97971, 1:500) and actin (Sigma a5441, 1:5000) for normalization of protein load. Other antibodies used were

SMI-32 (Covance Inc., Princeton, NJ, USA) (IF at 1:200 dilution; IB at 1:1000 dilution), drebrin (Abcam Plc, Cambridge, UK; ab12350, IF, 1:100), syntaxin-3 (Abcam ab4113, IF, 1:50), neurofilament (Abcam, ab 72997, IF 1:200), TDP-43 (Abcam, ab 545002, IF 1:2000), phospho-TDP-43 (Cosmobio Ltd, Carlsbad, CA, USA, Tip PTD.P05, IF 1:250 or Millipore P-TDP-43 (Ser409/Ser410), clone 1D3 (MABN14), IB 1:1000) and neuronal specific tubulin antibodies (Abcam ab18207, IF, 1:200; IB 1:1000).

Immunoreactivity images were analyzed with the Image J software. For area distribution of immunoreactive anti-drebrin particles, images were binary converted and analyzed with the particle analyses algorithm of the software (<http://rsbweb.nih.gov/ij/>), in a double blinded fashion. Distributional analyses of the particle areas was produced using the Prism 5 software (Graphpad Software, La Jolla, CA, USA).

Neuro2a (N2A), motor-neuron like (NSC34) cell and spinal cord organotypic culture

Oxidative stress has been recently related to TDP-43 pathology in ALS [17]. Thus, to study the potential link with DHA synthesis pathway in this condition, Neuro 2A (N2A) cells were incubated with 10 μM H_2O_2 for 2 h as previously described (62). TDP-43 plasmids and C-terminal fragments were obtained as indicated (18). Neuro 2A cells were transiently transfected with the empty pEGFP-C1 vector (GFP) or vector expressing the wild type (WT) human TDP-43 cDNA (1-414) or C-terminal fragments 162-414 (162), 218-414 (218) and 274-414 (274) using Lipofectamine-2000 Reagent (Invitrogen-11668) according to the manufacturer's instructions for 24 hours (depending on the experiment). Under these experimental conditions, the efficiency of transfection with pEGFP-C1 vector was ca 80%.

Spinal cord cultures were prepared from lumbar spinal cord of postnatal day 8 rat pups as previously indicated and maintained in culture media. Ten days after plating, to induce excitotoxicity the slices were incubated with the glutamate transport inhibitor D,L-threo-hydroxyaspartate (THA) (Sigma, St. Louis, MO, USA) at 100 μM , inducing a selective motor neuron death after 3 weeks (19). Experiments for each condition (n=30 slices per experimental group) were repeated at least three times. All animal experiments were approved by the Institutional Animal Care and Experimentation Committee, and followed EU Directive 2010/63/EU for animal experiments.

To analyse the potential neuroprotective role of antioxidants supplementation in combination of DHA in a cellular stress situation able to promote the ALS development, NSC-34 cells were incubated with fatty acids (as above) and antioxidants (α -tocopherol, hydroxytyrosol or p-HPEA-EDA) at final concentrations 100 μM , 25 μM and 5 μM , respectively) were added 48 hours before incubation with 10 μM H_2O_2 for 2 hours. Cell viability was evaluated 8 hours after with the 3-(4,5-Dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide test (MTT test, Sigma) according manufacturer instructions.

1056 Lipid analyses

Fatty acid profiles were established after whole lipid transesterification and gas chromatography analysis of methyl esters performed as previously described (64). The following indexes were calculated from the fatty acid composition: $\Delta^9 18:1/18:0$ ratio between C18:1(n-9) and C18:0 % contents; $\Delta^9 16:1/16:0$ ratio between C16:1 (n-9) and C16:0 % contents; $\Delta^2 20:4/20:3$ ratio between C20:4 (n-6,9,12,15) and C20:3 (n-6,9,12) % contents; 18:1/16:1 Elongase from ratio between C18:1(n-9) and C16:1 (n-9) % contents; and 22:4/20:4 Elongase from ratio between C22:4(n-6,9,12,15) and C20:4(n-6,9,12,15) as previously described (65).

For LC-Q-TOF-based lipid molecular species analyses, lipid extracts were subjected to mass-spectrometry using a HPLC 1200 series coupled to an electrospray-Q-TOF MS/MS 6520 (Agilent Technologies, Barcelona, Spain), using a reverse phase column and a methanol:water to 1-propanol:hexane:water gradient, following the method described in (67). Lipid class representative internal standards were added to the samples and after analyses; ionized lipids were processed for targeted and untargeted analyses. Briefly, the MassHunter Mass Profiler Professional Software (Agilent Technologies, Barcelona, Spain) was used to perform a non-targeted lipidomic analysis over the extracted features. Only common features (found in at least 75% of the samples of the same condition) were taken into account to correct for individual bias. Principal component analyses (PCA) was obtained using this software. The masses representing significant differences by Student T-test (fold change ≥ 2 , $p < 0.05$) were searched against the METLIN (metlin.scripps.edu), HMDB (www.hmdb.ca), LIPID MAPS (www.lipidmaps.org) and KEGG (www.genome.jp/kegg/) databases. Targeted lipidomic analysis was performed using the same chromatographic and spectrometric method as untargeted approach. MassHunter Qualitative Analysis Software (Agilent Technologies, Barcelona, Spain) was employed for integration and extraction of peak intensities of the different lipidic species. We looked for the following free fatty acids: docosahexaenoic acid, oleic acid, linolenic acid, stearic acid, arachidonic acid, lauric acid, palmitic acid, capric acid, myristic acid, palmitoleic acid and stearidonic acid. The m/z values used for quantification were: m/z 245.2486 [M-H]⁻ for oleic acid, m/z 283.2643 [M-H]⁻ for stearic acid, m/z 255.233 [M-H]⁻ for palmitic acid, m/z 227.2017 [M-H]⁻ for myristic acid and m/z 253.2173 [M-H]⁻ for palmitoleic acid. We detected no differences induced by chronic excitotoxicity in those fatty acids. The following lipids were also searched: 10-hydroxy-docosahexaenoic, 17-hydroxy-docosahexaenoic, 8-iso-PGF₂ α , 13-hydroxyoctadecadienoic acid (HODE), 9-HODE, HODE-cholesteryl

1089 ester, 1-palmitoyl-2-arachidonoyl-3-glycerophosphocholine, 1-palmitoyl-
1090 2-linoleyl-3-glycerophosphocholine, cholesterol, 4-hydroxynonenal,
1091 10-nitrooleate, cholesterol-5 α ,6 α -epoxide, 5-cholesten-3 β -ol-7-one, 7 β -
1092 hydroxycholesterol, resolving D1, cholesteryl linoleate hydroperoxide,
cholesteryl linoleate. The m/z values used for quantification were: m/z
1093 355.2479 [M+H]⁺ for 8-isoprostaglandin F2 α and m/z 377.2323 for resolvin
1094 D1. For d14 labelled linolenic acid (C18H16D14O2) and d5 labelled DHA
1095 (C22H27D5O2) the "Find by formula" (Agilent) algorithm was used.

Oxygen consumption

1096 Oxygen flux of sets of 5 slices of organotypic spinal cord cultures was
1097 measured at 37 °C in Hank's balanced salt solution with 20 mM Hepes
1098 (pH 7.4) by high-resolution respirometry using the Oroboros® Oxygraph-
1099 2k with chamber volumes set at 2 mL and at a slow stirring speed (150
1100 rpm) in order to avoid tissue disaggregation. DatLab software (Oroboros
1101 Instruments, Innsbruck, Austria) was used for data acquisition (2 s time
1102 intervals) and analysis, which includes calculation of the time derivative of
1103 oxygen concentration and correction for instrumental background oxygen
1104 flux (68). The experimental regime consisted of routine respiration, which is
1105 defined as respiration in cell-culture medium without additional substrates
1106 or effectors, and calculated as Steady-state respiratory flux in the time
1107 interval between 5 and 10 min after closing the chamber. In order to avoid
1108 oxygen limitations, all the experiments were performed above 50% oxygen
1109 saturation. Oxygen consumption was normalized by actual protein content in
the respirometer chambers and mitochondrial inhibitors were added as
described (68).

DHA synthesis flux experiments

1110 For evaluation of potential DHA synthesis under cell stress, N2A cells
1111 were seeded onto 6-well plates and grown in Advanced minimum essential
1112 media supplemented with 10% fetal bovine serum until 1 day postconflu-
1113 ence, the point at which fatty acid changes are maximized(69). Then, cells
1114 were incubated with medium containing 4.1 μ M d₁₄ labelled ALA (Cayman
1115 Chemical Company, 0000433) for 4 hours. After that, the medium was
1116 removed and cells were treated with H₂O₂ 10 μ M for 2 hours. Cells were
1117 washed and harvested in PBS using a cell scraper. Lipid extraction was carried
1118 out as described(70). Cells were pelleted by centrifugation (700 g, 4 °C, 5

1157 min) and dissolved in chloroform-methanol (2:1, v/v). They were incubated
1158 on ice for 10 min, vortexed, and centrifuged (1100 g, 4°C, 10 min). The lower
1159 organic phase was transferred to a new glass tube and dried completely
1160 under nitrogen, RT. Later, the fatty acid saponification was carried out by
1161 incubating lipid extracts in 2.5N KOH/MetOH (1/4, v/v) for 15 min at 72 °C
1162 in a heating block, as indicated (71). The pH of the solution was acidified
1163 with one-eighth of the volume of formic acid. The free fatty acids were then
1164 extracted with an equal volume of chloroform and after drying, extracts
1165 were reconstituted in chloroform and stored at -20°C until ready for LC-Q-
TOF analysis. Levels of d₁₄ labelled ALA, d₅ labelled DHA and oleic acid (used
for normalization) were quantified as indicated above.

Statistical and bioinformatical analysis

1166 All statistics were performed using the SPSS software (SPSS Inc., Chicago,
1167 IL, USA). Differences between groups were analyzed by the Student's
1168 t tests, One way and Two way ANOVA analyses, with post-hoc analy-
1169 ses, once normality of variables was tested by Kolmogorov-Smirnov test.
1170 The 0.05 level was selected as the point of minimal statistical signifi-
1171 cance in every comparison. For interatomic analyses, we selected as input
1172 nodes the genes *tardbp* and *dbnl*, and we used the GeneMANIA software
(<http://www.genemania.org>).

Acknowledgements.

1173 We are indebted to tissue donors and their families. We are grateful for
1174 the consortium of companies led by La Morella Nuts (Reus, Catalonia, Spain)
1175 with the following companies: BTSA, Selecció Batallé, Industrial Tècnica
1176 Pecuaría, Neuron BioPharma, Shirota Functional Foods, Grupo Leche Pascual,
1177 and Innaves. Supported by the Seventh Framework Programme of the
1178 European Commission, grant agreement 278486: DEVELAGE; by the Spanish
1179 Ministry of Science and Innovation [CENIT program, BFU2009-11879/BFI and
1180 AGL2006-1243] the Autonomous Government of Catalunya [2014SGR168] and
1181 the Spanish Ministry of Health [PI08/1843, 11/01532 and 13/00584]. DC is a
1182 predoctoral fellow from Spanish Ministry of Health [FI08-00707]. OR-N and
1183 RC are predoctoral fellows from the Autonomous Government of Catalonia.
1184 Supported also by the COST B-35 Action and the Fundació Miquel Valls.

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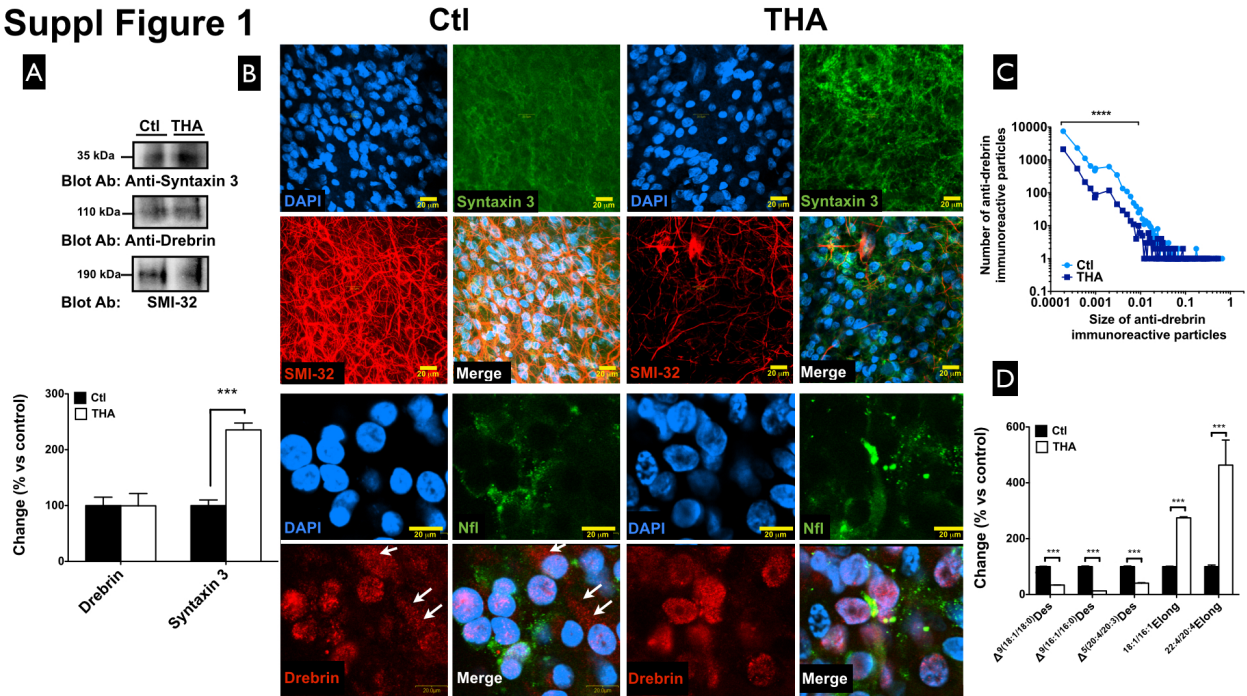
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Supplemental Figure 1

A) Representative western blot analyses reveal that chronic excitotoxicity leads to increased amount of syntaxin-3, but no major changes in drebrin amount, as quantified in the lower panel. B) Confocal microscopy revealed that chronic excitotoxicity induced increased syntaxin-3 immunoreactivity (green upper panels) concurrent with diminished SMI-32 immunoreactivity (red, upper panels). This was associated to a loss of drebrin compartmentalization (green, lower panels) since in control conditions anti-drebrin immunohistochemistry was distributed into several sizes with small granular-like particles (arrow), without apparent relationship with neurofilament marker (Nfl, green). C) The number of smaller particles was much lower in THA-treated spinal cord slices, compatible with a loss of drebrin compartmentalization. D) Estimation of desaturase and elongase activities in these samples suggest important changes in $\delta 9$, $\delta 5$ and elongase activities, according the ratios between products and precursors. Lower panels in A and D show the densitometric analyses of the above western-blots. Numbers in the left of blots show the approximate molecular weight. *** $p < 0,0001$ and **** $p < 0,00001$ between Ctl and THA-treated organotypic cultures (bars show means \pm S.E.M. for $n=11-15$ slices in each condition) by Student's t test.

Suppl Figure 1



Supplemental Table 1

Classification (Lipid Maps)	Compound	Regulation respect Ctl (at least $p < 0.05$ by Student's T test)
Glycerophospholipids	PS(16:0/18:1)	down
	PS(17:0/20:4)	down
	PS(18:2/18:0)/ PS(18:1/18:1)	down
	PS(21:0/22:6)	down
	PE(36:1)/PENMe2(44:1)	down
	PE(41:0)	down
	PE(18:2/18:2)	down
	PE(38:0)/PENMe2(36:0)	down
	PE(38:1)	down
	PE(38:2)/PENMe(36:2)	down
	PE(36:0)	down
	PE(39:0)	down
	PE(44:1)	down
	PE(44:0)	down
	PE(43:0)	down
	PE(O-38:5)	down
	PENMe(32:0)/PE(33:0)	down
	PENMe(16:0/18:1)	down
	PENMe(34:0)/PE (36:0)	down
	PG(17:0/20:4)	down
	PG(18:1/18:1)	down
PI(16:0/18:1)	down	
Sphingolipids	Cer (d18:1/20:0)	down
	Cer(d18:1/22:0)	down
	Cer(d18:1/24:1)	down
	GlcCer (d18:1/25:0)	down
	GlcCer(d18:1/26:0)	down
	GlcCer(d18:1/20:0)	down
	GlcCer(d18:1/22:0)	down
	GlcCer(d18:1/24:0)	down
	GlcCer(d18:1/18:0)	down
	GlcCer(d18:1/24:1)	down
	LacCer (d18:1/20:0)	down
	LacCer(d18:1/24:0)	down
	SM(d18:1/24:0)	down
	SM(d18:1/25:0)	down
	C18 Sulfatide	down
	C20 Sulfatide	down
	C22 Sulfatide	down
	C24 Sulfatide	down
	C22-OH Sulfatide	down
	Ganglioside GM3 (d18:1/24:1)	down
	Trihexosylceramide (d18:1/26:1)	down

Supplemental Table 2. Demographic characteristics of patients studied

Diagnostic	Gender	Age	Post-mortem delay
ALS	F	79	2h 10 min
ALS	F	75	4h
ALS	M	57	4h
ALS	M	64	16h 30 min
ALS	F	76	13 h
ALS	M	76	12h 40m
ALS	M	54	4h 50min
ALS	F	59	14h 15m
ALS	M	71	8h 45m
ALS	F	65	4h 10 min
Control	F	75	6h 10 min
Control	M	76	6h 30 min
Control	M	70	2 h
Control	F	82	3h 5 min
Control	M	76	6h 30min
Control	M	75	3h 25min
Control	M	64	8h 35m
Control	M	68	10h 55 min



4.3 Article 3

Title: “Dietary Lipid Unsaturation Influences Survival and Oxidative Modifications of an Amyotrophic Lateral Sclerosis Model in a Gender-Specific Manner”.

Authors: Cacabelos D, Ayala V, Ramírez-Núñez O, Granado-Serrano AB, Boada J, Serrano JC, Cabré R, Nadal-Rey G, Bellmunt MJ, Ferrer I, Pamplona R, Portero-Otin M.

Journal: Neuromolecular Medicine, 2014 Jul 1.

Received: 1 January 2014 / Accepted: 20 June 2014.

DOI 10.1007/s12017-014-8317-7

Dietary Lipid Unsaturation Influences Survival and Oxidative Modifications of an Amyotrophic Lateral Sclerosis Model in a Gender-Specific Manner

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Received: 1 January 2014 / Accepted: 20 June 2014
© Springer Science+Business Media New York 2014

Abstract The implication of lipid peroxidation in neurodegenerative diseases, including amyotrophic lateral sclerosis (ALS) derive from high abundance of peroxidation-prone polyunsaturated fatty acids in central nervous system and its relatively low antioxidant content. In the present work, we evaluated the effect of dietary changes aimed to modify fatty acid tissular composition in survival, disease onset, protein, and DNA oxidative modifications in the hSODG93A transgenic mice, a model of this motor neuron disease. Both survival and clinical evolution is dependent on dietary fatty acid unsaturation and gender, with high unsaturated diet, leading to loss of the disease-sparing effect of feminine gender. This was associated with significant increases in protein carbonyl and glycoxidative

modifications as well as non-nuclear 8-oxo-dG, a marker of mitochondrial DNA oxidation. Comparison of these data with γ H2AX immunostaining, a marker of DNA damage response, suggests that the highly unsaturated diet-blunted mitochondrial–nuclear free radical dependent crosstalk, since increased 8-oxo-dG was not correlated with increased DNA damage response. Paradoxically, the highly unsaturated diet led to lower peroxidizability but higher anti-inflammatory indexes. To sum up, our results demonstrate that high polyunsaturated fatty acid content in diets may accelerate the disease in this model. Further, these results reinforce the need for adequately defining gender as a relevant factor in ALS models, as well as to use structurally characterized markers for oxidative damage assessment in neurodegeneration.

Electronic supplementary material The online version of this article (doi:10.1007/s12017-014-8317-7) contains supplementary material, which is available to authorized users.

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Keywords Oxidative stress · Polyunsaturated fatty acid · DNA repair response · Gender dimorphism · Lipid peroxidation

Introduction

Amyotrophic lateral sclerosis (ALS, OMIM #105400) is a neurodegenerative, motor neuron-specific disease that causes death within 2–5 years after diagnosis. ALS sporadic forms account for most of the cases and despite much effort have been done, their causes remain unclear. However, familial forms of the disease (fALS) provide a valuable tool for the development of animal models to gain insight into disease mechanisms and therapy design, especially at preclinical stages. A breakthrough point in this line was the discovery by Rosen (1993), showing that mutations in Cu/ZnSOD were a primary cause for ALS. Since then, multiple mutations on Cu/ZnSOD (more than

100, reviewed in Gaudette et al. 2000) have been identified, thus leading to develop experimental models of fALS (Gurney et al. 1994; Oeda et al. 2001). In particular, transgenic mice bearing multiple copies of one of the fALS-linked mutations, a glycine for alanine substitution (G93A), has become the most used model to study the pathogenesis of ALS. Nevertheless, it is known that even a single mutation harbours an increasing disease complexity pointing novel roles of specific genes and proteins as disease modifiers (reviewed in Al-Chalabi et al. 2012).

Lipids account approximately for 50–60 % of the brain dry weight, from which polyunsaturated accounts around the 35 % (Lauritzen et al. 2001) being mostly long-chain polyunsaturated fatty acids (PUFAs). The majority of such lipids present in the central nervous system are structural, belonging to phospholipid bilayers in biomembranes. But apart from structural conformation in phospholipids and source of energy, lipids play key roles in different vital complex processes such as signalling. They act not only as direct messengers by signalling in paracrine communication but also in helping to correctly position cellular receptors (e.g. lipid rafts Simons and Toomre 2000) and also binding responsive elements to regulate DNA expression (e.g. PPARs; reviewed in Willson et al. 2000). They could also modulate reactive oxygen species (ROS) production and interact with those by generating reactive lipid species, which can be signalling intermediates (Niki 2012). Globally, PUFAs are essential for correct neuronal function. These data are behind the beneficial effects of an adequate intake of the n-3 series PUFAs, especially for DHA (C22:6, n-3). Accordingly, its deficiency leads to visual, cognitive and/or behavioural abnormalities in several animal models (Niu et al. 2004) as well as in humans (Deckelbaum and Torrejon 2012). DHA signalling is supposed to act: (1) through structural characteristics in lipid bilayers; (2) by DNA interaction through PPAR related genes enhancement (Willson et al. 2000); (3) also through its role as a source of signalling intermediates, since for instance, DHA is the metabolic source of docosanoids and resolvins, contrasted inflammatory resolution mediators (Serhan 2005); (4) and finally by oxidative signalling, since DHA oxidative derivatives also interact with PPARs family transcription factors (Itoh and Yamamoto 2008). Noteworthy, PUFA structure (n-3 vs n-6 families) is relevant, since they stimulate different genes (Barceló-Coblijn et al. 2003) as they share (and therefore compete) biosynthetic pathways for fatty acid itself, but also for its derivatives. This adds further complexity to the interaction of PUFA with central nervous system function.

Asides from these physiological roles, one potentially detrimental effect of PUFAs arises from their high

susceptibility to oxidation, which is believed to play a major role in ALS pathogeny (as hypothesized 20 years ago; (Bowling et al. 1993). An excess of ROS could interact with any of the surrounding biomolecules within the cell, ranging from DNA and proteins to lipids or carbohydrates, amplifying ROS damage. Particularly, after oxidative protein damage, several oxidatively modified amino acids are generated, which can be used as specific markers of distinct types of oxidative stress: (1) for direct, metal-catalysed, carbonylation, glutamic and amino adipic semi-aldehydes (GSA and AASA); (2) for glycooxidation, N Σ -carboxymethyl-lysine (CML) and N Σ -carboxyethyl-lysine (CEL) and finally, (2) for lipoxidation malondialdehyde-lysine (MDAL) (Portero-Otin et al. 2003; Thorpe and Baynes 2003). Similarly, ROS could modify DNA, by generating specific residues, such as 8-oxo-deoxyguanosine, between other (Weimann et al. 2001). In this line, dietary factors could modify 8-oxo-dG accrual (Zhu et al. 2000). In addition, it has not been studied whether PUFA intake could modify 8-oxo-DG accumulation in a neurodegeneration model, though positive role for dietary fish oil and vegetable PUFA was recently demonstrated related to a reduction of 8-oxo-dG accumulation both in colonic samples for a model of Crohn disease (Bancroft et al. 2003) or patients suffering type 2 diabetes (Müllner et al. 2013). Nonetheless, besides cytotoxic effects, a signalling role for ROS is known. Recent data show a crosstalk between mitochondrial-free radical production and nuclear DNA damage response (DDR), mediated by γ H2Ax (Passos et al. 2010), involved in cell and tissue homeostasis.

In the present work, we hypothesized that if extensive lipid composition and its susceptibility to peroxidation could be modified, ALS progression could be partially modulated. In this sense, regarding dietary intervention, previous works from our group showed that the fatty acid profiles of several organs, including brain, can be modified as a result of dietary modification (Pamplona et al. 2004), leading to significant effects in the concentration of protein oxidative markers. For this reason, in this study, diets with different degree of unsaturation were designed to evaluate their effects in the survival of an ALS model. Several diet-related outcomes (weight gain and lipid composition) as well as clinical score, coordination/strength (stride length) and distinct markers for oxidative damage to proteins along the disease progression were also measured. We also analysed the potential effect of PUFAs in the crosstalk between mitochondrial ROS production (assessed by 8-oxo-dG immunostaining) and DDR in lumbar spinal cords, in order to ascertain the potential role of lipid peroxidation and dietary lipid composition in ALS pathogenesis.

Methods

Animals and Diets

A colony of the strain B6SJL-Tg (SOD1-G93A)1Gur/J (JAX catalogue stock number 002726; from now on hSODG93A) was purchased at The Jackson Laboratories (Bar Harbor, MN, USA) and maintained in the B6SJL background, by male founder crossing with B6SJLF1/J. All mice were genotyped by using PCR-according procedures stated by the providers. For tail DNA extraction a kit for tissue DNA extraction was used (XNAT, Sigma-Aldrich, Saint Louis, MO, USA). PCR amplification was performed in a 2740 Thermal Cycler v2.08 (Applied Biosystems, Carlsbad, CA, USA) as follows: Pre-denaturation for 5 min at 95 °C, denaturation for 1 min at 94 °C, annealing for 45 s at 50 °C, elongation for 4 min at 72 °C and finally, after 35 cycles, elongation for another 7 min at 72 °C. The amplification products were stored at 4 °C before gel loading and electrophoresis, which was done in 1 % agarose gels and stained with Sybr safe (Molecular Probes, Carlsbad, CA, USA) following manufacture instructions. Products were electrophoresed for 30 min under constant 100 V and images were taken under (302 or 365 nm) UV light lamp from Alpha Innotech (Santa Clara, CA, USA) with a software acquisition Alpha Digidoc RT2 (Santa Clara, CA, USA).

After genotyping and weaning, animals were placed at 12:12 h dark/light cycle, at 22 ± 2 °C temperature, $50 \% \pm 10$ relative humidity, in individual cages, using the experimental diets (at 21 days). Whenever was possible by litter size of transgenic animals, gender and litter-matched animals were randomly distributed across the three diets. Animals were weighted weekly and daily for those under stride length analysis.

All diets used for experiments were purchased at Harlan Tekland (Madison, WI, USA) and stored at 4 °C until use. Diet composition was designed to be isocaloric and essential fatty acids requirements were completed (Table S3). We randomly assigned individual mice to either high unsaturated diet (Harlan reference number TD06154) or low unsaturated diet (Harlan reference number TD06155), whose compositions were as previously described (Pampolona et al. 2004). Those diets have extreme differences for peroxidizability indexes (fivefold), content of n-3 fatty acids (sixfold), content of arachidonic and docosahexanoic acids (100-fold) and double-bond indexes (threefold), with control diet values in-between. Importantly, low unsaturated diet does not lead to essential fatty acid deficiency, as shown by content of the n-3 and n-6 precursors linolenic and linoleic acids. Food pellets were weighted (for intake calculations) and removed weekly. As a control group, 40 animals (20 male, 20 female) were maintained and fed with

a regular rodent chow (AIN-93G, Harlan reference number TD94045) to ascertain survival homogeneity and standard growing curves. All experimental procedures were approved by the Institutional Animal Care Committee of Institut de Recerca Biomèdica de Lleida and were conformed to the Directive 2010/63/EU of the European Parliament.

Disability Score Assessment

Disability scores for both hind legs were assessed weekly for each mouse from 60 days of age to end point. The neurological score (Amyotrophic Lateral Sclerosis Therapy Development Institute and Jackson Laboratories) employed a scale where 0 points were given when full extension of hind legs away from lateral midline when mouse was suspended by its tail; one point when there was a collapse of leg extension towards midline or trembling of hind legs during this tail suspension; two points when toes

curled under at least twice during walking of 12 inch., or any part of foot was dragging along cage bottom/table; three points when it was present a rigid paralysis or minimal joint movement, foot not being used for forward motion and four points when mouse was not able to right itself within 30 s from either side (that was the endpoint of the measurement). Disease onset was considered the age at which an animal scored 2 in the above mentioned test. Observators for score were blinded to both diet and data analyses.

Stride Length Analysis

Stride length measurement was adopted from previously reported methods (Chiu et al. 1995). All animals were trained to walk freely along a U-shaped flat narrow corridor (5 cm wide, 70 cm long) three times per week before data collection (average age 70 days). Once trained, hindlimbs were stained with non-toxic poster children paints and their tracks were imprinted on paper (labelled with only with animal number and date) lining the floor of the corridor. Only continuous runs were measured among recorded and a minimum of 5–7 strides were measured per animal per day (three non-consecutive day measures were taken along week) to obtain daily mean. Since animals tended to walk faster when released and went slower at the end of the corridor, those areas were discarded for the stride measures, which were taken manually and were defined as the distance between successive right-to-right and left-to-left footprints. As the disease progresses, the painted footprints became increasingly smeared on the paper, which correlated with previous results (Chiu et al. 1995). Loss of stride length was quantified by determining the age at which

shortening of the stride length was lower than 10 % for two consecutive measures. Measurement of stride length was determined in a blinded manner since only number of the randomized animal and date identified the recorded tracks.

Analytical Measurements

Animals, after being fasted overnight, were anesthetised with 2.5 % isoflurane in air and finally sacrificed. Spinal cords and brain were rapidly excised, frozen in liquid N₂ and stored at -80 °C until further analyses. Samples were homogenized on ice in a buffer containing 180 mM KCl, 5 mM MOPS, 2 mM EDTA, 1 mM diethylenetriaminepentaacetic acid, and 1 μM of freshly prepared butylated hydroxyl toluene at pH 7.3 using a homogenizer device (T10 basic UltraTurraX, IKA, Staufen, Germany). Protein concentrations were measured by the Bradford method.

Measurement of Protein Oxidative (GSA, AASA), Glycoxidative (CML, CEL) and Lipoxidative (MDAL) Modifications

Gas chromatography–mass spectrometry (GC/MS) measurements of GSA, AASA, CEL, CML, and MDAL concentrations in total proteins from mice lumbar spinal cord homogenates were measured as routinely performed in our laboratory (Pamplona et al. 2005). Samples containing 0.5 mg of protein were delipidated using chloroform/methanol (2:1, v/v) (see below), and proteins were precipitated by adding 10 % trichloroacetic acid (final concentration) and subsequent centrifugation. Protein samples were reduced overnight with 500 mM NaBH₄ (final concentration) in 0.2 M borate buffer, pH 9.2, containing 1 drop of hexanol as an anti-foam reagent. Proteins were then precipitated by adding 1 ml of 20 % trichloroacetic acid and subsequent centrifugation. The following isotopically labelled internal standards were then added: [2H8]lysine (d8-Lys; CDN Isotopes); [2H4]CML (d4-CML), [2H4]CEL (d4-CEL), [2H8]MDAL (d8-MDAL), [2H5]5-hydroxy-2-aminovaleic acid (for GSA quantitation) and [2H4]6-hydroxy-2-aminocaproic acid (for AASA quantitation). The samples were hydrolyzed at 155 °C for 30 min in 1 ml of 6 N HCl, and then dried in vacuo. The *N,O*-trifluoroacetyl methyl ester derivatives of the protein hydrolysate were prepared as previously described (Pamplona et al. 2005). Then, GC/MS analyses were carried out on a Agilent model 6890 gas chromatograph equipped with a 30-m HP-5MS capillary column (30 m × 0.25 mm × 0.25 μm) coupled to a Agilent model 5973A mass selective detector (Agilent, Barcelona, Spain). The injection port was

maintained at 275 °C; the temperature programme was 5 min at 110 °C, then 2 °C/min to 150 °C, then 5 °C/min to 240 °C, then 25 °C/min to 300 °C, and finally hold at 300 °C for 5 min. Quantification was performed by external standardization using standard curves constructed from mixtures of deuterated and non-deuterated standards. Analytes were detected by selected ion-monitoring GC/MS. The ions used were: lysine and d8-lysine, *m/z* 180 and 187, respectively; 5-hydroxy-2-aminovaleic acid and d5-5-hydroxy-2-aminovaleic acid (stable derivatives of GSA), *m/z* 280 and 285, respectively; 6-hydroxy-2-aminocaproic acid and d4-6-hydroxy-2-aminocaproic acid (stable derivatives of AASA), *m/z* 294 and 298, respectively; CML and d4-CML, *m/z* 392 and 396, respectively; CEL and d4-CEL, *m/z* 379 and 383, respectively; and MDAL and d8-MDAL, *m/z* 474 and 482, respectively. The amounts of products were expressed as the ratio micromolar of GSA, AASA, CML, CEL, or MDAL/mol of lysine.

Fatty Acid Compositional Analyses

Fatty acid analysis in tissue samples and diets was performed as previously described (Pamplona et al. 2005). Total lipids from homogenates were extracted with chloroform/methanol (2:1, v/v) (3 times) in the presence of 0.01 % butylated hydroxytoluene. The chloroform phase was evaporated under nitrogen, and the fatty acids were transesterified by incubation in 2 ml of 5 % methanolic HCl for 90 min at 75 °C. The resulting fatty acid methyl esters were extracted by adding 2 ml of *n*-pentane and 1 ml of saturated NaCl solution. The *n*-pentane phase was separated, evaporated under nitrogen, re-dissolved in 80 μl of carbon disulphide, and 2 μl was used for GC analysis. Separation was performed by a DBWAX capillary column (30 m × 0.25 mm × 0.20 μm) in an Agilent GC System 7890A with a Series Injector 7683B and a FID detector (Agilent Technologies, Barcelona, Spain). The injection port was maintained at 220 °C, and the detector at 250 °C; the temperature programme was 2 min at 100 °C, then 10 °C/min to 200 °C, then 5 °C/min to 240 °C and finally hold at 240 °C for 10 min. Identification of fatty acid methyl esters was made by comparison with authentic standards (Larodan Fine Chemicals, Malmö, Sweden). Results are expressed as mol%.

From particular fatty acids, the following indexes were calculated as previously described (Pamplona et al. 2005). Saturated fatty acids (SFA) = Σ % of saturated fatty acids; unsaturated fatty acids (UFA) = Σ % unsaturated fatty acids; monounsaturated fatty acids (MUFA) = Σ % of monoenoic fatty acids; polyunsaturated fatty acids series n-3 (PUFA-n-3) = Σ % of polyunsaturated fatty acids n-3

series; polyunsaturated fatty acids series n-6 (PUFAn-6) = Σ % of polyunsaturated fatty acids n-6 series; average chain length (ACL) = $[(\Sigma \% \text{ Total } 14 \times 14) + \dots + (\Sigma \% \text{ total } n \times n)]/100$ (n = carbon atom number); peroxidizability index (PI) = $[(\Sigma \text{ mol\% monoenoic} \times 0.025) + (\Sigma \text{ mol\% dienoic} \times 1) + (\Sigma \text{ mol\% trienoic} \times 2) + (\Sigma \text{ mol\% tetraenoic} \times 4) + (\Sigma \text{ mol\% pentaenoic} \times 6) + (\Sigma \text{ mol\% hexaenoic} \times 8)]$; Double-bond index (DBI) = $[(\Sigma \text{ mol\% monoenoic}) + (2 \times \Sigma \text{ mol\% dienoic}) + (3 \times \Sigma \text{ mol\% trienoic}) + (4 \times \Sigma \text{ mol\% tetraenoic}) + (5 \times \Sigma \text{ mol\% pentaenoic}) + (6 \times \Sigma \text{ mol\% hexaenoic})]$; Antinflammatory index (AI) = $(20:3n-6) + (20:5n-3) + (22:5n-3) + (22:6n-3)/(20:4n-6)$; ratio PUFAs = (PUFAn-3)/(PUFAn-6).

Immunohistochemistry

Selected animals were anaesthetized by intraperitoneal injection (pentobarbital and ketamine, 20 and 60 mg/kg respectively on PBS). Animals were therefore exsanguinated by perfusion, firstly with saline solution (4 °C) and thereafter with ice cold 0.4 % paraformaldehyde (Sigma-Aldrich, Saint Louis, MO, USA) solution (freshly prepared with pH 7.4 phosphate buffer). After tissue collection (spinal cord) samples were immersed for 24 h in the same fixative to assure preservation. Samples were thereafter immersed in 30 % sucrose, (made in pH 7.4 phosphate buffer) for 48 h to achieve cryopreservation. Tissue was encased in a cubic recipient (Peel-A-Way Disposable Embedding Molds-S-22, Polysciences Inc., Warrington, PA, USA), labelled and embedded in tissue freezing medium (Triangle Biomedical Sciences Inc., Newcastle, UK) for easily cutting and better preservation and finally frozen (−80 °C). For immunofluorescence, 16 μ m wide sections of lumbar spinal cord were cut and carefully seeded along gelatine-coated slide. Selected sections were permeabilized with 0.4 % Triton \times -100 PBS. After blocking with 5 % normal horse serum in 0.4 % Triton \times -100 PBS for 2 h at room temperature (RT), the tissue was incubated for 24 h at 4 °C with the primary antibodies. Next day, the slices were washed with PBS three times for 10 min at RT. Then, the slices were incubated for 1 h at RT in darkness with corresponding secondary antibodies. Sections were finally counterstained with 4,6-diamidino-2-phenylindole dihydrochloride (DAPI, 1 μ g/ml) in PBS for 5 min at RT and mounted on slides with Vectashield (Vector Laboratories, Burlingame, CA, USA). In selected sections primary antibody was omitted to assure labelling specificity. Mounted slices were examined under a Fluoview 500 Olympus confocal laser scanning microscope (Olympus, Hamburg, Germany). For quantification of anti-ubiquitin, anti-syn-taxin3 and anti- γ H2Ax immunoreactivity images were analysed with the Image J software (<http://rsbweb.nih.gov/ij/>).

Statistical Analyses

All statistics were performed using the SPSS software (SPSS Inc., Chicago, IL, USA) or the Prism software (GraphPad Software, San Diego, CA, USA). Differences between groups were analysed by the Student's *T* tests or ANOVA with post hoc analyses, after normality of variable distribution was ensured by Kolmogorov–Smirnov test. Correlations between variables were evaluated by the Pearson's statistic. The 0.05 level was selected as the point of minimal statistical significance in every comparison.

Results

Survival and Clinical Evolution of ALS G93A Mice is Modified by Dietary Fatty Acid Unsaturation in a Gender-Specific Fashion

When compared with a regular rodent chow, low unsaturation in diet diminishes gender-related influence on median survival (Fig. 1a and Supplemental Figure 1). Survival analyses taking diet into account show that under control diet females survived longer (Fig. 1b), a fact maintained under low unsaturated diets (Fig. 1c), but not under high unsaturated diets (Fig. 1d). For males, results (Supplemental Figure 1) show that survival was highest in animals under low unsaturated diets ($p < 0.05$ for Log rank test), while as differences in females were not significant.

Phenotypic analyses for disease onset (as assessed both by a clinical score and stride length loss) revealed a similar trend: global analyses show that dietary fats did not affect disease onset (Fig. 1e). In contrast with survival, where feminine gender showed an evident protective effect under control diets, these diets did not show differences in disease onset (Fig. 1f). In contrast, low unsaturated diet delayed significantly disease onset in females (Fig. 1g), in contrast with highly unsaturated diet (Fig. 1h). If performed separately, no major differences were evidenced neither in males nor in females (Supplemental Figure 1). When evaluating loss of stride length preservation (defined by a consecutive decay of at least 10 % in stride length), we found that males under highly unsaturated diet reached this stage faster than those under low unsaturated or control ones (Fig. 1i). However, this phenomenon was not present in females (Fig. 1j). Rather, it appeared that both low and high unsaturated diets enhanced stride length preservation significantly in females, in comparison with control diets.

Food intake calculations were similar between dietary groups and comparable with a control diets with no major statistical differences along the experiment (data not shown). Mice gained weight as expected (Fig. 1k, l), reaching a maximum value at 100 days for males,

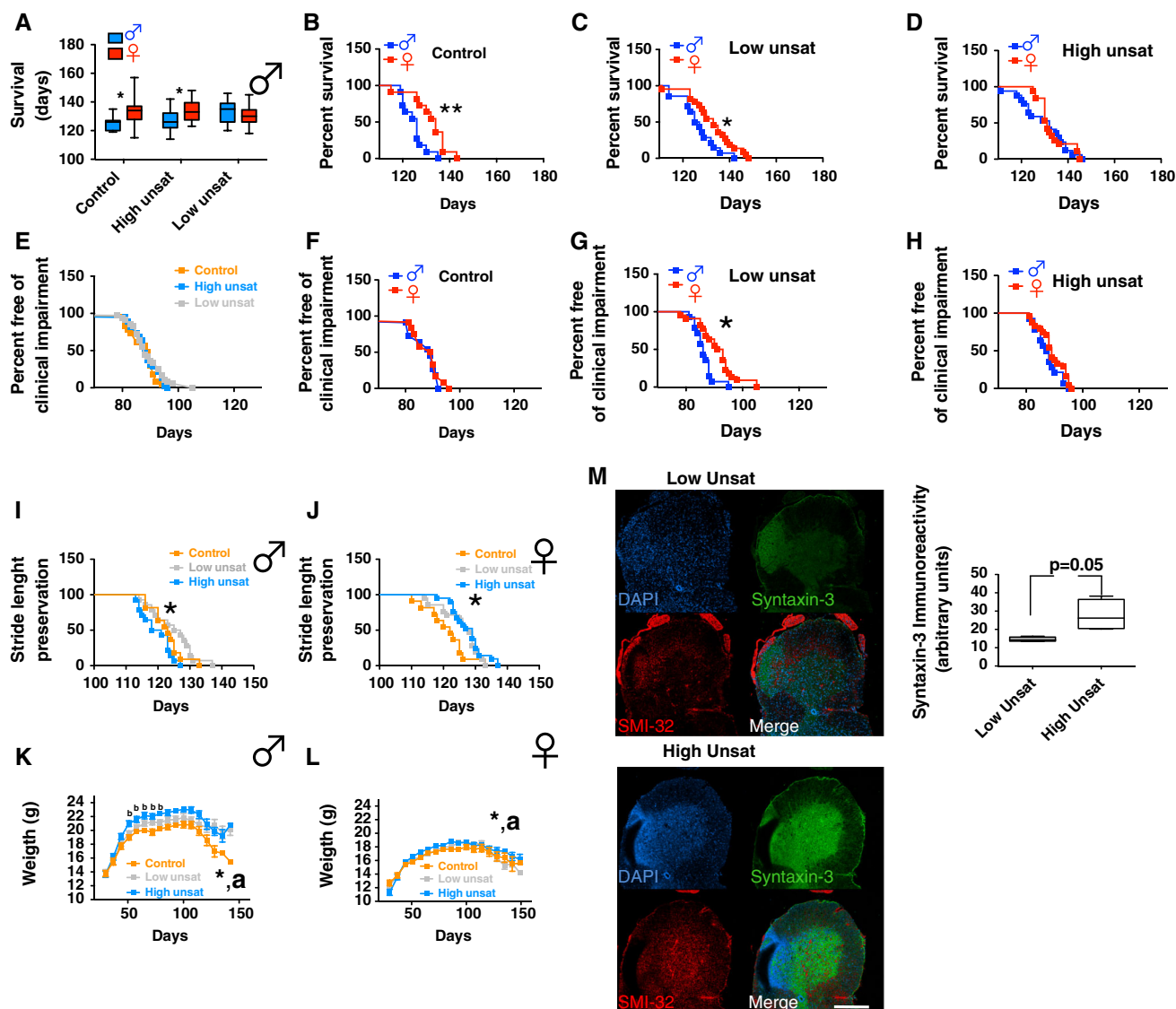


Fig. 1 Dietary fatty acid unsaturation induces a gender-specific effect in survival in the hSODG93A ALS mice model. **a** Low unsaturated fats (see text for description) maintained gender-related differences in median survival (seen under control conditions), while high unsaturated diet diminished this gender-induced difference. **b** Further, survival and gender-specific analyses demonstrated that under control (**b**) or low unsaturated diet (**c**), females lived longer than males, in contrast with the high unsaturation diet (**d**). Similarly, disease onset, as defined by changes in clinical score in the “Methods” section, was not affected by dietary fat unsaturation, as shown by global analyses (**e**). Disease onset in males was not affected by diets (**f**), in contrast with females (**g**) with significant differences ($p < 0.05$ by or that with high unsaturation (**h**). In line with this, disease progression proceeded faster in males under high unsaturation (**i**), while females were protected against this effect (**j**). Effects of dietary unsaturation in weight gain were similar for both genders (**k**, **l**). Males reached a maximum (23.04 ± 0.370 g, $n = 22$; 21.85 ± 0.559 g, $n = 22$; 20.83 ± 0.8 g, $n = 12$ for high, low and control unsaturation diets, respectively) at 100 days, meanwhile

females did it at 100 days for ones under high unsaturation and control (18.69 ± 0.327 g, $n = 22$; 17.9 ± 0.62 g, $n = 13$) and at 97 days those on low unsaturated diet (18.70 ± 0.270 g, $n = 28$). **m** Confocal microscopy images in lumbar spinal cord demonstrating increased biological availability of dietary unsaturated fatty acids in male animals (endpoint: 130 ± 7 days) as suggested by increased syntaxin-3 immunostaining, quantified in the whiskers plot in the left panel. In **a** asterisk indicates statistical differences between males and females survival by Bonferroni multiple test post hoc analyses after 2-way ANOVA. For **b–j** significant differences between diets and/or genders were evaluated by Kaplan–Meier survival statistic ($*p < 0.05$; $**p < 0.001$). For **k** and **l** * and ^asignificant differences by 2-way ANOVA of diet and age effects, respectively, while as ^bsignificant increases in weight at 50–80 days in males under high unsaturated diets by Bonferroni multiple test post hoc analyses after 2-way ANOVA. A total of 30 slices ($n = 3$ animals per treatment) were analysed for quantification in **m**, with differences induced by diet being evaluated by Student’s *T* test. Bars in **m** are 500 μ m

Table 1 Fatty acid composition (% of abundance) and derived indexes for whole brain homogenate (60 days)

	Male hSODG93A			Female hSODG93A		
	High unsat	Low unsat	<i>p</i> value	High unsat	Low unsat	<i>p</i> value
14:0	0.317 ± 0.092	0.542 ± 0.121	0.190	0.260 ± 0.027	0.420 ± 0.123	0.137
16:0	24.47 ± 0.592	16.32 ± 0.273	0.001	24.44 ± 0.239	13.05 ± 0.233	0.001
16:1n-7	0.593 ± 0.038	0.535 ± 0.099	0.604	0.556 ± 0.046	0.203 ± 0.114	0.024
18:0	22.67 ± 0.198	24.26 ± 1.177	0.230	23.21 ± 1.413	20.73 ± 1.701	0.352
18:1n-9	21.95 ± 0.848	22.00 ± 0.856	0.967	20.74 ± 0.521	18.82 ± 1.345	0.167
18:2n-6	0.690 ± 0.072	0.725 ± 0.053	0.732	0.621 ± 0.107	0.554 ± 0.077	0.698
18:3n-3	0.089 ± 0.010	0.035 ± 0.019	0.031	0.066 ± 0.085	0.446 ± 0.258	0.077
18:4n-6	0.905 ± 0.325	2.23 ± 0.130	0.009	0.685 ± 0.133	1.944 ± 0.385	0.015
20:0	0.365 ± 0.090	0.555 ± 0.048	0.100	0.330 ± 0.007	0.383 ± 0.008	0.384
20:1 n-9	1.142 ± 0.113	1.516 ± 0.140	0.084	1.203 ± 0.062	1.426 ± 0.520	0.538
20:2n-6	0.430 ± 0.145	0.726 ± 0.134	0.185	0.241 ± 0.015	0.948 ± 0.021	0.092
20:3n-6	0.094 ± 0.012	0.072 ± 0.018	0.175	0.081 ± 0.006	0.590 ± 0.329	0.066
20:4n-6	8.44 ± 0.796	10.09 ± 0.869	0.212	8.219 ± 0.255	8.965 ± 0.153	0.132
20:5n-3	0.276 ± 0.114	0.161 ± 0.073	0.440	0.314 ± 0.008	0.868 ± 0.427	0.103
22:0	1.522 ± 0.293	1.935 ± 0.197	0.289	0.478 ± 0.083	1.472 ± 0.122	0.002
22:4n-6	2.065 ± 0.339	2.976 ± 0.425	0.144	1.557 ± 0.065	2.567 ± 0.025	0.001
22:5n-6	0.365 ± 0.071	0.925 ± 0.186	0.030	0.363 ± 0.011	0.690 ± 0.011	0.001
22:5n-3	0.420 ± 0.018	0.680 ± 0.190	0.222	0.411 ± 0.005	1.177 ± 0.275	0.011
24:0	0.075 ± 0.015	0.152 ± 0.050	0.164	0.039 ± 0.006	0.769 ± 0.073	0.001
22:6n-3	12.741 ± 1.088	12.33 ± 1.807	0.654	15.77 ± 0.530	13.32 ± 0.619	0.039
24:5n-3	0.150 ± 0.049	0.485 ± 0.180	0.125	0.064 ± 0.016	0.928 ± 0.359	0.018
24:6n-3	0.290 ± 0.022	0.430 ± 0.115	0.279	0.325 ± 0.053	0.711 ± 0.175	0.045
SFA	49.46 ± 0.736	43.83 ± 1.402	0.012	48.77 ± 1.210	36.84 ± 1.625	0.004
UFA	50.06 ± 0.736	55.93 ± 1.345	0.013	51.22 ± 1.201	54.15 ± 0.128	0.130
MUFA	23.68 ± 0.760	24.07 ± 1.000	0.779	22.50 ± 0.576	20.45 ± 0.943	0.121
PUFA	26.87 ± 1.344	31.86 ± 2.238	0.105	28.72 ± 0.798	33.20 ± 1.071	0.016
PUFAn-3	13.98 ± 1.086	14.13 ± 1.049	0.917	16.95 ± 0.530	17.44 ± 0.901	0.637
PUFAn-6	13.10 ± 1.421	17.73 ± 1.221	0.045	11.77 ± 0.295	16.75 ± 0.169	0.001
ACL	18.43 ± 0.048	18.68 ± 0.798	0.209	18.46 ± 0.027	17.37 ± 0.247	0.005
DBI	156.97 ± 8.64	176.21 ± 10.10	0.133	168.88 ± 4.67	183.96 ± 2.85	0.105
PI	159.75 ± 11.6	179.91 ± 13.18	0.237	179.27 ± 4.40	192.71 ± 3.33	0.185
R/PUFAs	1.120 ± 0.155	0.795 ± 0.020	0.084	1.440 ± 0.023	1.071 ± 0.043	0.003
AI	163.04 ± 18.5	131.73 ± 9.19	0.192	200.74 ± 2.88	171.38 ± 2.18	0.001

p value reflects statistical significance between diets by Student's *T* test

irrespective of diet; meanwhile, females reached a maximum at 100 days for those under high unsaturated and control diets and at 97 days on low unsaturated one. Males under high unsaturated diet weighted significantly more than those of control during preclinical stages (from day 50 to day 75) (Fig. 1k, l).

To confirm fatty acid bioavailability, we measured both lipid composition and surrogate markers of n-3 availability. Since the profile of fatty acids in control-fed animals resemble strongly those present in low unsaturation diets (Supplemental Table 1 and 2), we focused to differences between high and low unsaturation fed animals. Thus, lipid profiles in brain (Table 1) and spinal cord (Tables 2, 3)

revealed that in this latter, the concentration of arachidonic acid (AA, 22:4n-6), under low unsaturation, was higher than those found in high unsaturated ones. In contrast, a major fatty acid (18:0) responsible for approximately 40 % of the total fatty acids measured was not affected by the diet.

Similarly, DHA levels were not severely altered. Anti-inflammatory index (AI) was always higher for animals under highly unsaturated diet independently of tissue or gender, including those from control-fed animals (Tables 1, 2, 3, Supplemental Tables 1 and 2). Double-bound (DBI) and peroxidizability (PI) indexes both reflecting susceptibility for lipid peroxidation were found

Table 2 Fatty acid composition (% of abundance) and derived indexes in spinal cord (lumbar region) for male hSODG93A

	60 days			90 days			120 days		
	High unsat	Low unsat	<i>p</i> value	High unsat	Low unsat	<i>p</i> value	High unsat	Low unsat	<i>p</i> value
	14:0	0.830 ± 0.085	0.824 ± 0.035	0.954	0.171 ± 0.014	0.454 ± 0.064	0.006	0.202 ± 0.021	0.696 ± 0.10
16:0	21.411 ± 0.373	19.934 ± 0.403	0.022	22.33 ± 2.372	26.57 ± 0.391	0.087	22.65 ± 1.171	20.54 ± 0.624	0.130
16:1n-7	0.838 ± 0.124	0.842 ± 0.042	0.974	0.558 ± 0.076	0.715 ± 0.049	0.114	0.806 ± 0.195	1.011 ± 0.075	0.321
18:0	15.528 ± 0.504	16.160 ± 0.388	0.335	15.86 ± 1.056	16.59 ± 1.681	0.742	16.169 ± 0.885	15.61 ± 0.611	0.612
18:1n-9	37.065 ± 0.706	35.94 ± 0.480	0.204	38.76 ± 1.572	33.03 ± 1.865	0.058	38.665 ± 0.581	36.575 ± 0.401	0.014
18:2n-6	1.529 ± 0.244	1.429 ± 0.094	0.692	1.002 ± 0.302	0.978 ± 0.040	0.931	0.903 ± 0.031	1.296 ± 0.11	0.013
18:3n-3	0.198 ± 0.051	0.177 ± 0.027	0.712	0.101 ± 0.013	0.164 ± 0.033	0.141	0.137 ± 0.028	0.449 ± 0.063	0.003
18:4n-6	0.395 ± 0.067	0.456 ± 0.061	0.519	0.110 ± 0.050	0.205 ± 0.055	0.262	0.166 ± 0.046	0.521 ± 0.104	0.018
20:0	1.608 ± 0.107	1.69 ± 0.092	0.569	1.467 ± 0.042	1.528 ± 0.082	0.564	1.273 ± 0.125	1.198 ± 0.094	0.637
20:2n-6	0.683 ± 0.041	1.092 ± 0.076	0.001	0.447 ± 0.065	0.721 ± 0.045	0.010	0.557 ± 0.036	0.720 ± 0.107	0.219
20:3n-6	2.007 ± 0.371	2.269 ± 0.216	0.543	1.345 ± 0.189	1.199 ± 0.180	0.598	1.671 ± 0.096	1.968 ± 0.222	0.283
20:4n-6	4.394 ± 0.139	5.917 ± 0.127	0.001	4.738 ± 0.289	5.296 ± 0.126	0.098	4.419 ± 0.055	5.637 ± 0.327	0.009
20:5n-3	0.271 ± 0.021	0.094 ± 0.013	0.001	0.048 ± 0.013	0.094 ± 0.014	0.057	0.493 ± 0.062	0.622 ± 0.113	0.317
22:0	0.264 ± 0.070	0.151 ± 0.023	0.132	0.114 ± 0.018	0.389 ± 0.067	0.010	0.321 ± 0.034	0.635 ± 0.052	0.001
22:4n-6	1.616 ± 0.101	2.292 ± 0.042	0.001	1.395 ± 0.0884	2.260 ± 0.126	0.001	1.126 ± 0.050	2.234 ± 0.073	0.001
22:5n-6	0.415 ± 0.075	0.569 ± 0.044	0.094	0.249 ± 0.089	0.287 ± 0.041	0.694	0.273 ± 0.033	0.691 ± 0.112	0.010
22:5n-3	0.543 ± 0.097	0.412 ± 0.064	0.275	0.998 ± 0.121	0.289 ± 0.042	0.001	0.948 ± 0.062	0.487 ± 0.033	0.001
24:0	0.117 ± 0.011	0.209 ± 0.026	0.007	0.630 ± 0.017	0.055 ± 0.027	0.001	0.178 ± 0.024	0.039 ± 0.016	0.001
22:6n-3	7.930 ± 0.482	6.954 ± 0.233	0.083	7.587 ± 0.356	6.620 ± 0.278	0.066	6.362 ± 0.117	6.269 ± 0.173	0.683
24:5n-3	0.053 ± 0.004	0.054 ± 0.004	0.887	0.095 ± 0.047	0.098 ± 0.014	0.943	0.158 ± 0.027	0.377 ± 0.108	0.058
24:6n-3	2.300 ± 0.172	2.522 ± 0.101	0.275	2.151 ± 0.065	2.440 ± 0.134	0.120	2.542 ± 0.160	2.400 ± 0.134	0.512
SFA	39.756 ± 0.702	38.972 ± 0.636	0.425	40.58 ± 1.970	45.59 ± 1.754	0.099	40.796 ± 0.781	38.73 ± 0.458	0.042
UFA	60.243 ± 0.702	61.027 ± 0.636	0.421	59.59 ± 2.123	54.40 ± 1.754	0.098	59.203 ± 0.781	61.262 ± 0.458	0.051
MUFA	37.90 ± 0.674	36.78 ± 0.506	0.204	39.32 ± 1.49	33.75 ± 1.85	0.059	39.471 ± 0.659	37.586 ± 0.337	0.025
PUFA	22.33 ± 0.261	24.24 ± 0.394	0.003	20.27 ± 0.958	20.65 ± 0.274	0.512	19.75 ± 0.212	23.676 ± 0.71	0.001
PUFAn-3	11.29 ± 0.164	10.21 ± 0.084	0.123	11.62 ± 0.318	9.28 ± 0.109	0.005	10.83 ± 0.259	10.59 ± 0.169	0.413
PUFAn-6	11.04 ± 0.661	14.02 ± 0.512	0.004	9.289 ± 0.833	10.94 ± 0.144	0.063	9.116 ± 0.209	13.06 ± 0.632	0.001
ACL	18.27 ± 0.030	18.35 ± 0.010	0.029	18.31 ± 0.085	18.16 ± 0.008	0.081	18.22 ± 0.024	18.31 ± 0.017	0.019
DBI	142.37 ± 1.92	146.35 ± 1.17	0.095	136.93 ± 4.35	130.49 ± 1.69	0.172	133.32 ± 1.50	145.36 ± 2.08	0.001
PI	122.82 ± 3.86	125.64 ± 1.64	0.482	116.51 ± 3.74	113.40 ± 2.06	0.538	111.32 ± 1.60	123.56 ± 2.06	0.002
R/PUFAs	1.067 ± 0.141	0.735 ± 0.041	0.038	1.270 ± 0.131	0.877 ± 0.080	0.006	1.190 ± 0.022	0.872 ± 0.009	0.002
AI	245.35 ± 7.41	164.6 ± 2.91	0.001	211.54 ± 6.26	155.11 ± 3.12	0.001	214.50 ± 3.54	169.4 ± 13.34	0.016

p value reflects statistical significance between diets by Student's *T* test

Table 3 Fatty acid composition (% of abundance) and derived indexes in spinal cord (lumbar region) for female hSODG93A

	60 days			90 days			120 days		
	High unsat	Low unsat	<i>p</i> value	High unsat	Low unsat	<i>p</i> value	High unsat	Low unsat	<i>p</i> value
	14:0	0.793 ± 0.068	0.761 ± 0.025	0.715	0.204 ± 0.012	0.364 ± 0.045	0.010	0.325 ± 0.040	0.246 ± 0.018
16:0	21.36 ± 0.514	19.82 ± 0.505	0.066	20.30 ± 0.706	24.96 ± 0.691	0.002	21.616 ± 0.462	21.730 ± 0.199	0.827
16:1n-7	0.904 ± 0.100	0.749 ± 0.071	0.278	0.583 ± 0.024	0.703 ± 0.043	0.043	0.920 ± 0.059	0.869 ± 0.037	0.488
18:0	15.90 ± 0.473	16.44 ± 0.174	0.379	18.960 ± 0.327	16.969 ± 0.273	0.002	16.476 ± 0.354	17.499 ± 0.287	0.055
18:1n-9	36.30 ± 0.485	36.89 ± 0.455	0.413	39.45 ± 0.384	34.03 ± 0.725	0.001	39.116 ± 0.555	37.338 ± 0.325	0.025
18:2n-6	1.401 ± 0.057	1.415 ± 0.048	0.862	0.817 ± 0.005	0.870 ± 0.033	0.427	0.816 ± 0.110	0.850 ± 0.037	0.783
18:3n-3	0.162 ± 0.022	0.219 ± 0.012	0.078	0.099 ± 0.009	0.104 ± 0.034	0.967	0.156 ± 0.013	0.100 ± 0.011	0.014
18:4n-6	0.461 ± 0.069	0.481 ± 0.042	0.830	0.129 ± 0.009	0.149 ± 0.035	0.590	0.189 ± 0.021	0.133 ± 0.009	0.041
20:0	1.581 ± 0.076	1.861 ± 0.089	0.039	1.329 ± 0.058	1.246 ± 0.111	0.529	1.115 ± 0.109	0.967 ± 0.100	0.348
20:2n-6	0.672 ± 0.057	0.927 ± 0.041	0.008	0.464 ± 0.014	0.673 ± 0.069	0.019	0.492 ± 0.025	0.435 ± 0.033	0.211
20:3n-6	2.193 ± 0.259	1.704 ± 0.130	0.169	1.183 ± 0.119	1.22 ± 0.128	0.810	1.537 ± 0.142	1.611 ± 0.067	0.655
20:4n-6	4.434 ± 0.200	5.254 ± 0.098	0.009	4.469 ± 0.103	5.508 ± 0.047	0.001	4.324 ± 0.155	6.366 ± 0.171	0.001
20:5n-3	0.154 ± 0.016	0.076 ± 0.008	0.005	0.096 ± 0.013	0.214 ± 0.033	0.011	0.552 ± 0.067	0.219 ± 0.011	0.001
22:0	0.110 ± 0.020	0.141 ± 0.042	0.488	0.202 ± 0.015	0.230 ± 0.034	0.485	0.269 ± 0.033	0.102 ± 0.004	0.001
22:4n-6	1.765 ± 0.086	2.635 ± 0.179	0.001	1.232 ± 0.060	2.636 ± 0.164	0.001	1.192 ± 0.089	2.100 ± 0.085	0.001
22:5n-6	0.557 ± 0.095	0.564 ± 0.044	0.960	0.214 ± 0.010	0.422 ± 0.090	0.053	0.297 ± 0.018	0.328 ± 0.026	0.365
22:5n-3	0.462 ± 0.078	0.440 ± 0.039	0.837	0.863 ± 0.012	0.269 ± 0.024	0.001	0.886 ± 0.030	0.522 ± 0.034	0.001
24:0	0.199 ± 0.021	0.237 ± 0.059	0.516	0.535 ± 0.024	0.025 ± 0.003	0.001	0.150 ± 0.036	0.031 ± 0.011	0.015
22:6n-3	7.916 ± 0.267	6.770 ± 0.203	0.010	6.819 ± 0.289	7.004 ± 0.079	0.557	6.724 ± 0.423	5.859 ± 0.201	0.102
24:5n-3	0.075 ± 0.017	0.041 ± 0.003	0.148	0.118 ± 0.016	0.137 ± 0.018	0.472	0.282 ± 0.036	0.106 ± 0.013	0.002
24:6n-3	2.572 ± 0.101	2.539 ± 0.096	0.862	1.922 ± 0.0466	2.252 ± 0.124	0.038	2.575 ± 0.057	2.581 ± 0.101	0.960
SFA	39.96 ± 0.901	39.27 ± 0.307	0.556	41.53 ± 0.735	43.79 ± 0.698	0.056	39.954 ± 0.598	40.577 ± 0.311	0.383
UFA	60.03 ± 0.901	60.71 ± 0.307	0.558	58.464 ± 0.735	56.200 ± 0.698	0.054	60.045 ± 0.598	59.422 ± 0.311	0.382
MUFA	37.20 ± 0.422	37.64 ± 0.517	0.508	40.034 ± 0.392	34.734 ± 0.699	0.001	40.036 ± 0.592	38.207 ± 0.292	0.024
PUFA	22.82 ± 0.643	23.03 ± 0.536	0.781	18.42 ± 0.469	21.46 ± 0.253	0.001	20.00 ± 0.153	21.21 ± 0.411	0.025
PUFAn-3	11.34 ± 0.297	10.09 ± 0.244	0.012	10.45 ± 0.309	10.00 ± 0.156	0.318	11.32 ± 0.378	9.42 ± 0.280	0.004
PUFAn-6	11.48 ± 0.552	12.98 ± 0.190	0.053	8.510 ± 0.206	11.47 ± 0.100	0.001	8.852 ± 0.297	11.85 ± 0.264	0.001
ACL	18.30 ± 0.033	18.34 ± 0.026	0.415	18.25 ± 0.033	18.21 ± 0.018	0.375	18.25 ± 0.019	18.24 ± 0.016	0.960
DBI	144.25 ± 2.83	143.06 ± 1.84	0.757	128.68 ± 2.85	135.73 ± 1.17	0.051	136.3 ± 1.280	136.6 ± 1.101	0.840
PI	125.74 ± 2.916	121.81 ± 2.413	0.379	105.58 ± 3.29	118.72 ± 1.71	0.008	114.92 ± 2.56	114.62 ± 2.72	0.946
R/PUFAs	1.007 ± 0.058	0.741 ± 0.008	0.006	1.227 ± 0.042	0.871 ± 0.013	0.001	1.281 ± 0.068	0.791 ± 0.010	0.001
AI	243.38 ± 6.03	171.88 ± 1.40	0.001	200.4 ± 2.818	158.2 ± 2.799	0.001	225.7 ± 14.42	129.23 ± 2.71	0.001

p value reflects statistical significance between diets by Student's *T* test

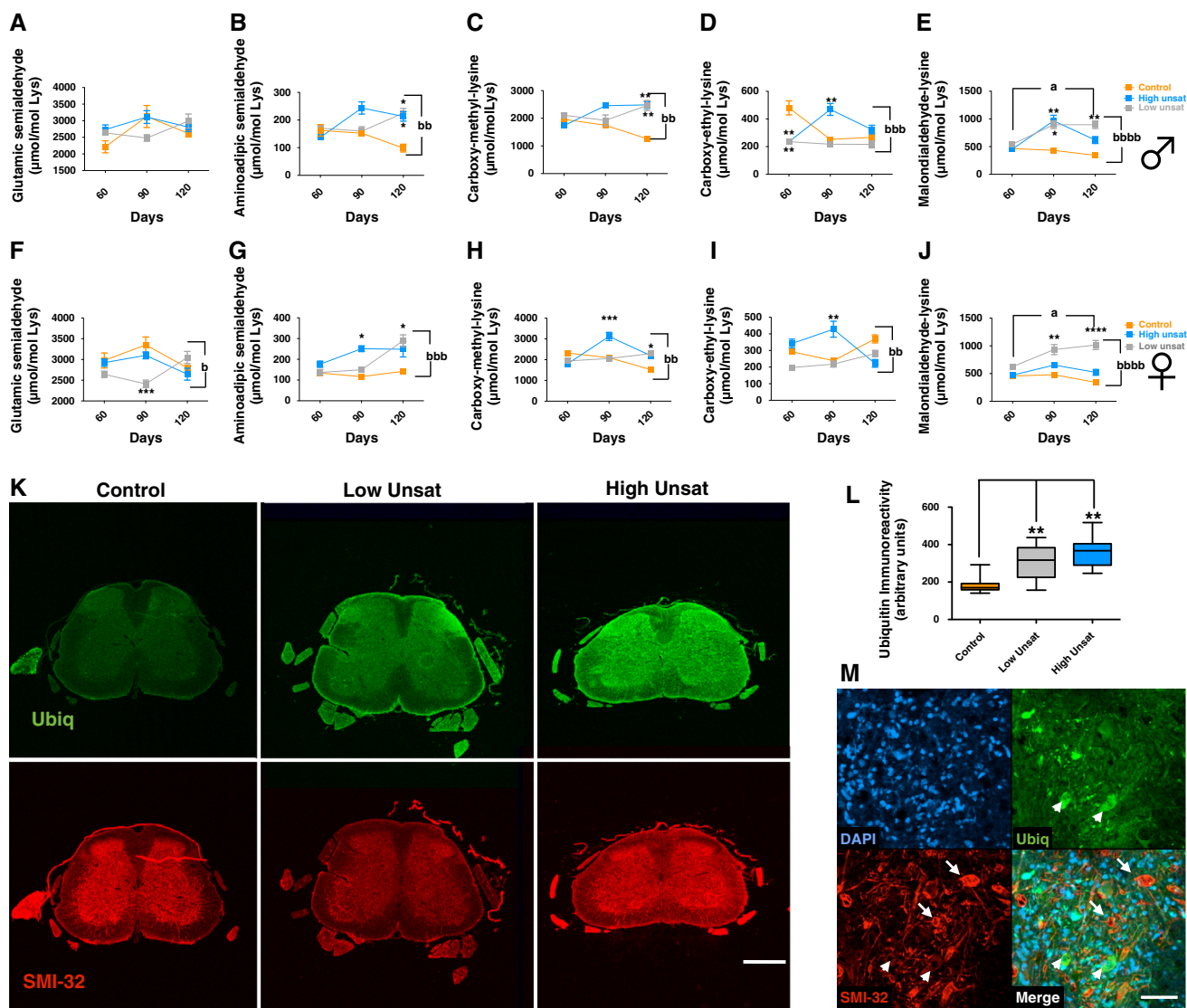


Fig. 2 Dietary unsaturation influences protein oxidative damage and ubiquitin aggregation in lumbar spinal cord. Protein carbonyls glutamic (a, f) and amino adipic semi-aldehydes (b, g) were influenced by diet (but not GSA in males). Similarly, protein glycoxidative markers carboxy-methyl-lysine (c, h) and carboxy-ethyl-lysine (d, i) were influenced by age. A marker of protein lipoxidative modification, malondialdehyde-lysine showed a paradoxical increase in low unsaturation fed animals (e, j), specifically in females and was the only marker affected significantly by age. In accordance with faster rate of disease onset and proteotoxicity in highly unsaturated diets, males (endpoint: 130 ± 7 days) showed significantly higher ubiquitin immunostaining in lumbar spinal cords by confocal microscopy (k) as quantified (l) in comparison to control diet. Higher

magnification images showed that ubiquitin immunostaining (arrowheads, m) was not restricted to SMI-32 positive neurons in anterior ventral horn (arrows, m). *, **, ***, and **** diet-related significant differences ($p < 0.05, 0.01, 0.001$ and 0.0001 , respectively) by post hoc Bonferroni multiple comparisons after two-way ANOVA, while as ^aage-related ($p < 0.05$) and ^{b,bb,bbb}diet-related ($p < 0.05, < 0.001$ and < 0.0001 , respectively) significant differences by two-way ANOVA. Bars in k and m are 500 and 50 µm, respectively. Number of animals used for each marker measure was $n = 7$ for each time point, both male and female. A total of 30 slices ($n = 3$ animals per treatment) were analysed for quantification in l, with differences evaluated by ANOVA post hoc Tukey’s multiple comparison test

surprisingly high on the spinal cord of animals under low unsaturation diets, most probably due to an increase of 20:4 and 22:4, both from the n-6 series, specially in females.

As surrogate marker of n-3 availability, we chose syntaxin-3 immunoreactivity (Darios and Davletov 2006), which showed that high unsaturated diet led to more

intense syntaxin-3 expression than low unsaturated one at similar ages (Fig. 1k).

All in all, these data demonstrated that highly unsaturated diets affected in a gender-dependent fashion the mean survival, the disease onset and the clinical evolution in the FALS model hSODG93A.

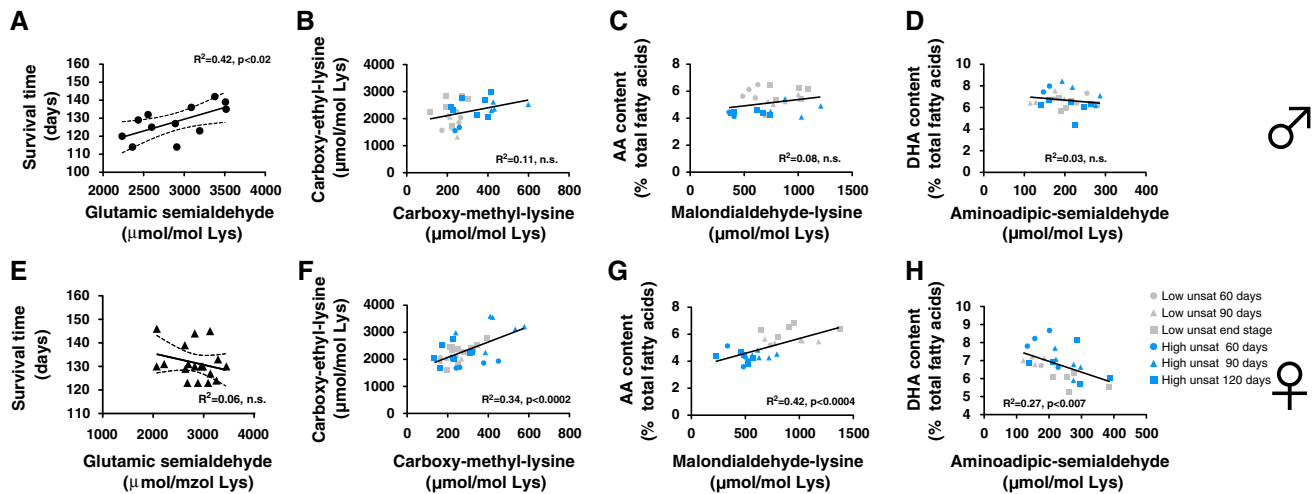


Fig. 3 Gender specific correlation between survival, protein oxidative damage and fatty acid contents. Glutamic semi-aldehyde is correlated with survival time in males (a) but not in females (e). Carboxy-ethyl-lysine is not correlated with carboxy-methyl-lysine modification in males (b) in contrast with females (f). Lipoxidative modification is not correlated with AA content in males (c) but it

shows a positive correlation in females (g). Amino adipic semi-aldehyde is inversely correlated with docosahexanoic acid content in spinal cord in females (h), but not in males (d). Inset show the linear regression statistic, with legend in h indicating the age and diets from individuals in the analyses from c to h

Protein Oxidative Damage in Neuronal Tissues of hSODG93A Transgenic Mice is Dependent on Dietary Fatty Acid Unsaturation

Potential causes of the deleterious effect of highly unsaturated diets comprise their high susceptibility to oxidative modification, though changes in DBI and PI suggested that highly unsaturated diets actually lowered PI. As shown in Fig. 2, the changes of unsaturation in diet induce significant changes in protein oxidative damage. For GSA, the most abundant marker among those detected belonging to direct oxidation pathway, changes in diet only induced significant effects in females, significantly lowering at early clinical stages. For AASA, both high and low unsaturated diets increased their concentrations, both in females and in males, being the changes more marked with high unsaturated diet. For CML, similar trends were seen in males and females, again showing that dietary unsaturation changes increased glycoxidative modifications at last stages, with reference to control diet. For CEL, significant increases were detected, induced by high unsaturated diet in males. Of note, at 90 days, levels of CEL were highest in males under high unsaturated diets, suggesting a key role for this modification in the determination of survival, as this is the group with faster disease progression and lower survival. Similarly, as females under highly unsaturated diets tended to have faster progression, significant CEL and CML increases at 90 days reinforce the role of glycoxidative modifications. Finally, for lipoxidative modifications (MDAL), significant increases induced by low unsaturated

and high unsaturated diet were evident, in line with PI changes. Interestingly, age was only a significant factor for changes in MDAL concentrations. Importantly, protein oxidative modifications are associated with aggregate build-up and increased ubiquitination (Shang and Taylor 2011). Reinforcing the mass spectrometry findings indicating protein modification with changes in unsaturation of diets, confocal immunohistochemistry revealed increased ubiquitin immunoreactivity in motor neurons and glial cells (Fig. 2k–m) in comparison to control diets.

Correlation analyses of these variables revealed strong gender specificity. In order to study the relationship between fatty acid composition and protein oxidative damage, we clustered all the values, irrespectively of diets. Following these analyses, in males, protein oxidative modification was directly correlated with survival, but not in females (Fig. 3a, e). Similarly, the two glycoxidation markers, CEL and CML correlated in females, but not in males (Fig. 3b, f). Supporting a significant role of inflammatory potential in protein oxidative modifications, AA content correlated with MDAL modification in females (Fig. 3g). Finally, reinforcing the potential protective role of DHA, its level was inversely correlated with one of the markers of protein oxidative modification in females (Fig. 3h).

All in all, these results suggest a lack of a general relationship between protein oxidative modifications and survival or disease onset. Interestingly, under control fatty acid diets, lower lipoxidative damage (measured by MDAL concentration) is found, in line with fatty acid

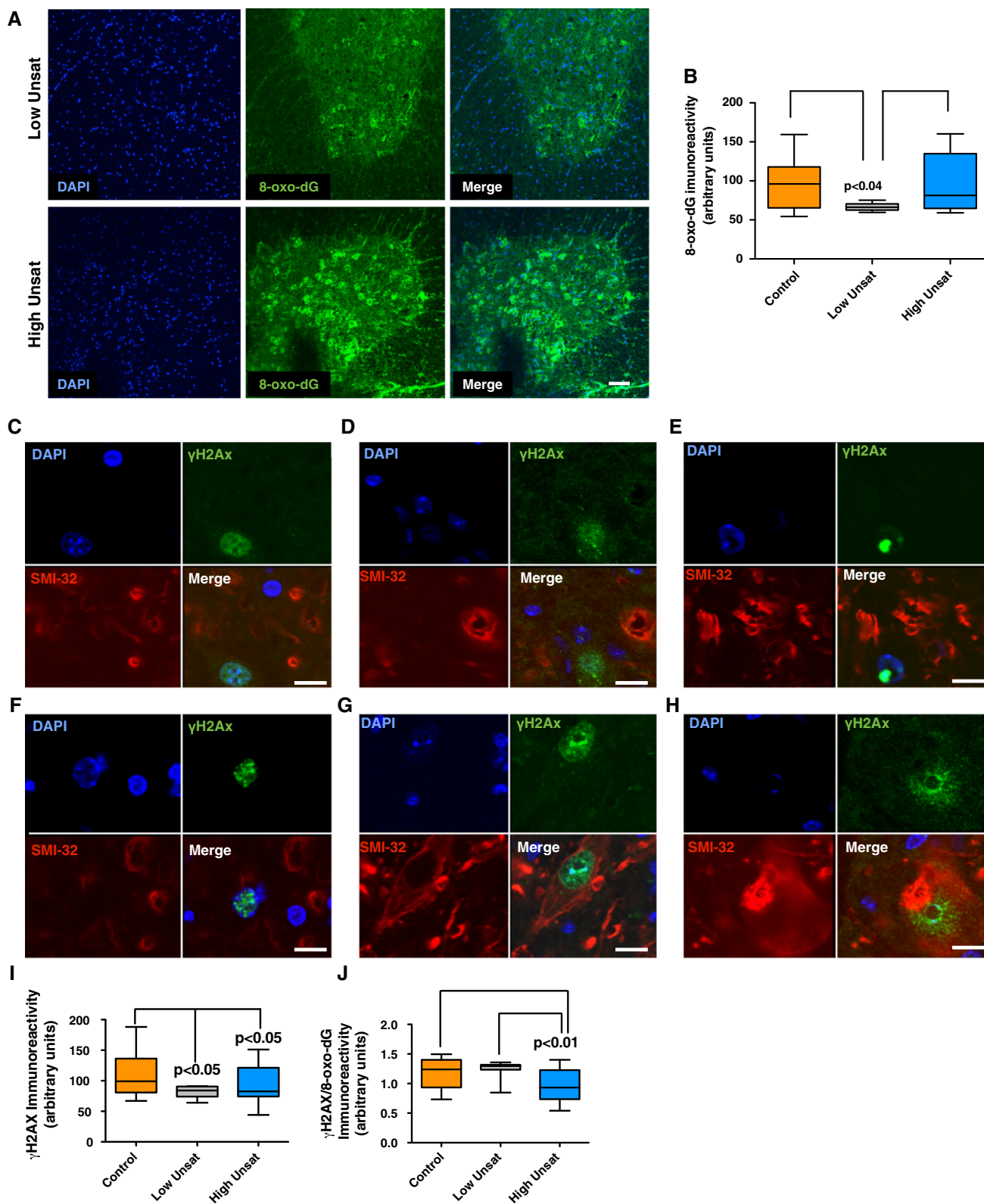


Fig. 4 Dietary fatty acid unsaturation changes 8-oxo-dG levels and its relationship with nuclear DNA damage response. The marker of oxidative DNA damage 8-oxo-dG was analysed by confocal immunohistochemistry in lumbar spinal cords from male mice in the preclinical stage (90 days) (a). Quantitative analyses demonstrated significantly decreased unsaturation in the low unsaturation group (b). Differential immunohistochemical pattern for γ H2Ax (90 days, male). Non-neuronal γ H2Ax appears as discrete patterning (c), as heterogeneous foci (d) or as a single aggregate (e). Similarly, motor neuron, (SMI-32 positive cells) had discrete foci (f) or general nuclear staining (g and h). Quantitative analyses of γ H2Ax and SMI-32 staining in whole sections are shown in the graph (i) and ratio between γ H2Ax and 8-oxo-dG in the graph (j). Bars in a and c are 10 and 5 μ m, respectively. A total of 30 slices (belonging to $n = 2$ –3 animals per treatment) were analysed for quantification in b and i, with differences evaluated by ANOVA post hoc Tukey's multiple comparison test

compositional changes, when compared to diets extreme in unsaturation. Rather, a potential protective role of lipid peroxidative-derived modifications can be defined in females.

Dietary Fatty Acid Unsaturation Blunts the Mitochondrial–Nuclear Crosstalk Based on Free Radical Production and DNA Damage Response

To extend oxidative damage measurements to nucleic acids, we evaluated the presence of 8-oxo-dG, a direct marker of oxidative modification of DNA, focused to male group and extreme unsaturation diets. In line with previous data demonstrating that 8-oxo-dG levels are higher in mitochondrial DNA than in nuclear DNA (Barja and Herrero 2000), 8-oxo-dG immunoreactivity was mainly localized in non-nuclear locations (Fig. 4a, c). 8-oxo-dG immunoreactivity was significantly higher in spinal cord from animals fed with highly unsaturated diet, reinforcing the importance of mitochondrial DNA modification in this transgenic model (Fig. 4a, b), in comparison to low unsaturated diet. Recent data show the crosstalk between mitochondrial-free radical production and nuclear DNA damage response, mediated by γ H2Ax (Passos et al. 2010). To evaluate whether this mechanism was affected by dietary fatty acid unsaturation, we evaluated by confocal microscopy the amount of γ H2Ax foci, a surrogate for DNA damage response. The results showed the presence of γ H2Ax in both non-neuronal (Fig. 4c–e) and neuronal cells (Fig. 4f–h). Quantitative analyses of anterior horns of whole sections (Supplemental Figure 2) showed that dietary fatty acid unsaturation influenced the mitochondrial–nuclear crosstalk, as increased 8-oxo-dG immunostaining in animals fed with high unsaturated diet was not associated to an increase in γ H2Ax staining in ventral horn of lumbar spinal cord (Fig. 4i), as reinforced by analyses of the γ H2Ax to 8-oxo-dG immunostaining ratio (Fig. 4j).

Discussion

The influence of dietary components in ALS progression has been a focus of wide research. It is well accepted that malnutrition is a negative prognostic factor (Greenwood 2013). A recent clinical trial evidence the relevant role of nutrition in ALS (Wills et al. 2014). Furthermore, it has been suggested (ALS Untangled 2012) that saturated fats, such as those present in coconut oil, could alleviate the disease course by means of increasing energy bioavailability towards mitochondrial pathways. The favourable effect of low unsaturated diet in comparison to high unsaturated one might be attributed to enhanced calorie availability. However, the fact that, under low unsaturated diets, mice had lower weight gain, suggests a potential disease-accelerating effect, even if it was not reflected in mean survival (at least for males). Previous data have linked fresh fish intake to ALS development (Sienko et al. 1990), although the mechanisms behind might be related to intake of contaminants including cyanobacterial-derived neurotoxins or metals (Roos et al. 2013; Vinceti et al. 2012). Nonetheless, a recent review reveals that PUFAs, if appropriately protected from peroxidation (e.g. by vitamin E) can be protective (Veldink et al. 2007). Indeed, in a different population, epidemiological studies have revealed that high intake of PUFAs, with other dietary fats, may have a preventive effect in ALS (Okamoto et al. 2007).

Our data and a recent report (Yip et al. 2013) have shown that this potential protective role is not easily reproduced in the same murine model. Previous results, both in the sporadic form of the disease (Ilieva et al. 2007; Shibata et al. 2004), as well as in the murine model (Perluigi et al. 2005) have suggested the accrual of lipid peroxidation-derived aldehydes (such as 4-hydroxy-2-hexenal or 4-hydroxy-2-nonenal), as well as the resulting modification of specific proteins. However, our present data have shown that the relationship between lipid peroxidation and disease evolution is not linear. Of note, despite diet was effective in changing the lipid profiles of several tissues (by comparison of previous data in liver (Herrero et al. 2001) using the same diets), central nervous system lipids were much more resistant to the introduced changes. Noteworthy, our low unsaturation diet was not intended to induce PUFA depletion. These formulations fulfil essential fatty acids requirements since it contained a sufficient amount of soybean oil. Interestingly, under the low unsaturation diet, we observed a paradoxical increase in the peroxidizability index, which is mainly attributable to the increased levels of AA. This increase is interpreted as an adaptive reaction to diet and disease, since diet composition for this particular fatty acid was in fact lower in the low unsaturated one. This may be related to the modulatory role of AA in inflammation. In any case, increased peroxidizability index

was associated with the increased load of protein lipoxidative damage (as evidenced by mass spectrometric measurements of MDAL). In contrast, the other protein oxidative modification markers measured (arising from direct oxidation or from glycooxidation) showed an increase under high unsaturated diets. This suggests that protein oxidative modifications such as GSA, AASA, CML and CEL could be more deleterious than MDAL. As a matter of fact, GSA shows a clear correlation with survival in males, a fact non present in females, suggesting that in these, protective mechanisms against protein oxidation could operate, as it has been suggested for ALS (Cervetto et al. 2013; Eschbach et al. 2013; Li et al. 2012) and in other diseases (Puertas et al. 2012).

Our results suggest that the relationship between lipid peroxidation and disease pathogenesis is not linear; i.e. lipid peroxidation is not always noxious. Previous data have demonstrated the important adapting role induced by lipid peroxidation-derived aldehydes, such as 4-hydroxy-2-nonenal and 15-deoxy- Δ -12,14-prostaglandin J₂. Thus, it is considered that lipid peroxidation may have a dual role in the pathogenesis of several diseases (Catalá 2009). In addition, protective roles of specific fatty acids can operate differently depending on diets and gender. The levels of a carbonyl damage marker (AASA), directly related to disease evolution, were inversely related to the content of DHA, supporting the potential protective role of this n-3 fatty acid. Docosahexanoic acid-derived molecules, such as resolvin D1, have been shown to be potentially protective in the process of phagocytosis which operates at later stages of ALS (Liu et al. 2012). Furthermore, previous data have revealed that while spinal cords with marked neuron loss showed diminished DHA contents, the cortex of the same individuals affected by ALS showed an increase in DHA (Ilieva et al. 2007). Interestingly, hSODG93A female transgenic mice at 90 d under low unsaturated diet (i.e. living longer than males) exhibited ca 6 % more DHA than males. However, DHA-dependent mechanisms could operate up to a certain point of pathological burden. Despite high unsaturated diet did not led to higher DHA content in males, biologically these diets allowed for higher accumulation of the DHA-dependent protein syntaxin-3 (Darios and Davletov 2006), supporting the notion that enhanced availability of DHA in high unsaturation diets may have some neurobiological impact. Our results support the notion that a trade-off for the high content of PUFAs in neuronal tissues, a high peroxidizability, may have a beneficial-adaptative role (i.e. accumulation of DHA-dependent proteins, enhanced responsiveness in terms of antioxidant mechanisms).

A similar trade-off is also evident from examining the potential implication of inflammation in the findings reported in our work. Neuroinflammation, just as lipid

peroxidation, is recognized to play a dual role, being neuroprotective in some stages to become neurotoxic in others (Consilvio et al. 2004). Our data, demonstrating a significant correlation between arachidonic acid content and MDAL only in females, suggest that lipid peroxidation adaptative mechanisms also affect arachidonic acid levels, and, consequently, inflammatory potential. Interestingly, reinforcing the potential protective role of neuroinflammation in some stages of the disease, high unsaturated diets in males, associated with a poor outcome-diminished survival, earlier onset, enhanced aggregation of ubiquitin proteins in spinal cord were consistently associated with higher anti-inflammatory index, as suggested by fatty acid profiles.

Both inflammation and oxidative stress can be inter-players in ageing basic mechanisms. Being ageing a clear risk factor for ALS, we explored whether mechanisms linking ageing, oxidative stress and inflammation could explain part of our results. In this line, the mitochondrial–nuclear crosstalk is relevant in cellular senescence (Passos et al. 2010). A resulting unbalanced response includes sustained DNA damage response and senescence-associated secretory phenotype, fuelled by mitochondrial-free radical production dependent on p21 activation and TGF β production. For this reason, we evaluated the presence of γ H2Ax foci, related to DNA damage, in spinal cord in this model. The present results have shown markers of DNA damage repairing in motor neurons and glial cells. Despite it has been previously hypothesized that these phenomena could be present in various in vitro models of neurodegeneration (Avramovich-Tirosh et al. 2007), our results demonstrate an unreported variability in the immunostaining of γ H2Ax. This morphological variety can be attributed to the several roles of this protein in cell homeostasis (Sharma et al. 2012) ranging from DNA replication to apoptosis, including also physiological neuronal activity (Suberbielle et al. 2013). Previous data have demonstrated that DNA in ALS is damaged in mitochondria (Kikuchi et al. 2002) and in the nuclei (Barbosa et al. 2010; Murata et al. 2008). Interestingly, recent data suggest a gender-specific difference in terms of DNA damage response/repair capacity (Trzeciak et al. 2008). The finding of increased mitochondrial DNA damage induced by high unsaturation, without a concomitant increase in γ H2Ax suggests that the mitochondrial–nuclear crosstalk based on p21 and free radical production is influenced by diet, specifically by PUFAs. Previous work has related G93A mutation to increased 8-oxo-dG accumulation (Barbosa et al. 2010) and also data from our laboratory (Herrero et al. 2001), revealed higher free radical production in mitochondria from animals fed with similarly high unsaturated diets, a finding that fits with enhanced 8-oxo-dG present in this work. Therefore, a logical response to

enhanced free radical production would be increased DDR, thought data presented here suggest that this is not the case. Reasons for this blunted response on mitochondrial–nuclear crosstalk may arise from several facts. It is known that enhanced levels of n-6 fatty acids (such as those present in low unsaturated fed animals) can be linked to higher production of TGF β , a key factor in the mitochondrial–nuclear crosstalk (Harbige and Sharief 2007). Similarly, it is known that docosa-hexanoic or eicosapentaenoic acids change the expression of p21 (Katakura et al. 2013; Slagsvold et al. 2010). When added to the fact that high unsaturated diets actually decreased lipid peroxidative modification in these experiments, our results reinforce a potentially protective role for lipid peroxidation. Thus, low unsaturated diets would sustain lipid peroxidation and reinforce mitochondrial–nuclear crosstalk via increased TGF β secretion and γ H2Ax foci formation and maintaining both an adequate antioxidant response—as evidenced by lower protein oxidative and glycoxidative damage—as well as diminished levels of mitochondrial DNA modification. In contrast, high unsaturated diets could act deleteriously in a double fashion: by increasing p21 expression, perhaps interfering with its activation and by increasing free radical production without an adequate response of cellular antioxidant systems, which will be focus of future studies.

As limitations of the present study, we recognize that other clinical measurements (e.g. Rotarod-based) may be also of interest. Further, establishment of standard methods for treatment testing is crucial in ALS models Ludolph et al. (2007, 2010). However, we hope that measurement of three indicators of disease evolution (i.e. weight changes, clinical score and stride length) could be helpful for global assessment of diet-induced changes. Importantly, these analyses show that values in animals fed with control diets were not always between the low unsaturated and high unsaturated groups: our suggestion is that survival, in relationship with changes in fatty acid composition present in spinal cord suggest the importance of an adequate lipid profile in neuronal resistance towards stressors. For instance, levels of AA are paradoxically lower in high unsaturated groups (irrespectively of the gender). A potential protective role of AA-derived bioactive compounds cannot be discarded based on these results. In line with this, fatty acids with a potential neuroprotective effects, such as DHA, are not altered in any of the groups, suggesting their importance and resilience towards dietary changes. We have also disclosed that in some terms, such as DNA modification and response to it, control animals behave differently to low unsaturated fed ones, demonstrating the complexity of the relationships behind.

Our data reveal that intervention on dietary fat unsaturation modulates the gender protective effect in females.

Highly unsaturated diet apparently diminished survival in females, while as maintenance of a diet with a low unsaturation allowed to differentiate gender-specific effects in survival of this ALS model. Taking into account the several mechanisms studied, particularly oxidative stress, our data suggest that despite PUFAs could have some potential benefits in specific stages of the disease, through a surprisingly protective lipid peroxidation, later on, the disease-sparing mechanisms are overwhelmed by pathology burden. A similar mechanism could operate for neuroinflammation. Further, our data suggest that highly unsaturated diet could blunt a mitochondria–nuclear crosstalk, essential for cell homeostasis. Together, these results reinforce the need for adequately defining gender as a modifying factor in ALS models, as well as to use structurally characterized and variegated markers for oxidative damage assessment in neurodegeneration.

Acknowledgments We are grateful to J. Pairada for excellent technical assistance. We thank D. Argilés and M. Martí for their skilful assistance. Supported by the Spanish Ministry of Science and Innovation [CENT Program, BFU2009-11879/BFI and AGL2006-1243] the Autonomous Government of Catalunya [2009SGR-735] and the Spanish Ministry of Health [FIS 08-1843, 11-01532 to M.P-O and FIS13-00584 to RP]. Supported also by the COST B-35 Action and the Fundació Miquel Valls. D.C. is a predoctoral fellow from Spanish Ministry of Health [FI08-00707]. O.R-N. and R. C. received a predoctoral fellowship from Autonomous Government of Catalonia.

Conflict of interest Daniel Cacabelos, Victoria Ayala, Omar Ramírez-Nunez, Ana Belen Granado-Serrano, Jordi Boada, Jose CE Serrano, Rosanna Cabré, Gisela Nadal-Rey, Isidro Ferrer, Reinald Pamplona and Manuel Portero-Otin have not financial relationship with the organizations that sponsored the research.

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Table S1: Fatty acid composition (% of abundance) and derived indexes in spinal cord (lumbar region) from hSODG93A male mice (90days).

	Control	High Unsat	Low Unsat	p value (Hi/Lo)	p value (Hi/Ctl)	p value (Lo/Ctl)
18:0	17,72±0,11	15,86±1,05	16,59±1,68	0,676	0,297	0,495
18:1n-9	38,91±0,269	38,76±1,57	33,04±1,86	0,017	0,942	0,011
20:4n-6	5,44±0,100	4,73±0,289	5,29±0,126	0,048	0,017	0,548
22:4n-6	2,34±0,074	1,39±0,088	2,26±0,126	0,001	0,001	0,543
22:6n-3	6,79±0,117	7,40±0,490	6,62±0,278	0,101	0,189	0,688
SFA	38,91±0,17	40,58±1,97	45,59±1,75	0,037	0,443	0,006
UFA	60,92±0,25	59,41±1,97	54,40±1,75	0,037	0,489	0,007
MUFA	41,99±0,31	39,32±1,49	33,75±1,85	0,018	0,210	0,001
PUFA	18,93±0,16	20,08±0,86	20,65±0,27	0,416	0,116	0,020
PUFA n-3	7,31±0,11	10,79±0,42	9,70±0,33	0,031	0,001	0,001
PUFA n-6	11,62±0,11	9,28±0,83	10,94±0,33	0,020	0,003	0,263
DBI	125,74±0,76	135,83±3,85	130,49±1,69	0,121	0,009	0,141
PI	95,62±1,06	115,10±4,18	113,41±2,96	0,688	0,001	0,001
AI	140,31±3,77	207,84±8,00	155,11±3,13	0,001	0,001	0,050

P value for Bonferroni multiple comparison tests after ANOVA analyses

Table S2: Fatty acid composition (% of abundance) and derived indexes in spinal cord (lumbar region) from hSODG93A female mice (90days).

	Control	High Unsat	Low Unsat	p value (Hi/Lo)	p value (Hi/Ctl)	p value (Lo/Ctl)
18:0	17,78±0,14	18,70±0,36	16,95±0,27	0,001	0,023	0,051
18:1n-9	39,42±0,26	39,29±0,35	34,03±0,72	0,001	0,822	0,001
20:4n-6	5,40±0,07	4,51±0,09	5,50±0,04	0,001	0,001	0,374
22:4n-6	2,31±0,027	1,21±0,052	2,63±0,164	0,001	0,001	0,020
22:6n-3	6,78±0,049	6,83±0,263	7,00±0,079	0,441	0,815	0,312
SFA	38,97±0,23	41,35±0,063	43,79±0,69	0,006	0,005	0,001
UFA	61,07±0,23	58,67±0,63	56,20±0,69	0,006	0,005	0,001
MUFA	42,45±0,28	39,93±0,33	34,73±0,69	0,001	0,001	0,001
PUFA	18,56±0,08	18,73±0,49	21,46±0,25	0,001	0,698	0,001
PUFA n-3	7,34±0,04	10,17±0,39	9,97±0,18	0,591	0,001	0,001
PUFA n-6	11,21±0,08	8,56±0,17	11,48±0,10	0,001	0,001	0,156
DBI	125,54±0,27	130,22±2,79	135,73±1,17	0,046	0,063	0,001
PI	95,47±0,53	107,88±3,40	118,55±1,32	0,001	0,004	0,005
AI	140,28±2,42	201,46±2,52	158,20±2,79	0,001	0,001	0,001

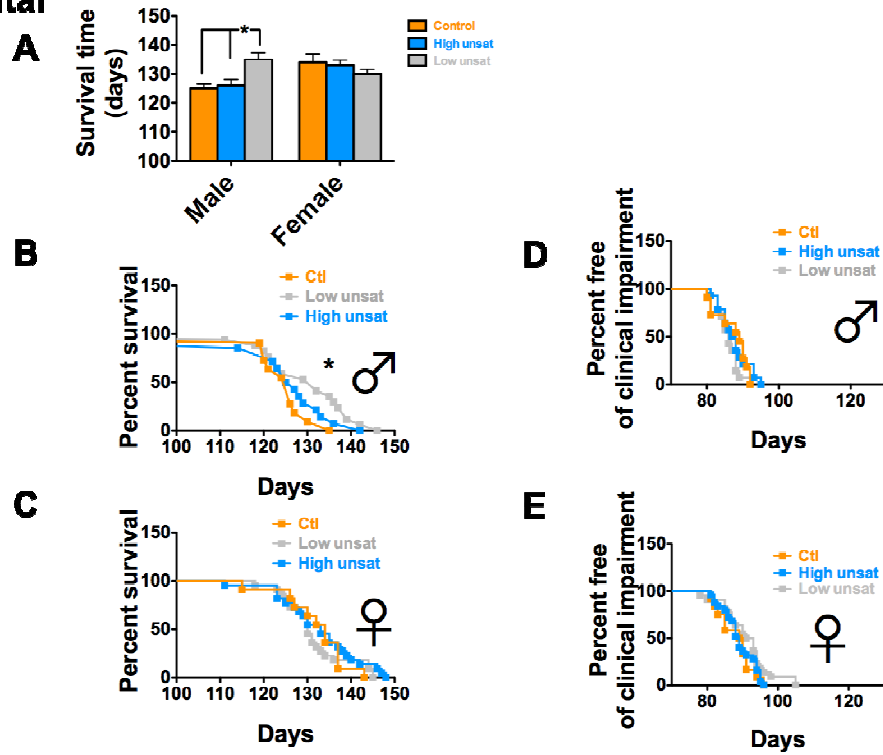
P value for Bonferroni multiple comparison tests after ANOVA analyses

Table S3. Fatty acid composition (mol%) of diets. Values are means \pm SEM from n=3 samples.

	High Unsat	Low Unsat	Control	p value (Hi/Lo)	p value (Hi/Ctl)	p value (Lo/Ctl)
14:0	10,04 \pm 0,173	29,67 \pm 0,422	0,404 \pm 0,040	0,001	0,001	0,001
16:0	17,78 \pm 0,113	18,14 \pm 0,018	11,95 \pm 0,011	0,102	0,001	0,001
16:1n-7	10,78 \pm 0,085	0,096 \pm 0,003	0,245 \pm 0,028	0,001	0,001	0,254
18:0	4,184 \pm 0,021	18,75 \pm 0,333	4,430 \pm 0,046	0,001	0,381	0,001
18:1n-9	14,44 \pm 0,012	8,854 \pm 0,062	23,88 \pm 0,629	0,001	0,001	0,001
18:2n-6	12,71 \pm 0,217	20,64 \pm 0,034	49,73 \pm 0,122	0,001	0,001	0,001
18:3n-3	3,397 \pm 0,069	2,987 \pm 0,032	7,501 \pm 0,085	0,064	0,001	0,001
18:4n-6	n.d.	0,061 \pm 0,007	0,155 \pm 0,015	-	-	0,047
20:0	1,352 \pm 0,142	0,262 \pm 0,008	0,350 \pm 0,009	0,001	0,001	0,604
20:1n-9	1,775 \pm 0,077	0,083 \pm 0,004	0,214 \pm 0,013	0,001	0,001	0,521
20:2n-6	1,302 \pm 0,194	0,030 \pm 0,005	0,080 \pm 0,014	0,001	0,001	0,061
20:3n-6	1,200 \pm 0,189	0,020 \pm 0,002	0,054 \pm 0,009	0,001	0,001	0,057
20:4n-6	1,876 \pm 0,176	0,021 \pm 0,002	0,053 \pm 0,008	0,001	0,001	0,060
20:5n-3	8,532 \pm 0,429	0,038 \pm 0,005	0,101 \pm 0,005	0,001	0,001	0,041
22:0	0,917 \pm 0,073	0,130 \pm 0,010	0,318 \pm 0,014	0,001	0,001	0,151
22:4n-6	0,735 \pm 0,094	0,031 \pm 0,015	n.d.	0,001	-	-
22:5n-6	0,963 \pm 0,140	0,043 \pm 0,003	0,095 \pm 0,001	0,001	0,001	0,031
22:5n-3	1,871 \pm 0,170	0,028 \pm 0,001	0,068 \pm 0,009	0,001	0,001	0,040
24:0	0,990 \pm 0,098	0,053 \pm 0,001	0,154 \pm 0,011	0,001	0,001	0,001
22:6n-3	4,790 \pm 0,363	0,040 \pm 0,003	0,109 \pm 0,014	0,001	0,041	0,080
24:5n-3	0,340 \pm 0,083	n.d.	0,024 \pm 0,002	-	0,001	-
24:6n-3	n.d.	0,006 \pm 0,001	0,061 \pm 0,003	-	-	0,001
SFA	35,27 \pm 0,323	67,01 \pm 0,094	17,61 \pm 0,084	0,001	0,001	0,001
UFA	64,72 \pm 0,320	32,98 \pm 0,095	82,38 \pm 0,084	0,001	0,001	0,001
MUFA	25,22 \pm 0,068	8,95 \pm 0,062	24,13 \pm 0,065	0,001	0,001	0,001
PUFA	37,75 \pm 0,457	23,95 \pm 0,043	58,04 \pm 0,155	0,001	0,001	0,001
PUFA n-3	19,96 \pm 0,690	3,153 \pm 0,040	8,027 \pm 0,110	0,001	0,001	0,001
PUFA n-6	18,79 \pm 0,120	20,84 \pm 0,017	50,17 \pm 0,098	0,001	0,001	0,001
DBI	164,77 \pm 3,08	60,60 \pm 0,228	149,75 \pm 0,22	0,001	0,001	0,001
PI	142,9 \pm 4,491	28,40 \pm 0,270	69,49 \pm 0,002	0,001	0,001	0,001
AI	893,6\pm109,6	617,9\pm76,3	659,9\pm117,2	0,001	0,001	0,812

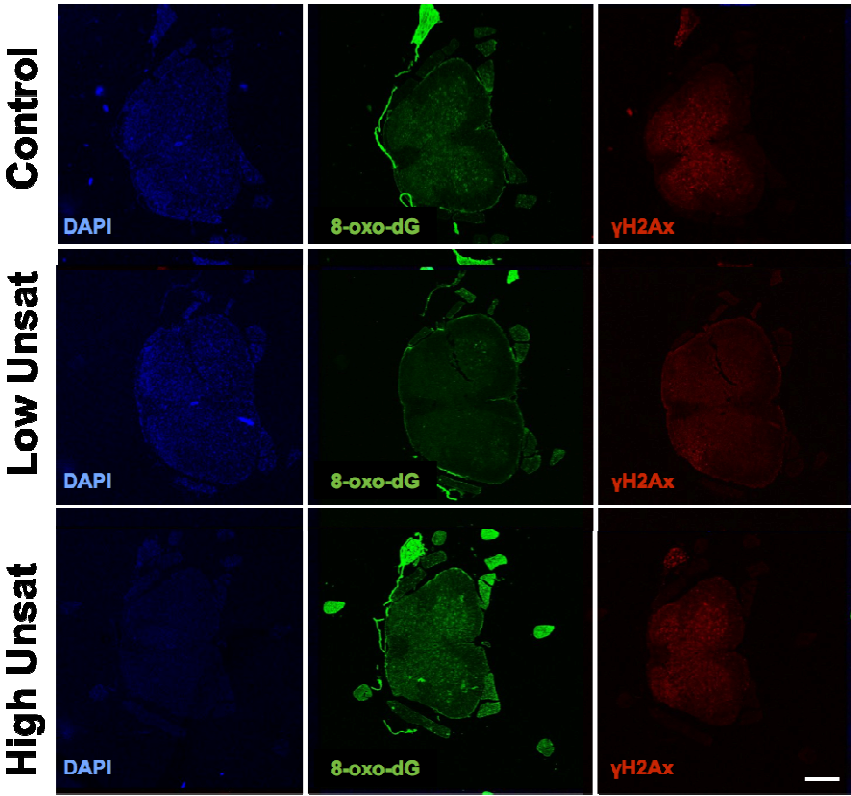
p value reflects statistical significance between diets by Bonferroni multiple comparison test after ANOVA analyses.

Supplemental Figure 1

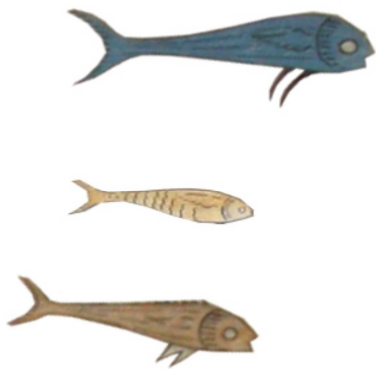


Supplemental Figure 1. Effect of diet and gender in median survival (A). B and C show the effect of experimental diets in survival curves separated by gender (middle for male and lower for female gender). * In A indicates significant difference by Bonferroni post hoc after 2 way ANOVA ($p < 0.05$ with reference to control or highly unsaturated diets). * In B indicates significant differences by Logrank test for trend between diets in males ($\chi^2 = 4.05$; $p < 0.04$). D and E show the effect of experimental diets in clinical onset, according to gender

**Supplemental
Figure 2**



Supplemental Figure 2. Effect of dietary unsaturation in oxidative DNA modification (8-oxo-dG) and its relationship with nuclear DNA damage response (γH2Ax). Bar is 0.5 μm.



4.4 Article 4

Title: “Gender Specific Differences in Spinal Cord Mitochondrial Function and Oxidative Damage Markers in a Mouse Model of ALS in Early Stages of Disease”.

Authors: Cacabelos D, Boada J

Gender specific differences in spinal cord mitochondrial function and oxidative stress markers in a mouse model of ALS in the early stage of disease

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Running title: gender and spinal cord mitochondria in G93A mice

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Abstract

Amyotrophic lateral sclerosis (ALS) is a motor neuron disease with a gender bias towards major prevalence in male individuals. Several data suggest the involvement of oxidative stress and mitochondrial dysfunction in its pathogenesis, though differences between genders have not been evaluated by state-of-the art analytical approaches. This study aimed to compare mitochondrial function in male versus female in spinal cord of a mouse model of ALS the G93A-hSOD1 overexpressing mice, by using high-resolution respirometry. This was measured both in the early pre-symptomatic and pre-symptomatic stages, at onset and near endpoint of the disease. Subsequently, we analyzed mass-spectrometric markers of protein oxidative damage and tissue lipid profile. Mitochondrial respiratory chain protein expression and high resolution respirometry were also analysed in Neuro 2A cell cultures transfected to overexpress G93A-hSOD1 after pretreatment with 17 β -estradiol. Overexpression of G93A mutated human SOD1 in transgenic mice decreased efficiency of mitochondrial oxidative phosphorylation, revealing a temporal delay in females respect to males associated to a parallel increase in protein oxidative damage. Neuro 2A cells overexpressing G93A-hSOD1 showed a reduction *in situ* mitochondrial complex I O₂ consumption prevented by 17 β -estradiol pretreatment. In conclusion, ALS associated SOD1 mutation leads to a delayed mitochondrial dysfunction in female mice in comparison with males partially attributable to the higher oestrogen levels of the former. This study may be important to further understand whether different degrees of spinal cord mitochondrial dysfunction are related to the earlier onset and faster disease progression in male ALS patients than in their female counterparts.

Introduction

Amyotrophic lateral sclerosis (ALS, OMIM #105400) is the motor neuron disorder with a higher occurrence in adult humans, characterized by a progressive loss of upper and lower motor neurons that leads to muscular atrophy, paralysis and death after median disease duration of 3 years (Leigh, 2007). The most common form of ALS is sporadic (sALS), having no apparent heritability, whereas the dominantly inherited familial ALS (fALS) accounts for only about 5 to 10% of all ALS patients (Al-Chalabi et al., 2012; Byrne et al., 2011). Among the genetic causes of ALS, Second to hexanucleotide repeat expansions in chromosome 9 open reading frame 72 (C9ORF72) (DeJesus-Hernandez et al., 2011; Renton et al., 2011), 15-20% of fALS cases and about 5% of sALS cases are associated to multiple mutations in the gene for Cu/Zn-superoxide dismutase (SOD1), which imparts a novel toxic function to this otherwise superoxide radical scavenging enzyme in normal condition (Rosen, 1993). Furthermore, mutated SOD1 forms appear misfolded, aggregated and accumulated primarily in spinal cord motor neurons and glial cells of ALS patients (Nagai et al., 2007). Transgenic mice overexpressing mutant forms of the human SOD1 (hSOD1) gene develop a progressive motor neuron syndrome similar to the human ALS phenotype (Gurney et al., 1994; Turner & Talbot, 2008) and have been extensively used as an experimental model to gain insight into ALS pathogenesis. Consequently, overexpression in animals and cultured cells of a mutated form of hSOD1 with a glycine for alanine substitution in amino acid 93 (G93A-hSOD1), has become the most used model to study pathophysiological ALS features.

Gender-related differences in many neurodegenerative diseases are observed across epidemiologic studies, pathophysiology and treatments (Crawford & Duncan, 2012; Członkowska, Ciesielska, Gromadzka, & Kurkowska-Jastrzebska, 2006). ALS not being an exception, its incidence (average male/female ratio 1.3) and prevalence are higher in men than in women, with a predominance of men with younger disease onset. Clinical phenotypes are also different in male and female patients, especially regarding to the site of onset of weakness, as well as cognitive impairment (Blasco et al., 2012; Portet, Cadilhac, Touchon, & Camu, 2001). The aforementioned gender differences have been reported in studies that included all ALS patients (sporadic and familial) but when fALS cases were studied separately, the gender ratio again was not equal to 1 (McCombe & Henderson, 2010), although according to some previous reports, fALS incidence was not significantly different between men and women, as theoretically expected with an autosomal dominant disease with complete penetrance (Orrell et al., 1999). However, supporting the higher occurrence of fALS in men than in women, data extracted from ALSod web site (www.alsod.iop.kcl.ac.uk) revealed a c. 1.5 male/female ratio for most mendelian ALS-related mutant genes, including SOD1. Moreover, it has been reported that gender can account for variations in the course of disease in fALS (H. Y. Kim et al., 2007).

Most of the neurodegenerative disorders involve either causally or consequently mitochondrial abnormalities (Federico et al., 2012; Lin & Beal, 2006; Martin, 2012) (reviewed in (Lezi & Swerdlow, 2012)). Although the underlying causes of motor neuron degeneration in ALS remain largely unknown, ALS-causing SOD1 mutations result in mitochondrial dysfunction, among multiple pathogenic pathways also present in sALS, such as oxidative stress and endoplasmic reticulum stress (Ayala et al., 2011; Cozzolino, Ferri, Valle, & Carri, 2013; Ilieva et al. 2007; Rothstein, 2009). A common trait of skeletal muscle biopsies of sALS and fALS patients, as well as transgenic animal models of ALS, is a mitochondrial electron transfer chain (ETC) dysfunction, leading to an impairment of ATP synthesis, metabolic stress, retrograde neurodegeneration and ultimately motor neuron cell death (Bowling, Schulz, Brown Jr, & Beal, 1993)(Vielhaber et al., 2000; Wiedemann et al., 1998). Being not restricted to

muscle mitochondria, similar deficits in the mitochondrial ETC have been reported in spinal cord of fALS patients, due to, among other causes, mitochondrial DNA mutations or binding of misfolded and aggregated SOD1 mutants to the voltage-dependent anion channel, dissipating the mitochondrial membrane potential (Jung, Higgins, & Xu, 2002; Mattiazzi et al., 2002). Moreover, besides its role in bioenergetics, buffering of intracellular calcium is one of the most important functions of the mitochondrion (Rizzuto, De Stefani, Raffaello, & Mammucari, 2012). Not surprisingly, mitochondrial dysfunction in spinal cord of ALS patients correlates with increased cytosolic calcium (Siklós et al., 1996). Likewise, SOD1-G93A transgenic mice exhibit a cytosolic calcium overload concomitant with a decrease in mitochondrial calcium loading capacity preceding neuromuscular alterations (Damiano et al., 2006) and a those changes are age-dependent (e.g. calpain activation and CaMKIV processing (Gou-Fabregas et al., 2014)).

Mitochondrial dysfunction may also directly provoke cell death by activating the apoptotic cascade, due to misfolded or aggregated SOD1 that results either in aberrant localization and release of proapoptotic factors, or binding to apoptotic inhibitors (Redler & Dokholyan, 2012). Studies in different species have reported that mitochondria in females are more differentiated, and, as a result, the mitochondria show a higher capacity and efficiency of substrate oxidation than in males. These features of female mitochondria have been described in nervous tissue, among other organs and tissues (Colom, Oliver, Roca, & Garcia-Palmer, 2007; Colom, Alcolea, et al., 2007; Guevara et al., 2009; Guevara, Gianotti, Roca, & Oliver, 2011; Justo et al., 2005). Results of several authors suggest a greater sensitivity of males to mitochondrial dysfunction compared to females. This includes higher permeability of the outer and inner mitochondrial membranes (whose occurrence is known to be affected by Ca^{+2} overload (Brustovetsky, Brustovetsky, Jemmerson, & Dubinsky, 2002)) with increased translocation of apoptosis-inducing factor (AIF) to the nucleus in neurons from immature rat brains submitted to hypoxia-ischemia (Weis et al., 2012). Moreover, male mitochondrial Ca^{+2} reuptake is known to be increased respect to females (Arieli, Gursahani, Eaton, Hernandez, & Schaefer, 2004).

In brain, other mitochondrial abnormalities related to neurodegeneration and more pronounced in males than females are an inhibition of mitochondrial electron transport chain complexes activities, a diminished mitochondrial mass and a lower mitochondrial membrane potential (Renolleau, Fau, & Charriaut-Marlangue, 2008; Renolleau, Fau, Goyenvallé, & Charriaut-Marlangue, 2007; Xia, Zhou, Huang, & Xu, 2006). Further, male mesencephalic neurons revealed a higher vulnerability to 6-hydroxydopamine compared with female cells. This difference in viability could be due to higher ROS generation and a more pronounced down-regulation of mitochondrial gene transcription, accounting for a more diminished ETC activity and subsequently lower ATP production in the male compared with female cells (Misiak, Beyer, & Arnold, 2010). Finally, focusing in gender relevance in the mitochondrial permeability transition pore formation in the SODG93A mouse model researchers (H. J. Kim, Magranè, Starkov, & Manfredi, 2012) demonstrated that deletion of cyclophilin D (a protein structurally linked to the mitochondrial permeability membrane transition pore (Doczi et al., 2011)) completely abolished the phenotypic advantage of female SODG93A, but no effect was found in males.

Taking this background into account, the aim of this paper was to study gender-related differences in spinal cord mitochondrial function of a mouse model of ALS, including the early pre-symptomatic stage of the disease. Several features of mitochondrial oxidative metabolism, lipid profile and protein oxidative stress markers have been analysed in SOD1-G93A transgenic mice and Neuro 2A cells overexpressing G93A-hSOD1. We hypothesized that differences in the

degree of spinal cord mitochondria dysfunction between male and female SOD1-G93A mice could explain, at least in part, their different clinical features. This study may be important to further understand whether different degrees of spinal cord mitochondrial dysfunction are related to the earlier onset and faster disease progression in male ALS patients than in their female counterparts. Moreover, understanding the causes of the sex differences in ALS could give clues to the pathophysiology of this devastating disease.

Materials and Methods

Chemicals

All reagents, unless stated otherwise, were purchased from Sigma Aldrich (St. Louis, MO). Media, sera, antibiotics and other media supplements and Lipofectamine 2000, were obtained from Invitrogen (El Prat de Llobregat, Catalonia). 17β -estradiol (E2) was dissolved in ethanol at a concentration of 1 mM, further diluted to 40 μ M with culture medium, aliquoted and stored frozen up to one month at -20°C . E2 stock solutions were used at a final concentration of 10 nM.

Animals

A colony of the strain B6SJL-Tg (SOD1-G93A)¹Gur/J (JAX catalogue stock number 002726; from now on G93A mice) was purchased at The Jackson Laboratories (Bar Harbor, ME) and maintained in the B6SJL background, by male founder crossing with B6SJL/F1/J females. All mice were genotyped as described in the Supplemental Methods section, and those non-transgenic littermates (from now on Control mice) were used as control. Animals were maintained under a constant 12h light–dark cycle in individual cages after weaning (day 21) with temperatures around $22\pm 4^{\circ}\text{C}$ and fed a standard rodent chow and water *ad libitum*. Animals were weighted weekly and daily for those under stride length analysis. A third-order polynomial curve was fitted to the age-body weight sets of data with Prism 6.0 software (GraphPad, La Jolla, CA) in order to calculate maximum weight and age of attaining maximum weight, and to interpolate age attaining a maximum weight minus 10%. Neurological scoring and paw print analysis were performed as previously reported (Cacabelos et al., 2014) in alternate days starting from day 60 and are further described in the Supplemental Methods section. All experimental procedures were approved by the Ethical Committee for Animal Testing of the Institut de Recerca Biomèdica de Lleida (IRBLleida) and were conformed to the Directive 2010/63/EU of the European Parliament.

Spinal cord sample preparation and homogenization

Animals were sacrificed by cervical dislocation at indicated times, after being fasted overnight. Spinal cord lumbar sections were rapidly excised, and kept in ice-cold saline, or frozen in liquid nitrogen and stored at -80°C , to perform respirometry or for other analysis, respectively.

Frozen samples were thawed on ice and homogenized at 0°C in a buffer containing 180mM KCl, 5 mM 3-[N-morpholino]propanesulfonic acid, 2mM ethylenediaminetetraacetic acid (EDTA), 1mM diethylenetriaminepentaacetic acid, 1 μ M freshly prepared butylated hydroxyl toluene (BHT), 10 $\mu\text{g}/\text{ml}$ aprotinin, and 1mMphenylmethylsulfonyl fluoride (PMSF), at pH 7.3 using a Potter-Elvehjem motor-driven glass-Teflon homogenizer. After a brief centrifugation (500 x g, 5 min) to pellet cellular debris, protein concentrations were measured in the supernatants using the Bradford assay.

The spinal cord slice permeabilization protocol was a modification of a previously published method (Safiulina et al., 2004). Fresh spinal cords were rinsed with ice-cold normal saline and cut into slices with a tissue chopper adjusted to a cut width of 300 μm . About 12-15

slices of the lumbar region were collected and transferred quickly into individual wells of a 6-well tissue culture plate with 2 ml of ice-cold permeabilization medium (in mM: 7.23 potassium ethylene glycol-bis(b-aminoethyl ether)*N,N,N',N'*-tetraacetate (K_2 EGTA), 2.77 CaK_2 EGTA, 60 *N,N*-bis[2-hydroxyethyl]- 2-aminoethanesulfonic acid (BES), 5.69 MgATP, 20 taurine, 3 K_2HPO_4 , 0.5 dithiothreitol and 81 potassium methanesulfonate, pH 7.1 at 25°C), rinsed and immediately transferred again into another well with the same medium containing 20 μ l of saponin stock solution (5 mg/ml; final concentration 50 μ g/ml). Lumbar spinal cord slices (LSCS) were shaken by gentle agitation at 4°C for 30 min. Afterwards, all samples were quickly transferred from the saponin permeabilization medium into 2 ml of respiration medium (in mM: 7.23 K_2 EGTA, 2.77 CaK_2 EGTA, 100 potassium salt of 2-(*N*-morpholino)ethanesulfonic acid (*K*-MES), 1.38 $MgCl_2$, 20 taurine, 3 K_2HPO_4 , 0.5 dithiothreitol, 20 imidazole and 5 mg/ml bovine serum albumine (BSA), pH 7.1 at 25°C), and shaken by gentle agitation for 10 min at 4°C before performing respirometry.

High resolution respirometry

Oxygen flux of sets of 5 mice LSCS (n=10-20 per genotype) or suspensions of Neuro-2A cells (100,000 cells/mL) was measured at 37 °C by high-resolution respirometry using an Oxygraph-2k (Oroboros Instruments, Innsbruck, Austria) with chamber volumes set at 2 mL. In order to avoid tissue disaggregation, LSCS required setting a slow bar stirring speed (150 rpm), but not too low to compromise homogeneity of substrate and oxygen concentrations in the measuring chambers, and therefore signal stability. Stirring speed for suspensions of Neuro-2A cells was set to 400 rpm after a trypan blue exclusion assay showed cell viability was > 95% (data not shown) after 1 h of agitation. DatLab software (Oroboros Instruments, Innsbruck, Austria) was used for data acquisition (2 s time intervals) and it was also used for analysis, which includes calculation of the time derivative of oxygen concentration and correction for instrumental background oxygen flux (Gnaiger, 2001).

Respiration of LSCS and Neuro-2A cells was analysed following two standardized protocols. The experimental regime for intact LSCS and Neuro-2A cells started with routine respiration, which we defined as the oxygen flux in Hank's balanced solution and cell culture medium, respectively, without additional substrates or effectors. After observing steady-state respiratory flux in the time interval between 5 and 10 min after closing the chamber, respiration was inhibited by sequential addition of rotenone at 0.5 μ M (to test for the effect of inhibiting complex I activity) and antimycin A at 2.5 μ M (inhibiting complex III). This titration method was completed within 30 min. In order to avoid oxygen limitations, all the experiments were performed above 50% oxygen saturation. Oxygen consumption was normalized by actual protein content and citrate synthase activity in the respirometer chambers.

The second experimental regime required tissue or cell permeabilization before placing the sample in the measurement chamber. Initially, we measured endogenous respiration in the absence of additional substrates. For evaluation of relative contributions of mitochondrial complexes to oxygen consumption, several specific mitochondrial inhibitors and substrates added sequentially as routinely performed in our laboratory (López-Erauskin et al 2013) and calculated as steady-state respiratory flux in the time interval between 5 and 10 min after its addition. First, we added glutamate (10mM) and malate (5mM) to increase NADH levels in order to measure the complex I non-phosphorylative activity, or state 2. 10 mM ADP was added to quantify the complex I-dependent phosphorylative activity, or state 3. Immediately afterwards, we added succinate (10mM), which is the substrate for complex II. At this point, the level of oxygen consumption corresponded to complex I- and II-dependent phosphorylative activity. The addition of 0.5 μ M rotenone inhibits complex I; therefore, oxygen consumption measured after the addition of rotenone only reflects complex II-dependent phosphorylative

activity (in absence of electron backflux to complex I). Then, complex III activity was inhibited with antimycin A (2.5 μ M), and finally complex IV maximal activity was measured after addition of the non-physiological substrate *N,N,N',N'*-tetramethyl-*p*-phenylenediamine (TMPD) at 0.5 mM, ascorbate (2mM) and cytochrome c (10 μ M). Maximal oxygen consumption rates of spinal cords were measured after addition of carbonyl cyanide-*p*-trifluoromethoxyphenylhydrazone (FCCP). In order to avoid oxygen limitations, all the experiments were performed above 50% oxygen saturation. Oxygen measurements media for permeabilized tissue was Mir05 (Pesta & Gnaiger, 2012) Oxygen consumption was normalized by actual protein content in the respirometer chambers.

Western blot analysis

The protein levels of Neuro-2A cells mitochondrial respiratory chain complexes, were estimated using Western blot analysis. Equal amounts of protein (10-25 μ g) were separated by SDS-PAGE gels. Proteins were transferred using a Mini Trans-Blot Transfer Cell (BioRad) to polyvinylidenedifluoride membranes (Immobilon-P, Millipore). Immunodetection was performed using specific antibodies for the 39kDa (NDUFA9; CI) subunit of complex I (1:1000), 70 kDa subunit (Flavoprotein) of complex II (1:500). (Ref. A21344 and A11142, respectively; Molecular Probes, Eugene, OR). Expression of mutant and wild type human SOD1 in mice spinal cords was immunodetected using a monoclonal antibody specific against human SOD1 (Abcam AB52950). An antibody to porin (1:5000, A31855, Molecular Probes) or α -actin (1:5000, AB20272, Abcam, Cambridge, MA) as a control for total mitochondrial mass or total protein charge were also used in order to determine the proportion of protein levels referred to total mitochondrial mass or total protein content. Appropriate peroxidase-coupled secondary antibodies anti-rabbit (1:40000, Pierce, Rockford, IL, USA) or anti-mouse (1:10000, GE Healthcare, UK) and chemiluminescence horseradish peroxidase (HRP) substrate (Millipore, Billerica, MA) were used for primary antibody detection. Signal quantification and recording was performed with Chemi-Doc equipment (Bio-Rad Laboratories, Inc., Barcelona, Catalonia). Protein concentration was determined by the Bradford method. Data were expressed as arbitrary units.

Oxidation-derived protein damage markers measurements by GC/MS

Gas chromatography-mass spectrometry (GC/MS) measurements of glutamic semialdehyde (GSA), amino adipic semialdehyde (AASA), N^{ϵ} -(carboxyethyl)-lysine (CEL), N^{ϵ} -(carboxymethyl)-lysine (CML), and N^{ϵ} -(malondialdehyde)-lysine (MDAL) concentrations in total proteins from mice lumbar spinal cord homogenates were measured as routinely performed in our laboratory (Vigerust et al., 2012) (See Supplemental Methods for further information). Samples were homogenized in 10 volumes of ice-cold homogenization buffer (0.32 mol/L sucrose, 10 mmol/L HEPES pH 7.4, 2 mmol/L EDTA, containing the protease inhibitor cocktail (Sigma P8340) and homogenized using 10 to 15 strokes of a motor-driven glass-Teflon homogenizer. Protein concentrations were measured by the Bradford method, and samples were stored at -80°C. Quantification was performed by external standardization using standard curves constructed from mixtures of deuterated and non-deuterated standards. Analytes were detected by selected ion-monitoring GC/MS and the amounts of products were expressed in μ mol of analyte per mol of lysine.

Lipid profile

Fatty acid analysis in tissue samples and diets was performed as previously described (Cacabelos et al., 2014). Total lipids from homogenates were extracted with chloroform/methanol (2:1, v/v) (3 times) in the presence of 0.01 % butylated hydroxytoluene. The chloroform phase was evaporated under nitrogen, and the fatty acids were transesterified by

incubation in 2 ml of 5 % methanolic HCl for 90 min at 75 °C. The resulting fatty acid methylesters were extracted by adding 2 ml of n-pentane and 1 ml of saturated NaCl solution. The n-pentane phase was separated, evaporated under nitrogen, re-dissolved in 80 µl of carbon disulphide, and 2 µl was used for GC analysis. Separation was performed by a DBWAX capillary column (30 m × 0.25 mm × 0.20 lm) in an Agilent GC System 7890A with a Series Injector 7683B and a FID detector (Agilent Technologies, Barcelona, Spain). The injection port was maintained at 220 °C, and the detector at 250 °C; the temperature programme was 2 min at 100 °C, then 10 °C/min to 200 °C, then 5 °C/min to 240 °C and finally hold at 240 °C for 10 min. Identification of fatty acid methyl esters was made by comparison with authentic standards (Larodan Fine Chemicals, Malmö, Sweden). Results are expressed as % of analyte from the total % of FAMES founded.

Cell culture and transfection

Neuro-2A cell line was obtained from ATCC (#CCL-131) and grown in MEM-Advanced medium without phenol red supplemented with 10% heat inactivated foetal bovine serum, 2 mM L-glutamine, 20 U/ml penicillin and 20 µg/ml streptomycin. Cells were kept at 37 °C in a humidified atmosphere with 5% CO₂. Neuro-2A cell permeabilization prior to respirometry and sample homogenization for protein expression and activity measurements were performed as described above for LSCS.

After 10 days of pre-treatment with 10nM E2 or vehicle, cells were harvested, counted, and subcultured in 6-well plates (200,000 cells per well) overnight. Transfection was performed by using Lipofectamine 2000 (Invitrogen, El Prat de Llobregat, Catalonia) according to manufacturer instructions. Briefly, lipofectamine and selected DNA plasmids were mixed (1 µg of DNA/1 µL of lipofectamine) with Optimen medium (Invitrogen) for 20 min and the resulting mixture was dispensed to the cell cultures (10 µg DNA per well). The plasmids pEGFP-G93A-hSOD1 and pEGFP-wt-hSOD1, expressing G93A mutant or wild type human SOD1 tagged with enhanced green fluorescent protein (EGFP) were kindly provided by Dr Josep Esquerda (Lleida, Catalonia). The pEGFP expression vector was used for mock transfection.

Cytotoxicity Assay and ATP content

Viability of Neuro-2A cells was assessed with a LDH Cytotoxicity Assay Kit (Promega, Madison, WI) according to manufacturer's instructions. Briefly, the amount of lactate dehydrogenase (LDH) released into the culture medium is measured using an enzymatic reaction that results in a red formazan product which can be measured spectrophotometrically. Lactate dehydrogenase (LDH) is a cytosolic enzyme that is an indicator of cellular toxicity. The cell viability was evaluated relative to the total LDH from whole cell lysate and the results were expressed as the percentage of viability versus treated with vehicle and/or mock transfected cells.

Adenosine triphosphate (ATP) content in Neuro 2A cell homogenates was measured with the ATP Bioluminescent Assay Kit (Sigma) according to the manufacturer's instructions. Results are expressed as nanomole ATP per milligram protein.

Statistical analysis

All statistics were performed using the SPSS software (SPSS Inc., Chicago, IL) or the Prism software (GraphPad Software Inc., La Jolla, CA). Differences between groups were analyzed by the Student's t tests or ANOVA with Post-Hoc analyses, after normality of variable distribution was ensured by Kolmogorov-Smirnov test. Correlations between variables were evaluated by the Pearson's statistic. The 0.05 level was selected as the point of minimal statistical significance in every comparison.

Results and discussion

Disease onset, clinical evolution and survival of G93A mice

Our G93A mouse colony exhibited a phenotype consistent with the overexpression of the G93A-hSOD1 transgene (Gurney, 1997). G93A-hSOD1 protein expression in spinal cord of transgenic mice was verified by Western-blot analysis, using a monoclonal antibody specific against human SOD1, which has been shown to recognize distinct mutated human SOD1 forms, including G93A-hSOD1 (Sotelo-Silveira et al., 2009), Figure S0. G93A mice gained weight as expected, reaching a higher ($p < 0.05$) maximum value for males (21.1 ± 0.2 g, $n=11$) than for females (18.0 ± 0.1 g, $n=12$) (Figure S1A). Control and G93A mice body weight was significantly higher in males than in females from weaning day. However, in G93A animals this difference is faded out along disease, with no differences found from 107 days between sexes. In control animals, both sexes continued gaining weight until endpoint (Figure S1B). Food intake was not significantly different between G93A mice of both genders at any age, neither between male and female control mice (Figure S1C, Figure S1D, respectively). Onset of clinical symptoms occurred by approximately 70–90 days of age, with body weight loss, abnormal gait, muscle weakness with decreased grip strength, and impaired coordination. As an estimation of disease onset, we used the interpolated value for age of attaining maximum weight after fitting a third-order polynomial curve to the weight evolution data. Maximum body mass was attained at a significantly younger age in males (87.9 ± 1.2 days, $n=11$) than in females (95.9 ± 1.0 days, $n=12$; $p < 0.05$; Figure 1A, bars on the left). Female G93A mice showed a significant delay in disease progression, as evidenced by the later age by which they dropped to 10% below their maximum weight (males, 120.2 ± 2.2 days; females, 135.5 ± 3.9 days, $P < 0.05$; Figure 1A, bars on the right). As a second estimation of disease progression, a paw print analysis was performed to measure stride length, indicating again a slower disease progression in female G93A mice, as previously reported (Cacabelos et al., 2014). Figure 1B shows that the median value of both right and left stride lengths in G93A females was attained at a significantly older age (116.2 ± 3.2 days, on average of both hindlimbs) than in their male counterparts (107.3 ± 4.1 days on average of both hindlimbs). Supporting this, overall clinical duration was greater in females (37.72 ± 2.01 days $n=11$ and 45.5 ± 2.52 days $n=12$ for male and female, respectively; $P < 0.001$, Figure 1D). However, the age reaching the different clinical score status (Figure S1E, S1F and S1G, respectively) was similar for both sexes. The animals were euthanized when it demonstrated hind limb paralysis or inability to right itself when placed on its side. Female G93A mice survived significantly longer than males ($P < 0.05$), with survival times of 134.1 ± 2.9 days ($n=11$, range 119–135) and 124.9 ± 1.5 days ($n=12$, range 115–157 days), respectively (Figure 1D).

Disease onset, neurological scores, disease progression and survival of our G93A mice were consistent with those reported in the literature (Gurney, 1997), so we considered validated our animal model of ALS. Moreover, gender differences in the aforementioned clinical features of the diseased mice were also confirmed. Indeed, sex appears to modify the course of disease and lifespan in animal models of ALS with mutations in the hSOD1 gene, with an earlier disease onset in male transgenic rats and mice overexpressing G93A-hSOD1 (Suzuki et al., 2007; Veldink et al., 2003), although sex appears to have no consistent effect on survival of ALS patients (Lee, Annegers, & Appel, 1995).

Preliminary experiments performed in our laboratory displayed a peak of G93A-hSOD1 protein expression at 60 and 90 days, and lower levels before and after (30 days and 120 days, respectively) in a mixed population of male and female G93A mice. After analysing separately male and female mice, the same pattern of mutated hSOD1 expression was observed (data not shown). Thus, we rule out different levels of aggregated or aberrant SOD1 activity between

male and female transgenic mice as the primary origin of gender differences in mitochondrial dysfunction and levels of protein oxidative modification markers.

Oxygen consumption of mice lumbar spinal cord slices

Respirometric analysis of mitochondrial function provides a tool to study changes in mitochondrial respiratory chain function and mitochondrial ATP production within tissue biopsies, cultured cells and isolated mitochondria (Hütter, Unterluggauer, Garedew, Jansen-Dürr, & Gnaiger, 2006). In order to assess gender-related differences in spinal cord mitochondrial function of a murine model of ALS both in presymptomatic and diseased stages, oxygen consumption in LSCS of male and female non transgenic and transgenic mice overexpressing G93A-hSOD1 were analysed in two standardized experimental regimes in 30, 60, 90 and 120 days old animals.

First, using intact (not permeabilized) slices, and therefore resembling *in vivo* spinal cord cell conditions, we found significant differences in routine respiration (measured in Hank's balanced salt solution containing 10mM Hepes, pH 7.4, without additional substrates, inhibitors or uncoupling agents) between control and transgenic mice at 120 days of age, with a reduced oxygen uptake for both genders (control *vs.* transgenic; males, 37.0 ± 3.8 *vs.* 22.5 ± 2.7 pmol O₂/min×mg protein, $P < 0.01$; females, 40.1 ± 1.5 *vs.* 31.9 ± 2.8 pmol O₂/min×mg protein, $P < 0.01$; Figures S2A and S2B). Interestingly, when comparing 120 days old male and female G93A mice, routine respiration was 41.7% higher in females ($P < 0.05$), while no differences appeared between control mice of both sexes (Figure 2A and Figure S4A, respectively). Then, rotenone was added to the measurement chambers in order to inhibit the mitochondrial complex I, followed by the inhibitor of complex III, antimycin A. When rotenone-resistant respiration is subtracted to routine respiration, an estimation of the contribution of the mitochondrial chain complex I to cell or tissue respiration is obtained. Likewise, when antimycin-resistant respiration is subtracted to rotenone-resistant respiration, the resulting value is an estimation of the contribution of mitochondrial chain complex II to total respiration. According to the aforementioned calculation, the estimated complex I respiration was lower in male G93A mice respect to control animals by 26.0% ($P < 0.05$), 26.7% ($P < 0.05$) and 33.9% ($P < 0.01$) at 60, 90 and 120 days, respectively (Figure S2C), whereas in females, complex I respiration in transgenic mice was significantly reduced (25.0%, $P < 0.001$) only at an age of 120 days, and, intriguingly, augmented by 28.7% ($P < 0.01$) at 30 days (Figure 2SD). When we compared complex I respiration between male and female G93A mice, the decrease in oxygen consumption was more pronounced in the former in all age groups, with the exception of 30 days. Specifically, complex I respiration in G93A females was significantly higher than in males at 90 days (31.4%, $P < 0.05$) and 120 days (25.6%, $P < 0.05$), and also at 60 days (20.3%), although the difference was not significant ($P = 0.0760$) (Figure 2B). In control animals, complex I respiration was 39.6% higher ($P < 0.01$) in 30 day old males, whereas in older animals the values were similar in both genders, lacking significant differences (Figure S4B). Regarding complex II, its estimated oxygen uptake in control mice intact LSCS was significantly higher for females at 30 days (Figure S4C). However no gender differences were found for G93A animals (Figure 2C) along disease. Confirming this, no differences were found for G93A respect to control ones, neither globally, nor separated by gender (Figure S2E and S2F for male and female, respectively). Residual oxygen consumption is the respiration due to oxidative side reactions remaining after application of mitochondrial chain complex III inhibitors, such as antimycin A. Addition of antimycin A to the measurement chambers provoked a sharp fall in oxygen uptake that revealed a similar pattern for both genders expressing SOD1G93A, hence no differences were found between them (Figure 2D). Antimycin

A-resistant respiration was higher in control mice LSCS of both genders at 30 days (control vs. transgenic; males, 15.4 ± 1.3 vs. 6.2 ± 1.1 pmol O₂/min×mg protein, $P < 0.001$; Figure S2G; females, 15.6 ± 0.7 vs. 9.8 ± 2.0 pmol O₂/min×mg protein, $P < 0.01$; Figure S2H) and 120 days (control vs. transgenic; males, 8.8 ± 1.2 vs. 4.6 ± 0.9 pmol O₂/min×mg protein, $P < 0.01$; Figure S2G; females, 9.7 ± 1.2 vs. 6.7 ± 0.7 pmol O₂/min×mg protein, $P < 0.05$; Figure S2H). Similar results were obtained when the total population of mice (males plus females) was analysed (data not shown). Interestingly, opposite results were obtained in residual respiration at 60 days and 90 days, displaying higher rates in male G93A mice at 60 days (control vs. transgenic; 8.0 ± 1.8 vs. 13.7 ± 1.0 pmol O₂/min×mg protein, $P < 0.01$; Figure 2G) and in female G93A mice at 90 days (control vs. transgenic; 7.2 ± 1.2 vs. 12.0 ± 1.0 pmol O₂/min×mg protein, $P < 0.01$; Figure 2H). When comparing antimycin A-resistant respiration in G93A mice of both genders, this rate was 53.9% ($P < 0.05$) higher in males than in females at 60 days (data not shown).

Consistent with previous reports (Mattiuzzi et al., 2002) routine (intact tissue, without any inhibitor) respiration only shows evident reduction of G93A animals at end stage of disease. This reduction was also verified when comparison between male and female was done in G93A overexpressors, but was abolished for control animals all studied points, suggesting that differences founded are attributable to G93A overexpression. Although the routine respiration of intact LSCS was not significantly different in males and female G93A mice (only at endpoint), the higher rotenone resistant respiration in males at 60 days suggests a lower Complex I contribution to overall respiration, as calculated by difference respect to routine respiration. Since routine respiration does not vary, a compensatory stimulation of Complex II respiration is plausible. Hence, we could demonstrate that G93A males consumed less oxygen than controls from day 60 (Figure S2), but females were protected (displaying even greater consumption than controls at 30 days) showing only a late reduction at endpoint.

Focusing in the G93A animals, females showed an upgraded Complex I oxygen consumption than males from 60 days (Figure 2). Nevertheless, this advantage was only significant for 90 and endpoint animals. Since rotenone mediated cytotoxicity was proved to be alleviated in female neuron primary cultures (Tao et al., 2012), this decreased respiration could lead cell survival demise in males. Studies from (Vinsant et al., 2013) showed that, in this mouse model, motor neuron abnormalities begins between 44 to 60 days. However, cytosol vacuolization and swollen and mega-mitochondrial were evident before (30 days, even P7). In line with this we also show in permeabilized slices early complex I dysfunction in males (Figure S3). On the contrary, females complex I-related reduced respiration was only evident under clinical symptoms. However, G93A-linked complex I malfunction was evident for early asymptomatic males respect to female's counterparts (Figure 2cont).

Underlying this gender dimorphism, studies from (Eschbach et al., 2013) show a male-specific protective mechanism of PGC-1 α (a master metabolic regulator (Chaturvedi & Flint Beal, 2013)) in this mouse model. Further, since PGC-1 α could enhance the transcriptional activities sex hormone receptors (e.g. androgen receptor (Shiota et al., 2010) or estrogen receptor (Tcherepanova, Puigserver, Norris, Spiegelman, & McDonnell, 2000)) this may result in a feed-back loop.

The second experimental regime required permeabilization of the LSCS with digitonin before the respirometry analysis in an artificial intracellular medium with sequential addition of mitochondrial substrates, uncouplers and inhibitors (SUIT protocol). Measurement of oxygen flux in permeabilized cells or tissues, in presence of saturating concentrations of substrates, ADP and P_i, provides an estimation of the in situ activities of the mitochondrial chain complexes, among other information, without the potential artefacts associated to the mitochondrial isolation procedure. Tissue permeabilization allows free diffusion of substances

through the cell membrane, while mitochondrial membrane integrity and permeability are not altered. Thus, the addition of substance to the measurement media allows direct manipulation of the chemical surround of the mitochondria. If the added substrates are added at saturating concentrations, its stimulating effect on its corresponding enzyme will be maximal. While this is not a physiological condition, it can give an estimation of the capacity of mitochondria to hold a metabolic challenge. Endogenous respiration is measured before addition of substrates, being supported by the remaining metabolites in the mitochondria, since the concentration of cytosolic metabolites has lowered to irrelevant levels due to its free diffusion through the permeabilized cell membrane. Under this situation no differences were found among male and female G93A overexpressors (Figure 2E), nor between control and transgenics for none sex (data not show) or even in control animals between sexes (Figure S4D). State 2 respiration (for Complex I) is achieved upon stimulation of those preparations with glutamate/malate. Hence, under this situation G93A females had higher oxygen consumption than G93A males only at early presymptomatic stages (30 days, Figure 2F). Differences between control and transgenic animals were also found for males (Figure S3A) and females (Figure S3E), but in this case, as expected, higher consumption was attributed to controls, only significant later in disease. Interestingly, male shows a dysfunction at 30 days which was not present in females. Finally, sexual dimorphism was confirmed for control animals, where at 60 and 90 days females displayed higher oxygen consumption (Figure S4E). Addition of ADP into the chambers reflects the oxygen consumption in state 3 (of complex I). Hence, in this situation, G93A females showed upgraded consumption compared with males all along disease (Figure 2G). Comparison of the overexpression separately between sexes shown G93A males (Figures S3B) underscored almost all along disease in contrast to females where decreased oxygen consumption was only evident at end stage (Figure S3F). For control animals, females showed increased complex I state 3 levels at 60 days when compared with males (Figure S4F). Succinate (substrate for the Complex II) addition serves us for complex I/II state 3 measurements. Thus, estimated measures showed early disruption in G93A females compared with males (Figure 2H) which was faded out along disease. No differences were found for males and (Figure S3C) only higher consumption was detected in controls females (Figure S3G) when compare the transgenic effect between sexes. Finally, as previously commented, rotenone addition blockades complex I and an estimation of complex II state 3 is obtained. In this situation, at 30 days there is an almost significant difference ($P=0.065$) between males and females overexpressing G93A which disappears along disease (Figure 2I). Splitting measures between sexes and comparison for G93A effect showed no differences for males and only endpoint G93A females had a reduced oxygen consumption compared with control littermates (Figures S3D and S3H for male and female, respectively).

Oxidative stress markers in spinal cord

To offer an accurate quantitative measurement of protein oxidation in spinal cord proteins, we measured structurally defined oxidation products by isotope-dilution GC/MS (Pamplona et al., 2005). Proteins from spinal cord samples contain oxidation products resulting from metal-catalysed oxidation (MCO), glycooxidation and lipoxidation. A general trend to decrease spinal cord levels of the five markers analyzed (GSA, AASA, CML, CEL and MDAL) with age can be observed in mice of both genders, either control or transgenic, with the exception of AASA and MDAL in female G93A mice and male control mice, respectively, at 120 days. (Figure 3) GSA and CML levels in transgenics of both genders were not different across disease (Figures S5A, S5B for males and Figures S5C and S5D for females). The comparison between male and female mice revealed that mutated hSOD1 overexpression was associated with differences in the steady-state levels of protein oxidative damage markers.

AASA, a MCO marker, displayed significantly 47.5% ($P < 0.01$; Figure 3A) and 39.5% ($P < 0.01$; Figure 3D) higher levels in spinal cord proteins of G93A mice at 60 days in males, and at 90 days in females, respectively, than in control mice. CEL is a glycooxidation marker whose levels were found surprisingly higher in spinal cord of female control mice at 90 days (Figure 3E). Finally, levels of the lipoxidation marker MDAL were augmented in spinal cord of males by 30.5% ($P < 0.01$) in G93A mice at 90 days, and, unexpectedly, by 23.5% ($P < 0.01$) in control mice at 120 days (Figure 3C).

ROS formation is particularly high when Complex I is inhibited (Votyakova & Reynolds, 2001). Therefore, its blockade may account for higher ROS production, and probably increased oxidative products accretion. Antimycin-resistant cell respiration has been used as an estimation of mitochondrial ROS production. In G93A mice spinal cord, the rise in AASA levels, a marker of metal-catalyzed oxidation (MCO) of proteins, occurred after the peak of antimycin-resistant respiration suggests the mitochondrion as the origin of the cellular protein oxidative damage. This delay in protein oxidative damage with respect to mitochondrial dysfunction is observed in mice of both genders. Interestingly, there is a shift of both mitochondrial-related and oxidative stress-related pathophysiological findings in female G93A mice respect to their male littermates. These results could explain, at least in part, the delayed clinical features observed in G93A female mice respect to male mice and, possibly, also in male patients respect to the female counterparts. In any case, higher oxidative damage was expected due to the G93A overexpression. Early studies already pointed for a nonlinear oxidative accretion in this animal model (accretion of MDA in spinal cord at 30 and 60 days, whole sections, by HPLC; greater MDA immunoreactivity in lumbar spinal cord at 100 and 120 days (Hall, Andrus, Oostveen, Fleck, & Gurney, 1998); carbonylated products early accretion -30 days- for G93A animals (Andrus, Fleck, Gurney, & Hall, 1998)) and were more recently confirmed (decreased ROS production for SODG93A animals in isolated mitochondrial preparations respect to controls, 100 days age (Vinsant et al., 2013); increased spinal cord 4-HNE and MDA at 100 and 130 respect to controls by spectrophotometry; DNP-carbonylated products accumulation was similar to controls along disease; whole spinal cord sections, no gender consideration (Miana-Mena et al., 2011); MDA accumulation at 30 and 120 days in G93A respect to controls, no gender consideration, measured by colorimetry (Kirkinetzos et al., 2005)). Even when our results do not completely fit this previous findings, our measures are lumbar specific (nor cervical or thoracic sections), we split by gender and methodology applied to the measurements were different. Hence, this could explain little variations with previous reports. This goes in line with our previous publication (Cacabelos et al., 2014) (focusing only in control diet) indicating that, among oxidative modification studied, most of them (but CEL in females) have greater accretion at early clinical stages (90-100 days), rather than end stage. And in any case, one should bear in mind that those animals are overexpressing an oxidant-scavenging enzyme (SOD1), which, even with less efficiency, is functional (Yim et al 1996).

Fatty acid profile in spinal cord

Since fatty acid profile strongly influences membrane peroxidizability, and consequently protein lipoxidative damage, we analysed fatty acid content in G93A mice spinal cord at early presymptomatic (30 and 60 days), disease onset (90 days) and symptomatic (120 days) ages as well as in control animals for both gender. Those analyses revealed significant differences in the G93A-hSOD1 colony between males and females (Figure 4) as well as differences among overexpressors and controls (Figure S6) along disease. The two most remarkable changes involve the highly peroxidizables docosahexaenoic acid (DHA) and arachidonic acid (AA). Levels of DHA decreased along time (Figures 4A, S6B, S6E and S6F),

with lower levels of this fatty acid at endpoint regardless sex or transgene. Focusing in gender dimorphism of G93A animals, interestingly DHA levels, despite being significantly higher in females early in disease, this difference is faded out along it. On the other hand, for non transgenic animals, even when decreasing along the experiment, AA and DHA levels were similar for males and females (Figure S6A and S6A, respectively). AA levels was severely affected by transgen, since for both sexes at preclinical ages (30, 60 days) non transgenic animals accumulated more than G93A ones, but this difference turned to be the opposite at endpoint (Figures S6A, S6C and S6D). Furthermore, focusing in G93A animals, AA levels turned from being significantly lower in males at 30 days, to be significantly higher at endpoint (Figure 4B), respect to females. This different FA handling goes in line with previous reports indicating a differential n-3 synthesis for both sexes. Studies from Alessandri and collaborators showed that females have a preference towards n-3 synthesis. Greater circulating DHA levels were reported for females plasma (Astorg et al., 2008)(Welch et al., 2006) and in tissues and neuronal cell lines (Alessandri et al., 2008). However, for our control animals, we could not observe any difference across the study for this particular FA (Figure S6B). Behind this differential lipid metabolism could rely an altered desaturase activity for males and females, as reported Extier and collaborators in a model of n-3 replenishment (Extier et al., 2010). Consistent with this DHA spinal cord depletion in this animal model, previous results from our group (Ilieva et al. 2007) had also reported decreased DHA accretion in spinal cord of patients (this study was carried out in ALS male patients, n=7). However in this report, even when levels are greater as in animals model, this deference was not significantly altered than controls.Finally,

Overexpression of G93A-hSOD1 in Neuro 2A cells: cell viability and ATP content, oxygen consumption and mitochondrial ETC complexes protein expression.

To evaluate the effect of estrogens on mitochondrial function of isolated neuronal cells overexpressing a mutated form of SOD1, Neuro-2A cells were treated with 17 β -estradiol prior to transfection with aG93A-hSOD1 plasmid (for 10 days,10 nM final concentration). The G93A mutated form of hSOD tagged to an EGFP expression vector was transiently transfected in Neuro-2A cells using Lipofectamine (from now on G93A cells). Mock transfected cells expressing EGFP were used as a control (Control cells). Direct visualization of GFP fluorescence was analysed using fluorescence microscopy to ensure transfection (efficiency \approx 80-90%, data not shown) or to denote differential expression between transfectants (Figure S7). To evaluate the cytotoxic effect of hSOD1 and mutant hSOD1 overexpression, alone and combined with E2 treatment in Neuro-2A cells, we compared the viability of WT and G93A cells vs. mock transfected cells, pre-treated during 10 days with 10 nM E2 or vehicle, after 24h of transfection. We found that there was no significant difference in the cell viability between the three transfectants either with or without exposure to estrogen (Figure 5A). The intracellular ATP content measurements neither revealed variations between transfections and E2 pretreatment or their mock and vehicle controls, respectively (Figure 5B).

As previously shown, we analysed oxygen consumption in two standardized experimental regimes. Neuro 2A cells transfected with an EGFP plasmid were included as a second control. First, using intact (i.e. not permeabilized) cells, we did not find significant differences in routine respiration (measured in standard culture medium without additional substrates, inhibitors or uncoupling agents) or in non-phosphorylating respiration (measured after inhibition of mitochondrial chain complex V F₀-ATP synthase with oligomycin). However, maximal respiratory capacity (measured after uncoupling with FCCP) in G93A cells was significantly reduced (P < 0.05) compared with control cells and wt cells by 27.6% and 18.2%,

respectively (Figure 5C). Respiration was inhibited by antimycin A to an equal extent in the three transfectants, pointing to a Complex I malfunction.

To further confirm this, the second experimental regime included cell permeabilization with saponin before the respirometry analysis in an artificial medium with sequential addition of mitochondrial substrates and inhibitors, quite similar to the protocol used to analyse respiration in permeabilized LSCS as described above. Neither endogenous respiration (before addition of substrates, data not shown) nor Complex I state 2 respiration stimulated by glutamate/malate, were significantly different between the three transfectants (data not shown). However, after addition of ADP, in order to achieve complex I state 3 respiration, oxygen uptake rose to a lower level in G93A cells than in wtSOD cells and GFP cells (Figure 5D, Complex I). This respiration difference was enhanced after addition of succinate (Figure 5D, Complex I-II), but disappeared when rotenone was injected in the measurement chambers (Figure 5D, Complex II). As in the non-permeabilized cell protocol, oxygen consumption was inhibited by antimycin A to an equal extent in the three transfectants (data not shown). Hence, all in all, similar to the respirometric measurements performed with intact cells, the aforementioned differences in oxygen uptake dependent on ADP and glutamate/malate, or ADP and glutamate/malate plus succinate, were abolished when cells were pre-treated with 10nME2 before the transfection.

In order to assess the origin of the reduced mitochondrial chain complex I state 3 respiration in G93A cells, we estimated the protein expression of the complex I (39KDa, NDUFA9) as well as Complex II (70KDa, Flavoprotein) subunits. Figure 5E shows that levels of expression of two peptides representative of mitochondrial chain complex I and complex II are not significantly different neither among transfects, nor E2 treatment.

Because the contribution of motor neurons, despite being large cells, in whole spinal cord is relatively minor, these results suggest that the decrease rate of respiration in G93A mice is present in different cell types, and not motor neuron specific. In fact previous result from our group (under revision) already reported a decreased respiration in an *in vitro* (tissular) model of ALS, particularly attributed to a Complex I malfunction. In any case, most functional experiments performed with nervous tissue provide a mixed result arising from its two major cell types. While much work showing glial involvement in the pathophysiology of the SOD1-G93A genetic mouse model has been done, the ultimate result is (motor) neuron dysfunction and death. On the other hand, the above-described differences in mitochondrial dysfunction between genders in SOD1-G93A mice could be attributable to the higher levels of estrogens in female mice. Taking these two points in mind, we aimed to investigate the effect of estrogen exposure on the mitochondrial dysfunction due to SOD1-G93A expression in neuronal cells. We found the mouse neuroblastoma N2A cell line a suitable model for this part of the study because: a) cells exhibit a differentiated neuronal phenotype (Graham, Gonatas, & Charalampous, 1974), b) expression of estrogen receptors (Mendez & Garcia-Segura, 2006)(Li, Hao, Cheng, & Li, 2014) , and c) it is a suitable transfection host. As a potential limitation of the present study, it may be argued that the Neuro-2A cell line is not derived from motor neuron. However, it has been demonstrated that not only spinal and upper motor neurons are degenerated in ALS, but also interneurons and glia. Here we show that SOD1 gene mutation did not induce harmful effects on cell viability of Neuro-2A cells under basal conditions, in accordance with a previous report by Pyo (Pyo et al., 2010) using stably transfected cells of the motoneuron–neuroblastoma hybrid (VSC 4.1) cell line. Although it has been reported that expression of mutant SOD1 (G37R) resulted in a time and dose-related death of differentiated neuroblastoma cells (Flanagan, Anderson, Ross, & Oberley, 2002; Gurney, 1997) and protein expression blockade (by RNAi against hSODG93A) resulted in disease alleviation (Ralph et al., 2005).Therefore, neuro-2A cells transfected transiently with mutated SOD1 for a relatively

short time previous to their analysis, could be considered a model comparable to spinal cord neurons of early pre-symptomatic hSOD1-G93A mice. Moreover exposure to 17- β -estradiol during 10 days did not alter significantly cell survival. Supporting this, G93A cells did not exhibit differences respect to their controls in viability or metabolism, measured as mitochondrial function and ATP content.

Finally, accounting the lesser extent of early oxidative damage in spinal cord of female G93A mice could be related to the higher levels of UCP4 protein expression compared to males. Thus, our results showing an increase in complex II state 3 respiration in female G93A mice, but not in males, and a higher efficiency in terms of ATP production in females (resulting from the subtraction of , altogether with the lack of difference in complex II peptide expression (at least in the cell line), suggest a role of UCP4 in the compensatory mechanisms against bioenergetic failure in spinal cord of G93A mice and possibly ALS patients. This would be a interesting question to be addressed since the neuroprotective effect of UCP4 and UCP5 has been reported in aged rat brain (Guevara et al., 2009). In this paper, researchers have found lower oxidative damage in proteins and lipids that correlated with higher protein levels of UCP4 and UCP5 in female rats compared with their age-matched male littermates. On the other hand, as reported by Ho and colleagues, UCP4 overexpression increased ATP synthesis by specifically interacting with mitochondrial complex II in SH-SY5Y with complex I deficiency induced by 1-methyl-4-phenylpyridinium (MPP(+)) treatment (Ho et al., 2012). However, these results could also be related to the fact that all complex II subunits are encoded in the nuclear genome, and therefore its DNA would be less exposed to the ROS generated by the dysfunctional mitochondria, contrary to complexes I, III and IV, all of them containing several subunits encoded in the mitochondrial DNA. But in any case, those results in terms of an upgraded mitochondrial physiology, concomitant to an increased UCP decoupling mechanism to reduce mitochondrial ROS should be revisited in this mouse model. In a recent publication model (Peixoto et al., 2013) researchers co-expressed hUCP2 into the SOD1G93A mouse model. Even when they demonstrated a protective effect in terms of ROS production with the co-overexpression, they also reported shortened lifespan and worst mitochondrial dysfunction (more sensitive to Ca^{+2} -induced mitochondrial depolarization, in purified brain mitochondria of 100 day). They also showed an accelerated disease progression when co-expressed in the SOD1G93A background. In line with our results (even taking in to account different methodology were used), their G93A animals showed a decreased peroxide production respect to controls, when complex I is in state 2 (Figures S2A and S3B).

However, besides UCPs, other proteins may contribute to the gender-related differences. In a recent publication (H. J. Kim et al., 2012) researchers focused in gender relevance in the mitochondrial permeability transition pore formation in the SODG93A mouse model. Hence, they demonstrated that ablation of cyclophilin D (a protein structurally linked to the mitochondrial permeability membrane transition pore (Doczi et al., 2011)) completely abolished the phenotypic advantage of female SODG93A, but no effect was found in males. In fact, they showed that 17 β -estradiol protected SODG93A cortical neurons and spinal cord motor neurons against glutamate toxicity in brain mitochondria, but the protection was lost in neurons lacking cyclophilin D.

In summary, we have described an early mitochondrial defect during the pre-symptomatic stage associated to the expression of G93A mutated human SOD1 that appears at a younger age in males mice than in females, correlating with the delay in their clinical features. These data support a role for dysfunctional mitochondrial function control of spinal cord neurons in ALS pathogenesis and, in particular, the gender bias towards males observed in ALS. Thus, mitochondrial enzymes, such complex I or malate dehydrogenase, may represent viable

targets for novel treatments of a range of disorders affecting motor systems. This possibility underscores the importance of further studies investigating the role of sexual hormones or related molecules in the face of injury and disease as well as their potential contribution to motor recovery.

Figure Captions

Figure 1.- Disease onset and progression (A), stride length analysis (B), clinical progression (C) and survival curves (D) of the G93A colony, depicted by sex. Bars in (A) represented means \pm SEM of the age at maximum weight, expressed in days. Bars in (B) represented means \pm SEM of the age of clinical onset measured after stride length analysis, expressed in days. Dots in (C) represented disease duration among the G93A colony, depicted by sex, expressed in days. (D) represented a Kaplan-Meyer survival curve. *, $P < 0.05$, between male and female mice of the same age by Student's t test. **, $P < 0.01$ after a Kaplan-Meyer analysis.

Figure 2.- Oxygen flux of sets of 5 intact lumbar spinal cord slices from male and female G93A mice measured at 30,60, 90 and 120 (endpoint) days of age. Experimental procedures allows show basal (A), complex I (B), complex II (C) or residual (D) oxygen consumption differences between male and female. Measurements were taken at 37 °C in Hank's balanced salt solution containing 10mM Hepes, pH 7.4, and corrected for instrumental background oxygen flux. Values were normalized by actual protein content in the respirometer chambers. Means \pm SEM, expressed as pmol O₂/s·mg protein. *, $P < 0.05$, between male and female mice of the same age by Student's t test.

Figure 2cont.- Oxygen flux of sets of 5 lumbar spinal cord slices from male and female G93A mice measured at 30,60, 90 and 120 (endpoint) days of age. Permeabilized LSCS measures on endogenous (E), Complex I state 2 (F), complex I state3 (G), complex I/II state 3 (H) and complex II state3 (I) oxygen consumption conditions between males and females overexpressing G93A. Measurements were taken at 37 °C in Mir05 media. Values shown are means \pm SEM expressed as pmol O₂/min·mg protein for 4-6 independent measures. *, $p < 0.01$ respect to females of the same age by Student's t test.

Figure 3.- GC/MS analyses of protein oxidation products in LSCS from male and female G93A and control littermates measured at 60, 90 and 120 (endpoint) days. (A) and (D) represented levels of AASA, for male and female, respectively. (B) and (E) represented levels of CEL for male and female, respectively. (C) and (F) represented MDAL levels for male and female, respectively. Values shown are means \pm SEM expressed as μ mol of analyte per mol lysine. *, $p < 0.01$ respect to non transgenic group of the same age by Student's t test.

Figure 4.GC analyses of lipids in LSCS from male and female G93A measured at 30, 60, 90 and 120 (endpoint) days. (A) Shows DHA levels along disease. (B) Shows AA levels along disease course. Bars represented mean values \pm SEM expressed as % of abundance of analyte among the total FAME identified. *, $p < 0.01$ respect to female group, of the same age by Student's t test.

Figure 5. Overexpression of mutated SOD1 in Neuro-2A cells and treatment with E2. Neither cell viability (A) nor ATP content (B) were altered as a consequence of transfection or E2 treatment. (C) Oxygen flux measurements in intact N2A cells pretreated with E2 and transfected with pEGFP-G93A-hSOD1 and pEGFP-hSOD-wt showed a reduction on the maximal oxygen capacity in G93A transfected cells which was abrogated by E2 treatment. (D) Oxygen flux measurements in permeabilized-above mentioned cells showed a Complex I impairment for cells transfected with G93A respect to control cells which was abolished by the E2 treatment. In the same experimental regime, western blot analysis (E) for mitochondrial complex protein expression (complex I and complex II) confirmed an unaltered protein expression among the E2 treatment and transfects. Bars in (A) represent % of survival \pm SEM

respect to control cells for 4-6 independent experiments. Bars in (B) represented ATP mean values \pm SEM expressed as nmol/mg protein for 4-6 independent experiments. Oxygen consumption in (B) was measured at 37 °C in culture medium containing 10mM Hepes, pH 7.4, and corrected for instrumental background oxygen flux. In (D) culture medium was MIR05. Values were normalized by actual protein content in the respirometer chambers, expressed as pmol O₂/ min \times mg protein. *, P<0.05; ** P<0.01;*** P<0.001 between control cells and G93A cells for 4-6 independent experiments. Bars in (E) represent means \pm SEM densitometric analysis of the corresponding complexes relativized by actual porin content in each lane for 4-6 independent experiments

SUPPLEMENTAL FIGURES

Figure S0.- Time course of G93A-hSOD1 protein expression in G93A mice spinal cord.

Western-blot analysis of transgenic male and female mice at 30 and 60 days, leads to the expression of a protein with an apparent MW of 16 kDa, whereas, as expected, the protein was not detected in control mice. Overexpressors of non mutant SOD1 (WT) was used as control. These results provided evidence that the mutated form of the enzyme were expressed at similar levels in mice of both sexes, at least at preclinical ages.

Figure S1.- Clinical and metabolic features of G93A colony and control littermates, depicted by sex. (A) Weigh evolution across the study for G93A animals. (B) Weigh evolution across the study for controls. (C) Food intake calculations for G93A colony. (D) Food intake calculations for controls. Along disease, animals were studied every other day for clinical symptoms, been classified accordingly. As a result (E) shows the age at which animals reached clinical score 2, (F) shows the age at clinical score 3 and (G) shows the age at clinical score 4. Dots represented means \pm SEM values in grams of weakly measurements in (A to D), n=at least, 11-12. In (E-F) boxes represented mean \pm SEM expressed in days, n=11-12. *, P<0.05 between male and age matched females.

Figure S2.- Oxygen flux of sets of 5 intact LSCS from male and female G93A and control mice measured at 30,60, 90 and 120 (endpoint) days of age. Experimental procedures allows show basal (A-B), complex I (C-D), complex II (E-F) or residual (G-H) oxygen consumption differences between G93A and controls, depicted by sex. Measurements were taken at 37 °C in Hank's balanced salt solution containing 10mM Hepes, pH 7.4, and corrected for instrumental background oxygen flux. Values were normalized by actual protein content in the respirometer chambers. Means \pm SEM, expressed as pmol O₂/s \cdot mg protein. *, P<0.05, between male and female mice of the same age by Student's t test.

Figure S3.- Oxygen flux of sets of 5 LSCS from male and female G93A and control mice measured at 30,60, 90 and 120 (endpoint) days of age. Permeabilized LSCS measures on complex I state 2 (A and E), Complex I state 3 (B and F), complex I/II state 3 (C and G) and complex II state 3 (D and H) oxygen consumption conditions between G93A overexpressors and controls depicted by sex. Measurements were taken at 37 °C in Mir05 media. Values shown are means \pm SEM expressed as pmol O₂/min \times mg protein for 4-6 independent measures. *, p < 0.01 respect to controls of the same age by Student's t test.

Figure S4.- Oxygen flux of sets of 5 LSCS from male and female control mice measured at 30,60, 90 and 120 (endpoint) days of age. In the upper panel, intact measures

showed basal (A), complex I (B) and complex II (C) oxygen consumption differences between males and age matched females in the control colony. Measurements were taken at 37 °C in Hank's balanced salt solution containing 10mM Hepes, pH 7.4, and corrected for instrumental background oxygen flux. On the lower panel, permeabilized LSCS measures on endogenous (D), Complex I state 2 (E), complex I state 3 (F) and complex I/II state3 (G) oxygen consumption conditions between male and age matched females in the control colony. Measurements were taken at 37 °C in Mir05 media. Values shown are means \pm SEM expressed as pmol O₂/min \times mg protein for 4-6 independent measures. *, p < 0.01 respect to females of the same age by Student's t test.

Figure S5.- GC/MS analyses of protein oxidation products in LSCS from male and female G93A and control littermates measured at 60, 90 and 120 (endpoint) days. (A) and (C) represented levels of GSA, for male and female, respectively. (B) and (D) represented levels of CML for male and female, respectively. Values shown are means \pm SEM expressed as μ mol of analyte per mol lysine. *, p < 0.01 respect to non transgenic group of the same age by Student's t test.

Figure S6.-GC analyses of lipids in LSCS from male and female G93A and controls, measured at 30, 60, 90 and 120 (endpoint) days. Upper panel shows absence of sexual dimorphism in the control colony regarding DHA (A) or AA (B) levels in spinal cord. Lower panel indicates the differences founded among G93A colony and controls depicted by sex. (C) and (D) shows levels of AA along disease course for male and female, respectively. (E) and (F) shows levels of DHA along disease course in male and female, respectively. Bars represented mean values \pm SEM expressed as % of abundance of analyte among the total FAME identified. *, p < 0.01 respect to female group in the upper panel and respect to the control littermate in the lower panel. All of them age-matched, by Student's t test.

Figure S6.- Phase contrast and fluorescence microscopy images of the N2A culture after pEGFP-hSOD-wt (A) and (C) or pEGFP-G93A-hSOD1 (B) and (D) transfection. Approximately, 80-90% trasfection efficiency was found.

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Supplementary material

Mice Genotyping

Mice were identified by PCR with tail genomic DNA as templates. The REDExtract-N-Amp Tissue PCR Kit (XNAT; Sigma-Aldrich, St. Louis, MO) was used to extract genomic DNA from mouse tails and amplify targets of interest by PCR according to manufacturer's instructions. Four primers (a pair for wild type forward: 5'-CTA GGC CAC AGA ATT GAA AGA TCT-3' and reverse: 5'-GTA GGT GGA AAT TCT AGC ATC ATC-3' and for G93A forward: 5'-CAT CAG CCC TAA TCC ATC TGA-3' and reverse: 5'-CGC GAC TAA CAA TCA AAG TGA-3') were used to amplify a bands from the inserted targeting vector. Briefly, the DNA is released from the tail tissue by incubating the sample with a mixture of the Extraction Solution and the Tissue Preparation Solution at room temperature for 10 minutes. After adding Neutralization Solution B, the extract is ready for PCR. A 4 μ L aliquot of the neutralized extract is then combined with 10 μ L of 2x REDExtract-N-Amp PCR Reaction Mix (buffer, salts, dNTPs, Taq polymerase, JumpStart Taq antibody and REDTaq® dye) and adequate volumes of each primer and water (PCR grade; Sigma-Aldrich, St. Louis, MO). PCR conditions were: after 1 cycle of 5 minutes at 95°C, 35 cycles of 30 seconds at 94°C, 45 seconds at 50°C, and 4 minute at 72°C, with a final extension at 72°C during 7 min, using an Applied Biosystems 2740 v.2.08 (Carlsbad, CA) thermal cycler. As a control of effective PCR amplification, housekeeping gene interleukin 5 was used. The resulting PCR products were stored at 4°C until direct loading onto an agarose gel. Products were electrophoresed for 30 minutes under constant voltage (100V) and imaged under UV light (302 or 365 nm) lamp from Alpha Innotech (Santa Clara, CA) and analysed with Alpha Digidoc RT2 software (Santa Clara, CA).

Neurological scoring

Neurological scoring was performed every other day for both hind legs for each mouse from 60 days of age. The neurological score employed a scale of 0 to 4 and was a slight variation of which was developed by observation at Amyotrophic Lateral Sclerosis Therapy Development Institute (ALSTDI). Criteria used to assign each score level were as following: score 0, full extension of hind legs away from lateral midline when mouse is suspended by its tail, and mouse can hold this for 2 seconds, suspended 2–3 times; score 1, collapse or partial collapse of leg extension towards lateral midline or trembling of hind legs during tail suspension; score 2, toes curl at least twice during walking a distance of 40cm, or any part of the foot is dragged along the cage bottom or table (if one hind leg is scored as 2, food pellets are left on bedding and a long sipper tube is placed on the water bottle); score 3, rigid paralysis or minimal joint movement, foot not being used for forward motion; and, score 4, mouse cannot right itself within 30 seconds from either side. When mice achieved a score of 4 for two alternate days, they were euthanized.

Paw print analysis

Mice were trained to walk freely along a U-shaped plastic corridor (5 cm wide, 70 cm long) three times per week before data collection (average age 70 days). Once trained, to perform stride length measurements, hind limbs were stained with non-toxic children paint and their tracks were imprinted on paper lining the floor of the corridor. Only continuous runs were selected among recorded paw prints and a minimum of 5-7 strides were measured per animal per day (measures were taken three times per week). Since animals tended to run when released and walk slowly at the end of the corridor, those sections of the paw print were discarded for the stride length measurements. Three stride length measurements were taken manually as described previously (Chiu et al., 1995) front and back stride, and front-to-back distance. 10 total measures were taken for each measurement. Front stride and back stride were collected as a straight line from paw print to the following paw print. Front-to-back distance was collected as a straight line from back paw print to corresponding front paw print. Correspondence was based on closest front footprint. The distance was recorded as length of line from paw to the stride line opposite the paw print. Since only number of the randomized animal and date identified the recorded tracks, measurement of stride length was determined in a blinded manner. As the disease progresses, the painted footprints became increasingly smeared on the paper, which correlated with previous results (Marx, 1994). The

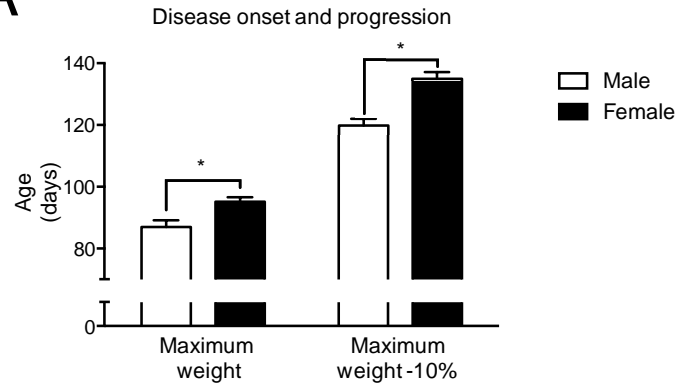
onset of clinical weakness was quantified by determining the age at which shortening of the stride length was lower than 40% for two consecutive measures.

Oxidation-derived protein damage markers measurements by GC/MS.

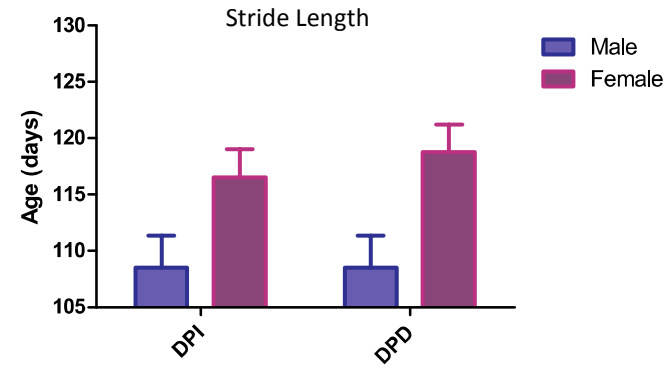
Glutamic semialdehyde (GSA), amino adipic semialdehyde (AASA), N^ε-(carboxyethyl)-lysine (CEL), N^ε-(carboxymethyl)-lysine (CML), and N^ε-(malondialdehyde)-lysine (MDAL) concentrations in total proteins from spinal cord homogenates were measured by gas chromatography/mass spectrometry (GC/MS) as previously described (Cacabelos et al., 2014). Samples containing 0.75-1 mg of protein were delipidated using chloroform:methanol (2:1 v/v), and proteins were precipitated by adding 10% trichloroacetic acid (final concentration) and subsequent centrifugation. Protein samples were reduced overnight with 500 mM NaBH₄ (final concentration) in 0.2M borate buffer, pH 9.2, containing 1 drop of hexanol as an anti-foam reagent. Proteins were then reprecipitated by adding 1ml of 20% trichloroacetic acid and subsequent centrifugation. The following isotopically labelled internal standards were then added: [2H8]Lysine (d8-Lys; CDN Isotopes); [2H4]CML (d4-CML), [2H4]CEL (d4-CEL), and [2H8]MDAL (d8-MDAL), prepared as described (8,26); [2H5] 5-hydroxy-2-aminovaleric acid (for GSA quantization) and [2H4]6-hydroxy-2-aminocaproic acid (for AASA quantization) prepared as described in (Pamplona et al., 2005). The samples were hydrolysed at 155°C for 30 min in 1ml of 6N HCl, and then dried in vacuo. The N,O-trifluoroacetyl methyl ester derivatives of the protein hydrolysate were prepared as previously described (Pamplona et al 2005). GC/MS analyses were carried out on a Hewlett-Packard model 6890 gas chromatograph equipped with a 30m HP-5MS capillary column (30m x 0.25mm x 0.25 μm) coupled to a Hewlett-Packard model 5973A mass selective detector (Agilent, Barcelona, Catalonia). The injection port was maintained at 275°C; the temperature program was 5 min at 110°C, then 2°C/min to 150°C, then 5°C/min to 240°C, then 25°C/min to 300°C, and finally hold at 300°C for 5 min. Quantification was performed by external standardisation using standard curves constructed from mixtures of deuterated and non-deuterated standards. Analytes were detected by selected ion-monitoring GC/MS. The ions used were: lysine and d8-lysine, m/z 180 and 187, respectively; 5-hydroxy-2-aminovaleric acid and d5-5-hydroxy-2-aminovaleric acid (stable derivatives of GSA), m/z 280 and 285, respectively; 6-hydroxy-2-aminocaproic acid and d4-6-hydroxy-2-aminocaproic acid (stable derivatives of AASA), m/z 294 and 298, respectively; CML and d4-CML, m/z 392 and 396, respectively; CEL and d4-CEL, m/z 379 and 383, respectively; and MDAL and d8-MDAL, m/z 474 and 482, respectively. The amounts of products were expressed as the ratio μmol GSA, AASA, CML, CEL or MDAL per mol lysine.

Figure 1

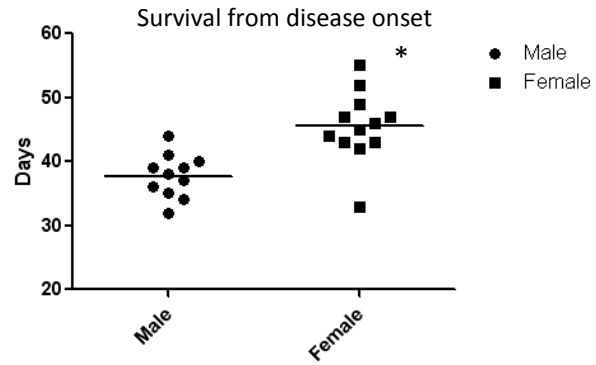
A



B



C



D

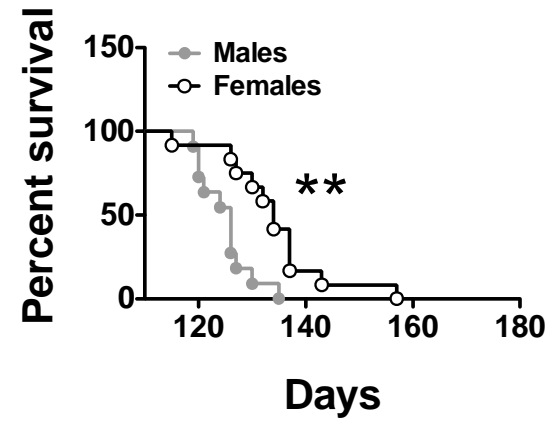
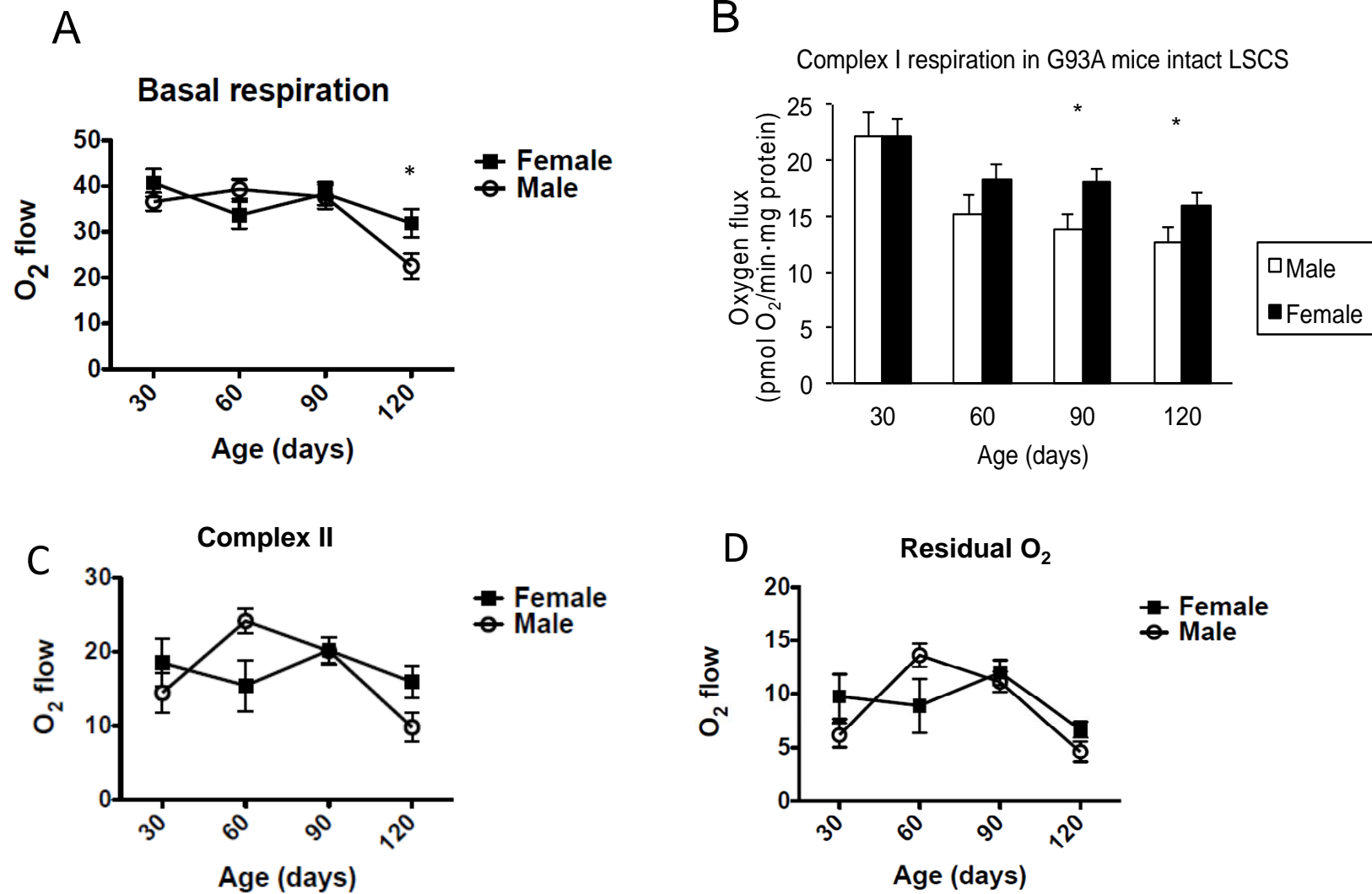
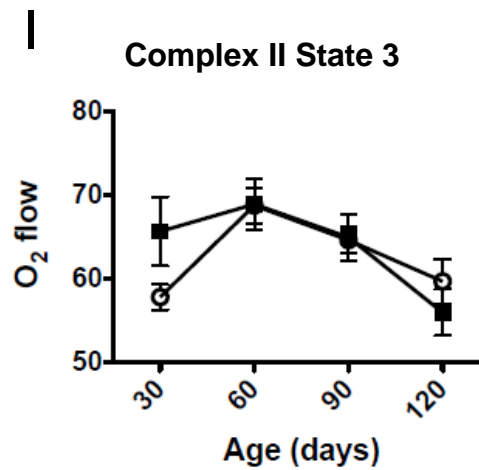
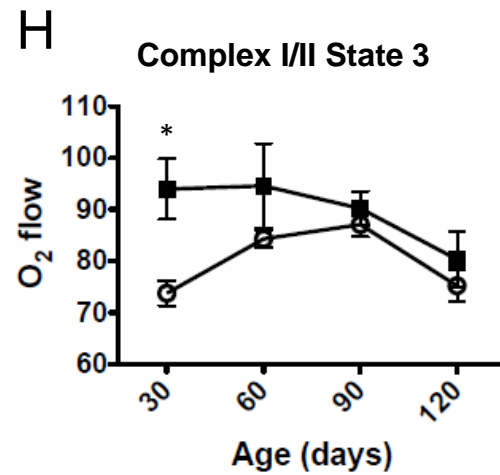
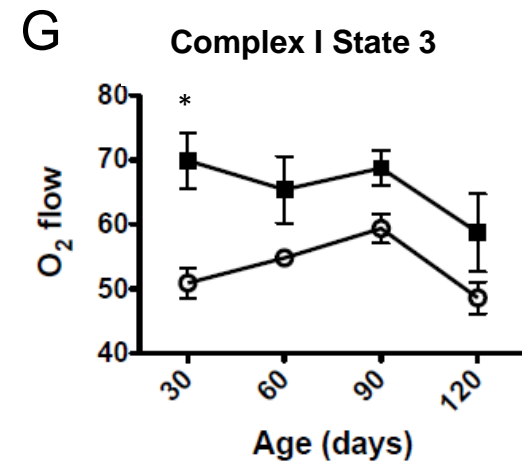
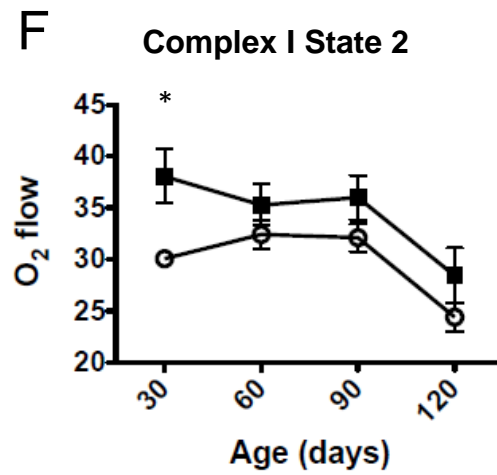
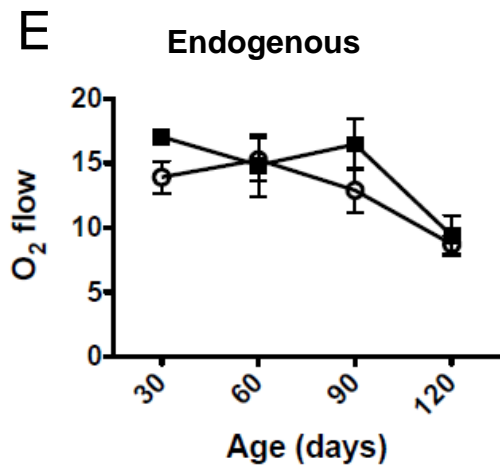


Figure 2





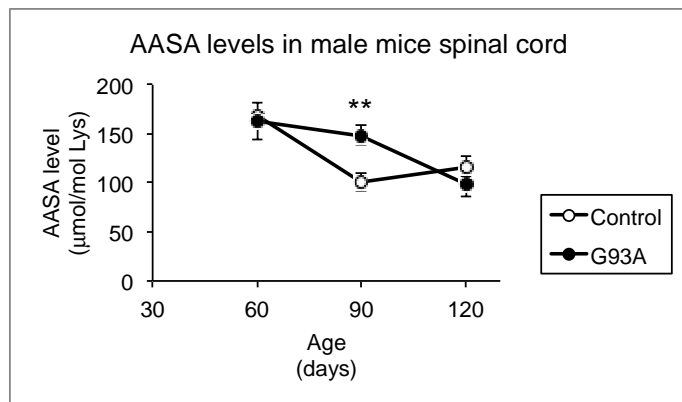
■ Female
○ Male

Figure 2 cont

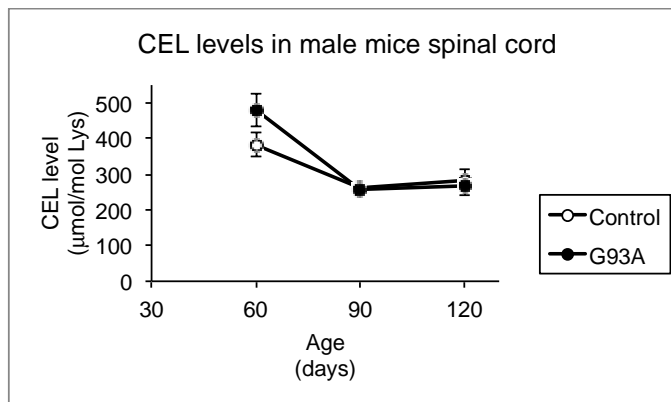
Figure 3

Male

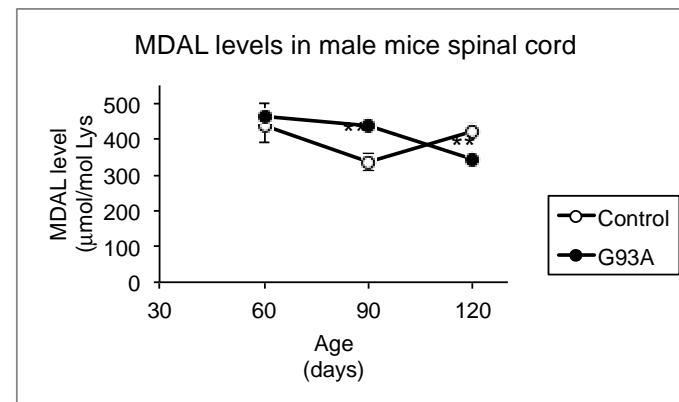
A



B

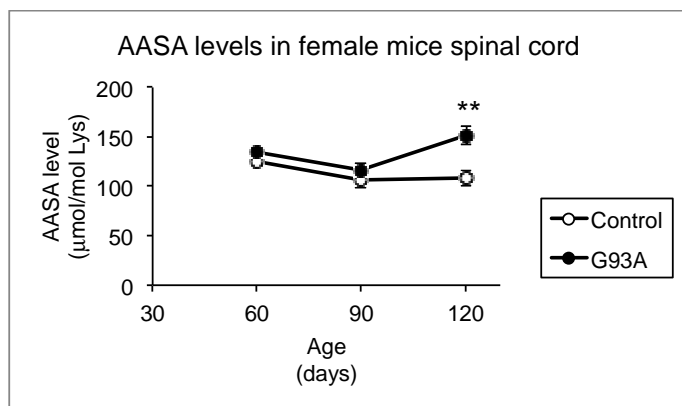


C

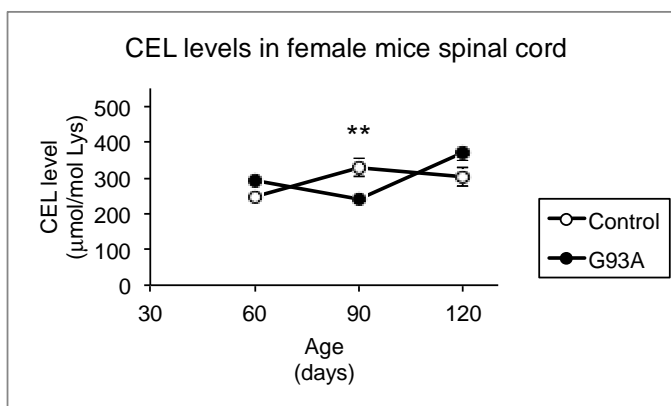


Female

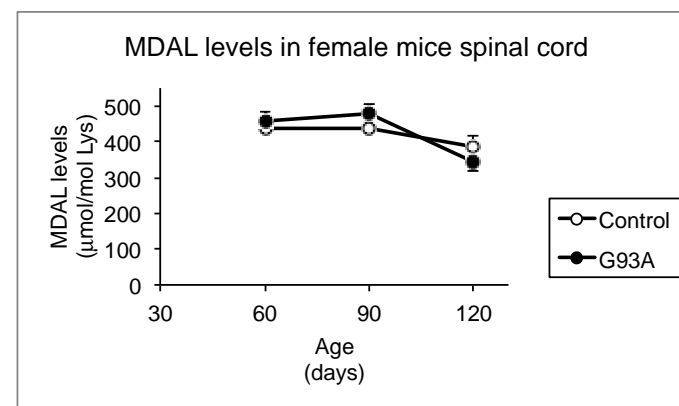
D



E

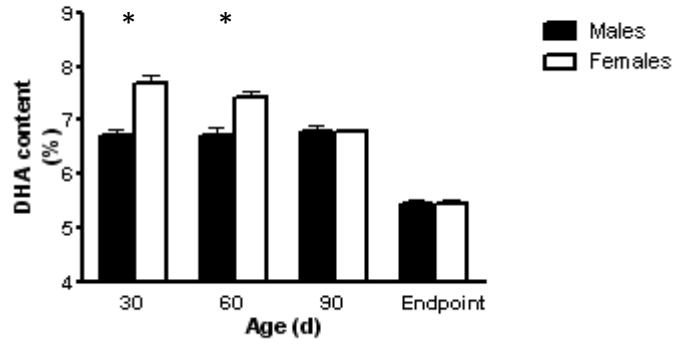


F



A

Effect of gender on spinal cord DHA (G93A)



B

Effect of gender on spinal cord AA (G93A)

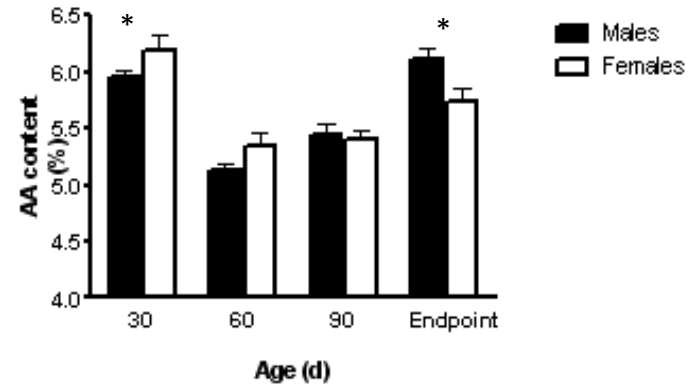
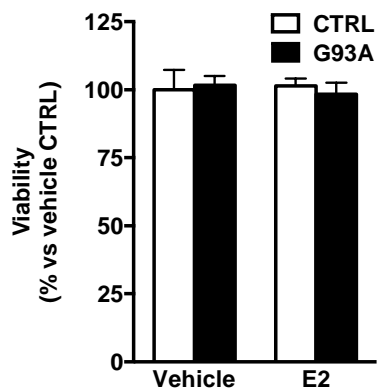


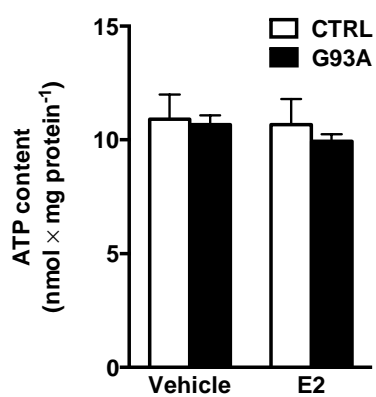
Figure 4

Figure 5

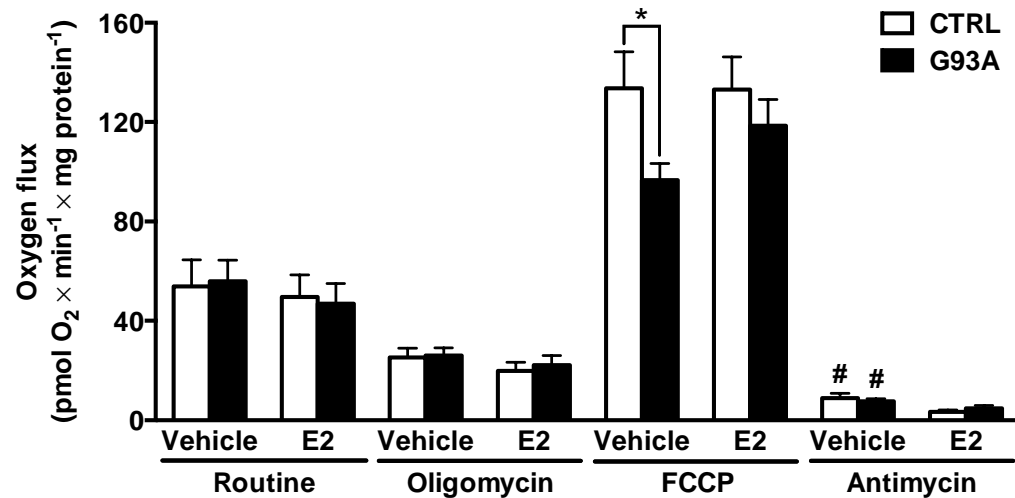
A



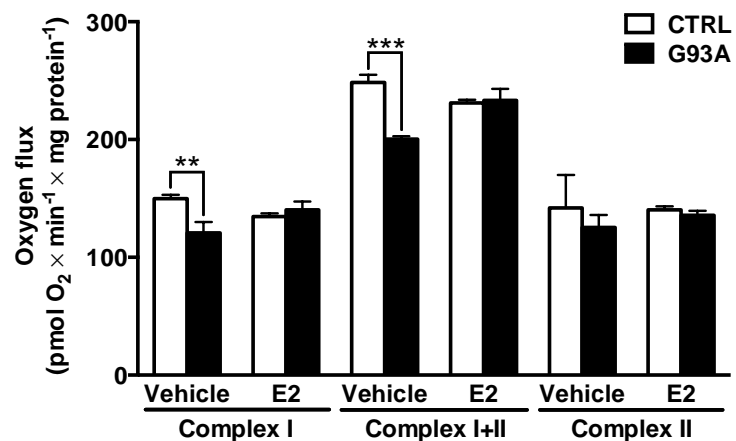
B



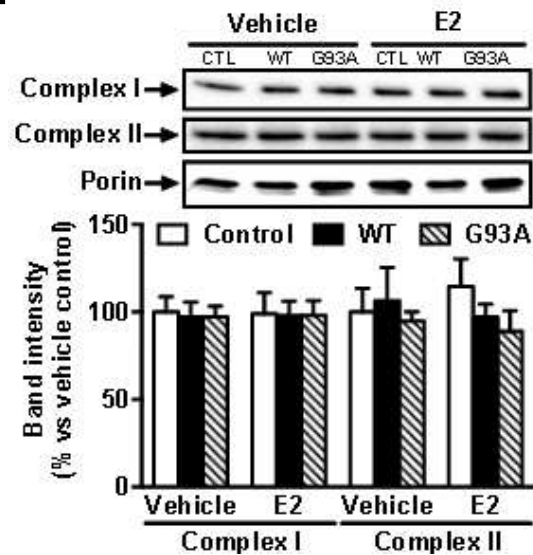
C



D



E



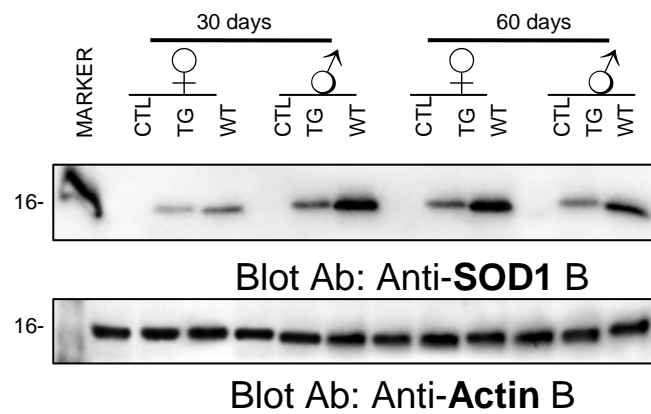
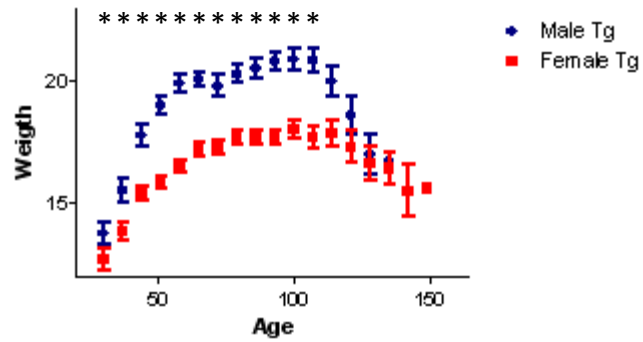


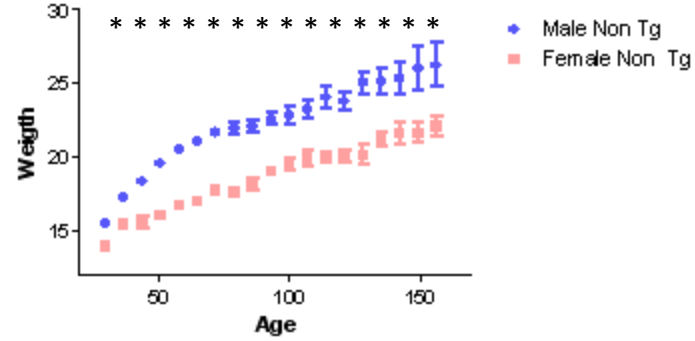
Figure S0 (supplemental)

Figure S1 (supplemental)

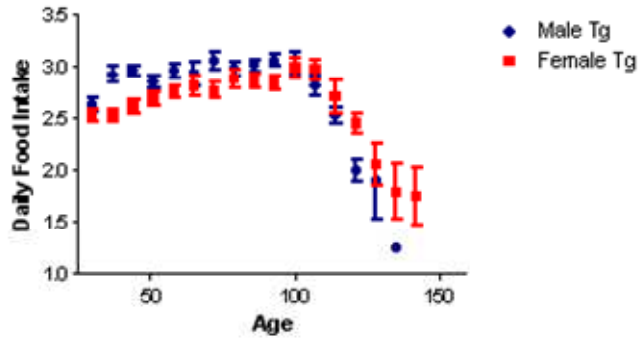
A
Weigh Evolution Gender Dimorphism CTL



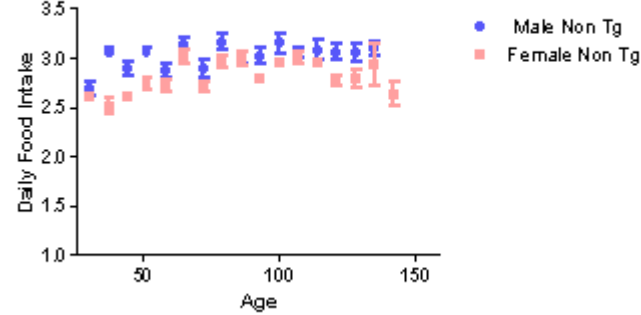
B
Weigh Evolution Gender Dimorphism CTL2



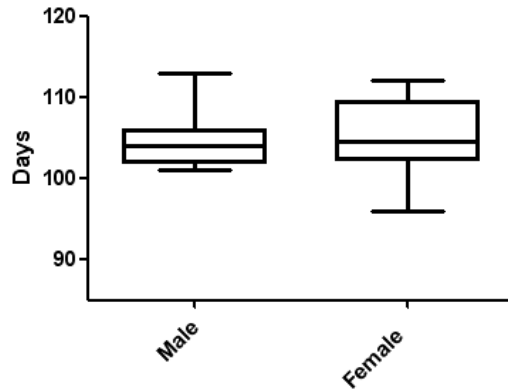
C
Food Intake CTL Gender dimorphism2



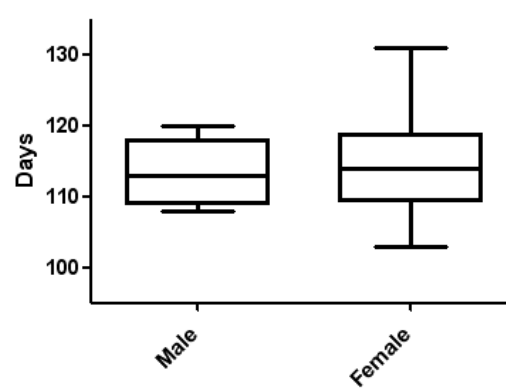
D
Food Intake CTL Gender dimorphism3



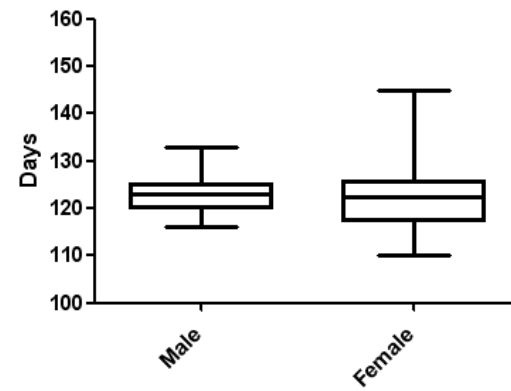
E
Clinical Score 2 Male vs Female



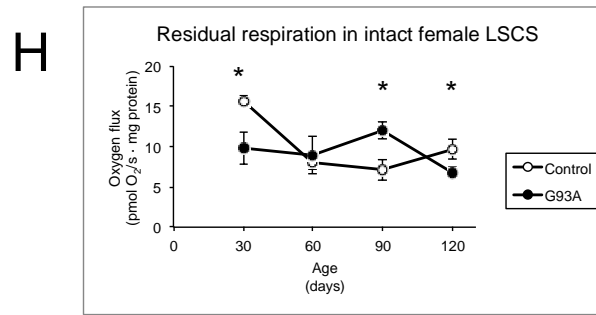
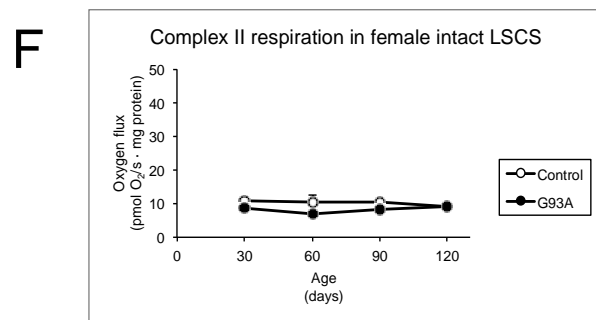
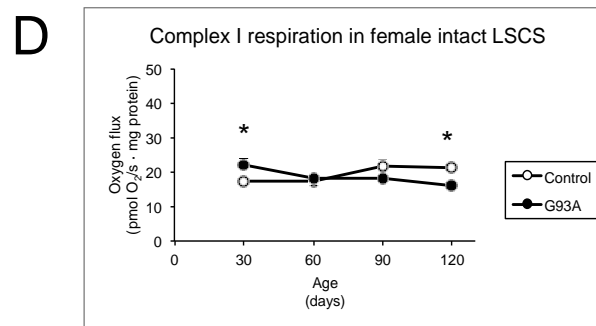
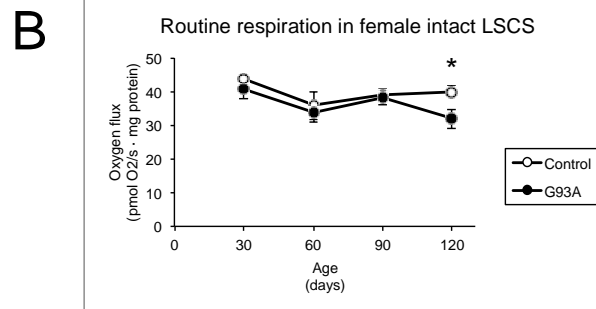
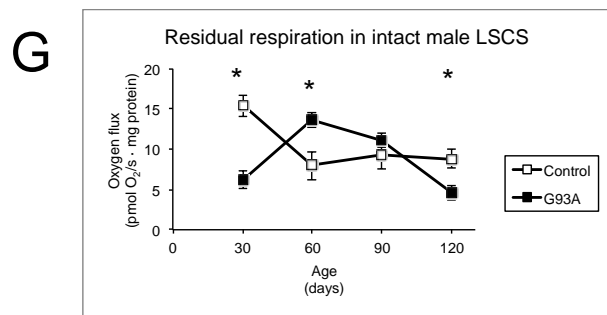
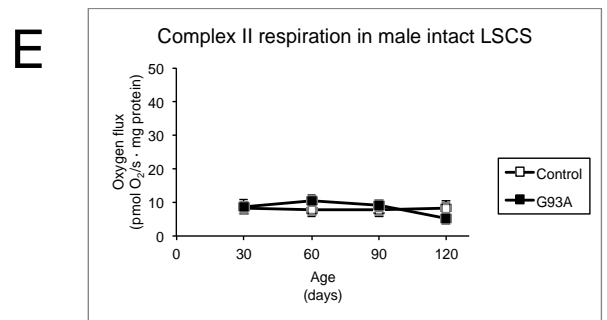
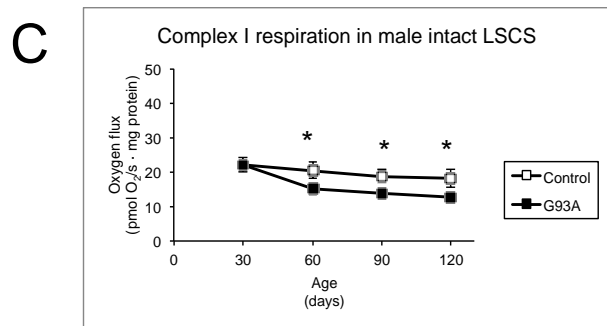
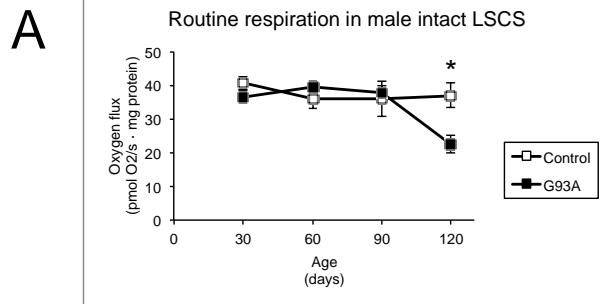
F
Clinical Score 3 Male vs Female



G
Clinical Score 4 Male vs Female



Male

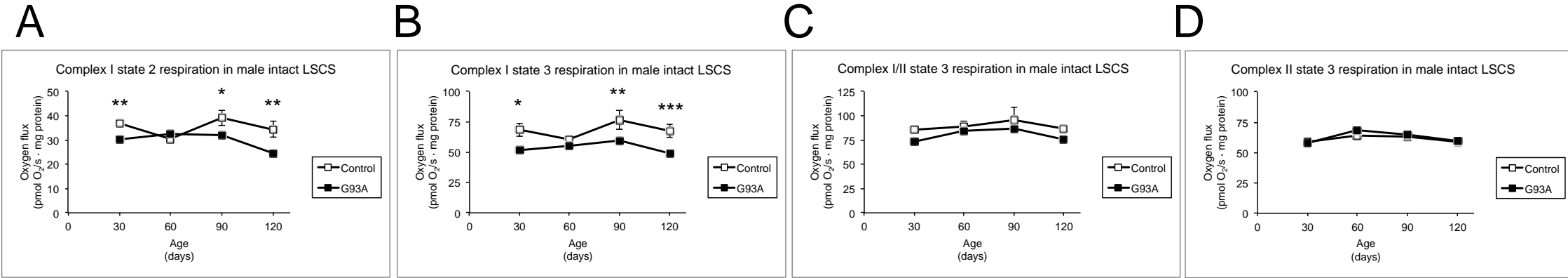


Female

Figure S2 (supplemental)

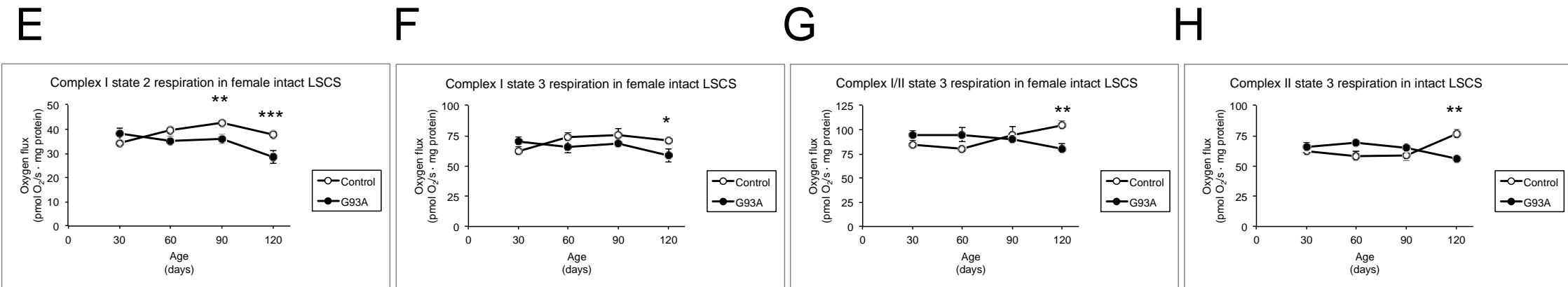
Figure S3 (supplemental)

Male



200

Female



Control Animals

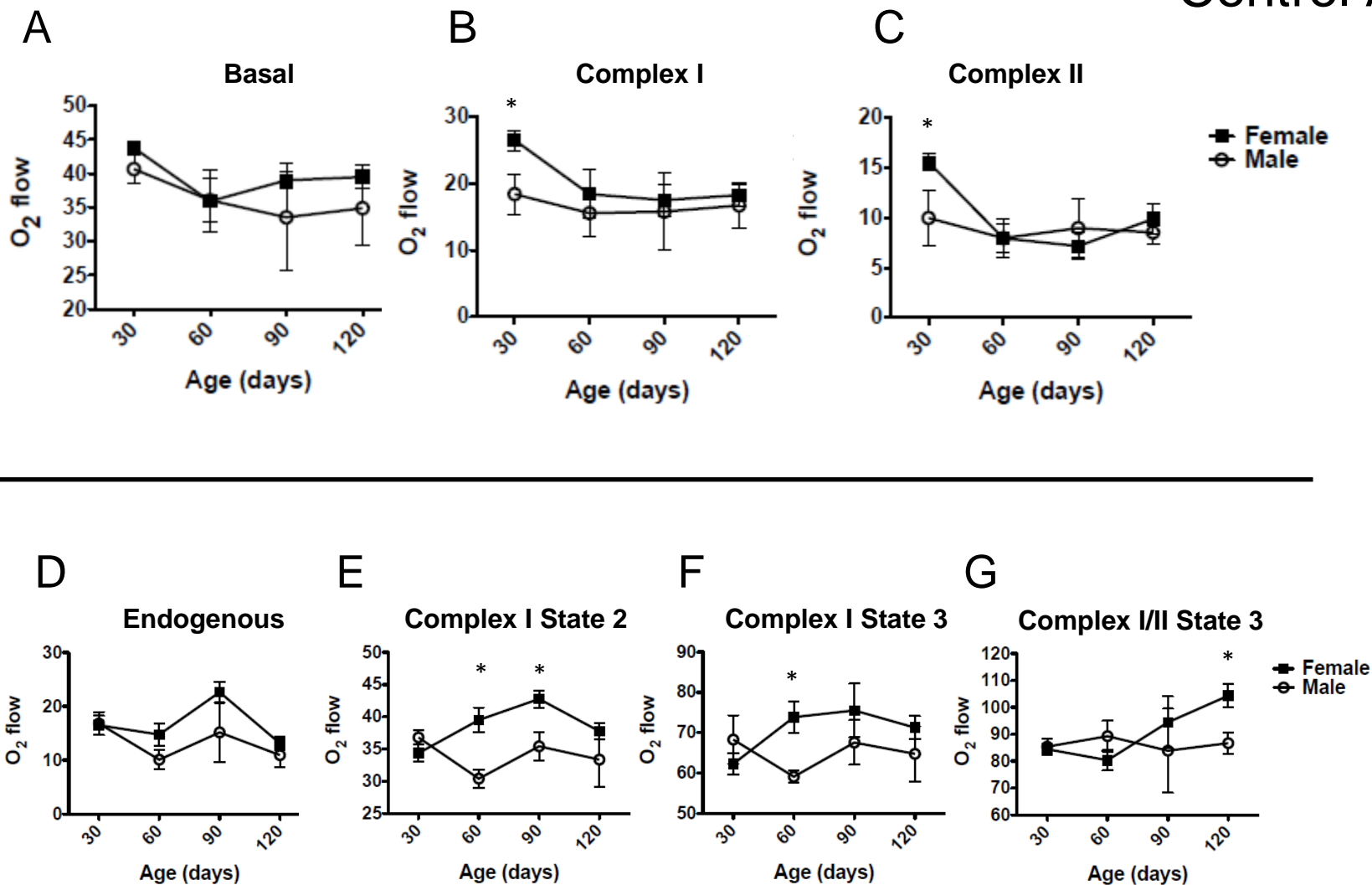
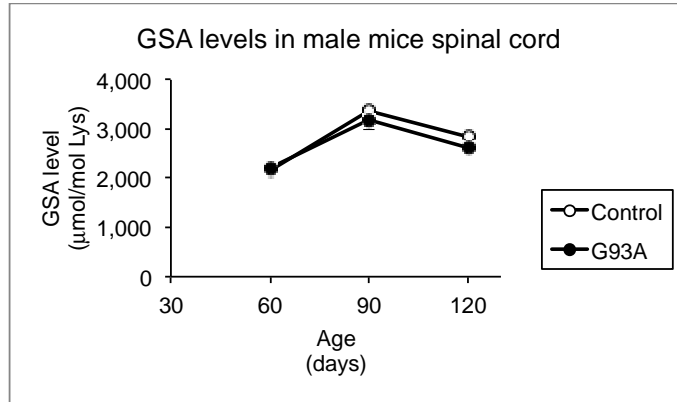


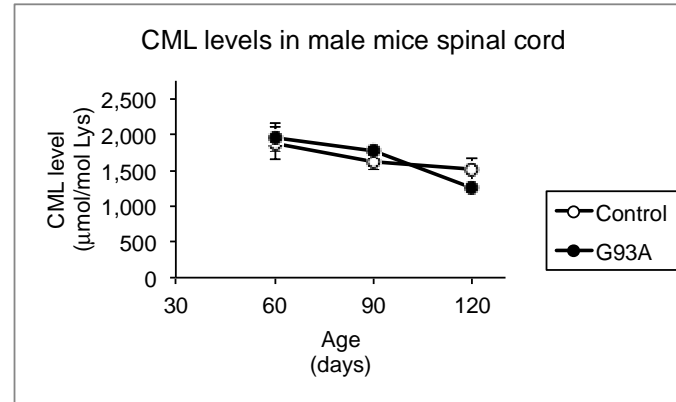
Figure S4 (supplemental)

Figure S5 (supplemental)

A

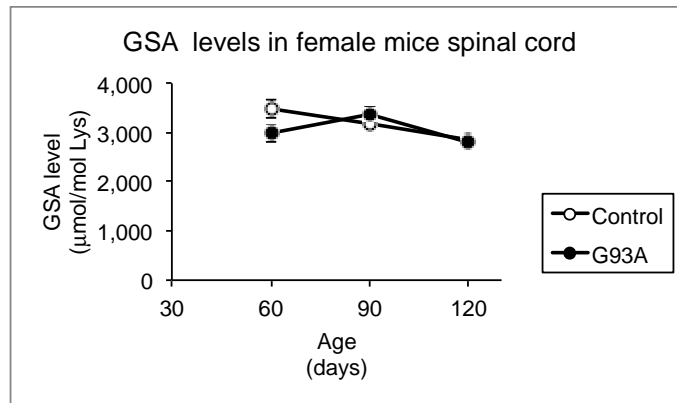


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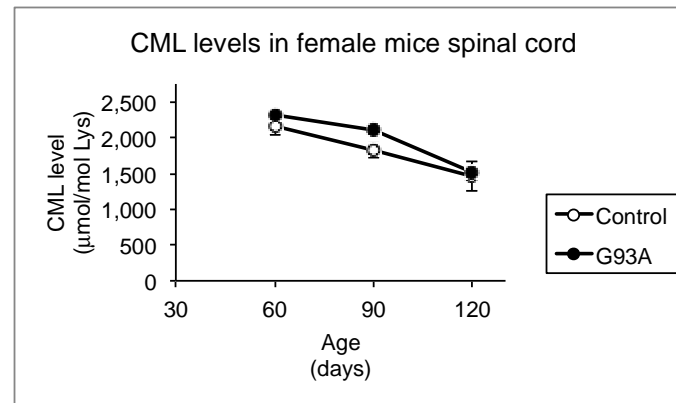


Male

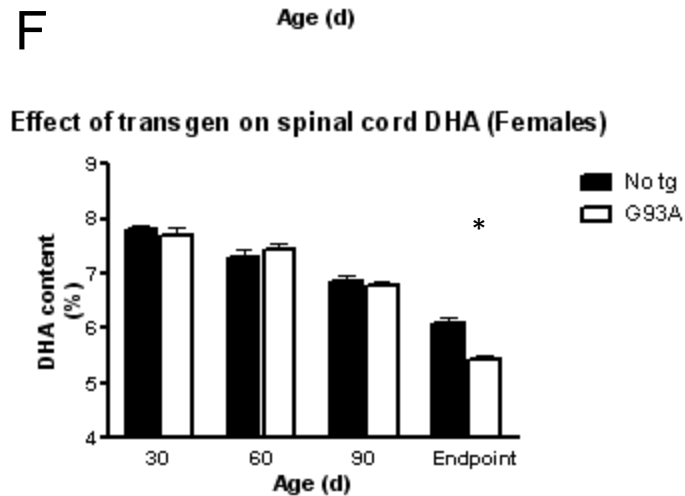
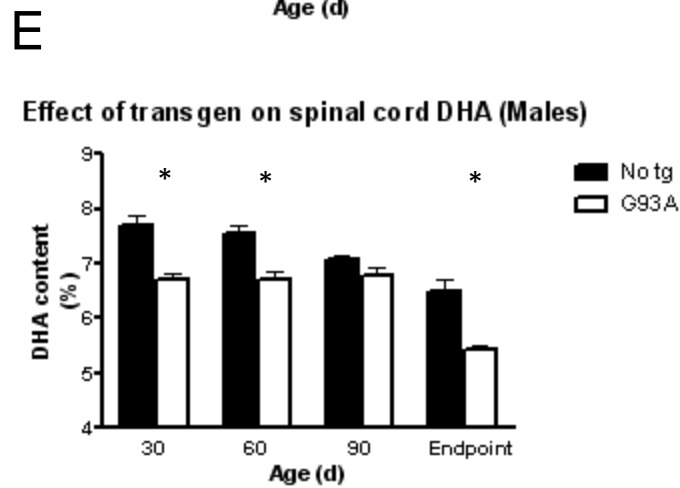
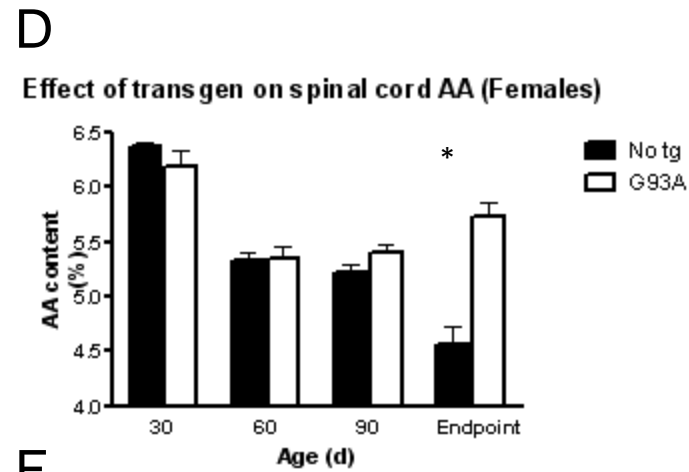
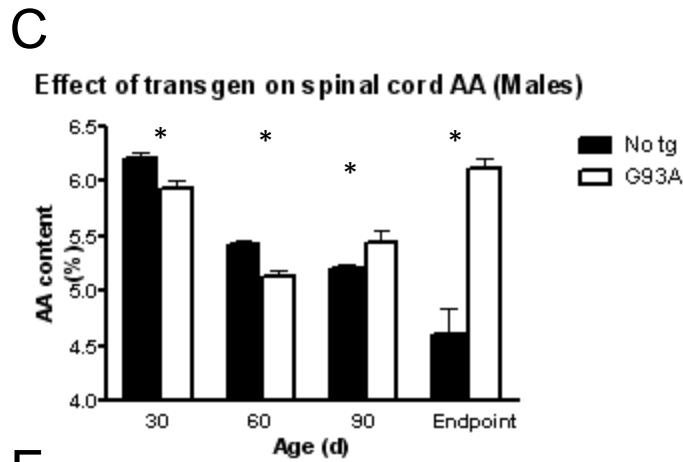
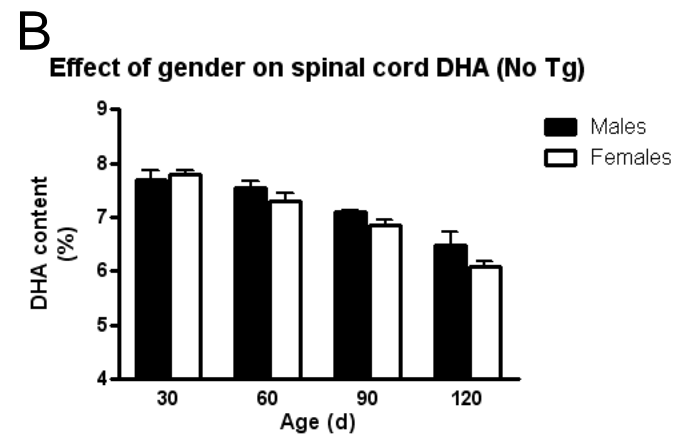
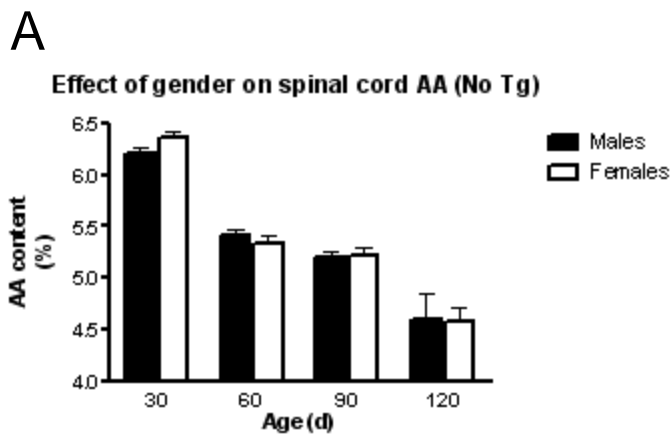
C



D



Female



Male

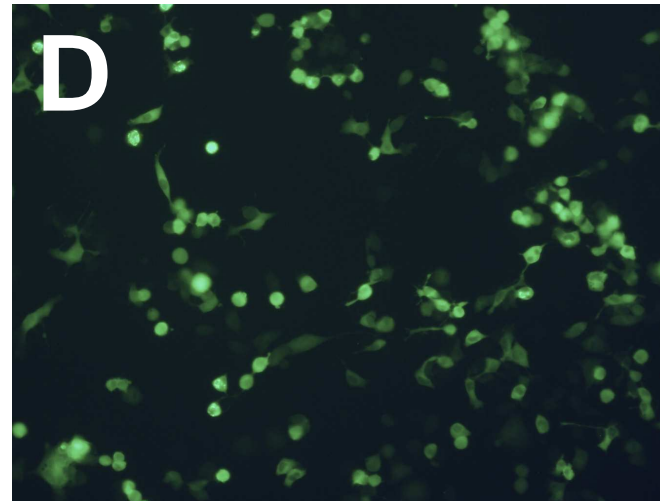
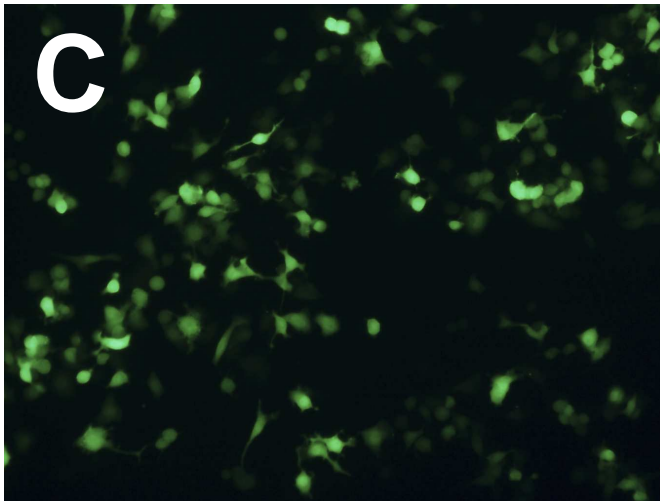
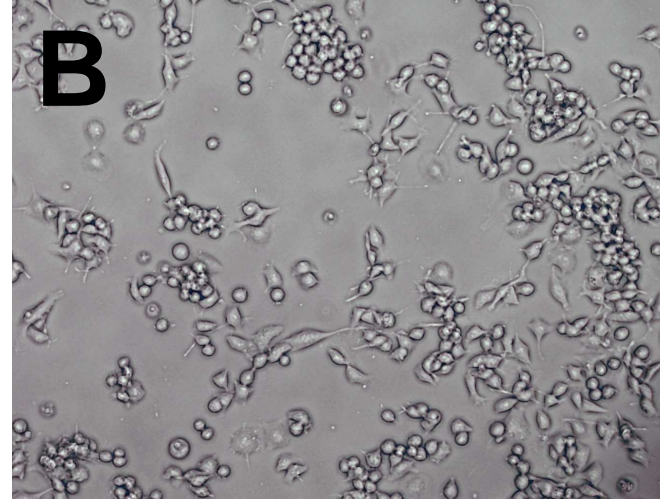
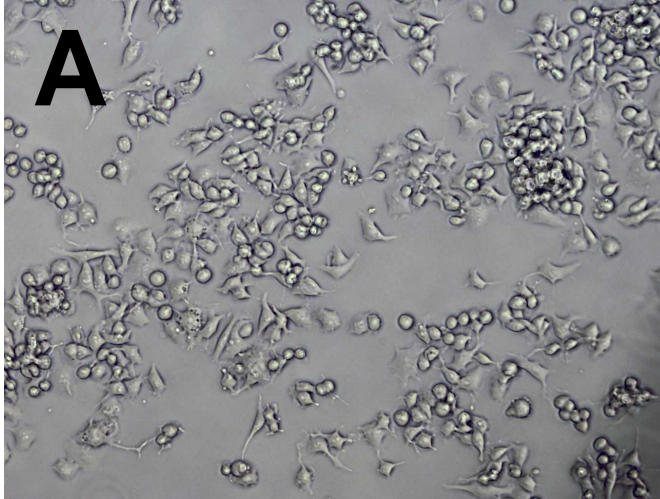
Female

Figure S4 (supplemental)

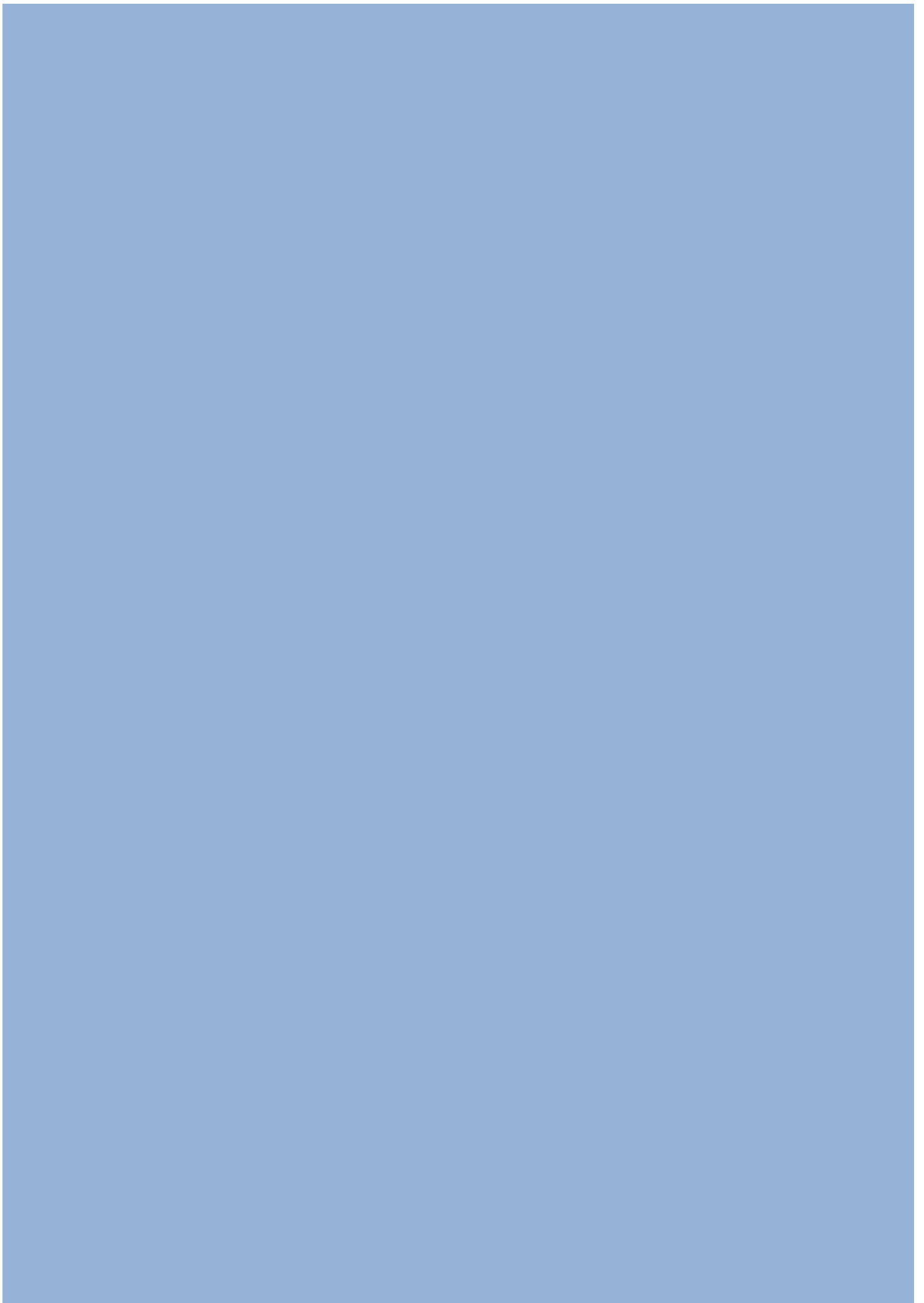
Figure S7 (supplemental)

Control (pEGFP-wt)

G93A (pEGFP-hSODG93A)



5. Discussion



5. Discussion

The work presented here summarized different methodological approaches aimed to shed some light on FA dietary interventions to better understand pathophysiology of ALS. Also relevant, we tried to increase the knowledge of a variety of well-established models of the disease (e.g. cell lines, OT, SODG93A), involving FA handling or sexual dimorphism, which were found altered in human patients.

For this purpose, we started with a very simplistic models of biomolecule substrates (lipid but also proteic) trying to define and characterize a suitable natural dietary antioxidant and its possible improved outcome (by means of reduced oxidative accretion and upgraded cell survival) when being co-treated against different oxidative stimuli. As many others had pointed before (reviewed in (Benzie and Choi 2014)), the heterogeneity encountered, which could be related to the different sources of oxidative stress, made the election of a single antioxidant substance very complex (to protect against those multiple situations). Those variable results could be therefore explained in terms of altered antioxidant properties of a specific compound as well as the different model involved. Thus, this capacity would greatly vary, sometimes based on antioxidant chemical structure. In fact, hyperconjugation and proton dislocation properties, like those obtained thanks to orto-dihydroxyl structures (e.g. those found in secoiridoids), phenol radical cation and phenoxy radical delocalization (e.g. phenolic acids) (Joshi et al. 2004) and/or α/β unsaturated structures (e.g. flavonoids and lignans among others) (Brown et al. 1998) have been proved to counteract oxidative-damage spread.

Anyway, antioxidant potential would also rely on the possible interaction with the substrate (e.g. lipid or aqueous media) and, in a complete animal model, its inherent natural dietary bio-availability (e.g. the chance to be in the right time and location). Therefore, the election of a suitable antioxidant would depend on the specific mechanism of oxidation that intercepts and the particular environment where it takes place, for those reasons being very difficult to find a broad-field one.

In any case, in general, luteolin and hydroxytyrosol showed a better response to oxidative stress (by multiple oxidative methodological approaches), in terms of oxidative carbonylation accretion (as shown by WB against DNP adducts in ox LDL) and alleviated oxidative mediated-cell death in HEMC-1 and HepG2 cell lines (*tert*-butoxide and Cu^{+2} incubation, respectively). But in the other hand, luteolin failed to reduce PC-oxidative derivatives (chromatographically measured, e.g. PLPC, SGPC, PGPC) in oxLDL, when compared, for instance, with hydroxytyrosol. Former specie also failed to help improving the FA preservation in the LDL, as was shown thanks to lipid profile measurements, with a better behavior of hydroxytyrosol, pinoresinol or gallic acid under those conditions. Thus, luteolin action could be more relevant in terms of protein modification reducer than in truly lipoxidative prevention.

Interestingly, specific oxidative signature was found *in vivo* (as suggested by the lipidomic profile of hamsters' plasma and the oxLDL GC/MS data). Hence, lipidomic analysis of hamster plasma revealed lower accretion of oxidized PL (e.g. PLPC, OGPC, PGPC) when animals consumed a polyphenol extract diet, even when total antioxidant capacity (FRAP measured) was unchanged. Furthermore, DNP accretion was reduced *ex vivo* when plasma was incubated

under Fe⁺³-Asc methodology and, similarly, human plasma was also protected with the luteolin incubation.

Either way, this first work established a noticeable relation between oxidative status, antioxidant action and specific lipid signature, which was useful in further research, even when, probably due to its intrinsic complexity, we failed to find a universal antioxidant.

Characteristic for ALS, as well as in other neurodegenerative diseases (Pamplona et al. 2008), it is known to have an increased oxidative accumulation (Shaw et al. 1995). Whether this fact is cause or consequence is still under debate, but strategies aimed reduce or control the spread of the damage showed positive outcomes, at least in some animal models (Gurney et al. 1996; Reinholz, Merkle and Poduslo 1999). Hence, for such a complex disease was worth to try to define a possible upgrade in terms of lipoxidative damage, both in cellular models (N2A, NSC34), tissular (organotypic) and animal models (SODG93A), before shifting to human scale. For this purpose, the election of GC/MS methodology, as well as WB against carbonylated adducts to assess the relevant accretion of damage to proteins was judged to be adequate. Moreover, we could depict the source of this damage, as we could relate it to specific metabolic damage *vias*, determining metal catalyzed -AASA and GSA- purely lipoxidative -MDAL-, glycooxidative -CEL-, mixed lipo-glycooxidative -CML- or even subcellular location (e.g. mitochondrial; 2-SC) as different origins protein oxidative damage. Furthermore, thanks to chromatography, whole lipidomic analysis as well as lipid percentage profiles of studied tissues/experimental situations we could ascertain whether “dietary” intervention is achieved (e.g. flux experiments, DHA accretion, AA depletion) and/or if an specific analyte is accumulated in response to a determined situation (e.g. NPD1, 8-iso-PGF_{2α}). In a recent publication (Zhang et al. 2010) researchers showed an intriguing novel role of 15-deoxy PJ₂ (mostly derived from the AA) a PG derivative derived to exert anti-inflammatory actions (Shibata et al. 2002). They demonstrated that *in vitro* treatment of this PG in cell lines altered TDP-43 proteolysis, solubility and subcellular localizations, resulting in a general better status.

Hence, these two approaches (e.g. oxidative damage to proteins and lipid composition) were therefore very helpful for a better description of such situations and were completed with IHQ analysis. Expression of a determined protein in relation to others (which could be confirmed by WB) is relevant for a precise description, but more complete information could be obtained when the expression is also localized within a cell. Hence, for most enzymes is not sufficient to exist, but rather to exist in the right place and this is especially relevant for CNS where very different cell population (with completely different functions, thus protein expression) is found. Finally, measures of oxygen consumption (high resolution respirometry) may help to both, describe a particular malfunction situation along ETC and justify a greater ROS production. Therefore, all those techniques, plus animal behavioral test for precise clinical evolution measurement, were aimed to shed some light over this devastating disease and its relation with lipid status.

Admitting the multiple limitations of co-cultured experiments: FA/cell line; FA/primary cultures (e.g. multiple cell types, bioavailability, delivery, metabolic degradation, albumin crosslink), but aiming to minimize complexity, flux/incorporation experiments (exposure of FA or mixtures of them to single cell and/or organotypical cultures) were designed to ascertain PUFA supplementation effects in relation to various cellular functions (i.e. O₂ consumption, antioxidant activity potential, survival against oxidative stressors, excitotoxicity, synaptic

protein expression, among others). In those measures, lipidic products (and antioxidants) dosages were designed according to an homeostatic range. Similarly, in animal models (e.g. hypercholesterolemic-feed hamsters supplemented with a polyphenol extract and FA unsaturation degree of in ALS model) isocaloric diets fulfill essential FA necessities. In both cases, particular compositions were aimed to, up to an extent, “stretch” the metabolic machinery, trying to observe subtle differences rather than big dietary alterations that would completely change the regular functioning. Anyway, in fact, accomplishing *in vivo* tissular modification is rather difficult, especially in CNS with exquisite nutrients necessities. Reinforcing this, only discrete modifications were found in response to the diet (WT animals) and few more due to the transgene expression (WT vs. SOD1G93A, data not shown).

Hence, since previous works claimed for an altered DHA homeostasis in ALS patients (Ilieva et al. 2007), it was interesting to pay special attention in its synthetic machinery. Interestingly, we found FASD1 and FASD2 altered expressions in spinal cord MNs. Further, thanks to IHQ, we showed a previously unreported FASD1, ACOX1 and AACA1 decrease in MN where pTDP-43 accumulates aberrantly. Surprisingly, those findings were not so evident when total protein extract (WB) was used. In fact, general increased AACA1 and FASD2 accumulation, indicating a potential higher DHA synthesis, was insufficient (Ilieva et al. 2007), pointing that cell specific mechanism may be operating. Thus, by switching to cellular models, our interest was in trying to define how this cellular relation could be altered in terms of DHA synthetic machinery and surrogates (STX-3, Drebrin) status. Undoubtedly, cell lines (N2A) transfected with aggregation prone TDP-43 fragment suffer from FASD2 depletion. Apart from the commented conversion of ALA to stearidonic acid (C18:4 ω -3) along the ω -3 synthesis of DHA, this enzyme is also responsible for the generation of DGLA (C20:3 ω -6, through the previous synthesis of γ -Linolenic -18:3 ω -6) in the ω -6 series. Interestingly, DGLA derivatives (with just one double bound along the aliphatic residues, thus named 1 series PG, e.g. PGF_{1 α} , PGE₁) even when less abundant, exerted mainly anti-inflammatory properties (Fan and Chapkin 1998; Kapoor and Huang 2006; Xu et al. 2014). Hence, FASD2 loss could result not only in less DHA synthesis (and consequently its anti-inflammatory derivatives depletion) but also for reduced non-DHA-related anti-inflammatory intermediates.

Also important, drebrin (but not STX-3) expression was reduced in these cells too (WB and IHQ measures) in response to TDP-43 aggregation, but again, a tissular variation was found in human samples. Spinal cord (where DHA is depleted) demonstrated drebrin and STX-3 reduction (the latter not significant), whereas brain cortex (with DHA accretion in patients) did not show those changes. However, MN drebrin reduction in patients was not linked with increased pTDP-43 accumulation, as shown by IHQ, even when drebrin function was altered in oxidative stress (Li, Wang and Zuo 2013). Furthermore, reduced mitochondrial Ca⁺² buffering capacity was found under ω -3 supplementation (at least in in CD₄⁺ T cells, (Yog et al. 2010)) although other reports showed no relation of dietary FA with the Ca⁺² capacity, nor response to oxidative stimuli and, importantly, stress the importance of a correct dosage for supplements (Stavrovskaya et al., 2012). Nevertheless, altered lipid metabolism and TDP-43 have been recently linked (Heck et al. 2014), since deletion of the latter caused membrane alterations as well as fat storage disarrangements. And further, we could confirm in our model that TDP-43 phosphorylation and aggregation preceded PUFA's synthesis changes (measured after 2h) and drebrin loss, after an H₂O₂ challenge.

In more a complete model (in terms of intercellular relationships), the OT primary culture, increased DHA (concomitant with increased AA and a drastic depletion of ω -3 DPA, a DHA precursor) was found thanks to GC. Further, specific lipid signature (lipidomic measurements) and increased oxidative damage was confirmed under THA treatment. This is, significant accretion of 8-iso-PGF_{2 α} and higher NPD1 (DHA derivative) as well as a positive correlation among them was confirmed. Several works showed increased NPD1 production in response to an insult (Bazan 2013; Bazan 2005; Mukherjee et al. 2007), but to our knowledge, this is among the first linking excitotoxicity and NPD1 production (and excitotoxicity and oxygen resepirometry reduction too). In addition, OT tissue composition (higher DHA under THA conditions) supports the possibility of this production, reinforced by the fact that in a neuronal cell line (N2A) chooses DHA synthesis as an initial response when confronted to oxidative stress (as show in flux experiments) and oxidative stress and mitochondrial dysfunction is known to be increased in excitotoxicity (Nguyen et al. 2011). Further explanation of an increased NDP1 production could be understood in terms of upgraded survival, which may involve PI3K/Akt signalling (Halapin and Bazan, 2010), know to be influenced by DHA (Akbar et al 2005) and by PLA₂ (Lukiw et al. 2005) action too. In any case, thanks to the previous studies (Ilieva et al. 2007), spinal cord DHA depletion was found, which is inconsistent with this increased DHA in cells and OT. However, this may be understood as an end point result. sALS samples are probably the most valuables ones since they are not a model, it's real life. But on the other hand, these patients have suffered for a long period of disease. Hence, their decreased levels could possibly indicate an insufficient synthesis or depletion due to disease-related-expenses. Beside this, models would reflect a more "acute" situation, whereas a possible correction to attain a new homeostasis may be achieved yet. Interestingly, co-culture with precursors (linen seed fatty acid extract) rather than final products (fish oil extract) showed better MN preservation. Altogether, these two facts (increased oxidative stress and better survival with lower peroxidability index -PRI- and double bound index -DBI- FA mixture -e.g. linenseed extract) could respond to an adaptative mechanism. Hence, this fact was reinforced by the upgraded MN survival when those explants are co-treated with DHA plus tocopherol (optimally preserved from oxidation), which goes in line with a recent publication demonstrating a reduced neuroinflammation in terms of decreased COX-2 activation and cell death prevention in a spinal cord cultures co-treated with a saturated FA (instead highly unsaturated DHA) and luteolin as antioxidant (Paterniti et al. 2013).

Finally, mitochondrial implication was proved, since lower (c.a. 30%) oxygen consumption was found under excitotoxicity. This may be explained in terms of complex I malfunction, because rotenone (complex I inhibitor) faded out this difference, but also due to oxidative modifications, since tocopherol treatment along the culture protected from this event. This is relevant because previous studies had link CI blockade with increased ROS production (Votyakova and Reynolds, 2001). Of note, interestingly mitochondrial permeability transition pore induction (discussed latter) and excitotoxicity-ROS production was linked too (Hansson et al. 2008). This is supported by the upgraded MN survival when DHA and tocopherol are combined. Interestingly, UCP2 overexpression, which is been related to a ROS reduction in various systems (Andrews and Horvath 2009), shortened lifespan, worsens mitochondrial dysfunction and accelerates disease progression when co-expressed in the SOD1G93A mouse model (Peixoto et al., 2013). This surprising finding may indicate that a minimal oxidative damage is required and we probably need deeper studies for the understanding of ROS production and survival interdependences.

Gender dependence among neurodegenerative diseases is observed (Członkowska et al 2006), as well in ALS incidence and some animal models recapitulated this effect. Recent neuroimaging studies in patients showed significant gender differences in the anatomical patterns of cortical and subcortical pathology in ALS (mostly localizing to extramotor, frontotemporal and cerebellar regions; (Bedeet al. 2014)). However, specific description of this dimorphism was not deeply described in preclinical models. In particular, how this relation could be dietary modified. Similar to a recently published paper (Yip et al. 2013), we demonstrated that potential preventive and beneficial responses attributed to PUFA are not easily reproduced in the SODG93A mouse model. Hence, as previously shown (Herrero et al. 2001), FA had an influence on the specific oxidative stress markers accretion. We demonstrate that this dietary difference was linked to survival differences (with high unsaturation diet diminishing the feminine-gender life sparing extension effect). However, one of the more striking results was the surprisingly lower lipoxidative damage marker founded in animals under lower unsaturation diet. Those animals had similar values of DHA in their spinal cords along disease (with a clear reduction along its course for both sexes), but in the contrary higher levels of AA and one of its derivatives (C22:4 ω -6) and those levels raised general higher PRI and DBI for animals under low unsaturation diet. In a detailed vision of this FA profile, males under low unsaturation diet were the ones with better DHA preservation along disease progression (estimated as % ratio of initial DHA content-60 days- respect to endpoint; 95,57% and 79,65% for males under low and high unsaturation diets respectively, 84.89% and 86,56% for females under low and high unsaturation diets respectively) and this group corresponds with the one with longer survival and lower UPR response.

Reinforcing this possible influence in survival with a correct DHA preservation, females, with general longer survival also conserve more tenaciously this FA. On the other hand, the AA accretion along disease of animals under low unsaturated diets should be viewed as a response to disease demands as well dietary influence, since this FA is in fact lower in this diet, compared with the high unsaturated one. Reinforcing this, results from animals under a control diet (the last paper) showed an increased AA accumulation latter in disease, in both genders, but more remarkable in males. Finally, correlation analysis showing a positive relation among spinal cord MDAL and AA content and a inverse relation of DHA and AASA, but just for females, emphasize the idea that lipoxidative damage could have a more deleterious effect in females even when they were preserved in terms of stride length preservation under high usaturation diet. Interestingly, correlation analysis of those variables in males only show a positive relation for GSA and survival, indicating again that deeper studies focusing in the oxidative modifications and survival interdependences should take gender as another variable.

Further, we showed an unreported relation of diet on UPR (e.g. ubiquitin), DNA oxidation (e.g. 8-oxo.dG) and DSB (e.g. γ H2Ax) responses. Males under low unsaturation diet demonstrated lower DNA oxidative damage but an unaltered mitochondrial-nuclear crosstalk concomitant to a reduced UPR response and a slower disease progression (in terms of stride length preservation). All those findings could serve as an explanation for the upgraded survival of males under such diet.

For a deeper understanding of mitochondrial function, ROS generation and damage to different biomolecules focusing in the sex as a modulator character we performed experiments in intact tissue (previous work had described mitochondrial preparation (Mattiuzzi et al. 2002) but not intact tissue) as well as permeabilized fibers of spinal cords. This helped to better describe a

natural occurring situation as well as what happened when mitochondria functioning at maximal capacity. Sample collection across all animal lifetime served us to show differential (late onset in females) respiration defects along it and, more importantly, how those changes were related with increased oxidative protein modification accretion. In fact a single sample collection, instead a cross-sectional study would only show a static frame and not those interesting outcomes.

Mitochondrial permeability transition pore is a protein “hole” in the inner mitochondrial membrane. It was originally discovered linked to neurodegeneration (Haworth and Hunter, 1979) and upon its formation, among others features, decreased membrane potential linked to cell death, mitochondrial swollen and mitophagy (reviewed in (Dagda et al. 2013) is found. Furthermore, its occurrence is known to be affected by Ca^{+2} overload (Brustovetsky et al. 2002), and to be induced by some FA derivatives (García-Ruiz et al. 2000). Therefore, excitotoxicity severely affects its formation and better outcomes are expected when this pore is abolish (e.g. its blockade -by cyclosporin A- allows complete recovery of membrane potential and therefore prevents cell death in cultured neurons (Schinder, Olson and Spitze 1996)). Hence mitochondrial pore formation could serve as a link between decreased respiration founded in the OT model and the exitotoxicity, and gender could modulate this. However, gender implication in the OT model remains to be elucidated and could be an interesting point to be address which could account for differential survival of the MN and impinge many other outcomes and could also rely under the upgraded survival and decreased oxidative modification and better mitochondrial function founded in females overexpressing SOD1G93A. In fact there is controversy whether hormones could alter this survival. A recent publication shows progesterone neuroprotection after spinal cord injury (Labombarda et al. 2013) but previous works demonstrated androgen-related positives outcomes (Hauser and Toran-Allerand 1989 and Levy et al. 1996). However, male Ca^{+2} reuptake was showed increased respect to females, rendering them more sensible to overload, at least in heart mitochondria (Arieli et al. 2004)).

Thus, linking those issues, in a recent publication (Kim, Magranè and Manfredi 2012) researchers focused in gender relevance in the mitochondrial permeability transition pore formation in the SODG93A mouse model. Hence, they demonstrated that ablation of cyclophilin D (a protein structurally linked to the mitochondrial permeability membrane transition pore (Doczi et al. 2011)) completely abolished the phenotypic advantage of female SODG93A, but no effect was found in males. In fact, they showed that 17β -estradiol protected SODG93A cortical neurons and spinal cord motor neurons against glutamate toxicity in brain mitochondria, but the protection was lost in neurons lacking cyclophilin D. This could be under the positive outcome founded in terms of upgraded oxygen consumption in females, since our results showed that the mitochondrial dysfunction was not linked to specific mitochondrial complex protein expression (e.g. Complex I and II, at least in cell lines). Further research will focus in the role that uncoupling proteins and their previously commented ROS reducing potential.

In the animal model, we found a gender-shift of both mitochondrial-related and oxidative stress-related pathophysiological outcomes and clinical features in female G93A mice respect to their male littermates. This different mitochondrial dysfunction onset could be, at least in part, underneath the delayed clinical features observed in G93A female mice respect to males, and more importantly, in male patients respect to the female counterparts. From literature, a greater oxidative modification could be expected under G93A overexpression. However, in a closer

look, we are not among the first to unveil a non-linear progression in the oxidative damage for this model (Andrus et al. 1998; Hall et al. 1998; Vinsant et al. 2013; Miana-Mena et al. 2011; Kirkinetzos et al. 2005; Cacabelos et al. 2014). Even when our results do not completely fit this previous findings, our measures are lumbar specific (nor cervical or thoracic sections), we split by gender and methodology applied to the measurements were different. Hence, this could explain little variations with previous reports.

Regarding lipid measurements in this model, the most remarkable feature was the reduction along disease founded for DHA. Animals expressing the G93A mutation demonstrated a DHA reduction in spinal cord content, concomitant to an increase of AA. This fact was also present in the dietary study previously commented, even when for those animals; the diet was in fact defective in this specific FA. Taking this two fact into account, and previous findings related to FA synthetic machinery, altogether seems clear that particular FA composition do play a role along disease and it would be hot topic for research in further works. In fact, even knowing that females displayed a differential FA regulation and metabolism (or probably due to this) any information on the gender-specific disease modification is welcome to try to apply a more personalized treatment.

Finally, trying to give some lighth regarding the estrogen interference, we used Neuro 2A cells overexpressing G93A-hSOD1 with a “feminization” treatment (This cell already express the estrogen receptor (Li, Hao and Li 2014)). Treatment with 17 β -estradiol for long period of the culture (10 days) did not show to be detrimental in terms of survival. In the same line, GFP_{hSOD1G93A} transfection do not comprise cell viability. However, estradiol treatment resulted in a similar oxygen consumption recovery, with “females” transfected with de G93A mutation showing an upgraded functionality. On the contrary, untreated “males” were unprotected against SOD_{G93A}-mediated mitochondrial malfunction. For this model, no protein expression modification was found between the mitochondrial complex subunits (I and II) to account for this reduced mitochondrial capacity, hence, we still miss a mechanisms to explain the altered functioning.

However, in a recent work (Tao et al. 2012) Tao and collaborators linked mitochondrial malfunctioning (rotenone mediated) and estradiol signaling in neuron primary culture. Hence, researchers showed altered gene induction in response to mitochondrial stress for male and female embryos. Furthermore, they detailed an upgrade survival of female primary cultured neurons rather than male when submitted to rotenome mediated cytotoxicity. Interestingly, they proved that the N2A cell line can be protected against oxidative stress through estrogen signaling (although they linked to a reduction of its protein receptor expression) and that under rotenome cytotoxicity, estradiol treatment both gender of primary-cultured neurons were protected. Altogether this results support our findings of feminine gender upgraded protection against mitochondrial dysfunction. Further analysis of these issues in relation to ALS and its potential therapeutical approaches should be considered in future works.

So globally, results in this thesis showed a relevant influence of sex on ALS outcome. FA metabolism seems to be altered (DHA and the enzymatic machinery) in patients, and cellular and tissular models could help to explain this difference. Furthermore, gender handling of FA is also different in animal models of the disease when confronted to saturated or unsaturated enrich diet, leading to differential survival and clinical features. Also relevant, oxidative modifications are dietary-altered and could help to understand survival differences

(lower ubiquitin inclusion, decreased 8-oxo-dG accretion upgraded DHA retention for males under low unsaturation diet). Finally, in line with previous works, mitochondrial implication was demonstrated also in intact tissue as well as in permeabilized tissue in the animal model (SODG93A), with a complex I deficiency, linked to a decreased oxidative accretion (MDAL) specially relevant in male and those reduced oxygen consumption was not attributed to a deficient protein expression nor activity of those.

... but may be related to a sexual-dependence Ca^{+2} excitotoxy ROS-interference ... which would be further explored.

6. Conclusions

the fact that the *Journal of Applied Behavior Analysis* is the most widely read journal in the field of behavior analysis.

It is my hope that this special issue will provide a valuable resource for researchers and practitioners alike.

Thank you to the reviewers for their helpful comments and to the staff of the journal for their assistance.

Finally, I would like to thank my family for their support and encouragement throughout this process.

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Received 10/15/03; accepted 11/15/03.

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This article is intended to be a review of the literature and is not intended to be a primary source of information.

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6. Conclusions

As a result of this research, we can consider the following conclusive statements:

One.- *In vitro* antioxidant capacity of a given nutritionally available substance is severely influenced by the oxidative methodology used and its definite action upon a substrate; however, a specific signature in terms of oxidative modification accretion and fatty acid protection preference in LDL and other biomolecules, could be described.

Two.- Endothelial and hepatocyte cell line cultures complement the above mentioned data for the biological relevance in terms of survival in front oxidative stress; hence, election of a single antioxidant to protect against those diverse situations can be challenging.

Three.- *Ex vivo* oxidative accumulation in hamsters serum under a grapeseed-derived, polyphenol-enriched diet showed an specific lipidomic (POVPC, PGP) and proteic (DNP measured) signature, whereas overall antioxidant status (FRAP measured) remains steady.

Four.- sALS is associated with spinal cord specific changes in DHA synthetic machinery (FADS2, ACAA1, ACOX-1) and Drebrin. IHQ measurements show that these changes are related to TDP-43 aggregates in motor neurons.

Five.- Neuron cell culture with TDP-43 aggregates partially reproduced sALS findings (reduced FADS2 and Drebrin). However, sALS changes are cell and site specific since WB levels do not correlate to IHQ.

Six.- Drebrin depletion in sALS spinal cords is cell specific; *in vitro* experiments showed that oxidative-derived TDP-43 aggregates precede decreased Drebrin expression. Furthermore, DHA synthesis from its precursors could be trigger by H₂O₂ incubation.

Seven.- Chronic excitotoxicity in organotypic spinal cord cultures promoted lipidomic and fatty acid profile changes compatible with altered DHA synthesis, highlighting the relevance of this model to mimic the pathophysiological features that lead to motoneuron death.

Eight.- Gender dimorphism is a relevant factor influencing lipid handling in the hSODG93A ALS animal model in terms of survival and clinical outcome.

Nine.- DHA-related synaptic machinery (syntaxin3) and UPR (Ubuquitin inclusions) responses in hSODG93A male mice is altered in response to high unsaturation degree diet.

Ten.- Dietary intervention aimed at modulating the FA composition by changes in FA sources evoked expected tissular FA modification and influenced protein and DNA oxidative damage with an altered nuclear-to-mitochondrial damage responses.

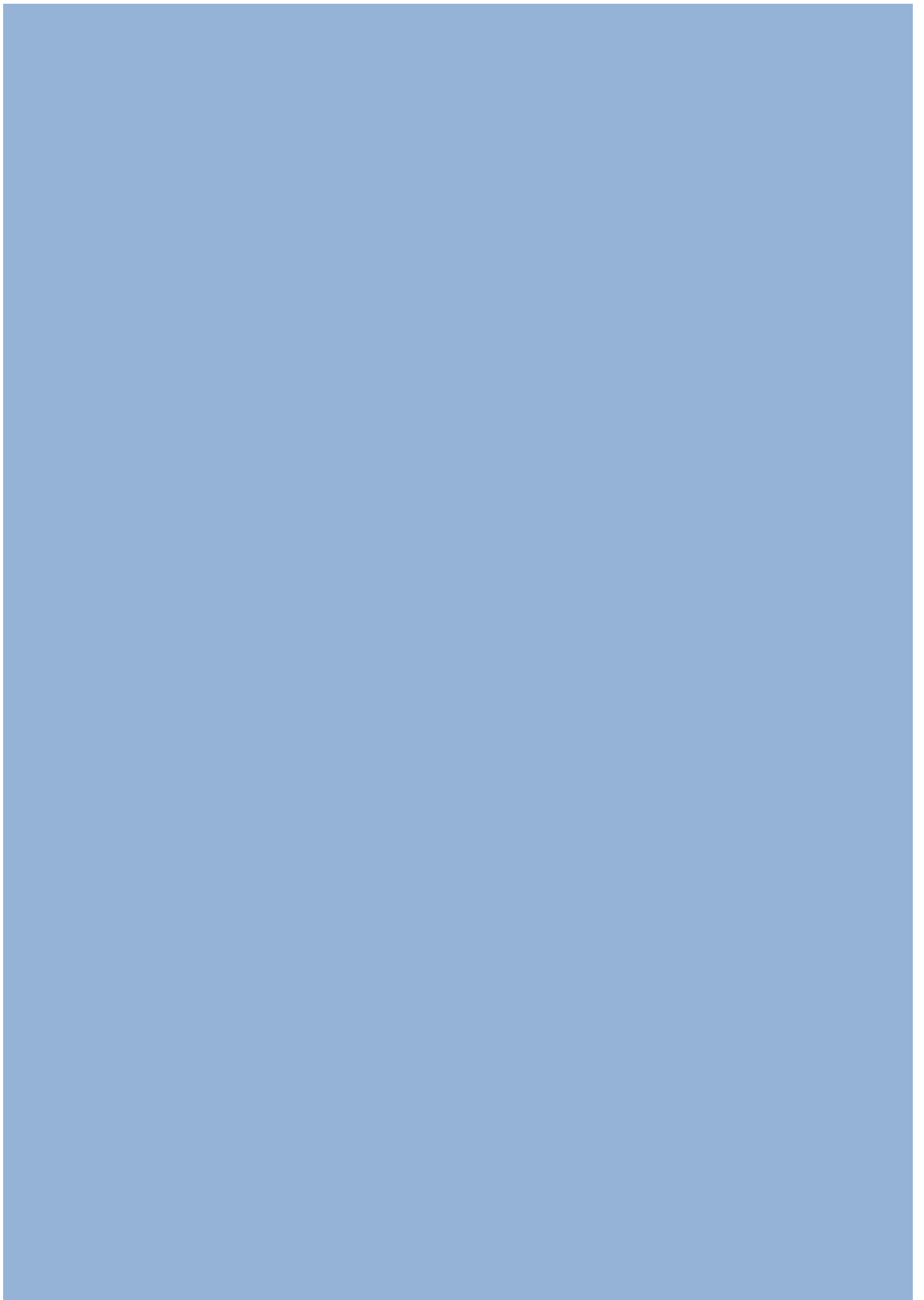
Eleven.- Mitochondrial dysfunction in hSODG93A mouse model (assessed by oxygen consumption measurements) is variable throughout disease. Females had a later oxygen consumption reduction.

Twelve.- Gender dimorphism in oxygen consumption correlated with female later onset and lower oxidative modifications as well as optimized lipid content.

Thirteen.- Overexpression of mutant SOD1 in cell cultures recapitulate oxygen consumption reduction in hSODG93A mouse model.

Fourteen.- Estrogen treatment (10nM) on those cells is able to reproduce female-outcome, protecting from CI dysfunction, without changes in expression of peptides belonging to CI or CII.

7. Bibliography



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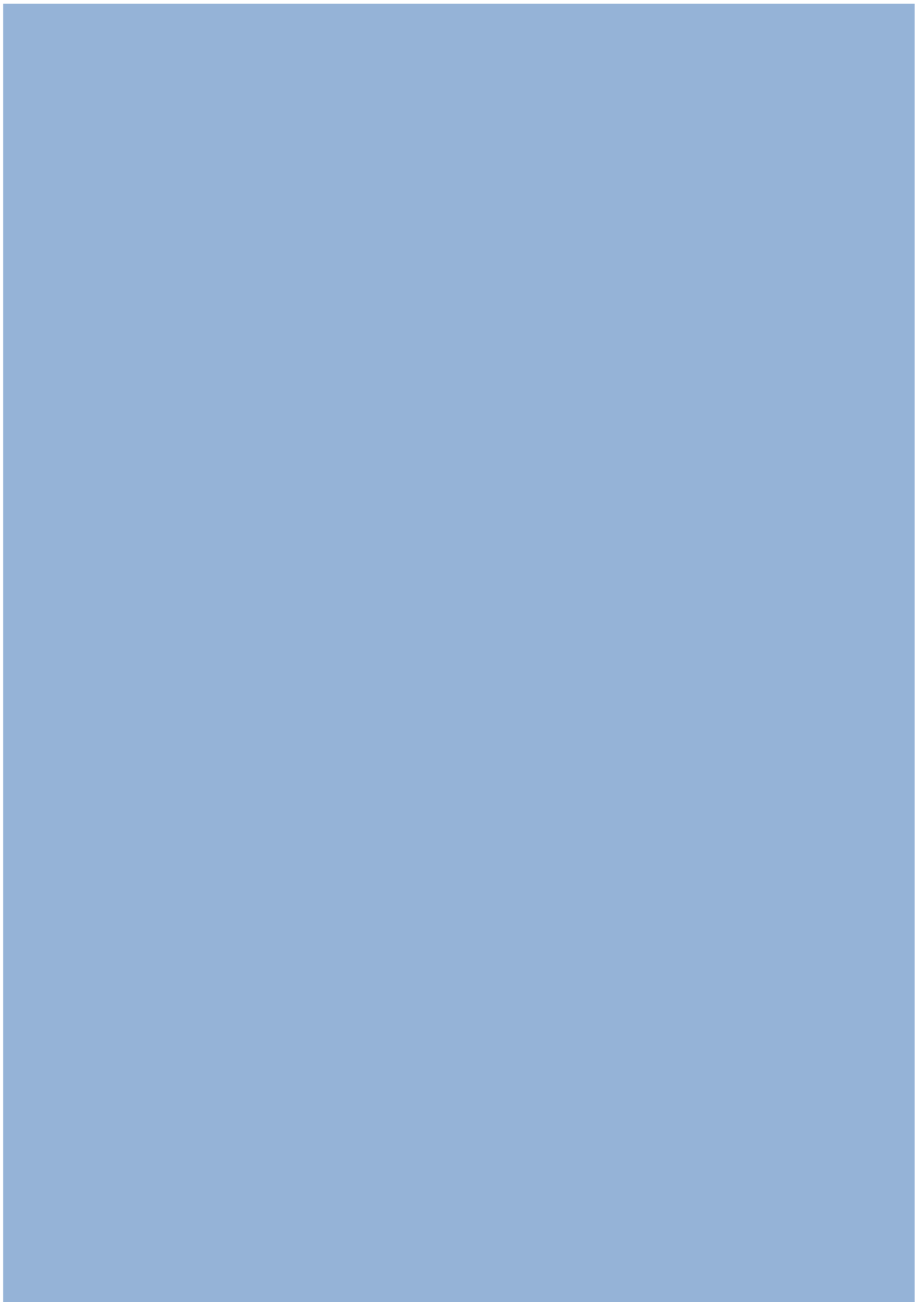
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8. Annexes



8. Annexes

For further immersion on PUFA's relevance and implications in different pathophysiological conditions (e.g. neurodegeneration and dietary interventions in chronic inflammatory models), we harvested relevant contributions for a better understanding of some hallmarks of oxidative reactions and its relevance in various neurodegenerative diseases in a paper entitled "*Maillard reaction versus other nonenzymatic modifications in neurodegenerative processes*", endorsed as an annex at the end of this book.

Furthermore, to increase the knowledge of PUFA's influence in various biological parameters (e.g. oxidative status, synthesis machinery, CHO status) in animals under a distorted diet (high fat diet). Various experiments were performed along my stay at the University of Bergen and were successfully published in "*Fish oil and 3-thia fatty acid have additive effects on lipid metabolism but antagonistic effects on oxidative damage when fed to rats for 50 weeks*" and could be also found below.

Finally, for a more comprehensive view of the pathophysiology of ALS, different models (cell lines confronted to oxidative and endoplasmic reticulum stressors and chronic excitotoxicity in OT spinal cord primary culture) as well as sALS samples were investigated trying to depict a new activation route which connects MN degeneration and TDP-43, together with ER and oxidative stress and an unreported role calpain and CaMKIV along disease progression as relevant factors in ALS. The experiments performed were successfully published in "*Cell stress induces TDP-43 pathological changes associated with ERK1/2 dysfunction: implications in ALS*", "*Oxidative and endoplasmic reticulum stress interplay in sporadic amyotrophic lateral sclerosis*" and "*Calpain activation and CaMKIV reduction in spinal cords from hSOD1G93A mouse model*" and could be found in the annex section.



Maillard Reaction versus Other Nonenzymatic Modifications in Neurodegenerative Processes

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Nonenzymatic protein modifications are generated from direct oxidation of amino acid side chains and from reaction of the nucleophilic side chains of specific amino acids with reactive carbonyl species. These reactions give rise to specific markers that have been analyzed in different neurodegenerative diseases sharing protein aggregation, such as Alzheimer's disease, Pick's disease, Parkinson's disease, dementia with Lewy bodies, Creutzfeldt-Jakob disease, and amyotrophic lateral sclerosis. Collectively, available data demonstrate that oxidative stress homeostasis, mitochondrial function, and energy metabolism are key factors in determining the disease-specific pattern of protein molecular damage. In addition, these findings suggest the lack of a "gold marker of oxidative stress," and, consequently, they strengthen the need for a molecular dissection of the nonenzymatic reactions underlying neurodegenerative processes.

Key words: advanced glycation end products; advanced lipoxidation end products; Alzheimer's disease; amyotrophic lateral sclerosis; Creutzfeldt-Jakob disease; energy metabolism; free radicals; mitochondria; oxidative stress; Parkinson's disease; Pick's disease; reactive carbonyl species

Nonenzymatic Oxidative Protein Modification

As a rule, chemical reactions in living cells are under strict enzymatic control and conform to a tightly regulated metabolic program. One important factor implicit in evolution, from a biomolecular view, is the minimizing of unwanted side reactions. Nevertheless, uncontrolled and potentially deleterious reactions occur, even under physiological conditions. Free radicals (reactive oxygen species [ROS] and reactive nitrogen species [RNS]) are generated by both enzymatic and nonenzymatic sources and have been implicated in a multitude of physiological processes including aging and disease initiation and/or progression.¹ Oxidative stress occurs when the net flux of free radical production during normal aerobic metabolism exceeds the antioxidant defenses of the cell. Emerging evidence indicates that this stress causes specific protein modifications that may lead to a change in the structure and/or function of the oxidized protein.^{2,3} Carbonylation is one of those changes, altering the conformation of the

polypeptide chain and determining the partial or total inactivation of proteins. This can have a wide range of downstream functional consequences and may be the cause of subsequent cellular dysfunctions and tissue damage.

Structurally, carbonylation may arise from direct oxidation of amino acid side chains, mainly Pro, Arg, Lys, and Thr, resulting in the formation, among others, of glutamic semialdehyde (GSA) and amino adipic semialdehyde (AASA), the main carbonyl products of metal-catalyzed oxidation of proteins. In addition, carbonyl groups may be introduced into proteins by secondary reaction of the nucleophilic side chains of Cys, His, and Lys residues with reactive carbonyl species (RCS) produced during lipid peroxidation (lipoxidation reactions) or generated as a consequence of the reaction with highly reducing sugars, such as glyoxal and methylglyoxal (an usual byproduct of glycolysis) or their oxidation products (glycation and glycoxidation reactions). Most of the biological effects of intermediate RCS are attributed to their capacity to react with the nucleophilic sites of proteins, forming advanced lipoxidation end products (ALEs) and advanced glycation end products (AGEs).² Compared to free radicals, RCS are stable and can diffuse within or even escape from the cell and attack targets far from the site of formation. Therefore, these soluble reactive intermediates are not only cytotoxic per se but

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also behave as mediators and propagators of oxidative stress and tissue damage, acting as second cytotoxic messengers.⁴

Oxidative decomposition of polyunsaturated fatty acids (PUFAs) initiates chain reactions that lead to the formation of a variety of RCS which, by reacting with nucleophilic sites in proteins, generate specific ALEs, such as MDA-Lys, HNE-Lys, and N ϵ -(hexanoyl)lysine, among others. These adducts have been detected by chemical and immunohistochemical methods in a broad range of tissues and species during physiological aging⁴ and specific pathological states. The involvement of toxic RCS as products and propagators of oxidative damage in neurodegenerative diseases is currently under study.

The residual aldehyde group in some ALEs can further react to give protein cross-links and fluorescent products that are very similar to AGEs. Lipofuscin, the nondegradable intralysosomal fluorescent pigment that accumulates with age in postmitotic cells, is a recognized hallmark of aging.⁴ Other important toxic products formed during nonenzymatic modification of proteins in aging and disease are referred to as “either advanced glycation or lipoxidation end products,” so named because they may be formed from either carbohydrates or lipids. N ϵ -(carboxymethyl)lysine (CML) and N ϵ -(carboxyethyl)lysine (CEL) are, on a molar basis, the major modifications that have been measured in tissue proteins among these mixed-origin products, emphasizing the importance of the intersection between carbohydrate and lipid chemistry.²

Protein Damage and Neurodegenerative Diseases

The nervous system is potentially sensitive to oxidative modifications because i) the particular fatty acid composition of neuronal tissues that is rich in PUFA (hence easily peroxidizable); ii) the high O₂ consumption; and iii) the relatively poor expression antioxidant systems.⁵ Also, nervous tissue is considered a postmitotic tissue and therefore highly susceptible to aging.⁶ Cells in all regions of the nervous system are affected by aging, as indicated by the decline of sensory, motor, and cognitive functions with time. As this process is involved as a risk factor in most neurodegenerative diseases—there is a dramatic increase in the probability of developing a neurodegenerative disorder (e.g., Alzheimer’s disease [AD], Parkinson’s disease [PD], or amyotrophic lateral sclerosis [ALS], among others) during the sixth, seventh, and eighth decades of life—and oxidative modifications play a key role in aging,

it is often accepted that these diseases should have increased oxidative damage.

Cells in the nervous system are affected by, and respond to, aging much as cells in other organ systems do, and so cells in the brain experience increased amounts of oxidative stress, impaired mitochondrial function and perturbed energy homeostasis, accumulation of damaged proteins, and lesions in their nucleic acids.^{5,6} These changes during normal aging are exacerbated in vulnerable populations of neurons in neurodegenerative disorders. Therefore, some diseases might be viewed as a syndrome of accelerated aging in selected neurons.

The interest in the molecular dissection of each of these three pathways (i.e., direct oxidative modification, glyoxidation, and lipoxidation) clearly exceeds an academic context. An appropriate knowledge in this sense could help to rationally design therapeutic approaches aimed either at diminishing oxidative damage in a nonselective way (provided each oxidative pathway is increased in a similar extent) or at pinpointing those processes selectively increased. With this goal in mind, tissues from human tauopathies (AD and Pick’s disease [PiD]), synucleopathies (PD and dementia with Lewy bodies [DLB]), and other neurodegenerative processes linked to protein misfolding and/or deposits (Creutzfeldt-Jakob disease [CJD] and ALS) were studied (TABLE 1). The concentration of selected markers of each pathway of protein oxidative damage was analyzed by gas chromatography coupled to mass spectrometry by using authentic deuterated internal standards, according to previously described procedures.⁷ Tissues located in “target” zones of the diseases (showing pathological abnormalities) and “control” zones (without morphological changes) were evaluated in order to offer a biochemical correlate of the disease (TABLE 1). These diseases were chosen by the fact that all share accumulation or involvement of structurally modified protein deposits, which have been detected as modified with oxidation products using immunohistochemical procedures.

Tauopathies: Alzheimer’s Disease and Pick’s Disease

Alzheimer’s disease is the more studied and prevalent neurodegenerative disease and is associated with β -amyloid deposits either in neurofibrillary tangles or hyaline bodies. The measurement of oxidative protein modifications⁷ reveals that GSA and AASA contents are higher in the frontal cortex (area 8) of AD patients than in age- and sex-matched healthy controls. These increases (around 50% over control values) are larger than those present for well-known

TABLE 1. Changes in specific markers from oxidation-, glycooxidation-, and lipoxidation-derived reactions in human neurodegenerative diseases: a comparative molecular pathology approach

Disease	Number of cases	Location	GSA	AASA	CEL	CML	PI	DHA	MDAL
AD ⁷	13	FC	↑	↑↑	↑	↑	↑	↑	↑↑
PiD ⁸ (1)	7	FC	↑	↑↑	↓	↓	↓	↓	↑
	7	OC	↑	↑	↑	↑	↑	↑	↑↑
PD ¹⁰	7	SN	=	=	=	=	↓	↓	↑
	7	FC	=	=	↓	=	↑	↑↑	↑↑
DLB ¹⁰	4	FC	=	=	↓	=	↑	↑	=
CJD (2)	10	FC	↑	↑	↑	↑	↓	↓	↑
ALS ¹²	11	SC	↑	↑	↑	↑	↓	↓↓	↑↑
	11	FC	↑	↑	↑	↑	↑	↑	↑

Abbreviations: AD, Alzheimer's disease; ALS, amyotrophic lateral sclerosis; CJD, Creutzfeldt-Jakob disease; DLB, dementia with Lewy bodies; PD, Parkinson's disease; PiD, Pick's disease. Location: FC, frontal cortex; OC, occipital cortex; SC, spinal cord; SN, substantia nigra. (1) unpublished results; (2) Pamplona, Naudi, Gavin, *et al.*, University of Lleida, Lleida Spain AASA, amino adipic semialdehyde; CEL, *N*ε-(carboxyethyl)lysine; CML, *N*ε-(carboxymethyl)lysine; DHA, docosahexaenoic acid; GSA, glutamic semialdehyde; MDAL, *N*ε-(malondialdehyde)lysine; PI, peroxidizability index.

AGE markers (CEL and CML), which roughly increase 15% over control values. As suggested by changes in peroxidizability, which is significantly increased in these AD patients (basically because of changed contents of docosahexaenoic acid [DHA]), the most affected marker of protein oxidative modification is *N*ε-(malondialdehyde)lysine (MDAL), which doubles its content in samples from AD patients. By using a combination of two-dimensional electrophoresis, Western blot, and peptide fingerprinting with matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF), several cytoskeletal proteins, metabolic enzymes, and heat shock proteins were identified as modified by MDAL.⁷

To ascertain whether those phenomena are specific to AD, we analyzed PiD (unpublished results and Ref. 8). PiD is another tauopathy, characterized by the specific involvement of the frontotemporal cortex. In common with AD, significant increases were found in AASA, GSA, and MDAL, suggesting increased direct oxidative and lipoxidative damage, although at a lower extent than in AD. However, concentrations of lipoxidative and glycooxidative protein modifications were decreased (both CEL and CML), a fact that can be related to the loss of glycolytic potential, well described in this disease.

The occipital cortex is usually viewed as a location without morphological evidence of involvement of the disease, and hence morphological evidence serves as controls for measurements. In this case, we evidenced increased oxidative, glycooxidative, and lipoxidative damage in this location, supporting the fact that oxidative stress may be an early-stage change in the pathogenesis of this disease. Most interestingly, there was a direct and significant correlation between

CEL concentration and DHA levels, suggesting that DHA is increased in response to neuronal stress. This would involve both oxidative stress and increased glycolysis, leading to increased CEL through potentially increased methylglyoxal efflux in the occipital cortex, whereas in the frontal cortex, because of neuronal loss and consequent decreased glycolysis, decreased values in both DHA and CEL content are present. Concerning the targets of oxidative damage, five different proteins exhibit increased anti-DNP staining: reduced form of nicotinamide adenine dinucleotide phosphate (NADPH) carbonyl-reductase, glial fibrillary acidic protein, heat shock protein 70, cathepsin D precursor, and vesicle-fusing ATPase (unpublished results).

Synucleopathies: Parkinson's Disease and Dementia with Lewy Bodies

Parkinson's disease is the most prevalent synucleopathy. Despite previous results describing increased immunoreactivity to anti-AGE and oxidative damage adducts,⁹ no chemical evidence of protein oxidative damage was available. When evaluating the content of the above-mentioned markers in substantia nigra from incidental DLB,¹⁰ MDAL was the only marker that was significantly increased in PD (approximately 100%). Similar increases were also found in the frontal cortex and amygdala, suggesting the importance of lipoxidation. In clear contrast, CEL levels were significantly decreased in both the amygdala and the frontal cortex, a fact that can be in accordance with a described loss of glycolysis in PD.¹¹ Targets of lipoxidative damage comprise several antioxidant enzymes, proteasome components, α-synuclein, and other proteins not shared with AD or PiD. To shed further light

on the potential relationship of oxidative damage in synucleopathies, we analyzed cortex samples from patients with DLB, which showed a lack of increased MDAL content but, again, significant decreases in CEL content.¹⁰

Other Neurodegenerative Processes Linked to Protein Misfolding and/or Deposits

Creutzfeldt-Jakob disease is a neurodegenerative spongiform disease, linked to transmissible prionopathies. The protein oxidative profile in the frontal cortex shows similarities to AD: increased direct oxidative, glycoxidative, and lipoxidative damage, but in this case a decrease in n-3 fatty acids is present. (Pamplona, Naudi, Gavin, *et al.*, University of Lleida, Lleida, Spain) All increases are in the same range, suggesting a general change in the modified protein turnover. This would be compatible with reported alterations in proteasome present in related prion-induced diseases. Concerning targets of glycoxidative damage, we evidenced two key enzymes in glycolysis to be highly modified in CJD samples: glyceraldehyde-3-phosphate dehydrogenase and fructose-1,6-bisphosphate aldolase. As the activity of this latter enzyme involves the formation of a Schiff's base in its active site, we hypothesize that some of those bases may be transformed, under increased oxidative conditions, to CEL.

Amyotrophic lateral sclerosis is characterized by the selective loss of motor neurons in spinal cord and in brain cortex, associated with highly ubiquitinated deposits of proteinaceous material. Spinal cord lysates from ALS patients showed significant increases in direct oxidative, glycoxidative, and lipoxidative damage.¹² Analogous to samples from the brain cortex in AD, the more sensible marker was MDAL, suggesting the importance of lipoxidative modification in this context. Similar to substantia nigra samples in PD and frontal cortex samples in PiD, lipoxidative damage was accompanied by a strong loss in the content of DHA. As observed from other locations without morphological evidence of pathology, samples from the brain cortex of ALS patients also showed increased oxidation, glycoxidation, and lipoxidation, associated with reactive increases in the content of n-3 fatty acids, particularly DHA. All these features are reproducible *in vitro* by the generation of chronic excitotoxicity—a mechanism linked to selective neuronal loss by disturbed intracellular Ca⁺⁺ homeostasis—in a spinal cord organotypic culture, supporting the involvement of this neurodegenerative pathway *in vivo*.¹²

Final Remarks

In conclusion to these analyses, no single marker of protein oxidative modification (among those used here) can be viewed as a gold standard for assessment of oxidative damage in neurodegenerative processes. The same applies to targets of oxidative damage that show disorder-specific differences. Moreover, in some cases CEL levels decreased, supporting CEL relationship with glycolysis potential. There are significant associations between changes in fatty acid composition (especially DHA) and protein oxidative damage. Most interestingly, when tissue from pathologically preserved locations was available, the tissue analyses indicated that protein oxidative modifications take place before potential morphological and clinical changes appear, suggesting an early involvement of protein oxidative damage in neurodegenerative process.

Acknowledgments

This study was supported in part by I+D grants from the Spanish Ministry of Education and Science (BFU2006-14495/BFI), the Spanish Ministry of Health (ISCIII, Red de Envejecimiento y Fragilidad, RD06/0013/0012), and the Generalitat of Catalunya (2005SGR00101) to R.P.; the Spanish Ministry of Health (FIS 04-0355 and 05-2241), Spanish Ministry of Education and Science (AGL2006-12433), and “La Caixa” Foundation to M.P.O. and E.D., E.I. and D.C.; and Field-initiated Studies Program grants 020004 and 03-006, Spanish Ministry of Education and Science (CICYT SAF-2001-4681E), and European Union project Brain Net Europe II to I.F.

Conflict of Interest

The authors declare no conflicts of interest.

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Fish oil and 3-thia fatty acid have additive effects on lipid metabolism but antagonistic effects on oxidative damage when fed to rats for 50 weeks[☆]

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Received 23 February 2011; received in revised form 5 August 2011; accepted 18 August 2011

Abstract

The 3-thia fatty acid tetradecylthioacetic acid (TTA) is a synthetic modified fatty acid, which, similar with dietary fish oil (FO), influences the regulation of lipid metabolism, the inflammatory response and redox status. This study was aimed to penetrate the difference in TTA's mode of action compared to FO in a long-term experiment (50 weeks of feeding). Male Wistar rats were fed a control, high-fat (25% w/v) diet or a high-fat diet supplemented with either TTA (0.375% w/v) or FO (10% w/v) or their combination. Plasma fatty acid composition, hepatic lipids and expression of relevant genes in the liver and biomarkers of oxidative damage to protein were assessed at the end point of the experiment. Both supplements given in combination demonstrated an additive effect on the decrease in plasma cholesterol levels. The FO diet alone led to removal of plasma cholesterol and a concurrent cholesterol accumulation in liver; however, with TTA cotreatment, the hepatic cholesterol level was significantly reduced. Dietary FO supplementation led to an increased oxidative damage, as seen by biomarkers of protein oxidation and lipoxidation. Tetradecylthioacetic acid administration reduced the levels of these biomarkers confirming its protective role against lipoxidation and protein oxidative damage. Our findings explore the lipid reducing effects of TTA and FO and demonstrate that these bioactive dietary compounds might act in a different manner. The experiment confirms the antioxidant capacity of TTA, showing an improvement in FO-induced oxidative stress.

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Keywords: Reactive oxygen species; Oxidative damage; UCP; β -oxidation

Abbreviations: AASA, α -amino adipic semialdehyde; *Acaca*, acetyl-coenzyme A carboxylase α ; *Acadm*, acyl-coenzyme A dehydrogenase, medium chain; *Acadvl*, acyl-coenzyme A dehydrogenase, very long chain; ACOX1, acyl-CoA oxidase 1; *Arbp*, acidic ribosomal protein, P0; CPT, carnitine palmitoyltransferase; CEL, *N* ϵ -carboxyethyl-lysine; CML, *N* ϵ -carboxymethyl-lysine; DBI, double-bond index; DHA, docosahexaenoic acid; DPA, docosapentaenoic acid; EPA, eicosapentaenoic acid; FO, fish oil; *Gapdh*, glyceraldehyde 3-phosphate dehydrogenase; GSA, γ -glutamic semialdehyde; *Hadha*, hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase, α -subunit; MDAL, *N* ϵ -malondialdehyde-lysine; PL, phospholipids; PPAR, peroxisome proliferator-activated receptor; PUFA, polyunsaturated fatty acid; SFA, saturated fatty acid; TTA, tetradecylthioacetic acid; UCP, uncoupling protein.

[☆] Grants and funding: This study was financially supported by grants from NordForsk, grant 070010, MitoHealth; the Research Council of Norway, grant 190287/110; and the European Community's Seventh Framework Program (FP7/2007-2013), grant 201668, AtheroRemo. Work carried out at the Department of Experimental Medicine was supported in part by R+D grants from the Spanish Ministry of Science and Innovation (AGL2006-12433 and BFU2009-11879/BFI), the Spanish Ministry of Health (RD06/0013/0012 and PI081843), the Autonomous Government of Catalonia (2009SGR735), and COST B35 Action of the European Union. D.C. received a fellowship from the Spanish Health Institute Carlos III. The authors declare no conflict of interest.

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1. Introduction

The body's inability to handle excess energy intake leads to metabolic abnormalities such as hyperglycemia and dyslipidemia. The coexistence of these risk factors with overweight and hypertension represents the metabolic syndrome [1,2]. Thus, the discovery and testing of dietary supplements that can improve lipid metabolism and maintain homeostasis, and consequently, prevent the development of risk factors of metabolic syndrome, is of great importance.

Both fish oil (FO) and tetradecylthioacetic acid (TTA) have been widely used in *in vivo* experiments. FO has been shown to inhibit lipogenesis and exert a hypolipidemic effect by lowering plasma cholesterol and triacylglycerol (TAG) levels [3], as well as having an anti-inflammatory effect beneficial against both atherosclerosis [4] and arthritis [5,6]. The effects of FO are attributed to ω -3 polyunsaturated fatty acids (PUFAs), such as eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA), which are thought to bind and activate peroxisome proliferator-activated receptors (PPARs) [7]. They act upon ligand activation by controlling networks of target genes and therefore serve as lipid sensors because they can be triggered by metabolic derivatives of fatty acids in the body.

Tetradecylthioacetic acid, a structurally modified 16-carbon saturated fatty acid (SFA) with a sulfur atom inserted in the third position of the alkyl chain, has been documented as a pan-PPAR ligand in several cell lines [8–10]. Tetradecylthioacetic acid has a particularly high affinity for PPAR α [9–11] and exerts its hypolipidemic effect by inducing gene expression of enzymes involved in hepatic fatty acid β -oxidation. It thereby reduces the availability of fatty acids for very-low-density-lipoprotein synthesis and secretion and lowers plasma TAG and cholesterol levels. In addition, TTA has been shown to have an important role in diminishing of inflammation [12–16].

Both physiological processes and externally induced oxidative stress reactions can lead to formation of reactive oxygen species (ROS) in the body. It is well-known that dietary FO supplementation can increase lipoxidative damage due to the high amount of unsaturated fatty acids [17–19]. Tetradecylthioacetic acid has a potent capacity to attenuate the oxidative stress and protect the cellular membrane lipids from oxidative damage. Based on this, we hypothesized that a dietary TTA supplementation to the high-fat diet would be able to reduce the oxidative stress induced by FO.

Thus, the main focus in this 50-week-long *in vivo* experiment was to investigate the effects of TTA and FO, given separately or in combination, on body weight gain, plasma and liver lipid levels, as well as fatty acid composition in plasma and several genes encoding important enzymes involved in fatty acid metabolism. Further, despite the similar ability to act through PPAR-activation, we revealed principal differences in the mechanisms of action of TTA and FO. Finally, we confirmed that TTA can act as an antioxidant and prevent the FO-caused oxidative damage.

2. Methods

2.1. Animals and diets

This animal study was conducted according to the Guidelines for the Care and Use of Experimental Animals, and the protocol was approved by the Norwegian State Board of Biological Experiments with Living Animals. Eight- to 10-week-old male Wistar rats, weighing 200–250 g, were obtained from Taconic Europe (previously Møllegaard and Bomholtgaard, Ry, Denmark). Throughout the experiment, the rats were housed in Makrolon III cages in an open system and kept under standard laboratory conditions with temperature $22^{\circ}\text{C}\pm 1^{\circ}\text{C}$, dark/light cycles of 12/12 h, relative humidity $55\pm 5\%$ and 20 air changes per hour. The animals were housed five per cage and had free access to food and water during the study. They were acclimatized under these conditions with standard chow for 1 week before the experiment started. All rats were divided into four groups. The first group of animals (control group) was fed a high-fat diet with 25% fat, consisting of 23% lard and 2% soybean oil. The second group (TTA group) was fed a high-fat diet supplemented with TTA (0.375%). The third group (FO group) was

fed a diet supplemented with 10% FO (EPAX 4020 TG) (12.6% lard and 2% soy oil). The fourth group (TTA+FO group) was fed both diet supplements. The amount of ω -3 fatty acids in FO-containing diets was 8% (where the EPA content was 4.5% and DHA was 2.3%). All diets were isocaloric in their energetic value (4900 kcal).

The animals were part of a larger study described elsewhere, and all animals underwent a jejuno-gastric reflux surgical procedure (manuscript in preparation). An additional 2-month feeding experiment on male Wistar rats with and without surgery was performed to determine if the procedure had an effect on the nutritional state of the animals. There was no difference in body weight or plasma lipids between the groups (data not shown), and thus it could be assumed that the surgery had no adverse effect on nutritional uptake.

Tetradecylthioacetic acid was synthesized as previously described [20]. The rats were anaesthetized with isoflurane (Forane; Abbott Laboratories, Abbott Park, IL) inhalation under nonfasting conditions. Blood was drawn by cardiac puncture and collected in BD Vacutainer tubes containing EDTA (Becton-Dickinson, Plymouth, UK), and the organs were immediately removed and frozen in liquid nitrogen.

2.2. Quantification of lipids and fatty acids

Plasma and liver lipids were measured on the Hitachi 917 system (Roche Diagnostics, Mannheim, Germany). Quantification of TAGs and total cholesterol in plasma and liver were obtained by using kits from Roche Diagnostics. Choline-containing phospholipids (PLs) in plasma and liver were measured by PAP150 from bioMérieux (Lyon, France). Hepatic lipids were analyzed in cytoplasmic extracts. Lipids from plasma and liver were extracted before the fatty acid composition was analyzed as described previously [21,22].

From the fatty acid profile, the double-bond index (DBI) of lipid susceptibility to oxidative modification [23] was calculated: $\text{DBI} = [(1 \times \sum \text{mol\% monoenoic}) + (2 \times \sum \text{mol\% dienoic}) + (3 \times \sum \text{mol\% trienoic}) + (4 \times \sum \text{mol\% tetraenoic}) + (5 \times \sum \text{mol\% pentaenoic}) + (6 \times \sum \text{mol\% hexaenoic})]$.

2.3. Enzyme activities

Fresh liver tissue samples were homogenized in ice-cold sucrose medium and centrifuged. The resulting three postnuclear fractions, a mitochondrial-enriched fraction (M), a peroxisome-enriched fraction (L) and a cytosolic fraction (S), were isolated as previously described and frozen at -80°C [24]. Then the activities of fatty acyl-CoA oxidase 1 (ACOX1) [25], carnitine palmitoyltransferase II (CPT-II) [26], 3-hydroxy-3-methylglutaryl-coenzyme A synthase (HMG-CoA synthase) [27] and fatty acid synthase (FAS) [28,29] were measured.

2.4. Gene expression analysis

Liver samples were frozen in liquid nitrogen immediately after dissection and stored at -80°C . Total cellular RNA was purified from 20- to 30-mg tissue using RNeasy Mini Kit (Qiagen). RNA was quantified spectrophotometrically (NanoDrop 1000; NanoDrop Technologies, Boston, MA), and the quality was evaluated by capillary electrophoresis (Agilent 2100 Bioanalyzer; Agilent Technologies, Palo Alto, CA). For each sample, 400 ng total RNA was reversely transcribed in 20- μl reactions using Applied Biosystem's High Capacity cDNA Reverse Transcription Kit with RNase inhibitor according to the manufacturer's description. Real-time polymerase chain reaction was performed with custom-made 384-well microfluidic plates [Taq-Man

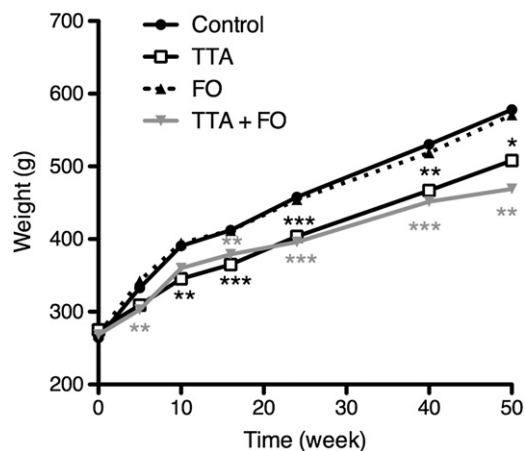


Fig. 1. Average weight of rats on high-fat diets supplemented with 3-thia fatty acid TTA and/or FO for 50 weeks. Data represent means ($n=10$). Values that were significantly different from control by *t* test are indicated by black (TTA) or gray (TTA+FO) asterisks (* $P<.05$, ** $P<.01$, *** $P<.001$).

Low Density Arrays (TLDA), Applied Biosystems, Foster City, CA). The genes selected were acyl-coenzyme A dehydrogenase, medium chain (*Acadm*), acyl-coenzyme A dehydrogenase, very long chain (*Acadvl*), carnitine palmitoyltransferase 1A and 2 (*Cpt1a* and *Cpt2*, respectively), acetyl-coenzyme A carboxylase α (*Acaca*), uncoupling protein 2 and 3 (*Ucp2* and *Ucp3*, respectively), glyceraldehyde 3-phosphate dehydrogenase (*Gapdh*) and hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase, α -subunit (*Hadha*). All probes and primers were obtained from Applied Biosystems. The reference gene was chosen according to the MIQE guidelines [30,31]. Three different control genes were included: *18s* (Kit-FAM-TAMRA, reference RT-CKFT-18s from Eurogentec, Seraing, Belgium), *Gapdh* (Rodent GAPDH Control Reagents, part 4308313) and *Arbp* (from Applied Biosystems). In a comparative analysis using the programs geNorm and Normfinder, *Arbp* was found to be the best. The expression value of each gene in each sample was normalized against this endogenous control.

2.5. Oxidative damage markers

Glutamic semialdehyde (GSA), amino adipic semialdehyde (AASA), carboxymethyl-lysine (CML), carboxyethyl-lysine (CEL) and malondialdehyde-lysine (MDAL) concentrations in total proteins from liver homogenates and mitochondrial fraction were measured by gas chromatography/mass spectrometry (GC/MS) as previously described [18]. Samples containing 0.5 mg of protein were delipidated using chloroform/methanol (2:1, v/v), and proteins were precipitated by adding 10% trichloroacetic acid (final concentration) and subsequent centrifugation. Protein samples were reduced overnight with 500 mM NaBH₄ (final concentration) in 0.2 M borate buffer, pH 9.2, containing 1 drop of hexanol as an antifoam reagent. Proteins were then reprecipitated by adding 1 ml of 20% trichloroacetic acid and subsequent centrifugation. The following isotopically labeled internal standards were then added: [²H₈]lysine (d₈-Lys; CDN Isotopes); [²H₄]CML (d₄-CML), [²H₄]CEL (d₄-CEL) and [²H₈]

MDAL (d₈-MDAL), prepared as described [32,33]; [²H₅]5-hydroxy-2-aminovaleric acid (for GSA) and [²H₄]6-hydroxy-2-aminocaproic acid (for AASA) were prepared as described [34]. The samples were hydrolyzed at 155°C for 30 min in 1 ml of 6 HCl and then dried in vacuo. The *N,O*-trifluoroacetyl methyl ester derivatives of the protein hydrolyzate were prepared as previously described [34]. Gas chromatography/mass spectrometry analyses were carried out on a Hewlett-Packard model 6890 gas chromatograph equipped with a 30-m HP-5MS capillary column (30 m × 0.25 mm × 0.25 μ m) coupled to a Hewlett-Packard model 5973A mass selective detector (Agilent, Barcelona, Spain). The injection port was maintained at 275°C; the temperature program was 5 min at 110°C, then 2°C/min to 150°C, then 5°C/min to 240°C, then 25°C/min to 300°C and finally held at 300°C for 5 min. Quantification was performed by external standardization using standard curves constructed from mixtures of deuterated and nondeuterated standards. Analytes were detected by selected ion monitoring GC/MS. The ions used were lysine and d₈-lysine, *m/z* 180 and 187, respectively; 5-hydroxy-2-aminovaleric acid and d₅-5-hydroxy-2-aminovaleric acid (stable derivatives of GSA), *m/z* 280 and 285, respectively; 6-hydroxy-2-aminocaproic acid and d₄-6-hydroxy-2-aminocaproic acid (stable derivatives of AASA), *m/z* 294 and 298, respectively; CML and d₄-CML, *m/z* 392 and 396, respectively; CEL and d₄-CEL, *m/z* 379 and 383, respectively; and MDAL and d₈-MDAL, *m/z* 474 and 482, respectively. The amounts of products were expressed as the ratio of micromole of GSA, AASA, CML, CEL, or MDAL/mol of lysine.

2.6. Statistical analysis and presentation of data

The results are presented as mean values with their standard deviations for 7 to 10 rats per group. The data were evaluated by one-way ANOVA and Tukey test or by unpaired Student *t* test with the level of statistical significance set at *P* < .05 (GraphPad Prism version 4.01; GraphPad, San Diego, CA). Single outliers (significance level >0.05) were removed using Grubb test (www.Graphpad.com).

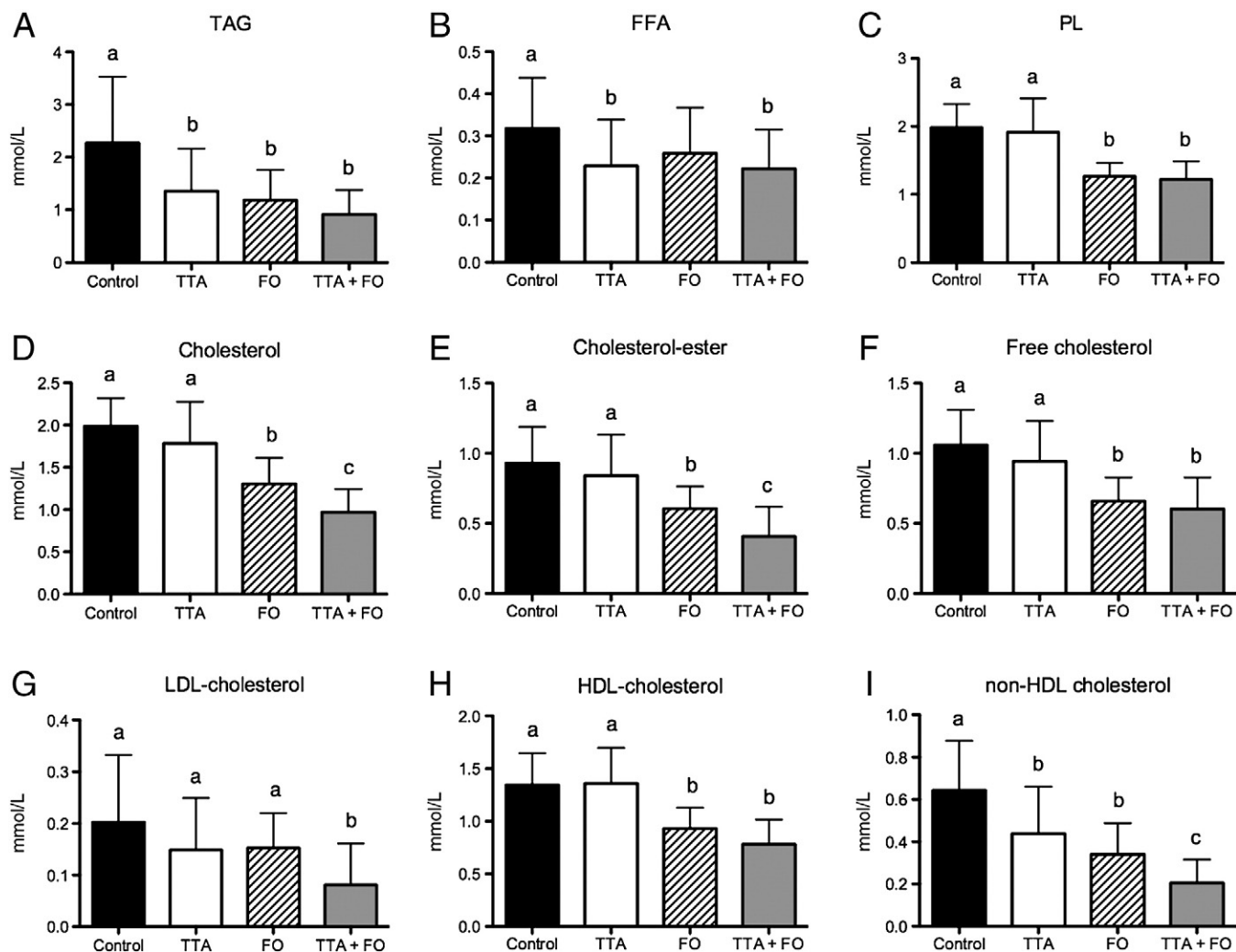


Fig. 2. Plasma lipid concentrations in male Wistar rats after 50 weeks of high-fat diets supplemented with 3-thia fatty acid TTA or FO. Values are means \pm S.D. (*n* = 31–38). Results were analyzed by ANOVA, and means with the same letter are not significantly different from each other (Tukey–Kramer test, *P* < .05).

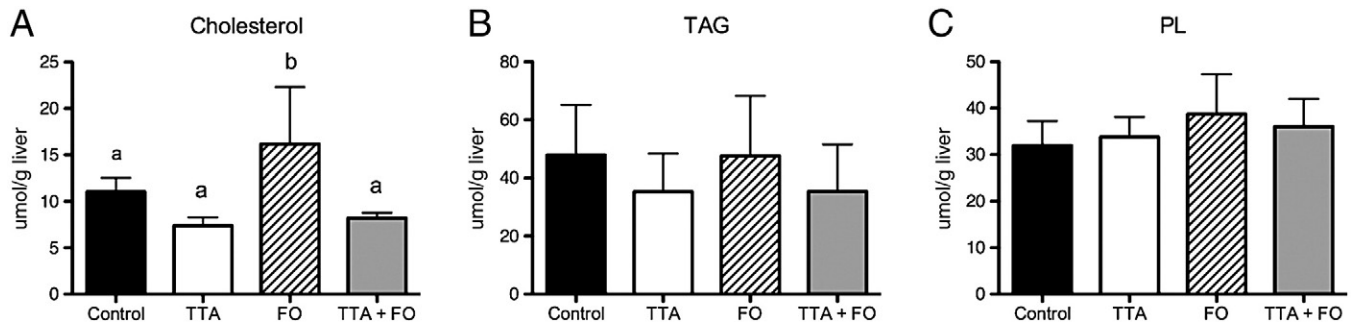


Fig. 3. Liver lipid concentrations in male Wistar rats after 50 weeks of high-fat diets supplemented with 3-thia fatty acid TTA or FO. Values are means \pm S.D. ($n=10-11$). Results were analyzed by ANOVA and means with the same letter are not significantly different from each other (Tukey–Kramer test, $P<.05$).

3. Results

3.1. Animal body weight

The addition of FO to a high-fat diet (25%) had no effect on the growth rate of rats, while the combined treatment led to a significant reduction in weight gain compared to the control group already after 5 weeks of treatment (Fig. 1). Moreover, the diet that contained both bioactive lipids seemed to reduce body weight more than TTA alone after 50 weeks of treatment but not significantly ($P=.23$). The weight loss caused by TTA stabilized over time. In this study, all groups demonstrated the same average feed intake. Thus, animals from TTA and TTA+FO groups had a reduced body weight compared to control group animals with the same energy intake over a 50-week period.

3.2. Plasma lipids

We studied the impact of TTA and FO on key parameters in lipid metabolism. Analysis of plasma lipids at the end point of the experiment demonstrated that all treatments had a substantial lipid-lowering potential (Fig. 2). The plasma TAG level was significantly improved by all the treatments (Fig. 2A). Only TTA and the combination of TTA and FO were able to lower the free fatty acids (FFAs, Fig. 2B). In contrast, FO and the combination with TTA were able to reduce plasma PL levels by 30%, while TTA had no effect compared to the control diet (Fig. 2C).

FO treatment alone or in combination with TTA was effective in lowering of the total plasma cholesterol, cholesterol esters and free cholesterol (Fig. 2D–F). While the FO-containing diet alone reduced cholesterol by 35% compared to the control high-fat diet, the cotreatment with TTA and FO reduced it by 49%, indicating an additive effect of the supplements (Fig. 2D). Likewise, a significant decrease in the cholesterol ester level was obtained after TTA+FO treatment compared to either treatment alone (Fig. 2E). The additive effect of TTA and FO was mainly on LDL cholesterol (Fig. 2G) and non-HDL cholesterol (Fig. 2I).

3.3. Liver lipids

The hepatic cholesterol concentrations had a tendency to decrease after administration of TTA and TTA+FO (Fig. 3) but increased significantly with FO treatment compared to control. In addition, in rats fed a TTA diet, the total hepatic TAG concentration was 26% lower than in control. In contrast, FO treatment did not influence the TAG concentration in liver and caused an insignificant rise in PL levels.

3.4. Fatty acid composition in plasma

The fatty acid composition in plasma is shown in Table 1. Compared to control animals, the plasma levels of SFAs and monounsaturated fatty acids (MUFAs) were marginally changed by TTA treatment alone, except for an increase in C20:3n–9 ($P<.0005$). In contrast to that, FO supplementation caused the significant reduction in amounts of SFAs ($P<.0005$), MUFAs ($P<.0005$) and n–6 PUFAs ($P<.0005$) in plasma from FO-treated animals. $\omega-3$ PUFAs

Table 1
Plasma fatty acid composition of male Wistar rats after 50 weeks of feeding with high-fat (25% w/v) diets supplemented with TTA, FO or TTA+FO

	Dietary supplementation			
	Control	TTA	FO	TTA+FO
SFAs	35.20 \pm 0.88 ^a	34.98 \pm 1.36 ^a	30.82 \pm 2.06 ^b	32.66 \pm 1.65 ^c
C16:0	21.22 \pm 1.49 ^a	22.41 \pm 1.23 ^b	17.72 \pm 1.28 ^c	20.35 \pm 1.44 ^a
C18:0	12.12 \pm 1.43 ^a	10.78 \pm 0.81 ^b	11.27 \pm 1.26 ^b	10.40 \pm 0.96 ^b
MUFAs	24.65 \pm 4.75 ^a	25.87 \pm 3.73 ^a	16.79 \pm 1.62 ^b	20.28 \pm 2.74 ^c
C16:1n–7	1.05 \pm 0.29 ^{a,b}	1.20 \pm 0.65 ^b	0.77 \pm 0.13 ^c	0.91 \pm 0.18 ^{a,c}
C18:1n–7	1.96 \pm 0.28 ^a	1.65 \pm 0.29 ^b	1.49 \pm 0.14 ^c	1.50 \pm 0.17 ^{b,c}
C20:1n–7	0.17 \pm 0.08	0.13 \pm 0.08 ^a	0.19 \pm 0.09 ^b	0.16 \pm 0.07
C22:1n–7	0.03 \pm 0.01 ^a	0.02 \pm 0.01 ^b	0.04 \pm 0.02 ^a	0.03 \pm 0.01 ^a
C16:1n–9	0.26 \pm 0.06 ^a	0.36 \pm 0.07 ^b	0.24 \pm 0.03 ^a	0.32 \pm 0.06 ^c
C18:1n–9 (OA)	20.46 \pm 4.23 ^a	21.70 \pm 3.49 ^a	12.99 \pm 1.37 ^b	16.29 \pm 2.50 ^c
C22:1n–9	0.02 \pm 0.00 ^a	0.02 \pm 0.01 ^a	0.04 \pm 0.01 ^b	0.04 \pm 0.01 ^b
C24:1n–9	0.27 \pm 0.11 ^a	0.46 \pm 0.14 ^b	0.48 \pm 0.11 ^b	0.53 \pm 0.14 ^b
n–9 PUFAs				
C20:3n–9 (MA)	0.23 \pm 0.03 ^a	0.85 \pm 0.33 ^b	0.12 \pm 0.01 ^c	0.13 \pm 0.02 ^c
n–6 PUFAs	36.26 \pm 4.61 ^a	33.76 \pm 3.59 ^b	22.72 \pm 2.63 ^c	22.38 \pm 2.50 ^c
C18:2n–6 (LA)	17.94 \pm 1.76 ^a	15.16 \pm 3.22 ^b	12.32 \pm 1.03 ^c	13.07 \pm 0.97 ^c
C18:3n–6	0.22 \pm 0.05 ^a	0.46 \pm 0.10 ^b	0.11 \pm 0.02 ^c	0.22 \pm 0.04 ^a
C20:2n–6	0.26 \pm 0.04 ^a	0.20 \pm 0.04 ^b	0.16 \pm 0.03 ^c	0.16 \pm 0.03 ^c
C20:3n–6	0.56 \pm 0.12 ^a	1.11 \pm 0.22 ^b	0.37 \pm 0.08 ^c	0.74 \pm 0.18 ^d
C20:4n–6 (AA)	16.76 \pm 4.69 ^a	16.57 \pm 3.69 ^a	9.45 \pm 1.89 ^b	7.95 \pm 1.83 ^b
C22:4n–6	0.34 \pm 0.07 ^a	0.14 \pm 0.03 ^b	0.07 \pm 0.02 ^c	0.05 \pm 0.01 ^c
C22:5n–6	0.16 \pm 0.04 ^a	0.12 \pm 0.06 ^b	0.22 \pm 0.04 ^c	0.17 \pm 0.02 ^a
n–3 PUFAs	3.55 \pm 0.5 ^a	2.30 \pm 1.03 ^a	29.48 \pm 4.19 ^b	22.90 \pm 3.14 ^c
C18:3n–3 (ALA)	0.61 \pm 0.16 ^a	0.45 \pm 0.16 ^b	0.59 \pm 0.14 ^a	0.50 \pm 0.17 ^b
C18:4n–3	0.02 \pm 0.01 ^a	0.01 \pm 0.02 ^a	0.54 \pm 0.19 ^b	0.53 \pm 0.22 ^b
C20:4n–3	0.12 \pm 0.02 ^a	0.09 \pm 0.02 ^b	0.39 \pm 0.06 ^c	0.30 \pm 0.05 ^d
C20:5n–3 (EPA)	0.02 \pm 0.01 ^a	0.01 \pm 0.02 ^a	16.52 \pm 3.38 ^b	12.58 \pm 2.82 ^c
C22:5n–3 (DPA)	0.47 \pm 0.11 ^a	0.17 \pm 0.08 ^b	1.32 \pm 0.30 ^c	0.79 \pm 0.10 ^d
C22:6n–3 (DHA)	2.01 \pm 0.49 ^a	1.28 \pm 0.58 ^a	9.84 \pm 2.27 ^b	8.02 \pm 1.03 ^c
TTA	ND	1.36 \pm 0.38 ^a	ND	1.04 \pm 0.17 ^b
TTA:1n–8	ND	0.79 \pm 0.28 ^a	ND	0.55 \pm 0.25 ^b
n–3 PUFA/n–6 PUFA ratio	0.10 \pm 0.01 ^a	0.07 \pm 0.03 ^a	1.34 \pm 0.37 ^b	1.04 \pm 0.22 ^c
DBI	1.52 \pm 0.16 ^a	1.43 \pm 0.13 ^b	2.38 \pm 0.15 ^c	2.04 \pm 0.11 ^d
$\omega-3$ index	2.33 \pm 0.52 ^a	1.58 \pm 0.94 ^a	26.36 \pm 3.83 ^b	20.59 \pm 2.85 ^c

Data are given as mol% \pm S.D. ($n=31-38$).

Results were analyzed by ANOVA, and means with the same letter are not significantly different from each other (Tukey–Kramer test, $P<.05$).

AA, arachidonic acid; ALA, α -linolenic acid, LA, linolenic acid; ND, not detectable; OA, oleic acid.

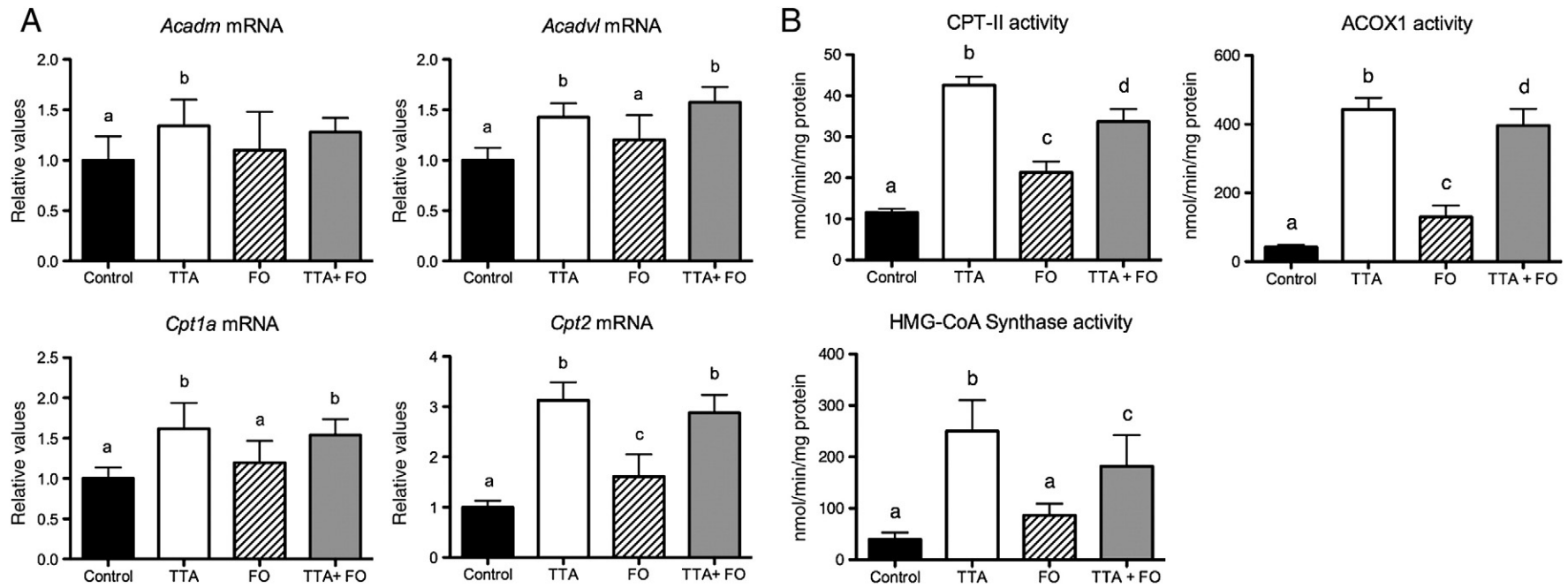


Fig. 4. Effect of 3-thia fatty acid TTA and FO on hepatic fatty acid β -oxidation. (A) Gene expression of *Acadm*, *Acadvl*, *Cpt1a*, and *Cpt2*. Data are shown as relative values. (B) Activity of ACOX1, measured in postnuclear fractions, CPT-II and HMG-CoA synthase, measured in crude mitochondrial fractions. Values are means \pm S.D. ($n=8-10$). Results were analyzed by ANOVA, and means with different letters are significantly different from each other (Tukey-Kramer test, $P<.05$).

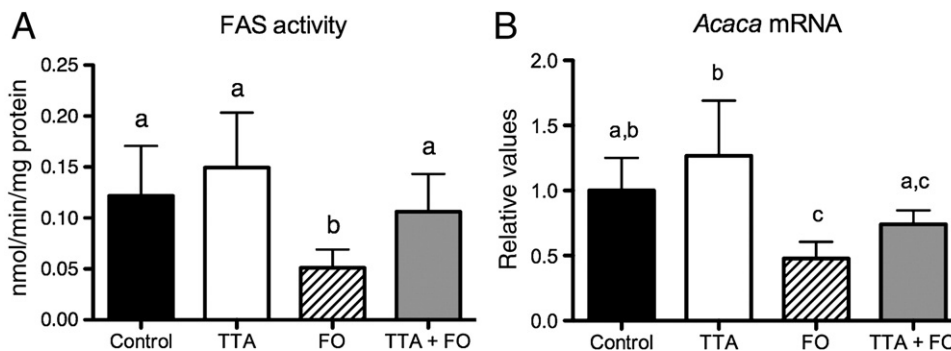


Fig. 5. Effect of 3-thia fatty acid TTA and FO on hepatic FAS activity (A) and hepatic gene expression of *Acaca* (B). Values are means \pm S.D. ($n=8-10$). Results were analyzed by ANOVA, and means with different letters are significantly different from each other (Tukey–Kramer test, $P<.05$).

[C20:5 $n-3$ (EPA), C22:5 $n-3$ (docosapentaenoic acid, DPA), C22:6 $n-3$ (DHA)] were decreased after TTA treatment [35,36], leading to a significantly reduced DBI. We also found a significant ($P<.0005$) reduction of $\omega-3$ PUFA in TTA+FO-treated animals compared to FO treatment alone. However, the combined treatment increased the $n-3/n-6$ PUFA ratio, as well as the $\omega-3$ index (DHA+EPA) (Table 1), by over 10-fold compared to TTA alone.

3.5. Genes and enzymes involved in fatty acid metabolism

Several of the PPAR-controlled genes involved in the mitochondrial fatty acid β -oxidation pathway, such as *Acadm*, *Acadvl*, *Cpt1a*, and *Cpt2* were induced in liver by the TTA diet (Fig. 4A). The FO diet seemed to give an induction of PPAR-activated genes; however, only *Cpt2* was significantly increased.

Hepatic ACOX1, CPT-II and HMG-CoA synthase activities indicated a high induction of fatty acid β -oxidation after 50 weeks of TTA diet (Fig. 4B). The addition of FO caused the less pronounced effect on hepatic enzyme activities in combination group compared to TTA group.

The activity of lipogenic enzyme FAS was significantly reduced by FO administration (Fig. 5A). Tetradecylthioacetic acid gave an insignificant increase in FAS activity and counteracted the FO effect in the combined treatment.

We also investigated the messenger RNA (mRNA) expression of *Acaca* (Fig. 5B). This gene encodes the enzyme acetyl-coenzyme A carboxylase, which catalyzes carboxylation of acetyl-CoA to malonyl-CoA. *Acaca* mRNA level in liver tended to be up-regulated by TTA compared to control group. The FO-supplemented group had a significantly lower *Acaca* mRNA expression than both TTA group and control group ($P<.001$). Also, in the TTA+FO group,

Acaca expression was significantly lower than in the TTA group ($P<.01$).

3.6. Differential effects of TTA and FO on *Ucp* mRNA expression

In the liver samples, differential effects of TTA and FO were observed on the gene expression of *Ucp2* and *Ucp3* mRNA, which are suggested to act as regulators of mitochondrial energy metabolism and ROS. Both TTA and TTA+FO diets resulted in the down-regulation of hepatic *Ucp2* mRNA levels, in contrast to FO alone (Fig. 6A). We revealed a substantial up-regulation (1500 \times) of *Ucp3* in rats fed a TTA-supplemented diet (Fig. 6B). The combination of TTA with FO also led to an up-regulation of *Ucp3* mRNA levels, while the FO diet had no significant effect on this mitochondrial uncoupling protein.

3.7. Oxidative damage in homogenate of whole liver and mitochondria

We evaluated the relationship between different oxidative biomarkers (representing different oxidative damage pathways) between whole-liver vs. mitochondrial fraction (Fig. 7).

γ -Glutamic semialdehyde is a marker that is related to direct metal catalysed oxidation on proline and arginine residues in proteins. Interestingly, the diet supplementation with FO led to non-significantly higher levels of GSA than in the control group in both mitochondrial extract and whole-liver homogenate, which indicated an increase in protein oxidative damage (Fig. 7A). In contrast to this, the dietary supplementation of TTA significantly reduced protein oxidative damage in mitochondrial extracts obtained from TTA- and TTA+FO-fed animals.

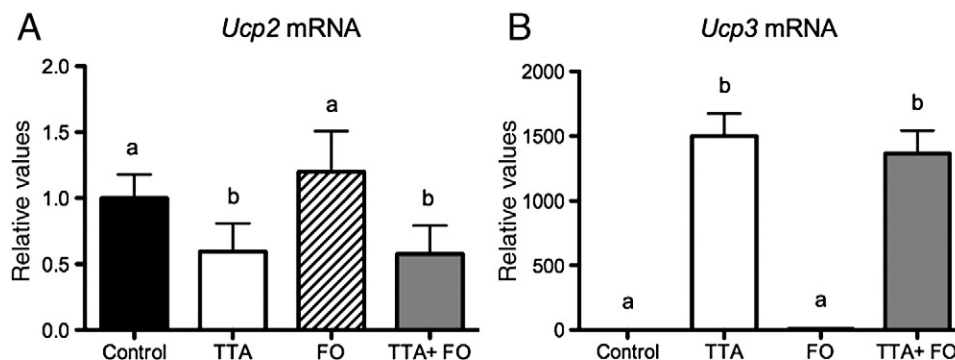


Fig. 6. Effect of 3-thia fatty acid TTA and FO on the hepatic gene expression of mitochondrial uncoupling proteins *Ucp3* (A) and *Ucp2* (B). Values are means \pm S.D. ($n=10$). Results were analyzed by ANOVA, and means with different letters are significantly different from each other (Tukey–Kramer test, $P<.05$).

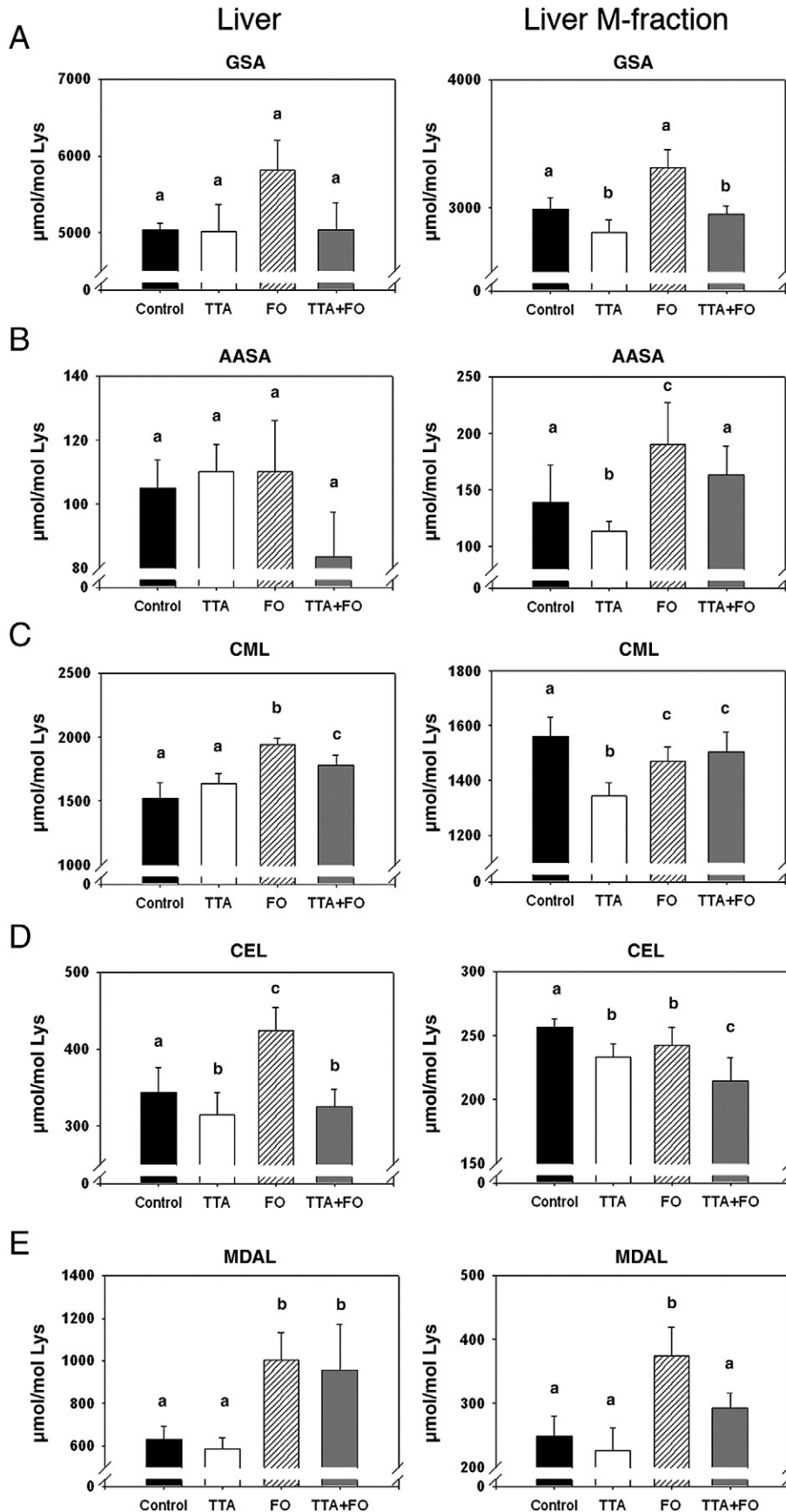


Fig. 7. Protein oxidative damage amongst different dietary interventions. GSA, AASA, CEL, MDAL and CML measured in liver (left) and liver mitochondrial homogenate (liver M-fraction, right). Values are means \pm S.D. ($n=7$ or 8 animals in each group). Results were analyzed by ANOVA, and means with different letters are significantly different from each other (Tukey–Kramer test, $P<0.05$).

The other marker of protein oxidative damage, α -AASA, was also significantly higher in mitochondrial samples from the FO group than in animals from the control group and groups treated with TTA or the combination (Fig. 7B). The TTA supplementation led to reduction of protein oxidative damage mitochondrial extract.

The nonenzymatic glycation and subsequent irreversible oxidation of proteins cause formation of glycoxidation products. *N* ϵ -Carboxymethyl-lysine is known to be formed from the oxidation of both carbohydrates and lipids, making it a biomarker of general oxidative stress. The whole-liver samples from the FO group showed significantly increased lipoxidation and TTA diminished this potentially deleterious effect of FO in animals from the TTA+FO group (Fig. 7C). In mitochondrial extracts, both FO and TTA treatment resulted in reduced levels of CML compared to the control group.

N ϵ -Carboxyethyl-lysine is a homolog of CML, which is formed by the reaction of lysine residues in proteins with methylglyoxal as well as with triose phosphates and other sugars. Our results showed that FO increased oxidative (nonenzymatic) sources of methylglyoxal, while the addition of TTA into the diets reduced CEL levels in whole-liver homogenates (Fig. 7D). In mitochondrial extracts, both bioactive compounds resulted in lower levels of CEL compared to control group. The cotreatment with TTA and FO demonstrated significantly lowered CEL compared with control, TTA, and FO groups in mitochondrial extract.

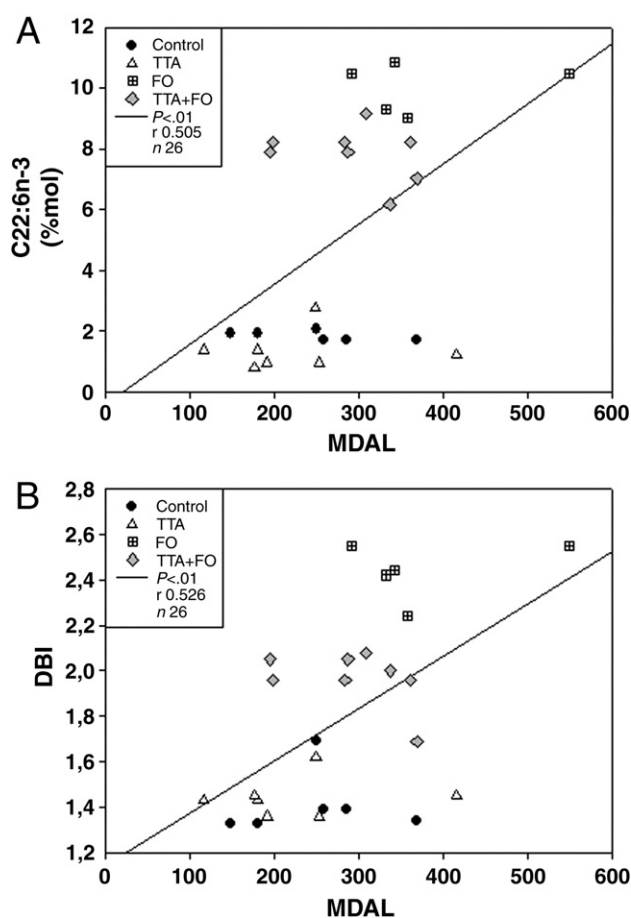


Fig. 8. Correlations for the fatty acid composition in plasma and the lipoxidative damage marker MDAL measured in mitochondrial extracts. (A) Correlation between DHA (C22:6n-3) and MDAL. C22:6n-3 values are shown as mole percent of the total lipid content. (B) Correlation between the DBI and MDAL. DBI values are expressed as \sum % of unsaturated fatty acids \times number of double bonds per unsaturated fatty acid. MDAL values are expressed in μ mol MDAL/mol Lys.

N ϵ -Malondialdehyde-lysine is a biomarker of lipoxidation. FO supplementation showed an increased oxidative damage compared to control group in both whole-liver and mitochondrial homogenate samples (Fig. 7E). We found that TTA cotreatment diminished the FO-induced lipoxidative damage in mitochondrial homogenates.

Furthermore, there is a significant positive correlation between MDAL concentration and the DHA content, as well as the DBI (Fig. 8).

4. Discussion

Contrary to earlier performed animal experiments on the effects of bioactive lipids such as TTA and ω -3 PUFAs, the distinguishing factor of our study was its duration of 50 weeks. The extended duration gave us the possibility to evaluate and compare the effectiveness of combined treatment vs. mono supplementation with TTA or FO. The prolonged beneficial effects observed were changes in expression of genes involved in fatty acid metabolism and activities of corresponding key enzymes, improvement of plasma lipid parameters and liver lipid composition and not the least weight reduction. A 50-week period of feeding with TTA resulted in a significantly reduced body weight gain during the whole study period, apparently reflecting increased energy expenditure due to TTA. In agreement with other studies, FO did not affect the overall body weight of male Wistar rats given a high-fat diet [37]. Further, the rise in activities of CPT-II, HMG-CoA synthase and ACOX1 (Fig. 4B) combined with the enhanced expression of hepatic *Cpt1*, *Cpt2*, *Acadm* and *Acadvl* (Fig. 4A) as well as *UCP3* (Fig. 6) suggests that TTA both increases the β -oxidation and induces the energy consumption via intensification of uncoupling in the liver (45).

The diets had a differential effect on the lowering of plasma lipid levels. While the TTA diet mainly lowered TAG, FFAs and LDL cholesterol in this long-term treatment, FO supplementation showed substantially more lowering of TAG, PLs, cholesterol and HDL cholesterol than TTA alone. The combined supplementation with TTA and FO demonstrated the additive effect of both components on the decrease in several plasma lipids and especially in a significantly enhanced reduction in plasma cholesterol.

In agreement with the results obtained by Duan et al. [38], our 50-weeks-long experiment showed that high-fat feeding can induce elevation in hepatic TAG levels (Fig. 3B). The accumulation of TAG was probably due to inability of the liver to handle the increased import of plasma lipids and indicated the development of liver steatosis. The diet with TTA showed a potential to improve the hepatic TAG and cholesterol levels, whereas the FO diet did not. This could be due to the high induction of hepatic β -oxidation by TTA that enhances lipid metabolism and consequently results in pronounced removal of lipids from both plasma and liver [13]. In addition, TTA has previously been shown to drain lipids from specific adipose tissue depots [39]. It might be possible that both FO and TTA diets are able to increase cholesterol and TAG transport to the liver, but animals given the FO diet are less able to metabolize the excess hepatic lipid levels. The stimulated activities of CPT-II and ACOX1 were much more pronounced with TTA than with FO feeding (Fig. 4B). Thus, TTA seemed to lower plasma lipid levels by an increased hepatic β -oxidation, while FO redistributed lipids without affecting the total lipid level and body weight.

We have revealed a tendency to decrease in the hepatic cholesterol concentrations after administration of TTA and TTA+FO, whereas FO supplementation alone gave a significant increase in hepatic cholesterol compared to controls. Consequently, the observed lowering effect of hepatic cholesterol by TTA+FO combination might be due to the TTA effect.

In this long-term experiment, TTA supplementation caused several changes in the plasma fatty acid composition, particularly, the decrease in ω -3 PUFA content (Table 1). The observed reduction in ω -3 PUFA levels can be explained by TTA-induced stimulation of

mitochondrial and peroxisomal fatty acid oxidation (36). Furthermore, the *n*–9 fatty acid, mead acid (MA, C20:3*n*–9), was up-regulated in the plasma of TTA-fed rats (approximately fourfold). Notably, both FO and the combined treatment led to a twofold reduction of MA compared to control. As an increased production of the nonessential MA may be linked to a poor PUFA status in humans [40], the FO-induced decrease in MA supports a similar regulation of MA in rats.

The addition of both TTA and FO to the high-fat diet induced genes linked to fatty acid metabolism and increased the corresponding enzyme activity levels. Tetradecylthioacetic acid was far more potent than FO, and the combination of TTA and FO did not further increase the effect. The pattern of enzyme activity implicated in fatty acid metabolism was similar to previous findings [19,36,39], demonstrating that the metabolic effects of FO and TTA supplementation are long-lasting.

Tetradecylthioacetic acid and FO seem to affect the factors involved in lipogenesis in a different manner. The significant reduction in hepatic FAS activity in rats fed the FO diet could contribute to the registered changes in plasma lipid content. In contrast, the TTA diet showed an insignificant increase in hepatic FAS activity ($P=.24$). Moreover, the FO diet significantly decreased *Acaca* expression in liver compared to TTA. Thus, comparing the effect of combination of both supplements with the effect of TTA treatment, the reduction of *Acaca* mRNA level could be a result of the competing modes of action of TTA and FO.

The study with Wistar rats fed a low-fat TTA-supplemented diet for 7 days showed an enhanced *Ucp2* mRNA expression in liver [41], and it has been suggested that this early, transient induction in hepatic *Ucp2* may contribute to increased energy expenditure. However, our long-term experiment and the 7-week study performed by Wensaas *et al.* [39] demonstrated a significant decrease in *Ucp2* expression caused by TTA-supplemented diets.

Ucp3 is usually not expressed in the liver, except in response to PPAR activation during situations with a high level of fatty acid metabolism [42]. The increase in hepatic *Ucp3* mRNA expression caused by TTA treatment alone (over 1500-fold) and the combined treatment (over 1300-fold) was the most striking results in our experiment. As discussed previously, the stimulated hepatic expression of *Ucp3* due to TTA administration could be related to an increased metabolism, possibly also through energy uncoupling (Fig. 6B). Altogether, these findings indicate that the induction of *Ucp2* becomes less pronounced over a longer period, while the induction of *Ucp3* is a prolonged effect by TTA.

A hypothesis about a possible protective role of endogenous UCP3 against oxidative damage by ROS in skeletal muscle mitochondria was proposed and tested by Brand *et al.* [43]. They discovered that down-regulation of *Ucp3* was associated with increased oxidative damage through higher ROS generation, while the *Ucp3* up-regulation was not. Based on findings from our study and in accordance with previous observations [44,45], we could propose that such pronounced effects might represent an adaptive response to protect the mitochondria and their host cells from oxidative stress in situations characterized by intensive lipid metabolism and consequently further support the theory of the defensive role of *Ucp3* against lipid-induced mitochondrial damage.

In agreement with previous data [46–48], we confirm that dietary FO supplementation increased lipoxidative damage. Our experiment revealed marked changes in CML and MDAL, which are markers related to lipoxidative status, in both liver homogenate and mitochondrial extracts. Since liver is a crucial organ in lipid metabolism, the fatty acid profile in liver is sometimes assumed to reflect the fatty acid composition in plasma. Therefore, it is not unreasonable to think that the profile might reflect the membrane lipid composition of liver cells. From that point of view and being

demonstrated by a 1.5-fold increase of DBI for FO-treated animals compared with the control group (Fig. 8), one can postulate that the different degree of unsaturation in liver membranes may account for the increased damage observed and could achieve enough amplification without ROS production being raised. In other words, FO diet is not necessarily responsible for an increased ROS production but for a major ROS susceptibility, since membrane composition is slightly altered and the degree of unsaturation is increased. Finally, both CML and MDAL were reduced by addition of TTA into the diets. Thus, TTA was able to partially prevent those FO-induced changes. This fully agrees with the hypothesis of TTA as an antioxidant.

The results also demonstrate that a dietary manipulation comprising changes in the amount of fatty acids induce a significant change in the steady state levels of GSA and AASA, markers of direct oxidative damage. Reinforcing the implication of mitochondria in this change, only mitochondrial proteins show those changes, whereas liver homogenates did not. Fish oil effects could be due to increased free radical production as recently demonstrated in other tissues and experimental models, implicating Ca^{+2} transit between mitochondria and endoplasmic reticulum [49–51]. Most interestingly, the fact that TTA significantly lowers direct oxidative damage supports the notion that TTA increases mitochondrial efficiency (irrespective of FO) and may reproduce beneficial effects of caloric restriction.

To conclude, this study provides evidence that the long-term effects of TTA are similar to those seen in experiments of shorter duration. We report that TTA and FO are efficient dietary supplements in improvement of plasma lipid profile, despite differences in their mechanisms of action. While TTA increased energy expenditure and lipid metabolism, FO seemed to lower plasma lipid levels mainly by a redistribution of lipids, as well as a reduced fatty acid synthesis. Through our experiment, we confirmed that, during long-term FO diets, the proper supplementation of antioxidants, such as TTA, is essential.

Acknowledgments

The authors are grateful to Kari Williams, Liv Kristine Øysæd, and Svein Krüger for excellent technical contribution and to the staff at the Laboratory Animal Facility, University of Bergen. We thank Professor Jon Skorve for helpful discussions.

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Cell stress induces TDP-43 pathological changes associated with ERK1/2 dysfunction: implications in ALS

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Received: 18 March 2011 / Revised: 2 June 2011 / Accepted: 9 June 2011 / Published online: 25 June 2011
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Abstract TDP-43 has been implicated in the pathogenesis of amyotrophic lateral sclerosis and other neurodegenerative diseases. Here we demonstrate, using neuronal and spinal cord organotypic culture models, that chronic excitotoxicity, oxidative stress, proteasome dysfunction and endoplasmic reticulum stress mechanistically induce mislocalization, phosphorylation and aggregation of TDP-43. This is compatible with a lack of function of this protein in the nucleus, specially in motor neurons. The relationship between cell stress and pathological changes of TDP-43 also includes a dysfunction in the survival pathway mediated by mitogen-activated protein kinase/extracellular signal-regulated kinases (ERK1/2). Thus,

under stress conditions, neurons and other spinal cord cells showed cytosolic aggregates containing ERK1/2. Moreover, aggregates of abnormal phosphorylated ERK1/2 were also found in the spinal cord in amyotrophic lateral sclerosis (ALS), specifically in motor neurons with abnormal immunoreactive aggregates of phosphorylated TDP-43. These results demonstrate that cellular stressors are key factors in neurodegeneration associated with TDP-43 and disclose the identity of ERK1/2 as novel players in the pathogenesis of ALS.

Keywords Oxidative stress · Proteasome stress · Endoplasmic reticulum stress · Excitotoxicity · ALS · TDP-43 · ERK1/2

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Electronic supplementary material The online version of this article (doi:10.1007/s00401-011-0850-y) contains supplementary material, which is available to authorized users.

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Introduction

Transactive response DNA binding protein (TDP-43) is a 414-amino acid protein with two highly conserved RNA recognition motifs, a nuclear localization signal at the protein N-terminus, and a glycine-rich region mediating protein-protein interactions at the C-terminus [8, 9, 29, 31, 38]. TDP-43 was discovered as the gene encoding a 43-kDa protein that binds to the transactive response DNA sequence of human immunodeficiency virus type 1 [38]. Subsequently, it was demonstrated that TDP-43 regulates DNA transcription, RNA splicing and microRNA biogenesis in physiological conditions [9]. Recently, the discovery of TDP-43 cytosolic aggregates in sporadic amyotrophic lateral sclerosis (ALS), a progressive and deadly motor neuron disease, has prompted its research in neurodegeneration [2, 35]. TDP-43 ALS-associated forms characteristically exhibit ubiquitination, phosphorylation and fragmentation, together with abnormal subcellular localizations [35].

Neurodegeneration in ALS involves many different cellular stress mechanisms: oxidative stress, mitochondrial dysfunction, endoplasmic reticulum (ER) stress, proteasome stress and protein aggregation, glutamate excitotoxicity, cytoskeletal dysfunction, malfunctioning non-neuronal cells in the vicinity of motor neurons, and abnormal RNA processing [4, 14, 20, 22, 23, 25, 33, 47]. Some of them also originate after excitotoxicity caused by dysregulation of glutamate signaling [40]. In addition to ALS, there is a wide variety of neurodegenerative diseases (such as Alzheimer's, Parkinson's and Huntington's), that also show TDP-43 pathological forms, suggesting a potential association between TDP-43 and neurodegenerative processes [1, 15, 21, 34, 35, 42].

We have previously shown that ER stress, increased ubiquitination, protein oxidative damage and changes in fatty acid profile are associated with chronic excitotoxicity in organotypic spinal cord cultures [23], a well-supported model of the sporadic form of ALS [39]. However, it is not known if excitotoxicity or other ALS-involved cellular stressors induce TDP-43 pathological changes. Here, we report that oxidative, endoplasmic reticulum (ER) stress and proteasome dysfunction induce those changes. Furthermore, excitotoxicity leads to TDP-43 accumulation resembling the pathological aggregates shown in human disease. As oxidative stress impairs protein nuclear import, and this involves mitogen-activated protein kinase/extracellular signal-regulated kinases (ERK1/2) activation [11], we also investigated whether oxidative, ER and proteasome stress cause a ERK1/2 activation leading to cytosolic TDP-43 aggregation in neuronal cell lines. Paradoxically, the results indicate that inhibition of TDP-43 nuclear import associated with stress involves the inhibition of ERK1/2, which interestingly are also aggregated. Furthermore, we show the presence of abnormal phosphorylated ERK1/2 aggregates in motor neurons with p-TDP-43-positive inclusions in ALS.

Materials and methods

Cell culture

Neuro-2A and SH-SY5Y cell lines were incubated as detailed in the *Supplementary material*. To study the effects of oxidative stress, alteration of endoplasmic reticulum and inhibition of proteasome activity, cells were treated with 10 μM H_2O_2 (Sigma), 5 μM thapsigargin (Thp) (Sigma), or 2.5 μM epoxomicin (Epo) (Sigma), respectively, for 2 or 4 h. Similarly, the cells were incubated with 20 μM PD98059 (Sigma) for 2 h before any stress to specifically inhibit the ERK1/2 pathway. To avoid the influence of growth factors present in the fetal bovine serum on the results, the normal culture medium was replaced by Optimem (Invitrogen, Carlsbad, CA, USA)

12 h before all the assays. Cell viability was evaluated using the crystal violet assay as previously described [19] and detailed in the *Supplementary material* section.

Spinal cord organotypic cultures

Spinal cord cultures were prepared from lumbar spinal cord of postnatal day 8 rat pups as previously described [23, 39] and maintained in culture media as described in the *Supplementary material* section. One week after plating, to induce excitotoxicity the slices were incubated with the glutamate transport inhibitor D,L-threo-hydroxyaspartate (THA) (Sigma, St. Louis, MO, USA) at 100 μM . This treatment injures motor neurons with a morphology typical of excitotoxic degeneration after 3 weeks of treatment. Experiments for each condition ($n = 30$ slices per experimental group) were repeated at least three times. All animal experiments were approved by the Institutional Animal Care and Experimentation Committee.

Patients' information

The human spinal cord samples were from six males and five females aged between 54 and 76 years (mean age 62) affected with typical neurological and neuropathological characteristics of sporadic ALS. The post-mortem delay between death and tissue processing was between 3 and 13 h. Age- and gender-matched controls ($n = 11$) with no neurological disease and normal neuropathological study were processed in parallel. All samples were obtained from the Institute of Neuropathology and University of Barcelona Brain Bank following the guidelines of the local ethics committees. Extensive pathological studies were done for ALS diagnosis as previously described [23].

Immunohistochemical analysis

Detailed procedures, following previously described methods [23] for immunohistochemistry analysis of organotypic spinal cord cultures, cell lines and human samples are described in the *Supplementary material* section. Immunohistochemical controls, performed by omitting the primary antibodies, resulted in the abolition of the immunostaining in all cases. For quantitation of p-TDP-43 or p-ERK1/2 aggregates a minimum number of 1,000 cells were counted in each experimental situation.

Cell fractionation, protein electrophoresis and western blot

Tissue and cell lysis, protein electrophoresis and western blot were performed as previously described [23]. For details see the *Supplementary material* section.

Equal loading of western blot was ensured by β -actin or α -tubulin and blot quantification was carried out using the ChemiDoc XRS system and the softwares Quantity One (BioRad, Hercules, CA, USA) and Scion Image (Scion Corp., Frederick, MD, USA).

Statistical analysis

All statistics were performed using the SPSS software (SPSS Inc., Chicago, IL, USA). Differences between groups were analyzed by the Student's *t* tests or ANOVA analysis, once normality of variables was tested by Kolmogorov–Smirnov test. The 0.05 level was selected as the point of minimal statistical significance in every comparison.

Results

TDP-43 pathogenic alteration is induced by different ALS-related stressors in different neuronal cell lines

Previous results from our group showed that sporadic ALS is associated with increased protein oxidation, loss of proteasome activity and ER stress contributing to motor neuron death [23]. ALS-associated TDP-43 changes include increased fragmentation, increased cytosolic localization and aggregate formation with concurrent phosphorylation. To validate the relationship between cell stress and TDP-43 changes we measured TDP-43 changes in accepted models of each of those stress types in neuronal cell lines. Neuro 2A cultures were treated with either H_2O_2 to induce oxidative stress, thapsigargin to induce endoplasmic reticulum stress, or with epoxomicin to inhibit proteasome activity. Treatments were sublethal (Fig. 1a), so the presented changes in TDP-43 are not directly related to immediate cell death. Furthermore, none of the stress conditions used here increased cleaved caspase-3 levels (data not shown).

Western blot using the polyclonal antibody anti-TDP-43 (Sigma ref HPA017284), extensively validated in the Human Protein Atlas (<http://www.proteinatlas.org/>), showed a transient increase of an anti-TDP-43 immunoreactive 37-kDa band (putatively a TDP-43 fragment) after each one of the stress inducers for 2 h (Fig. 1b, c). All the stressors induced a significant increase in TDP-43 phosphorylation versus control cells, measured by using an antibody against the phospho-Ser410/409 in TDP-43 (p-TDP-43). In the case of a 25-kDa phosphorylated fragment, its presence was sustained after 4 h (Fig. 1b, d). According to p-TDP-43 immunoreactivities a general increase was seen at fragments with apparent molecular weights between 32–37 kDa and 22–25 kDa, even

comprising a very low molecular weight fragment of 15-kDa (Fig. 1b, d).

Subcellular fractionation and immunohistochemistry demonstrated that these stress inducers led to the accumulation of TDP-43 and p-TDP-43 in the cytosolic fractions (Figs. 1e–g, 2). Specifically, in the case of epoxomicin treatment, practically all TDP-43 were fragmented (37 kDa band) and localized in the cytosol after 4 h, as the TDP-43 immunoreactivity was practically lost in nuclear fractions of epoxomicin treated cells. Proteasome inhibition led to the highest accumulation of non-phosphorylated TDP-43 (Fig. 2a, b). In addition, both proteasome and ER stress inducers generated a high level of cytosolic p-TDP-43 aggregates (Fig. 2a, c). The highest labeling of epoxomicin is coincident with the suggestion that TDP-43 or some of its fragments are degraded by proteasome [37]. These results also show that TDP-43 phosphorylation is not always related to its cytosolic aggregation under cell stress. Most of these results were also observed in a human cell line (differentiated SHSY-5Y neuroblastoma cells), suggesting that oxidative, ER and proteasome stress-induced neuronal TDP-43 pathological changes are common mechanisms across different species (Fig. S1).

In summary, these data show that oxidative, ER and proteasome stress induce ALS-related TDP-43 pathogenic changes in neuronal cell lines. These include increased TDP-43 fragmentation, increased cytosolic localization and aggregate formation with concurrent phosphorylation.

Involvement of ERK1/2 in stress-induced ALS-related TDP-43 changes

ERK1/2 pathway is implicated in cellular death/survival signaling and is activated in response to certain situations of cellular stress [6]. Moreover, previous data have described that oxidative stress prevents nuclear import of transcription factors by activating ERK1/2 [11]. So this phenomenon could partially explain TDP-43 cytosolic accumulation observed after oxidative and ER stress, and proteasome inhibition. To demonstrate this hypothesis, the degree of ERK1/2 activation in all stress situations was analyzed and it was demonstrated that all cell stress—though at different rates—activated initially ERK1/2 (Fig. 3a–d). In fact, ERK1/2 inactivation by the specific inhibitor PD98059, not only failed to prevent TDP-43 abnormal distribution associated to stress, but it also increased cytosolic p-TDP-43 aggregation (Fig. 3e–h, S2) and it induced p-ERK1/2 aggregation (Fig. 3h, S2). Noteworthy, epoxomicin induced a cytosolic accumulation of p-ERK1/2 (Fig. 3h, Fig. S2), coincident (but not colocalizing) within cells showing p-TDP-43 aggregates. These

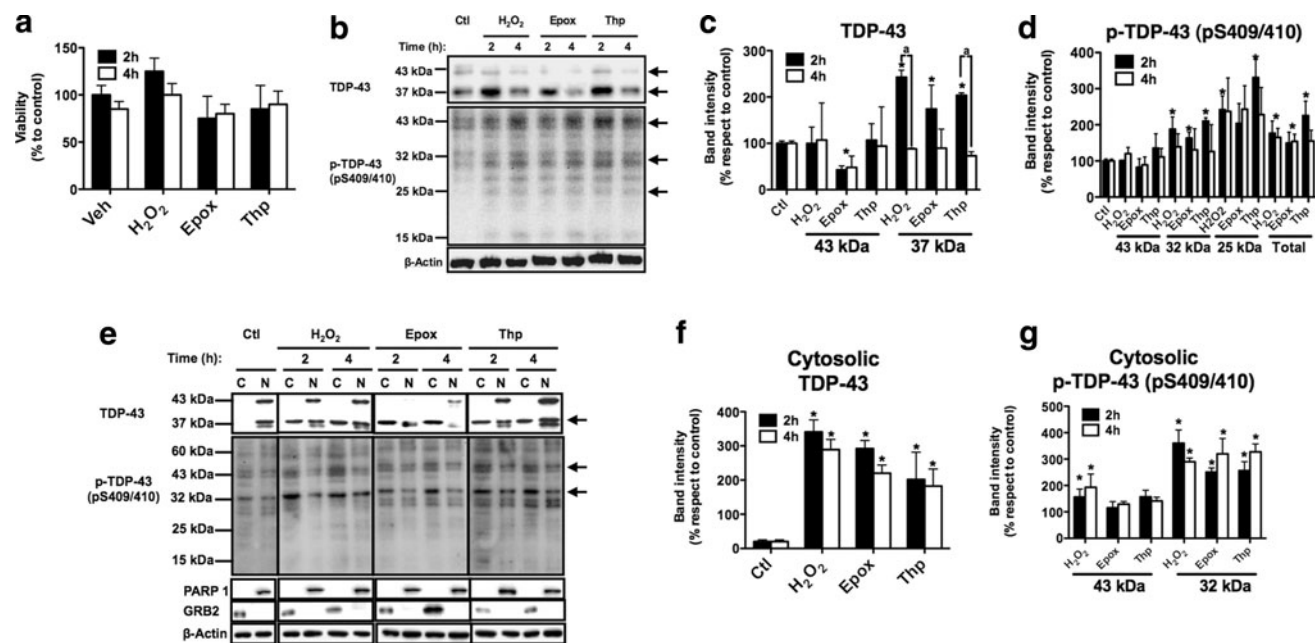


Fig. 1 TDP-43 pathogenic alteration is induced by different ALS-related stressors in neurons. **a** Treatments with oxidative stress, proteasome stress and ER stress did not induce a significant change in neuron cell line viability (neither at 2 nor at 4 h). **b** Representative immunoblots of TDP-43 and p-TDP-43 immunoreactivities of Neuro 2A cell lysates after induction of oxidative stress (10 μ M H_2O_2), proteasomal inhibition (2.5 μ M Epoxomicin, Epox) and endoplasmic reticulum stress (5 μ M Thapsigargin, Thp). Densitometric analysis of the anti-TDP-43 (**c**) and anti-p-TDP-43 (**d**) bands, adjusted to actin content, being the differences analyzed with reference to unstressed cells. **e** Representative immunoblots of cytosolic (C) and nuclear (N) fractions of Neuro 2A cells after induction of the above referred stress. Anti-growth factor receptor-bound protein 2 (Grb2)

immunoreactivity was used to ensure specificity of cytosolic isolation and anti-Poly (ADP-ribose) polymerase 1 (PARP1) immunoreactivity for nuclear isolation. Densitometric analyses of the anti-TDP-43 immunoreactivity (**f**) and anti-p-TDP-43 (**g**) in cytosolic fractions showed increased amount of TDP-43 protein (both phosphorylated and non-phosphorylated) after each stress with significant changes with reference to unstressed cells. Differences between control and H_2O_2 , Epox and Thp-treated samples were analyzed by Student's *t* test being $*p < 0.01$ (for different treatments) and a $p < 0.01$ (for differences between 2 and 4 h). Arrows at left of blots indicate bands whose intensity was quantified. Total in **d** indicates the summatory of individual immunoreactivities of anti-p-TDP-43 in **b**

data suggest that p-TDP-43 and p-ERK1/2 deposits may be present in different cellular compartments in the same cell. Importantly, those p-ERK1/2 cytosolic aggregates coincided with the lowest degree of ERK1/2 activation (Fig. 3a, b, h). These data suggest an association between aggregation/inactivation of ERK1/2 and TDP-43 abnormal localization. Noteworthy, cytosolic p-ERK1/2 did not colocalize with stress granules (anti-TIA immunoreactivity in cells treated with thapsigargin, Fig. S3).

To directly prove that ERK1/2 inactivation is sufficient for TDP-43 alteration, we submitted cells to pharmacological ERK1/2 inactivation without further stress, leading to a clear increase in nuclear TDP-43 fragmentation as well as an accumulation of total levels of cytosolic TDP-43 (Fig. 4a, b) and their appearance as perinuclear p-TDP-43 aggregates (Fig. 4c). Globally, these data demonstrate that ERK1/2 inactivation does not prevent the stress-induced changes in TDP-43. Furthermore, ERK1/2 inactivation is sufficient for ALS-related TDP-43 pathological changes in neurons (Fig. 4).

Chronic excitotoxicity leads to ALS-related TDP-43 pathogenic changes and ERK1/2 aggregation

Cell phenotype in neuronal lines is quite different from the spinal cord neurons. Moreover, these neuronal cell lines are grown in the absence of a natural cellular milieu (astrocytes, microglia), which plays a role in the development of ALS. Organotypic spinal cultures could solve these limitations, as glutamate excitotoxicity, a well-recognized mechanism of motor neuronal death in sporadic ALS, can be reproduced in vitro by exposing lumbar cord slices to the glutamate-uptake inhibitor THA [39]. We have previously shown that chronic excitotoxicity in this model induces ER stress, increased ubiquitination, protein oxidative damage and changes in fatty acid profile [23]. To evaluate whether cell stress-induced TDP-43 pathological changes were also present in chronic excitotoxicity, we measured potential fragmentation, cytosolic localization and aggregate formation of TDP-43 with concurrent phosphorylation with different antibodies, to avoid non-

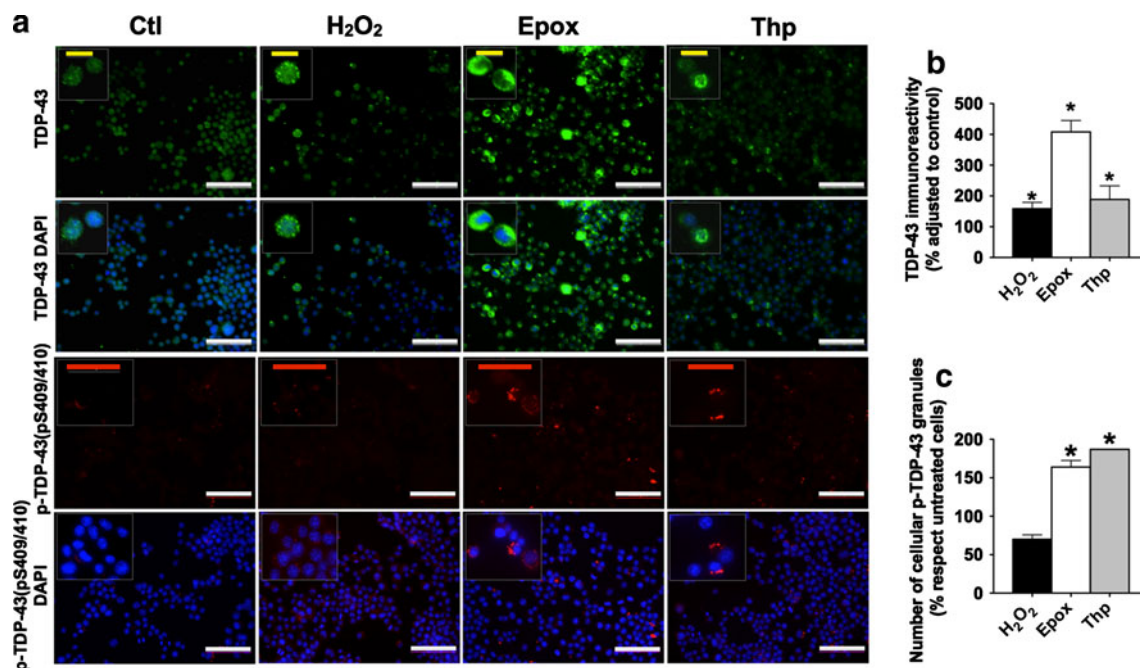


Fig. 2 TDP-43 cytosolic aggregation and phosphorylation is induced by different ALS-related stressors in neurons. **a** Both TDP-43 (green) and p-TDP-43 (red) aggregates were observed in Neuro 2A cells 2 h after induction of oxidative stress (10 μ M H₂O₂), proteasomal inhibition (2.5 μ M Epoxomicin, Epox) and endoplasmic reticulum stress (5 μ M Thapsigargin, Thp). Nuclei were stained with DAPI (blue). **b** Evidences the effect of cell stress in anti-TDP-43 immunoreactivity and **c** shows the effect of stress inducers in the

number of cellular anti-p-TDP-43 immunoreactive granules (number of aggregates for each 100 cells: 11.5 ± 1.6 ; 26.6 ± 5.8 and 30.3 ± 7.6 , mean \pm SD for H₂O₂, Epox and Thp-treated cells, respectively). Differences between control and H₂O₂, Epox and Thp-treated samples were analyzed by Student's *t* test being $*p < 0.01$ (for different treatments). Scale bars: white 50 μ m; yellow 10 μ m; red 25 μ m

specific recognition. This approach revealed different patterns of TDP-43 distribution in organotypic spinal cord culture. The use of the polyclonal antibody anti-TDP-43 (Sigma ref HPA017284) revealed decreased TDP-43 immunostaining, specifically in the nucleus of neuronal cells, compatible with the above-mentioned nuclear loss of TDP-43 induced by cell stressors. These neurons, localized in the ventral horn, show a morphology and SMI-32 immunoreactivity compatible with its identity as motor neurons and they exhibited a near-complete depletion of TDP-43 (Fig. 5a, Fig. S4). In contrast, glial cells do not exhibit this TDP-43 loss (Fig. S4). The use of another antibody raised against a peptide comprising the N-terminal region (1-261 aminoacids, Abnova ref H00023435-A01) evidenced TDP-43 accumulation in the cytoplasm after THA treatment (Fig. 5b), also showing a nuclear loss. Interestingly, in those cells with nuclear TDP-43 depletion, TDP-43 immunoreactivity was present in the cytoplasm, both in perinuclear areas and dendritic terminals (small panels, Fig. 5b). Strikingly, while as TDP-43 nuclear loss was neuron specific, cytosolic immunoreactivity was extended to both neuronal and glial cells.

Western blot analysis disclosed two major bands: a 43-kDa (native) and the 37-kDa (Fig. 5c). Densitometric

analysis demonstrated that excitotoxicity significantly increased the levels of this TDP-43 fragment while 43-kDa band tended to decrease, albeit non-significantly (Fig. 5d), a fact that might be explained by the contribution of non-neuronal TDP-43.

Chronic excitotoxicity also leads to increased p-TDP-43, specifically in the cytoplasm of cells in the ventral horn of spinal cord cultures (Fig. 6a–d). The resulting increased p-TDP-43 immunostaining showed two patterns: an aggregated and a diffuse one. Aggregates were not colocalized with ubiquitin (Fig. 6b upper panel), though they were restricted to cells showing ubiquitin inclusions. In contrast, the p-TDP-43 diffuse pattern was present in cells without increased protein ubiquitination (Fig. 6b lower panel). Western blot analysis evidenced that the presence of various immunoreactive bands, similar to neuronal cell lines (at apparent molecular weight 43, 37, 29, 25, 23 and 15 kDa), increased significantly after THA treatment, except the unfragmented 43-kDa band (Fig. 6c, d). P-ERK1/2 analyses revealed that chronic excitotoxicity increased extranuclear p-ERK1/2 immunoreactivity together with p-TDP-43 aggregates. p-ERK1/2 aggregates showed both fine granular and meshwork-like morphologies (Fig. 6e). In this specific case, and based on cell

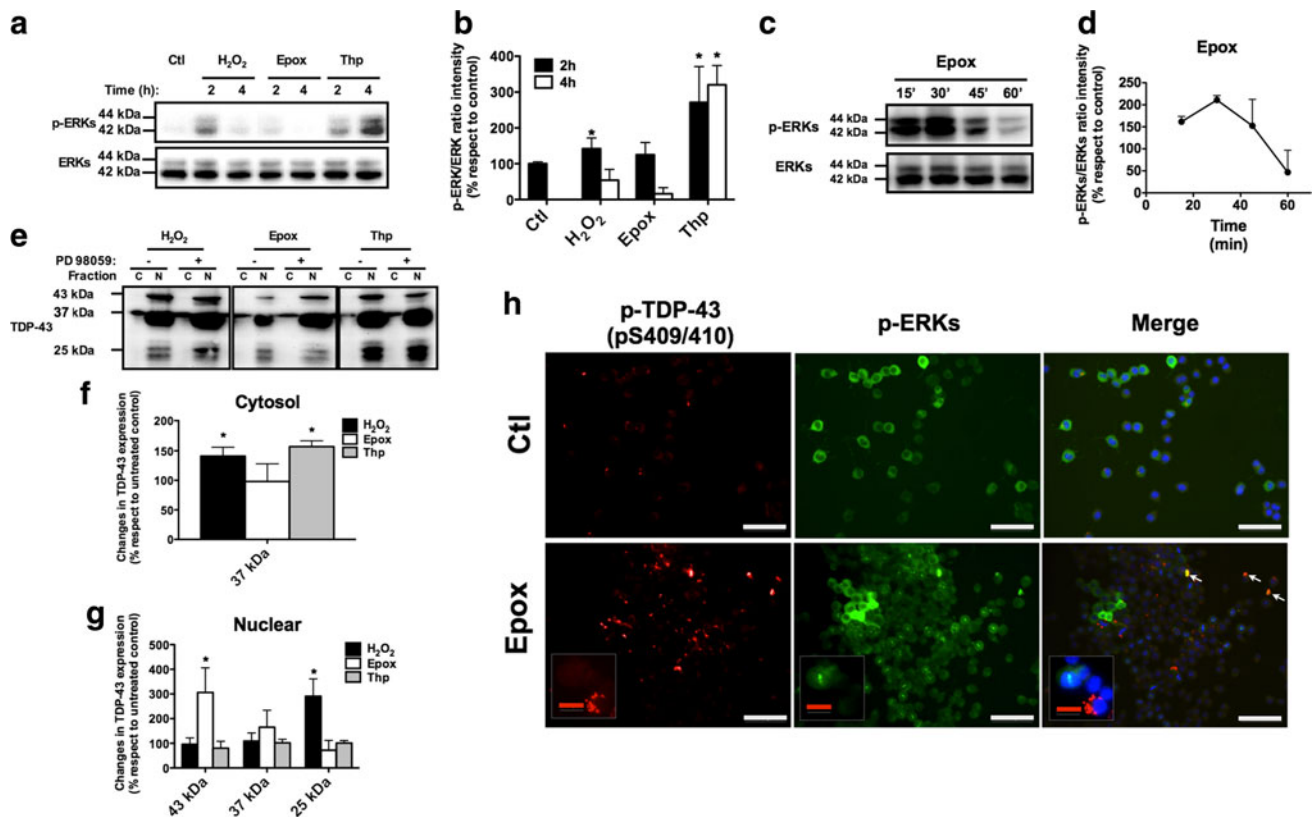


Fig. 3 Involvement of ERK1/2 in stress-induced ALS-related TDP-43 changes. **a** Representative immunoblots of total ERK1/2 and p-ERK1/2 immunoreactivities of Neuro 2A cell lysates after induction of oxidative stress (10 μ M H₂O₂), proteasomal inhibition (2.5 μ M Epoxomicin, Epox) and endoplasmic reticulum stress (5 μ M Thapsigargin, Thp). **b** Densitometric analysis of p-ERK1/2 bands, adjusted to total ERK1/2 content, being the differences analyzed with reference to untreated cells. **c** Time course analyses show that in the case of epoxomicin, 2 h inactivation (shown in **a**) was preceded by a marked acute activation of p-ERK1/2, with a maximum at 30 min, as evidenced by the densitometric analysis (**d**). **e** Representative immunoblots of cytosolic (C) and nuclear

(N) fractions of Neuro 2A cells after induction of the above referred stress under previous ERK1/2 inhibition induced by PD98059 treatment for 2 h. Densitometric analysis of the anti-TDP-43 immunoreactivity in cytosolic (**f**) and nuclear fractions (**g**). In the case of oxidative stress, PD98059 treatment increased nuclear TDP-43 fragmentation as evidenced by the accrual of a 25 kDa anti-TDP-43 reactive fragment (**e**, **g**). **h** Proteasome stress led to p-ERK1/2 aggregation (*green*) in association with p-TDP-43 aggregation (*red*), with some cells showing colocalization of both aggregates (*arrows*). Differences between control and H₂O₂, Epox or Thp-treated samples were analyzed by Student's *t* test being **p* < 0.01 (for different treatments). Scale bars: white 50 μ m; red 10 μ m

abundance, p-ERK1/2 aggregates were present in both neuronal and non-neuronal cells in ventral horn (Fig. 6f). Importin beta, a protein implicated in nucleocytoplasmic transport, was studied by immunostaining, showing that this protein is absent in cells showing p-ERK1/2 aggregates in THA-treated organotypic cultures (Fig. S5). This supports the hypothesis that impaired nuclear import due to excitotoxicity may be related to p-ERK1/2 aggregation.

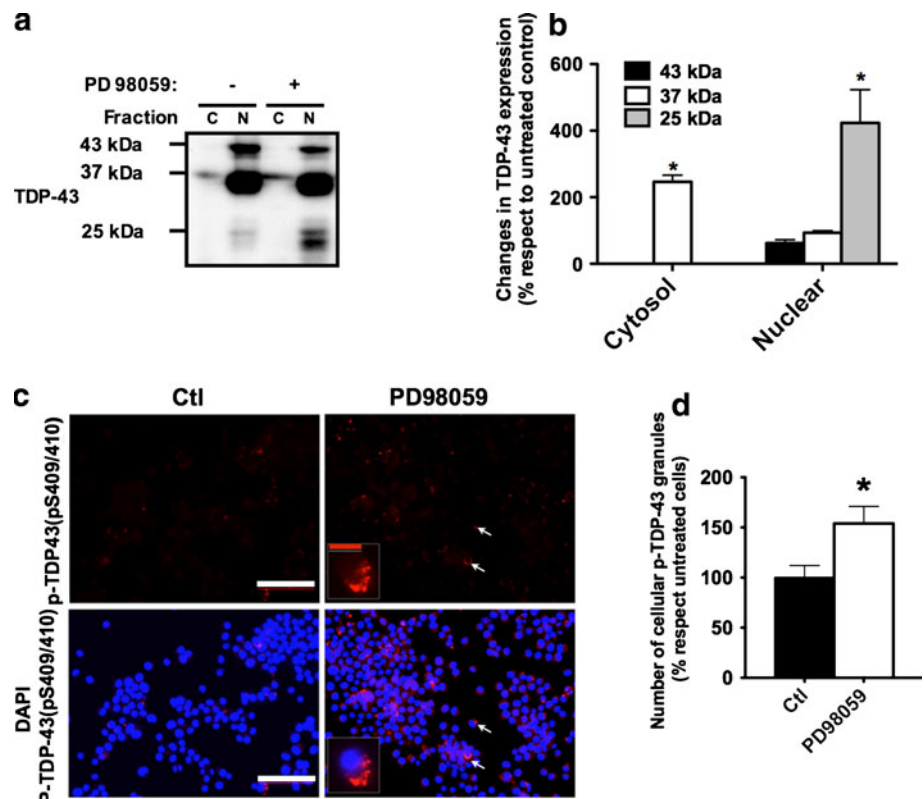
Globally, these results demonstrate that chronic excitotoxicity, which is known to induce ER, proteasome and oxidative stress, leads to TDP-43 pathogenic changes, namely increased fragmentation, increased cytosolic localization and aggregate formation with concurrent phosphorylation in cells of the ventral horn of lumbar

spinal cord. Furthermore, increased p-ERK1/2 deposition is also present, coincident with p-TDP-43 aggregates.

Altered p-ERK1/2 deposition is restricted to motor neurons with p-TDP-43 immunoreactive deposits in ALS

As already reported, TDP-43 immunoreactivity in normal motor neurons of the spinal cord was characterized as fine granular precipitate localized in the nuclei. However, TDP-43 immunoreactivity was altered in many motor neurons in ALS as fine granular deposits, skein-like inclusions and globular inclusions in the cytoplasm, at the time that TDP-43 immunoreactivity vanished in the nuclei of the same neurons, reproducing what is observed in the spinal cord

Fig. 4 ERK1/2 inactivation leads to ALS-related TDP-43 changes. **a** Representative immunoblots of cytosolic (C) and nuclear (N) fractions of Neuro 2A cells untreated after ERK1/2 inhibition by PD98059 treatment for 2 h. **b** Densitometric analysis of the anti-TDP-43 immunoreactivity in cytosolic and nuclear fractions. **c** ERK1/2 inactivation induces p-TDP-43 cytosolic aggregation, shown by arrows. Nuclei were stained with DAPI (blue). **d** Effect of ERK1/2 inhibition in the number of cell anti-p-TDP-43 immunoreactive granules (number of aggregates for each 100 cells: 16.1 ± 1.2 and 25.6 ± 5.8 for control and PD98059 treated cells, respectively). Differences between control and PD98059-treated samples were analyzed by Student's *t* test being $*p < 0.01$ Scale bars: white 50 μm , red 10 μm



organotypic cultures. Similar results were obtained with the two anti-TDP-43 antibodies used in samples from ALS patients (data not shown).

Phosphorylated form of TDP-43, as observed with both anti-p-TDP-43 antibodies, was only found in pathological inclusions whereas the normal nuclei were not stained. Thus, p-TDP-43 was a marker of altered TDP-43 localization in ALS motor neurons (data not shown). In those sections, p-ERK1/2 immunoreactivity was present in the nuclei of motor neurons in normal spinal cords and in apparently non-altered motor neurons in samples from ALS patients (Fig. 7a). Yet several motor neurons in the ALS showed abnormal p-ERK1/2 deposits in the form of dense nuclear aggregates (Fig. 7b, c) or dense (Fig. 7d–f), fine granular or rectilinear (Fig. 7g, h), skein-like (Fig. 7i, j) or meshwork-like (Fig. 7k, l) cytoplasmic inclusions. These were accompanied by a decrease or absence of nuclear p-ERK1/2 immunoreactivity.

Double-labeling immunofluorescence and confocal microscopy showed altered p-ERK1/2 deposition restricted to motor neurons with p-TDP-43 immunoreactive deposits in ALS cases (Fig. 7m–r). Subcellular colocalization of abnormal p-ERK1/2 and p-TDP-43 was also occasionally observed (Fig. 7s–x). These data reinforce a potential role for ERK1/2 dysfunction in ALS pathogenesis related to TDP-43 alterations, as the same motor neurons show both TDP-43 and p-ERK1/2 aggregates.

Discussion

Data presented here demonstrate that different paradigms of sporadic ALS, including organotypic culture of lumbar spinal cord slices under excitotoxic conditions [23, 39] reproduce TDP-43 abnormalities observed in sporadic ALS and frontotemporal lobar degeneration. In both diseases, TDP-43 shows increased fragmentation, hyperphosphorylation and ubiquitination [35]. Furthermore, its subcellular localization is changed from its physiological preferential nuclear localization to a cytosolic one, even showing aggregates [2, 3, 35]. Our data reinforces both the usefulness of organotypic culture as a valid model for sporadic ALS and the fact that chronic excitotoxicity could reproduce TDP-43 pathological findings in vitro.

Nuclear TDP-43 protein is decreased in ventral horn of glial and motor neurons of THA-treated cultures. ALS-associated extranuclear localization has been described in several subcellular fractions, including cytosol and ER [18, 41], concurrent with a loss in nuclear TDP-43 localization, potentially compatible with an impairment in its functions, mainly in the nucleus. Accordingly, in control conditions of organotypic cultures, nuclear TDP-43 seems considerably more accumulated in motor neurons than in other surrounding cells. This may be consistent with a neuron-selective functional dependency of TDP-43 [43]. Loss of nuclear TDP-43 in excitotoxic conditions may be related to

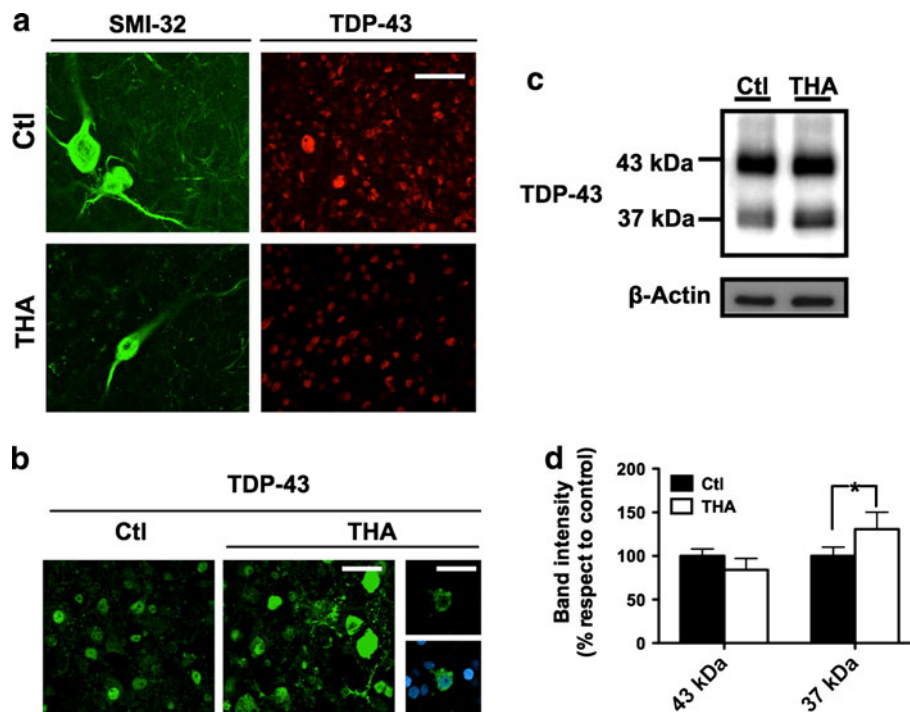


Fig. 5 Chronic excitotoxicity leads to ALS-related TDP-43 pathogenic changes. **a** Representative confocal microscope images showing decreased TDP-43 immunoreactivity in ventral horns of spinal cord slices cultured for 21 days with 100 μ M D,L-threo-hydroxyaspartate (THA) (lower panel) or vehicle (upper panel) using rabbit anti-TDP-43 (red). Immunostaining was combined with anti-SMI-32 (green) to visualize motor neurons. **b** Using a mouse anti-TDP-43 antibody (green), immunoreactivity distribution was markedly changed by THA treatment. Smaller panels in **b** show that in some cells TDP-43

immunoreactivity is present in the cytoplasm, excluding DAPI stained nuclei (blue). **c** Representative immunoblots of spinal cord homogenates using rabbit anti-TDP-43 show that THA induced a significant increase in the levels of a 37-kDa band. **d** Densitometric analysis of the bands, adjusted to actin content, being the differences analyzed with reference to control values. Scale bars **a** 50 μ m; **b** 25 μ m. Differences between control and THA-treated samples were analyzed by Student's *t* test being $*p < 0.01$

TDP-43 fragmentation by excitotoxic phenomena, concurrently to both native TDP-43 (43-kDa) diminished levels and increased amount of lower molecular weight TDP-43 fragments. In this sense, recent data supported the pathogenic importance of TDP-43 fragments, specially those of 25-kDa in nuclei [7, 13, 46]. Most interestingly, these nuclear fragments were also present in neuronal cell cultures under the stressors evaluated here, including ERK1/2 inhibition. These results reinforce the potential interaction between cell stress and TDP-43 pathology, independently on the neurodegenerative paradigm chosen. Using other antibodies for p-TDP-43, chronic excitotoxicity was associated with increased diffuse and aggregate cytoplasmic p-TDP-43 immunoreactivity. Cytosolic p-TDP-43 aggregates did not show a constant colocalization with ubiquitin, another marker of ALS. However, only cells showing increased ubiquitin immunostaining demonstrated cytosolic p-TDP-43 aggregation, suggesting a close link between these two phenomena (e.g. by proteasomal dysfunction).

It is accepted that oxidative stress could influence proteasome activity [24]. In turn, proteasomal stress is one of

the potential causes of ER stress [10]. In accordance with this, the increased TDP-43 aggregation linked to its fragmentation and cytosolic location which is observed in Neuro2A and SH-SY5Y cell lines could be explained by a combined effect of proteasomal dysfunction, oxidative and ER stress. Nevertheless, proteasomal activity impairment seems to be a key factor, as it induces the highest aggregation (in terms of immunohistochemical evidences) of both TDP-43 and its phosphorylated form, according to previous reports indicating TDP-43 fragmentation occurs mainly via proteasome [49], reproducing both the human disease and the organotypic culture under excitotoxicity.

The presented results demonstrate increased levels of p-TDP-43 induced by cell stress in several experimental models: chronic excitotoxicity (in spinal cord organotypic culture), and oxidative, ER and proteasome stress (in Neuro-2A and SH-SY5Y), suggesting that TDP-43 phosphorylation is a common feature in the potential for pathogenesis exhibited by this protein in stress-associated neurodegenerative disorders [17]. These results could be derived both from increased TDP-43 phosphorylating activity, depending on casein-kinase I or decreased

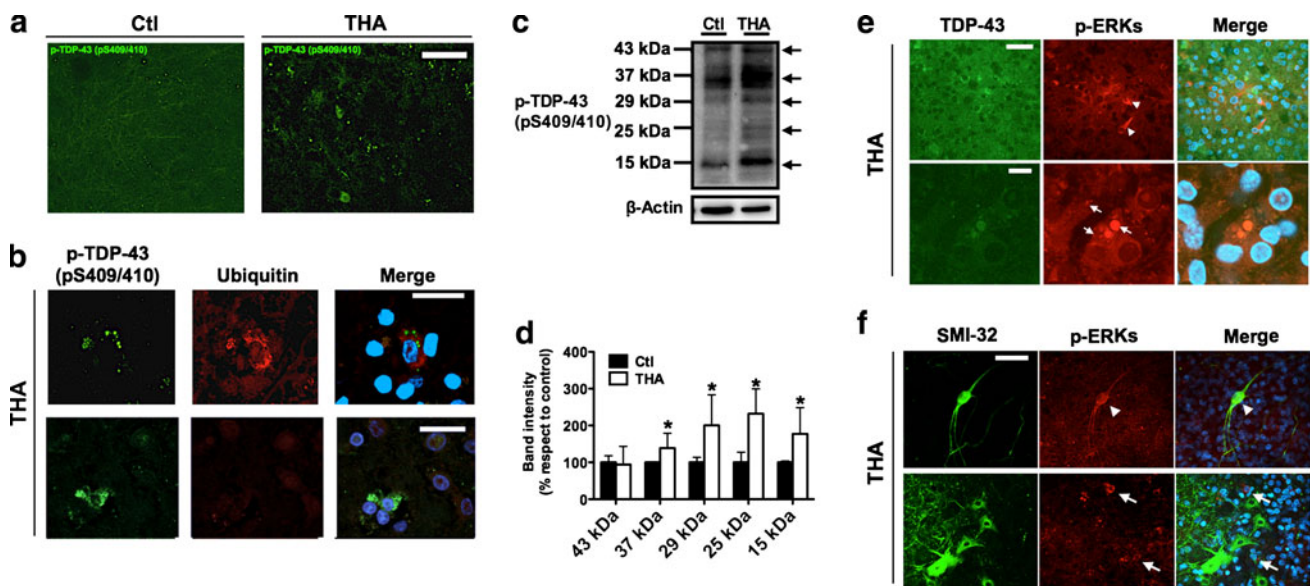


Fig. 6 Increased TDP-43 phosphorylation is associated with cytosolic p-ERK1/2 aggregation. **a** Representative confocal microscope images showing increased cytoplasmatic TDP-43 phosphorylation in ventral horns of spinal cord slices under chronic excitotoxicity. **b** Increased p-TDP-43 immunoreactivity was present both in aggregate form (upper panel, green) and in a diffuse pattern (lower panel, green), with no ubiquitin colocalization (red). Nuclei were stained with DAPI (blue). **c** Representative immunoblots of spinal cord homogenates using anti-p-TDP-43 shows that THA induced a significant increase in the levels of several bands. **d** Densitometric analysis of the bands, adjusted to actin content, being the differences analyzed with reference to control values. At least 30 hemi-slices from each condition were examined throughout the different

experiments. **e** Increased p-ERK1/2 immunoreactivity after THA treatment was distributed following cytosolic location (arrowheads, upper panels) or granular-globular patterns (arrows, lower panels), some showing colocalization with TDP-43 immunoreactivity (**f**). Increased p-ERK1/2 immunoreactivity (red) after THA treatment was distributed among SMI-32 positive cells (identified as neurons, arrowheads) and preferentially in non SMI-32 positive cells (arrows). Nuclei were stained with DAPI (blue). Scale bars: **a** 50 μ m; **b** 20 μ m; (**e** upper panel) 25 μ m; (**e** lower panel) 10 μ m; **f** 50 μ m. Arrows at left of blots indicate bands whose intensity was quantified. Differences between control and THA-treated samples were analyzed by Student's *t* test being $*p < 0.01$

phosphatase responses, depending on yet ill defined factors [26]. Furthermore, the relationship of TDP-43 aggregation–fragmentation and phosphorylation is still under evaluation, with recent data showing that p-TDP-43 (at Ser 409/410) is closely associated to aggregation [7]. However, we also evidence that increased phosphorylation is not always correlated with p-TDP-43 aggregation (e.g. while all stressors evaluated increased cytosolic p-TDP-43 levels, H_2O_2 failed to show increased aggregation by immunohistochemistry). This suggest the existence of stress-specific trends for TDP-43 pathogenetical changes. We recognize, as limitation of the cellular models used here, the fact that p-TDP-43 expression is present in “control” conditions. Nevertheless, in the tissular (organotypic) model and specially, in the human samples, p-TDP-43 expression is mostly restricted to the pathological conditions. Previous data show that SHSY-5Y cell lines using western blot reveal a very small, though visible, immunoreactivity over anti-p-TDP-43 in control conditions [5, 37, 48]. The mechanisms leading to this increased phosphorylation in cell lines are not currently known, but they may be related to the protecting role of TDP-43 over apoptosis

in human cells, accounting the fact that TDP-43 deletion increases p-Rb-mediated cell death [5].

In any case, the present report linking neurodegeneration-basic mechanisms to TDP-43 abnormalities supports the notion that TDP-43 mutations are not necessary for its pathological role. Thus, in rodent models, TDP-43 overexpression leads to TDP-43 inclusions and neurodegenerative phenotypes compatible with sporadic ALS [45, 46]. Furthermore, previous results demonstrating colocalization of “stress granules” with mutated TDP-43 [12, 16, 30, 32] are extended in the present study, where it is clearly shown that cell stress leads to native TDP-43 pathogenetical changes, without apparent participation of “stress granules”. Thus, neither p-ERK1/2 nor TDP-43 aggregates were colocalized with TIA-1 immunostaining, a marker of stress granules, in any of the stress conditions examined. The relationship between those different aggregates linked to pathology will be the focus of future studies. Nevertheless, our results with chronic excitotoxicity in organotypic cultures of spinal cord and stress induction in different neuronal cell lines from different species allows to propose their use as

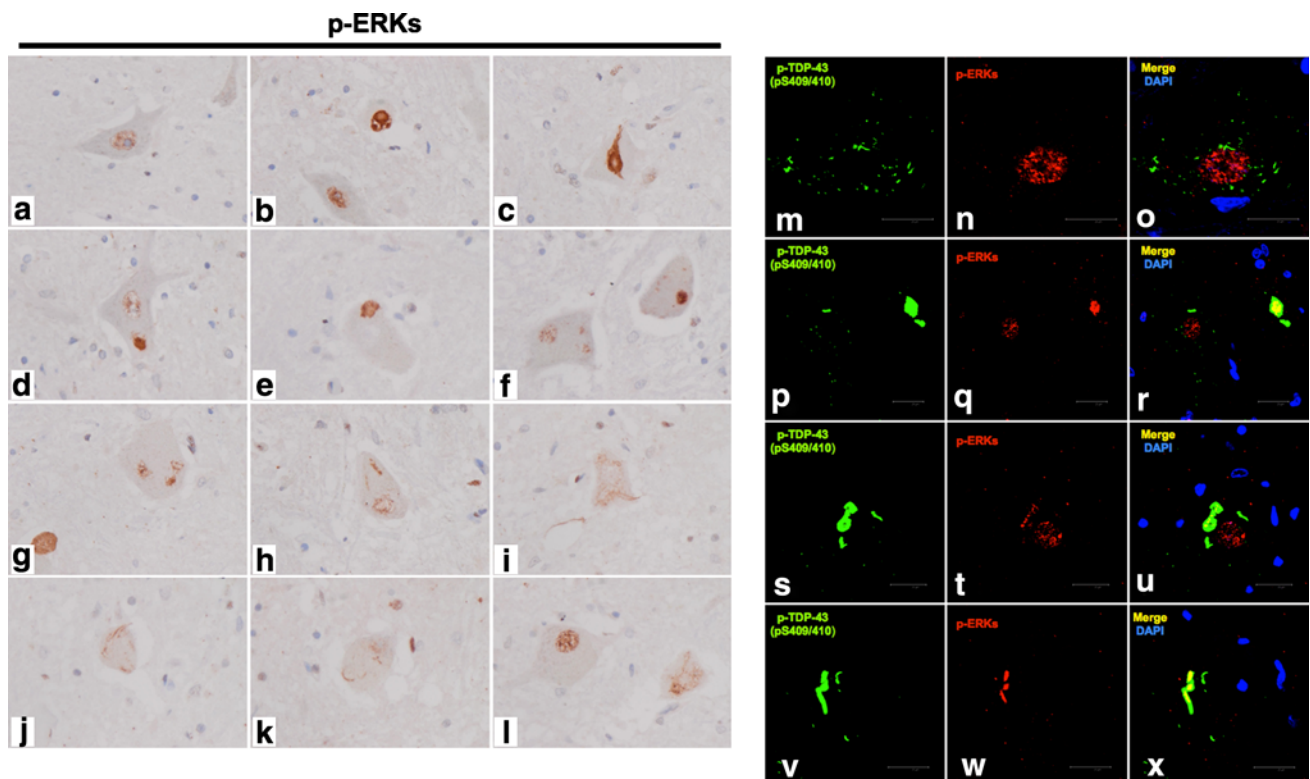


Fig. 7 Altered p-ERK1/2 deposition is restricted to motor neurons with p-TDP-43-immunoreactive deposits in ALS. *Left panel* p-ERK1/2 immunoreactivity in the nucleus of motor neurons in normal spinal cord (**a**) and abnormal, globular nuclear p-ERK1/2 inclusions in motor neurons in ALS (**b, c**), dense (**e, f**), fine granular or rectilinear (**g, h**), skein-like (**i, j**) or meshwork-like (**k, l**) cytoplasmic inclusions, accompanied by decreased or absence p-ERK1/2 immunoreactivity only

in spinal cord motor neurons in ALS cases. Paraffin sections slightly counterstained with hematoxylin. *Right panel* Double-labeling immunofluorescence and confocal microscopy showing altered p-ERK1/2 deposition in ALS motor neurons with p-TDP-43 immunoreactive deposits (**m–r**). Sub-cellular co-localization of abnormal p-ERK1/2 and p-TDP-43 is also observed in altered ALS motor neurons (**s–x**). Nuclei were stained with DAPI (*blue*). Scale bars 30 μ m

preclinical model in the screening of agents potentially affecting TDP-43 pathogenic changes.

An impairment of nuclear import mechanisms could play an important role in ALS pathogenesis, based on abnormal location of TDP-43 (a nuclear factor) [28, 36]. As it is known that oxidative stress impairs nuclear import by a mechanism depending on ERK1/2 activation [11], we tested whether ERK1/2 activation is related to TDP-43 pathogenic changes observed in our neuronal cell models exposed to different stress conditions. If this was the case, ERK1/2 pathway inhibition could relieve stress-associated TDP-43 pathogenicity. Oxidative and ER stress induced increased levels of p-ERK1/2 in a transient or sustained manner, in accordance with this hypothesis. However, inhibition of these kinases, far from avoiding these changes, exacerbated them, even in control conditions. In the case of proteasome stress, depletion of p-ERK1/2 is strongly associated with TDP-43 pathogenic phenomena. Our results suggest that ERK1/2 plays a previously unreported significant role in TDP-43 cellular homeostasis and cellular wellness, as specific ERK inhibition leads to TDP-43 fragmentation, cytosolic aggregation and increased

phosphorylation. So the initial activation of ERK1/2 promoted by cell stress in both neuronal cell lines could be related to the first cellular response to a stress situation, since its modulation has been associated with protection mechanisms in others neuronal cell lines [44]. These results are also compatible with the known physiological role of ERK1/2 regulated pathways, acting to promote survival or death, depending upon the cellular context in which they are activated [27]. In fact, our results show that ERK1/2 activation is needed for cell survival under stress, as shown by viability assays. Several neurological insults linked to excessive release of glutamate and neuronal death result in tyrosine kinase activation, including ERK1/2. Furthermore, oxidative stress is a known activator of ERK1/2 pathway [27] as in our hands seems to be ER stress [2] and proteasome stress. In line with the observations in vitro, the present study has also evidenced, for the first time, aggregation of phosphorylated ERK1/2 in motor neurons in ALS, with a close relationship with TDP-43 inclusions. Thus, abnormal p-ERK1/2 is only found in motor neurons with altered TDP-43 deposition, further supporting an association but not necessarily a causal relationship

between abnormal TDP-43 expression and ERK1/2 signaling in this disease. Concerning a potential direct interaction between TDP-43 and ERK1/2, it has been recently shown that interactome of TDP-43 consists of proteins implicated in pre-mRNA splicing and RNA stability and transport, as well as other neuron-enriched proteins, methyl CpG-binding protein 2 and polypyrimidine tract-binding protein 2, besides others. Nevertheless, no direct interaction with ERK1/2 was reported [43]. These data do not exclude that these identified proteins may interact with TDP-43 and ERK1/2, an issue that merits further exploration.

In conclusion, the present work evidences interactions between TDP-43 and stress mechanisms involved in ALS development. Furthermore, a novel finding, implicating ERK1/2 inhibition as a potential contributor to TDP-43 pathogenetical changes, is presented for explaining p-ERK1/2 aggregates in human motor neuron disease.

Acknowledgments We are indebted to tissue donors and their families. This work was supported by grants from Spanish Ministry of Education and Science [grant numbers BFU 2009-11879/BFI, AGL2006-12433, BFU 2009-06427/E]; the Generalitat of Catalunya [grant number 2009SGR-735]; the Spanish Ministry of Health [grant number PI08-1843 to M.P.O., BESAD-P and PI08-0582 to I.F.]; the ALS Catalan Foundation [to I.F.]; and “La Caixa” Foundation. Supported also by the COST B-35 Action. V.C has been supported by a predoctoral fellowship from Govern Balear, Conselleria d’Economia Hisenda i Innovació and D.C. by a predoctoral fellowship from the Instituto de Salud Carlos III.

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Oxidative and endoplasmic reticulum stress interplay in sporadic amyotrophic lateral sclerosis

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The occurrence of endoplasmic reticulum (ER) stress in the sporadic form of amyotrophic lateral sclerosis (ALS) is unknown, despite it has been recently documented in experimental models of the familial form. Here we show that spinal cord from patients with sporadic ALS showed signs of ER stress, such as increased levels of ER chaperones such as protein-disulfide isomerase, and increased phosphorylation of eukaryotic initiation factor 2 α (eIF2 α). Among the potential causes of such ER stress proteasomal impairment was confirmed in the same samples by demonstrating increased ubiquitin immunoreactivity and increased protein lipoxidative (125%), glycoxidative (55%) and direct oxidative damage (62%) over control values, as evidenced by mass-spectrometry and immunological methods. We found that protein oxidative damage was strongly associated to ALS-specific changes in fatty acid concentrations, specifically of *n*-3 series (as docosahexaenoic acid), and in the amount of mitochondrial components as respiratory complexes I and III, suggesting a mitochondrial dysfunction leading to increased free radical production. Oxidative stress was also evidenced in frontal cortex, suggesting that this region is affected early in ALS. As those events were partially reproduced by threo-hydroxyaspartate exposure in organotypic spinal cord cultures, we concluded that changes in fatty acid composition, mitochondrial function and proteasome activity, which may be driven by excitotoxicity, lead to oxidative stress and finally contribute to ER stress in sporadic ALS.

Keywords: Proteasome; glycation; lipoxidation; mitochondria; motor neuron

Abbreviations: ER = endoplasmic reticulum; GSA = glutamic semialdehyde; AASA = aminoadipic semialdehyde

Received February 9, 2007. Revised July 5, 2007. Accepted July 20, 2007. Advance Access publication August 23, 2007

Introduction

Amyotrophic lateral sclerosis is a multifactorial disease whose pathophysiological mechanisms include decreased availability to neurotrophic factors, disturbances in calcium metabolism, increased neuroinflammatory status, cytoskeletal changes and oxidative stress (Dupuis *et al.*, 2004; Rao and Weiss, 2004; Strong *et al.*, 2005; Boillee *et al.*, 2006). Recent data indicate (Atkin *et al.*, 2006; Turner and Atkin, 2006) that endoplasmic reticulum (ER) stress may be also involved in the familial form of the disease. ER stress, a complex pattern involving highly specific signalling pathways, ensures through the so-called unfolded protein response that protein folding capacities of ER are not

overwhelmed. However, prolonged ER stress could contribute to cell death, both by mitochondria-dependent and independent pathways (Lindholm *et al.*, 2006). In contrast with the familial form, no data was available on the occurrence of ER stress in the more common, sporadic form of the disease.

Some of the pathological hallmarks of ALS, such as increased ubiquitinated bodies, neuronal and astrocytic hyaline inclusions as well as axonal spheroids are protein aggregates that may be related to ER and oxidative stress. This fact is based on the relationship between protein oxidative damage and proteasomal activity following an inverted U shape, i.e. while moderate oxidative

modification of proteins increases their susceptibility for proteasome clearance, higher rates of oxidative modification actually inhibit proteasome activity (Grune *et al.*, 1996; Sitte *et al.*, 2000; Grune *et al.*, 2004). Such a decreased proteasomal activity has been previously recognized in other neurodegenerative processes, and it may explain ALS-characteristic increased ubiquitination and presence of proteinaceous aggregates. The disruption of the ER-associated degradation, a pathway which helps to clear misfolded protein species from ER, is a potential consequence of such proteasomal impairment, finally contributing to ER stress (Marciniak and Ron, 2006; Oyadomari *et al.*, 2006; Zhang and Kaufman, 2006).

Despite these data suggesting the importance of protein oxidative damage in ALS, its study by using selective, chemically characterized markers has not been reported, though immunohistochemical evidences support ALS-induced increased oxidative damage (Ferrante *et al.*, 1997; Pedersen *et al.*, 1998; Shibata *et al.*, 1999; Kato *et al.*, 2000; Kikuchi *et al.*, 2000; Shibata *et al.*, 2000; Kikuchi *et al.*, 2002). Such molecular dissection, allowing quantitative analyses of oxidative pathways should be useful for diagnostic and therapeutic approaches. The use of highly selective mass spectrometry-based techniques could help to further delineate the potential pathogenic role of oxidative stress in ALS. Several markers could be used, such as glutamic semialdehyde (GSA), which derives from the metal-catalysed oxidation of proline and arginine; or amino adipic semialdehyde (AASA) which results from lysine oxidation (Requena *et al.*, 1997, 2001, 2003; Dalfo *et al.*, 2005). Besides these direct modifications of protein structures, the effects of free radical efflux in proteins could also involve third-party molecules which also give rise to increased damage, such as carbohydrates and/or lipids, in processes termed glycooxidation and lipoxidation, respectively (Requena *et al.*, 1997; Baynes, 2003). Both carbohydrates and polyunsaturated fatty acids, when reacting with free radicals generate highly reactive dicarbonyl compounds, such as glyoxal, methylglyoxal, 4-hydroxynonenal and malondialdehyde, among others. These reactive carbonyl compounds can generate specific non-enzymatic adducts when reacting with proteins, such as N^{ϵ} -carboxymethyl-lysine (CML), N^{ϵ} -carboxyethyl-lysine (CEL) and N^{ϵ} -malondialdehyde-lysine (MDAL) (Baynes and Thorpe, 2000). The high content of polyunsaturated fatty acid in central nervous system and its elevated oxygen consumption support the possible significance of lipid peroxidation-derived processes in neurodegeneration, including ALS. However, there is no chemical evidence for lipoxidative or glycooxidative damage of proteins in sporadic or familial ALS based on structural identification and supported by mass-spectrometry.

For these reasons, in this work we have studied the development of ER stress in sporadic ALS. We examined ER stress causal factors such as proteasome function, protein oxidative damage, fatty acid composition and potential disturbances in mitochondrial respiratory

complexes (as the major sources of free radical efflux). These changes have been evaluated in human samples and in lumbar spinal cord organotypic cultures under chronic excitotoxicity, a well-supported model of the sporadic form of ALS (Rothstein *et al.*, 1993).

Patients and methods

Human spinal cord and brain specimens

Brain and spinal cord samples were obtained from the Institute of Neuropathology Brain bank following the guidelines of the local Ethics Committee. The brains and spinal cords of seven men and five age-matched controls (four men and one woman) were obtained from 3 to 6 h after death, and were immediately prepared for morphological and biochemical studies. The agonal state was short with no evidence of acidosis or prolonged hypoxia. The pH of the post-mortem brain was between 7 and 7.4. All ALS patients had suffered from clinical signs and symptoms of lower and upper motorneuron disease, finally involving motor nuclei of the medulla oblongata. Importantly, none of these patients had cognitive impairment or dementia. Although variable from one case to another, the terminal stage of the disease was characterized by predominant bulbar failure manifested as impaired swallowing and usually complicated by aspiration pneumonia, or by dominant respiratory insufficiency. Age-matched controls did not show clinical and neuropathological anomalies. Frozen samples of the spinal cord (lumbar enlargement) and frontal cortex area 8 were used for biochemical studies. Samples of control and diseased spinal cords and brains were processed in parallel. Summary of the main clinical and neuropathological aspects is shown in Table 1.

Organotypic cultures

Spinal cord cultures were prepared from lumbar spinal cord of postnatal day 8 rat pups as previously described (Rothstein *et al.*, 1993) and maintained in 50% minimal essential medium, 25 mM Hepes, 25% Hanks balanced salt solution with D-glucose 25.6 mg/l, 25% heat-inactivated horse serum, 2 mM L-glutamine. Incubation at DIV7 of the slices with the glutamate transport inhibitor D,L-threo-hydroxyaspartate (THA) at 200 μ M injures motorneurons with a morphology typical of excitotoxic degeneration after several weeks of treatment. In selected experiments, slices were also incubated with the ER stress inducers thapsigargin (32 ng/ml) and tunicamycin (500 and 5 ng/ml). After 15 or 30 days of treatment, cultures were harvested and fixed in 4% paraformaldehyde in 0.1 M phosphate buffer, pH 7.4, overnight at 4°C and processed for immunocytochemistry. For western-blot and mass-spectrometric measurements slices were washed with PBS containing 1 mM diethylenetriaminepentaacetic acid and 1 μ M butylated hydroxyl toluene, harvested and frozen at -80° C. Experiments for each condition ($n=30$ slices per experimental group) were repeated at least three times.

Immunohistochemistry

De-waxed sections 5- μ m-thick of the spinal cord were processed for immunohistochemistry following the streptavidin LSAB method (Dako). After incubation with methanol and H₂O₂ in PBS and normal serum, the sections were incubated with anti-phosphorylated eukaryotic initiation factor 2 α (eIF2 α) (1:100,

Table 1 Summary of clinical and pathological data in the present series

Case	Age	Gender	Diagnosis	Duration	Cause of death	p-m delay
1	41	M	ALS	3	Dysphagia, bronchopneumonia	3
2	68	M	ALS	5	Respiratory failure	3
3	76	M	ALS	4	Dysphagia, bronchopneumonia	3
4	69	M	ALS	4	Dysphagia, bronchopneumonia	2
5	40	M	ALS	3	Respiratory failure	2
6	73	M	ALS	4	Dysphagia, bronchopneumonia	4
7	71	M	ALS	4	Respiratory failure	6
8	75	M	Control		Neoplasia	6
9	76	M	Control		Cardiac infarction	4
10	67	F	Control		Cardiac infarction	3
11	51	M	Control		Bronchopneumonia	4
12	68	M	Control		Neoplasia	6

Note: ALS: amyotrophic lateral sclerosis; p-m delay: post-mortem delay (in hours); age and duration are in years.

Abcam, UK). Following incubation with the primary antibody, the sections were incubated with LSAB for 15 min at room temperature. The peroxidase reaction was visualized with diaminobenzidine and H₂O₂. Control of the immunostaining included omission of the primary antibody; no signal was obtained following incubation with only the secondary antibody. Sections were slightly counterstained with haematoxylin.

Confocal immunocytochemistry

The antibodies used are listed in the supplementary information (Table S1). Fluorescein-conjugated *Bandeiraea simplicifolia* lectin (type I) was used as a label for microglia. Appropriate secondary antibodies: Alexa Fluor 488 F(ab)₂ fragment of goat anti-mouse IgG (1:500, Molecular Probes, USA) and Alexa Fluor 546 goat anti-rabbit IgG (1:500, Molecular Probes, USA) were used for immunofluorescence. Image analyses were carried out by a single investigator who was blinded to the experimental conditions. Large (>25 µm in diameter) SMI-32-immunopositive neurons were identified as motorneurons. Immunocytochemical controls were performed by the omission of the primary antibodies, resulting in a negative immunostaining in all cases studied. Mounted slices were examined under a FluoView 500 Olympus confocal laser scanning microscope (Hamburg, Germany).

Protein electrophoresis and western blot

Samples (spinal cord, frontal cortex or organotypic spinal cord cultures) were homogenized in a buffer containing 180 mM KCl, 5 mM 3-[N-morpholino]propanesulfonic acid, 2 mM ethylenediaminetetraacetic acid (EDTA), 1 mM diethylenetriaminepentaacetic acid and 1 µM butylated hydroxyl toluene, 10 µg/ml aprotinin, 1 mM phenylmethylsulfonyl fluoride, pH 7.3 with a Potter-Elvehjem device at 4°C. After a brief centrifugation (500 × g, 5 min) to pellet cellular debris, protein concentrations were measured in the supernatants using the Lowry assay (BioRad Laboratories, München, Germany).

For detection of protein carbonyls, and prior to electrophoresis, samples were derivatized with 2,4-dinitrophenylhydrazine (DNP) as previously described (Pamplona *et al.*, 2005). Briefly, to 15 µl homogenates adjusted to 3.75 µg/µl protein SDS was added to a final concentration of 6%, and, after boiling for 3 min, 20 µl of 10 mM DNP in 10% trifluoroacetic acid were added. After 7 min at room temperature, 20 µl of a solution containing 2 M Tris base, 30% glycerol and 15% β-mercaptoethanol were added for neutralization and sample preparation for loading onto SDS-PAGE gels.

For immunodetection, after SDS-PAGE, proteins were transferred using a Mini Trans-Blot Transfer Cell (BioRad) to PVDF membranes (Immobilon-P Millipore, Bedford, MA). Immunodetection was performed using as primary antibodies those listed in supplementary information (Table S1): (i) for ER stress and proteasome function assessment: anti-KDEL, which recognizes KDEL-sequence containing proteins such as ER chaperones as protein disulfide isomerase (PDI), GRP78 and GRP94; anti-eIF2α anti-GRP78, anti-phosphorylated eIF2α (S52), anti-PDI and anti-ubiquitin; (ii) for protein oxidative damage: anti-DNP antibody, anti-CML, anti-neuroketal and anti-MDAL; and (iii) for mitochondrial studies: anti-NDUFA 9 antibody for respiratory complex I, anti-core II antibody for respiratory complex III and anti-apoptosis inducing factor (AIF) antibody. For detection of primary antibodies, the following peroxidase-coupled secondary antibodies were used: sheep anti-mouse (1:30 000, Amersham, USA); anti-rabbit (1:40 000, Pierce, USA) and anti-goat (1:7500, Abcam, Cambridge, UK) antibodies. Luminescence was recorded and quantified in a Lumi-Imager equipment (Boehringer, Mannheim, Germany), using the Lumianalyst software. Control experiments showed that omission of primary or secondary antibody addition produced blots with no detectable signal.

Measurement of specific, protein-oxidation-derived markers: GSA, AASA, CML, CEL and MDAL

GSA, AASA, CML, CEL and MDAL concentrations in total proteins from spinal cord, frontal cortex or organotypic culture homogenates were measured by isotope-dilution gas chromatography/mass spectrometry (GC/MS) as previously described (Pamplona *et al.*, 2005). Samples containing 500 µg of protein were delipidated using chloroform:methanol (2:1 v/v), and proteins were precipitated by adding 10% trichloroacetic acid (final concentration) and subsequent centrifugation. Protein samples were reduced overnight with 500 mM NaBH₄ (final concentration) in 0.2 M borate buffer, pH 9.2, containing 1 drop of hexanol as an anti-foam reagent. Proteins were then reprecipitated by adding 1 ml of 20% trichloroacetic acid and subsequent centrifugation. The following isotopically labelled internal standards were then added: [²H₈]Lysine (*d8*-Lys; CDN Isotopes); [²H₄]CML (*d4*-CML), [²H₄]CEL (*d4*-CEL) and [²H₈]MDAL (*d8*-MDAL); [²H₅] 5-hydroxy-2-aminovaleric acid (for GSA analysis) and [²H₄]6-hydroxy-2-aminocaproic acid (for AASA analysis). The samples were hydrolysed at 155°C for 30 min in 1 ml of 6 N HCl, and then dried *in vacuo*. The *N,O*-trifluoroacetyl methyl ester derivatives of the protein hydrolysate were prepared and GC/MS analyses were carried out on a Hewlett-Packard model 6890 gas chromatograph equipped with a 30 m HP-5MS capillary column (30 m × 0.25 mm × 0.25 µm) coupled to a Hewlett-Packard model 5973A mass selective detector (Agilent, Barcelona, Spain). The injection port was maintained at

275°C; the temperature program was 5 min at 110°C, then 2°C/min to 150°C, then 5°C/min to 240°C, then 25°C/min to 300°C and finally hold at 300°C for 5 min. Quantification was performed by external standardization using standard curves constructed from mixtures of deuterated and non-deuterated standards. Analytes were detected by selected ion-monitoring GC/MS. The ions used were: lysine and *d8*-lysine, *m/z* 180 and 187, respectively; 5-hydroxy-2-aminovaleric acid and *d5*-5-hydroxy-2-aminovaleric acid (stable derivatives of GSA), *m/z* 280 and 285, respectively; 6-hydroxy-2-aminocaproic acid and *d4*-6-hydroxy-2-aminocaproic acid (stable derivatives of AASA), *m/z* 294 and 298, respectively; CML and *d4*-CML, *m/z* 392 and 396, respectively; CEL and *d4*-CEL, *m/z* 379 and 383, respectively; and MDAL and *d8*-MDAL, *m/z* 474 and 482, respectively. The amounts of products were expressed as the ratio μmol GSA, AASA, CML, CEL or MDAL/mol lysine.

Fatty acid analysis

Distributional analysis of fatty acids was performed as previously described (Dalfó *et al.*, 2005; Pamplona *et al.*, 2005). Total lipids from spinal cord, frontal cortex or organotypic cultures were extracted with chloroform:methanol (2:1, v/v) in the presence of 0.01% butylated hydroxytoluene to avoid artifactual oxidation. The chloroform phase was evaporated under nitrogen, and the fatty acids were transesterified by incubation in 2.5 ml of 5% methanolic HCl for 90 min at 75°C. The resulting fatty acid methyl esters were extracted by adding 2.5 ml of *n*-pentane and 1 ml of saturated NaCl solution. The *n*-pentane phase was separated, evaporated under nitrogen, re-dissolved in 75 μl of hexane and 1 μl was used for GC/MS analysis. Separation was performed in a SP2330 capillary column (30 m \times 0.25 mm \times 0.20 μm) in a Hewlett Packard 6890 Series II gas chromatograph (Agilent, Barcelona, Spain). A Hewlett Packard 5973A mass spectrometer was used as detector in the electron-impact mode. The injection port was maintained at 220°C, and the detector at 250°C; the temperature program was 2 min at 100°C, then 10°C/min to 200°C, then 5°C/min to 240°C and finally hold at 240°C for 10 min. Identification of fatty acid methyl esters was made by comparison with authentic standards and based on mass spectra. Results are expressed as mol%.

From fatty acid composition, the following indexes were calculated: saturated fatty acids (SFA) = $\sum\%$ of saturated fatty acids; unsaturated fatty acids (UFA) = $\sum\%$ of unsaturated fatty acids; monounsaturated fatty acids (MUFA) = $\sum\%$ of monoenoic fatty acids; polyunsaturated *n*-3 fatty acids (PUFAn-3) = $\sum\%$ of polyunsaturated fatty acids *n*-3 series; Polyunsaturated *n*-6 Fatty Acids (PUFAn-6) = $\sum\%$ of polyunsaturated fatty acids *n*-6 series; average chain length (ACL) = $[(\sum\% \text{Total}_{14} \times 14) + \dots + (\sum\% \text{Total}_n \times n)] / 100$ (*n* = carbon atom number); peroxidizability index (PI) = $[(\sum \text{mol\% Monoenoic} \times 0.025) + (\sum \text{mol\% Dienoic} \times 1) + (\sum \text{mol\% Trienoic} \times 2) + (\sum \text{mol\% Tetraenoic} \times 4) + (\sum \text{mol\% Pentaenoic} \times 6) + (\sum \text{mol\% Hexaenoic} \times 8)]$.

Statistical analyses

All statistics were performed using the SPSS software (SPSS Inc., Chicago, IL). Once normality of distribution was assessed by Kolmogorov–Smirnov test, differences between groups (ALS samples versus control; THA treated versus vehicle) were analysed by the Student's *t*-tests and correlations between variables were evaluated by the Pearson's statistic. The 0.05 level was selected as the point of minimal statistical significance in every comparison.

Results

Samples from ALS patients evidence signs of ER stress: proteasomal impairment as a potential mechanism

Since ER stress has been implied in ALS experimental models we examined signs of ER stress by western-blot and immunohistochemistry in samples from ALS patients. The results demonstrated ER stress in ALS samples (Fig. 1). Thus, increased expression of chaperones PDI and KDEL-containing proteins were found in spinal cord from ALS patients (Fig. 1A), but not in frontal cortex samples (not shown). This was accompanied by a marked increase in eIF2 α phosphorylation (a sign of protein synthesis control after ER stress), both in spinal cord lysates (Fig. 1A) and in remaining neuronal bodies in spinal cord (Fig. 1B).

As proteasome is responsible for degradation of ER misfolded proteins, we examined whether its function was preserved. Accounting that ubiquitin-modified proteins are degraded by the proteasome, its function can be inferred by western-blot and immunohistochemical analyses of ubiquitin-modified proteins. The results of such approach showing increased protein ubiquitination in spinal cord from ALS patients, but not in frontal cortex, are compatible with compromised proteasomal function (Fig. 1C). It should be also considered that increased protein turnover due to massive protein degradation could saturate the ubiquitin-proteasome system in spite of proteasome preserved activity.

Proteins from spinal cord and frontal cortex present structurally characterized oxidation products and the amount of these modifications increases with ALS, favoured by changes in fatty acid composition

While moderate oxidative modification of proteins increases their susceptibility for proteasome clearance, higher rates of oxidative modification actually inhibit proteasome activity. Therefore, we evaluated protein oxidative damage in spinal cord and frontal cortex samples, to ascertain whether proteasomal dysfunction could be related to increased protein oxidative damage. GC/MS analyses demonstrated that those proteins contained oxidation-derived products resulting from metal-catalysed oxidation, glycooxidation and lipoxidation. The more abundant products were those derived from metal-catalysed oxidation, AASA and GSA assuming almost 95% of measured markers. GSA stood as the more frequent modification, with levels being 30-fold higher than those of AASA. The concentrations of both GSA and AASA were significantly higher in proteins from spinal cord ($P < 0.001$) and frontal cortex ($P < 0.01$) samples of ALS patients than in control age-matched individuals (Fig. 2A). Similarly to specific oxidation products, the concentrations of CEL and CML, glycooxidation products, were also significantly higher in

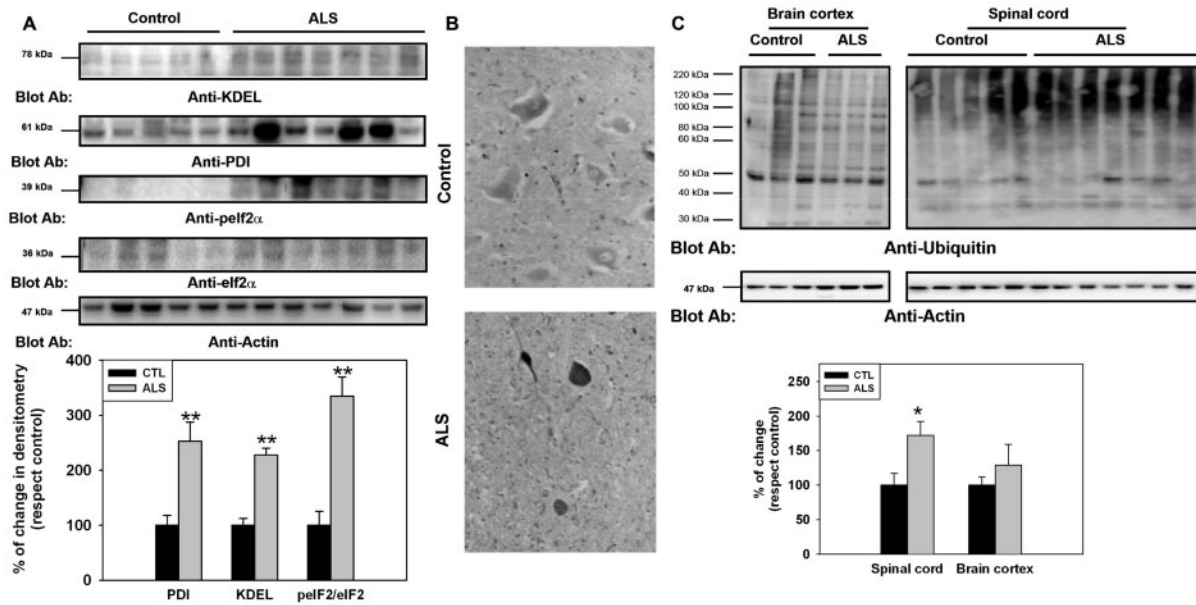


Fig. 1 ER stress and protein ubiquitination in spinal cords from ALS patients. **(A)** Representative western blot of spinal cord homogenates showing increased content of ER resident proteins containing KDEL motifs, PDI and phosphorylated eIF2 α in samples from ALS patients. **(B)** Representative immunohistochemical image of phosphorylated eIF2 α in the motor column of human lumbar spinal cords, showing increased staining in ALS samples. **(C)** Representative western blot of anti-ubiquitin, suggesting decreased ubiquitin degradation in spinal cord samples from ALS patients and control individuals, but not in frontal cortex. Right numbers of the blot indicate apparent molecular weight. Immunoblotting of actin is also shown. The lower panels shows the quantitation of those blots by densitometry, adjusted to actin content and differences were analysed respect to control group by Student's *t*-test being **P* < 0.01 and ***P* < 0.001.

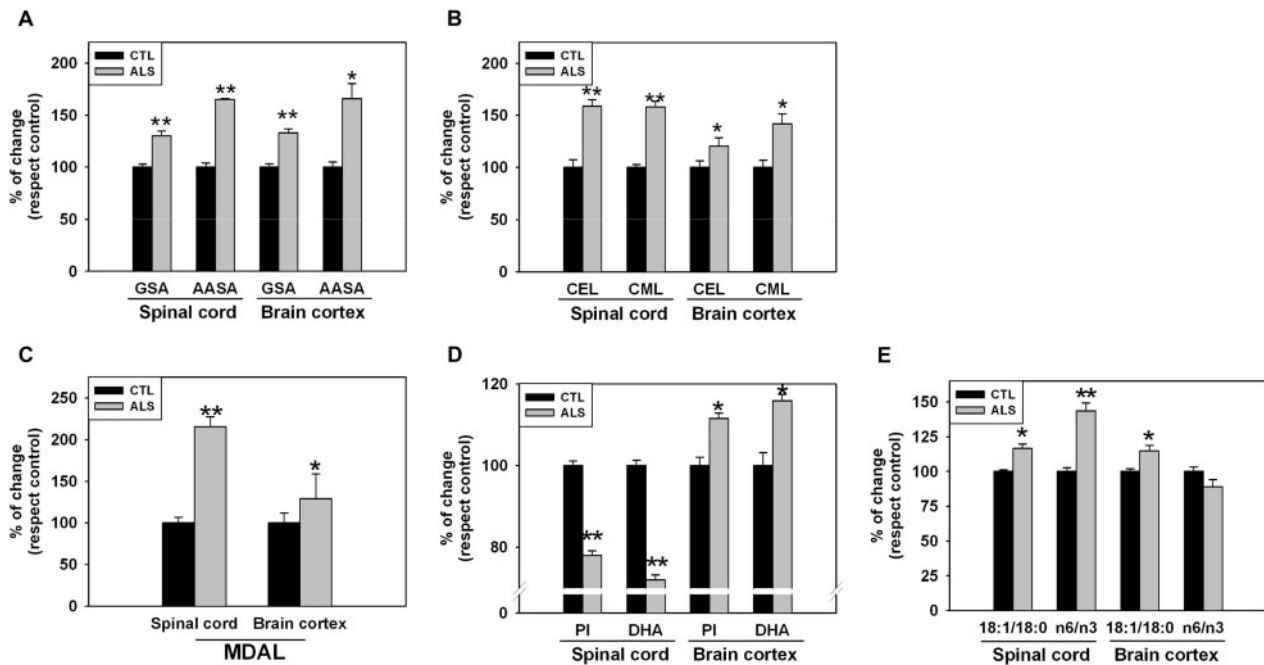


Fig. 2 Proteins from ALS samples show significant increases in the amounts of oxidation markers and changes in fatty acid composition. **A–C** show GC/MS analyses of GSA and AASA (markers of MCO), CML and CEL (arising from glycooxidation and lipoxidation) and MDAL, originated from lipoxidation. **(D)** Changes in PI and DHA levels associated with ALS in spinal cord differ from those present in frontal cortex. **(E)** ALS also leads to organ-specific changes in desaturation indexes (18:1/18:0) and *n*6/*n*3 ratios. Values shown are % changes of mean \pm SE over values from control samples (in spinal cord GSA: 21498 \pm 619 μ mol/mol lysine; AASA: 102 \pm 7 μ mol/mol lysine; CEL: 385 \pm 57 μ mol/mol lysine; CML: 521 \pm 30 μ mol/mol lysine and MDAL: 258 \pm 48 μ mol/mol lysine; PI: 116.24 \pm 4.23; DHA: 10.89 \pm 0.20%; 18:1/18:0 ratio: 1.36 \pm 0.025; *n*6/*n*3 ratio: 0.67 \pm 0.04; in frontal cortex GSA: 20512 \pm 638 μ mol/mol lysine; AASA: 82 \pm 4 μ mol/mol lysine; CEL: 249 \pm 16 μ mol/mol lysine; CML: 522 \pm 37 μ mol/mol lysine MDAL: 197 \pm 6 μ mol/mol lysine; PI: 155.31 \pm 1.55; DHA: 12.35 \pm 0.17; 18:1/18:0 ratio: 0.75 \pm 0.01; *n*6/*n*3 ratio: 1.1 \pm 0.034). **P* < 0.01 and ***P* < 0.001 respect to control group by Student's *t*-test.

Table 2 Fatty acid composition (mol%) of total lipids from spinal cord and frontal cortex

	Frontal cortex CTL	ALS	P<	Spinal cord CTL	ALS	P<
14:0	0.50 ± 0.03	0.59 ± 0.05	0.234	0.49 ± 0.04	0.58 ± 0.01	0.112
16:0	24.57 ± 0.48	23.97 ± 0.35	0.352	14.61 ± 0.25	15.47 ± 0.23	0.02
16:1n-7	1.63 ± 0.15	1.64 ± 0.25	0.980	1 ± 0.07	1.53 ± 0.15	0.005
18:0	25.20 ± 0.40	22.92 ± 0.39	0.007	23.95 ± 0.23	22.34 ± 0.68	0.027
18:1n-9	19.09 ± 0.15	19.90 ± 0.45	0.141	30.15 ± 0.25	32.82 ± 0.25	0.001
18:2n-6	1.02 ± 0.28	0.77 ± 0.13	0.458	0.33 ± 0.03	0.62 ± 0.05	0.001
18:3n-3	n.d	n.d	–	0.24 ± 0.02	0.27 ± 0.001	0.254
20:0	0.88 ± 0.20	0.57 ± 0.04	0.190	7.05 ± 0.43	6.28 ± 0.25	0.117
20:1	n.d	n.d	–	0.54 ± 0.03	0.78 ± 0.07	0.016
20:2n-6	0.47 ± 0.16	0.29 ± 0.07	0.345	0.31 ± 0.03	0.31 ± 0.05	0.997
20:3n-6	0.36 ± 0.04	0.25 ± 0.05	0.210	0.6 ± 0.08	0.98 ± 0.25	0.137
20:4n-6	7.39 ± 0.23	8.70 ± 0.22	0.007	2.9 ± 0.17	3.15 ± 0.11	0.508
22:4n-6	4.16 ± 0.22	3.78 ± 0.42	0.460	2.86 ± 0.05	3.05 ± 0.14	0.289
22:5n-6	0.72 ± 0.14	0.66 ± 0.18	0.794	0.27 ± 0.03	0.22 ± 0.03	0.173
22:5n-3	0.17 ± 0.01	0.20 ± 0.01	0.170	0.14 ± 0.02	0.19 ± 0.03	0.118
24:0	0.61 ± 0.07	0.54 ± 0.04	0.466	0.91 ± 0.13	0.81 ± 0.15	0.600
24:1n-9	0.47 ± 0.14	0.56 ± 0.05	0.557	2.26 ± 0.10	2.23 ± 0.10	0.793
ACL	18.41 ± 0.02	18.49 ± 0.02	0.055	18.67 ± 0.01	18.51 ± 0.01	0.001
SFA	51.78 ± 0.58	48.60 ± 0.56	0.008	46.21 ± 0.37	44.55 ± 0.65	0.001
UFA	48.21 ± 0.58	51.39 ± 0.56	0.008	52.59 ± 0.35	54.92 ± 0.45	0.001
MUFA	21.20 ± 0.04	22.11 ± 0.73	0.263	33.84 ± 0.31	37.6 ± 0.46	0.001
PUFA	27.00 ± 0.58	29.28 ± 0.60	0.037	18.7 ± 0.22	16.61 ± 0.4	0.002
PUFA n-6	14.13 ± 0.33	14.47 ± 0.69	0.676	7.46 ± 0.18	8.39 ± 0.19	0.005
PUFA n-3	12.87 ± 0.40	14.81 ± 0.22	0.006	11 ± 0.15	8.63 ± 0.12	0.001
DBI	152.18 ± 2.68	166.92 ± 1.70	0.004	127.82 ± 1.58	119.69 ± 1.59	0.003

Note: Values: mean ± SEM. N × group: for brain cortex (n = 4); for spinal cord (n = 5 for control and n = 7 for ALS). ACL, average chain length; SFA, saturated fatty acids; UFA, unsaturated fatty acids; PUFA n-6/n-3, polyunsaturated fatty acids n-6 or n-3 series; MUFA, monounsaturated fatty acids; DBI, double bond index; Docosahexaenoic acid levels are shown in Fig. 1.

proteins from spinal cord ($P < 0.001$) and frontal cortex ($P < 0.01$) of ALS patients than in control individuals (Fig. 2B). The concentration of MDAL, a lipoxidation product, was also increased in samples from ALS patients, both in spinal cord ($P < 0.001$) and in frontal cortex ($P < 0.01$) compared to control individuals (Fig. 2C). Nonetheless, the magnitude of difference between ALS and control samples was considerably higher in spinal cord (120%) than in frontal cortex (50%).

As fatty acid profile strongly influences membrane peroxidizability, and consequently protein lipoxidative damage, we analysed fatty acid content in ALS samples. Those analyses revealed significant differences associated with ALS in spinal cord and frontal cortex, both in individual fatty acids and in global indexes (Table 2). The most remarkable change involves the highly peroxidizable docosahexaenoic acid (DHA), which showed a significant decrease in spinal cord samples with ALS ($P < 0.01$), contrasting with the significant increase observed in frontal cortex ($P < 0.01$; Fig. 2D). With reference to the fatty-acid-derived indexes, spinal cords from ALS patients showed significant decreases in the content of PUFA of the n-3 family ($P < 0.001$; Table 2), while increases of this parameter were detected in frontal cortex ($P < 0.006$; Table 2). Changes in fatty acid profile led

to significant changes in double bond index ($P < 0.004$; Table 2), PI ($P < 0.003$; Fig. 2D), $\Delta 9$ -desaturase estimation ($P < 0.01$; Fig. 2E) and n6/n3 ratio ($P < 0.001$; Fig. 2E). Overall, these indexes could reflect the potential vulnerability of membranes to peroxidative damage. Since changes in double bond and PI in spinal cord were inverse to those observed in frontal cortex, these data suggest that spinal cord membranes are actively producing substrates for peroxidative modification of proteins, while as frontal cortex are not under this circumstance. Accordingly, analysis of MDAL/PI ratio, suggest that for a given PI, rates of MDAL formation are 3-fold higher in spinal cord than in frontal cortex from ALS patients.

Different kinds of protein oxidative damage are correlated together and are associated to changes in fatty acid content

After quantitations of protein oxidation and fatty acid analyses, several significant correlations were present among anatomically different locations (Fig. 3). GSA levels correlated significantly with AASA ($r = 0.918$; $P < 0.0001$; Fig. 3A), with MDAL ($r = 0.865$; $P < 0.0001$; Fig. 3B), with CEL ($r = 0.716$; $P < 0.002$) and with CML ($r = 0.878$; $P < 0.0001$). This suggests that protein carbonyl formation

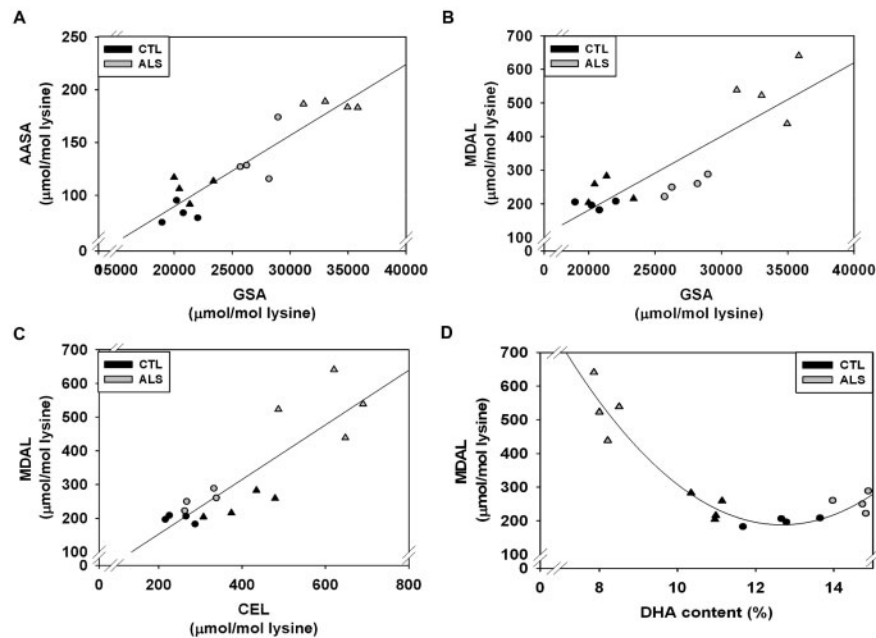


Fig. 3 Changes in protein oxidation indexes and fatty acid contents are strongly correlated. Indexes of protein carbonyl GSA and AASA are strongly correlated (upper panel, left; $r = 0.92$; $P < 0.0001$). Protein oxidative damage is also correlated with protein lipoxidative damage (upper panel, right; $r = 0.865$; $P < 0.0001$). Protein lipoxidative damage is correlated to glycoxidative modifications (lower panel, left; $r = 0.865$; $P < 0.0001$). DHA content shows a quadratic relationship with protein lipoxidative damage (lower panel, right; $r = 0.95$; $P < 0.0001$; model: $[\text{MDAL}] = 17.3 * [\text{DHA}]^2 - 440.3 * [\text{DHA}] + 2977$). Triangles (%) represent values from spinal cord samples and circles (○) represent values from frontal cortex. Results are only shown for those samples where both frontal cortex and spinal cord were available ($n = 4$ for each group).

is also associated to glycoxidative and lipoxidative modifications in spinal cord and frontal cortex. Furthermore, peroxidizability index was inversely correlated with CEL ($r = -0.816$; $P < 0.0001$) and MDAL ($r = -0.685$; $P < 0.003$) concentrations, suggesting an association between lipid peroxidizability, glycoxidation and lipoxidation modifications. Interestingly, levels of MDAL display a second-order relationship with DHA levels ($r = 0.961$; $P < 0.0001$; Fig. 3D), suggesting an intimate interplay between these two factors.

Protein oxidative damage, showing preferential targets in ALS spinal cord proteins can be associated to mitochondrial disturbances

It is known that an important determinant for oxidative damage of proteins, besides fatty acid content, is the mitochondrial free radical production. Therefore, we analysed the expression of representative subunits of mitochondrial respiratory complexes I and III, whose activity is counted among the major sources for mitochondrial free radical production (Herrero and Barja, 2000; Chen *et al.*, 2003), as well as the levels of AIF, shown recently to enhance the functional stability of complex I (Vahsen *et al.*, 2004). These analyses demonstrated that both complex I and III concentrations are significantly decreased in spinal cord samples from ALS patients ($P < 0.01$; Fig. 4A) while AIF expression is not changed in ALS (Fig. 4A). Reinforcing an apparently different pace of

ALS-induced changes between frontal cortex and spinal cord, these effects were not present in frontal cortex from ALS patients (data not shown).

Western-blot analyses of frontal cortex and spinal cord proteins showed differences in the distribution of oxidation (DNP-reactive), glycoxidation (anti-CML) and lipoxidation-derived (anti-neuroketal) protein modifications (Fig. 4B) supporting both diversity and specificity of protein oxidative damage. These findings agree with quantitative analyses by GC/MS as densitometric measurements revealed increased oxidative damage in ALS samples. Major targets of glycoxidation were proteins with apparent molecular weights ranging from 35 to 55 kDa, partially coincident with anti-DNP immunoreactivity (which was also evident for high-molecular weight bands). This pattern differs from targets of neuroketal formation (Fig. 4B), which showed more discrete targets (being targets of 40 and 60 kDa the more prominent). These differences were not present in frontal cortex samples (data not shown).

Chronic excitotoxicity in organotypic spinal cord cultures leads ER stress, ubiquitin alterations, protein oxidative damage and changes in fatty acid profile

Chronic excitotoxicity has been implied in the pathogenesis of ALS (Rothstein *et al.*, 1993; Boillee *et al.*, 2006). This can be reproduced *in vitro* by treatment with the pre-synaptic

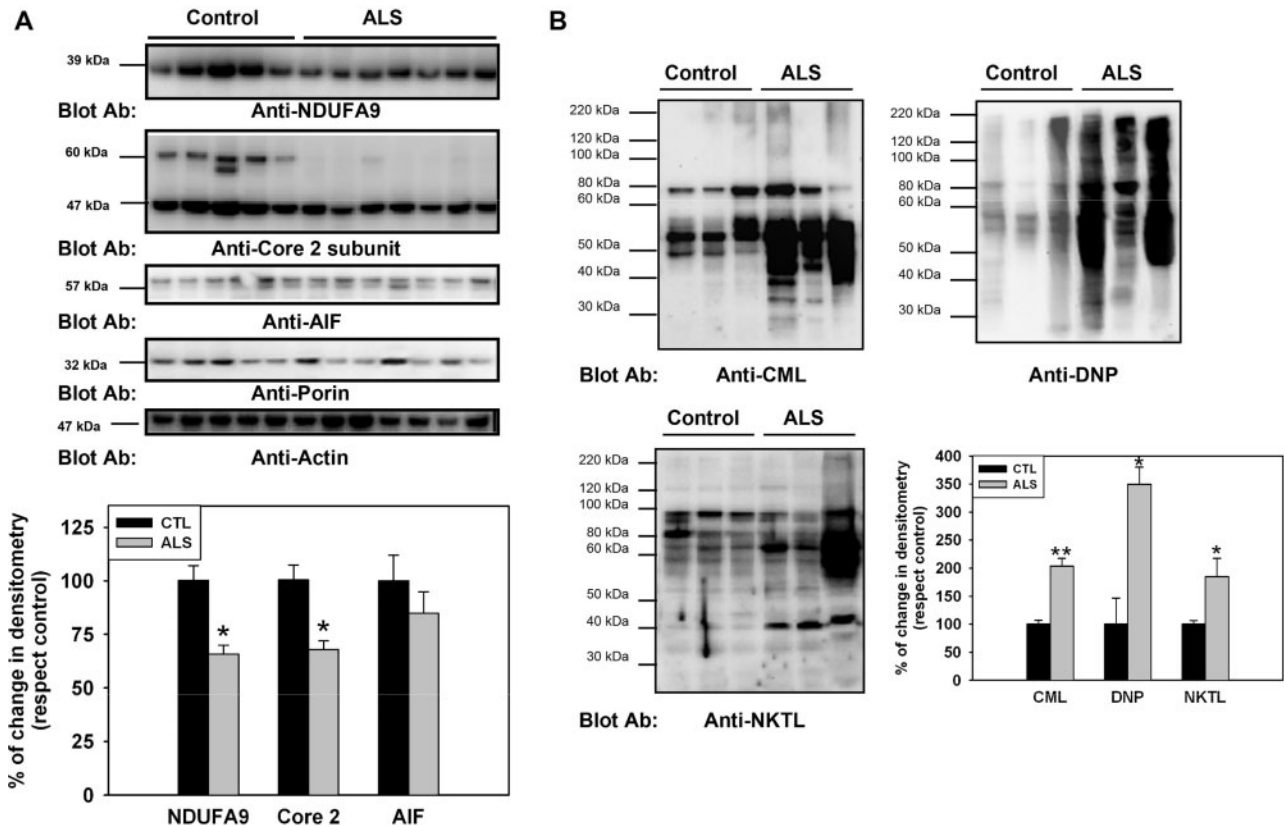


Fig 4 ALS-induced mitochondrial changes and protein-oxidation-specific targets in spinal cord. **(A)** Representative western blot of peptides NDUFA9 and core 2 subunits of mitochondrial respiratory chain complexes I and III, respectively, suggesting decreased complex III content in spinal cord samples from ALS patients compared to control individuals. This was not associated with increased amount of apoptosis-inducing factor (AIF). The lower panel shows the quantitation of these blots by densitometry, adjusted to porin density and differences were analysed respect to control group by Student's *t*-test being $*P < 0.01$. **(B)** Western blot for mixed glycoxidation/lipoxidation (CML), MCO (DNP) and lipoxidation [neuroketal (NKTL)] revealed differential targets for each of these oxidative pathways. Right numbers of the blots indicate apparent molecular weight. The lower panels show the quantization of these blots by densitometry, after densities of bands (ranging between 30 and 220 kDa) or actin (not shown, for B), and differences were analysed respect to control group by Student's *t*-test being $*P < 0.01$ and $**P < 0.001$.

glutamate transport inhibitor THA, leading to losses in the number of motoneurons, as assessed by SMI-32 immunoreactivity (data not shown). In accordance to findings in ALS samples, signs of ER stress were also found in spinal cord slices under chronic excitotoxicity after a 30-day period (Figs. S1A and S2A). Although eIF2 α phosphorylation was present in neuronal bodies of vehicle-treated slices, increased immunoreactivity was found along neuritic processes as well as in small cellular populations morphologically compatible with glia on THA-treated slices. Furthermore, demonstration of a markedly increased intracellular ubiquitin immunoreactivity excluding nucleus (Fig. S1B) suggest a role of proteasomal dysfunction in this phenomena at an earlier stage. Furthermore, incubation with the ER stress inducing agents tunicamycin and thapsigargin led to increases in chaperone expression (Fig. S2A) and to a marked decrease in the number of motoneurons, suggesting its preferential sensitivity to ER stress (Fig. S2B).

Since those analyses revealed ER stress and proteasome dysfunction in chronic excitotoxicity, we analysed whether

protein oxidative damage was also increased in these conditions. The results demonstrated that protein oxidative damage is increased by excitotoxicity (Fig. S3). All measured markers of oxidation, glycoxidation and lipoxidation, increased significantly after THA treatment ($P < 0.001$, Fig. S3A). As in the ALS cases, these increases in protein oxidative modifications were associated to changes in fatty acid composition (Table S2, Fig. S3B). Noteworthy, THA-induced changes resembled those present in frontal cortex, with 2-fold increases in the DHA content ($P < 0.0001$, Fig. S3B), PI increases—150% respect vehicle-treated slices—($P < 0.0001$, Fig. S3B) and decreased *n6/n3* ratios ($P < 0.0001$, Fig. S3B). Confocal microscopy of the most THA-sensitive marker, CEL, revealed that proteins modified with this product were present, in increased amounts, throughout glial and neuronal populations (Fig. S3C). Neuropil and star-shaped cells resembling microglia were major distribution sites of CEL immunoreactivity in THA-treated slices. Co-localization studies with *Bandiraea Simplicifolia* lectin supported the microglial origin of some of those cells (Fig. S3C).

Nevertheless, chronic excitotoxicity also led to increased AIF immunoreactivity in a non-nuclear distribution, suggesting common basis for mitochondrial dysfunction between sporadic ALS and chronic excitotoxicity both in neuronal and glial cells (Fig. S1C).

Discussion

Cells facing protein misfolding in the ER initiate the so-called unfolded protein response. As a part of this unfolded protein response, the initiation process in global protein synthesis is repressed by eIF2 α phosphorylation via PERK kinase. There is also increased expression of ER chaperones and, if ER stress cause is not corrected, apoptosis is induced (Marciniak and Ron, 2006; Zhang and Kaufman, 2006). The results reported here, showing both increased phosphorylation of eIF2 α and increased expression of ER chaperones (PDI and KDEL-containing proteins), strongly support the participation of ER stress in ALS pathogenesis. The relevance of this pathway was also evident in the chronic excitotoxicity paradigm, where both motorneurons and glial cells were stained for anti-phosphorylated eIF2 α . Noteworthy, the importance of this pathway is also demonstrated by immunohistochemical analyses, where remaining neuronal bodies of spinal cord ventral horns in ALS show intense anti-phosphorylated eIF2 α . Our data suggest that ER stress arises from oxidative stress and from a mitochondrial disturbance. Based on correlative data, we propose that this is a late phenomenon, when compared with protein oxidative damage, as we are able to detect increased protein oxidative damage, increased DHA amount and other fatty acid changes in brain cortex, without increased ubiquitination or any other noticeable change. Recent data demonstrates the occurrence of ER stress in familial ALS paradigms, associating PDI and mutated SOD in motorneurons (Atkin *et al.*, 2006; Furukawa *et al.*, 2006), showing also caspase-12 activation (Wootz *et al.*, 2004; Turner and Atkin, 2006). More interestingly, chronic excitotoxicity leads to protein aggregation in ER from motorneurons (Tarabal *et al.*, 2005), without inducing an upregulation of heat-shock proteins, as those cells have a characteristically high threshold for heat-shock proteins induction (Batulan *et al.*, 2003). This fact, when added to the increased chaperone expression and immunohistochemical data on organotypic cultures, strongly suggest that ER stress is also taking place in glial cells. Due to the important role of the proteasome in ER-directed disposal of misfolded proteins, ER stress could be caused by decreased ER-associated degradation (Bush *et al.*, 1997; Obeng *et al.*, 2006; Yamamuro *et al.*, 2006).

In agreement with our findings, previous data indicate a potential loss of proteasome activity in ALS (Urushitani *et al.*, 2002; Cheroni *et al.*, 2005; Ahtoniemi *et al.*, 2006; Basso *et al.*, 2006; Kabuta *et al.*, 2006; Koyama *et al.*, 2006; Mendonca *et al.*, 2006), specially in the familial forms of the disease. *In vitro* experiments and *in vivo* data show that

mutated SOD is associated with decreased amount of specific proteasome subunits, particularly LMP7 (Allen *et al.*, 2003). Furthermore, proteasome inhibition leads to the reproduction of the abnormal solubility properties shown by mutated SOD *in vivo* (Koyama *et al.*, 2006). However, the role of proteasome in sporadic ALS has received less attention. Recent data demonstrate increased proteasome immunoreactivity both in glia and motorneurons from spinal cords in sporadic ALS (Mendonca *et al.*, 2006). Accordingly, findings reported here, demonstrating increased amount of ubiquitinated proteins in spinal cord samples, is compatible to such proteasomal involvement. It should be recalled that ubiquitinated lesions are prominent in ALS morphology. Noteworthy, this increased ubiquitination was also evident under chronic excitotoxicity, being present both in neuronal and non-neuronal populations. This agrees with the previous works, showing that proteasome inhibition in organotypic cultures induce selectivity damage to motorneurons, as chronic excitotoxicity does (Tsuji *et al.*, 2005). As chronic excitotoxicity leads to increased oxidative damage (Rao and Weiss, 2004; Rival *et al.*, 2004), our data suggest that this condition could contribute to proteasome inhibition. Relating differences with frontal cortex, western-blot analyses did not reveal such changes in this latter location. Once a given protein is modified by oxidation, it is degraded by 20S proteasome in an ATP and ubiquitin-independent fashion (Shringarpure *et al.*, 2003; Grune *et al.*, 2005), as recently shown for metal-free SOD (Di Noto *et al.*, 2005). Nevertheless, a high degree of oxidative modification could even decrease proteasome activity (Sitte *et al.*, 2000).

For these reasons we evaluated whether, by using novel mass spectrometry measurements, ALS samples presented increases in protein oxidative damage, both in spinal cord and in frontal cortex. Nonetheless, the magnitude of changes with reference to control was higher in spinal cord than in frontal cortex. These results suggest an early selective involvement of oxidative stress in spinal cord during ALS pathogenesis. In addition, the involvement of frontal cortex agrees with previous reported data in other neurodegenerative diseases, such as Alzheimer disease or Parkinson disease, where pathologically preserved locations of nervous system show incipiently increases in protein oxidative damage, thought at a lower extent than classical targets of disease (Dalfo *et al.*, 2005; Pamplona *et al.*, 2005). Cognitive dysfunction and dementia have been reported as complications in a subgroup of patients with ALS, the majority of them presenting atrophy, neuronal loss and reactive gliosis in the frontal and temporal lobes (Kato *et al.*, 2003). Although the present study is not focused on ALS cases with frontotemporal dementia, these results point to the suggestion that frontal cortex is a vulnerable region to ALS. As a working hypothesis it can be proposed that modifications in the levels of certain lipids are predisposing factors to further cellular damage. Nevertheless, data presented here support the notion that

lipid peroxidation-associated processes seem to be the more sensible cellular oxidative phenomenon, based on MDAL values. Previous immunohistochemical evidences demonstrate increased lipid peroxidation in ALS (Hall *et al.*, 1998; Pedersen *et al.*, 1998). Furthermore, recent data showing accumulation of 4-oxo-2-nonenal DNA etheno adduct in brain cortex from ALS patients support the importance of lipid peroxidation-derived pathways (Shibata *et al.*, 2006). Interestingly, while PI is still increased in frontal cortex, basically due to increases in DHA content, a potential defensive response of nervous tissue (Akbar *et al.*, 2005), these indexes were decreased in spinal cord, suggesting a functional collapse and/or a lower content of neurons. Thus, while brain cortex could produce *n*-3-derived anti-inflammatory resolvins and docosatrienes (Hong *et al.*, 2003), spinal cord neurons would have decreased DHA availability due to increased lipoxidative consumption. Rather than being a general phenomena, the selectivity for changes in *n*-3 strongly suggest specific mechanisms of the disease depending on these fatty acids, maybe affecting biosynthetic pathways and/or membrane remodelling systems that deserve further studies. Nonetheless, long-chain unsaturated fatty acids contribute to the formation of cytotoxic aggregates of ALS-linked superoxide dismutase-1, thereby stressing the importance of fatty acid changes in ALS pathogenesis (Kim *et al.*, 2005). To shed further light on these issues we analysed a chronic excitotoxicity paradigm. The results demonstrated—at an early stage of the excitotoxic paradigm—changes partially resembling those present in frontal cortex, e.g. increases in all oxidative markers and increases in DHA content and PI. This was present at a time when motorneuron death is still not evident. In line with this, DHA induces resistance against excitotoxic degeneration of cholinergic neurones *in vivo*, leading to higher survival, lower dendritic involution and decreased axon degeneration (Hogyes *et al.*, 2003). Globally, these results suggest a pathological spectrum, driven by excitotoxicity, ranging between overt pathological manifestation (present in spinal cord) and more subtle changes, with variations in fatty acids as reactive changes and protein oxidative modifications as important signals of disease.

The significant correlations found between different types of protein oxidative damage suggest that ALS could influence general mechanisms determining protein oxidative modifications, such as free radical production (Pamplona and Barja, 2006). In most cells, the major sources of free radical production are mitochondrial respiratory complexes I and III (Herrero and Barja, 2000) although in brain some mitochondrial matrix enzymes also contribute to free radical production (Starkov *et al.*, 2004; Tretter and Adam-Vizi, 2004). The analyses performed in spinal cords suggest decreases in both respiratory complexes, as well to qualitative changes in complex III distribution. Due to the role of complex I and III as free radical generators (Chen *et al.*, 2003), the results may be compatible with increased free radical efflux by incorrect

assembly of complexes or to metabolic reprogramming (Iuso *et al.*, 2006). These data complements previous reports demonstrating decreased activities of respiratory chain complexes I+III, II+III and IV, suggesting a loss of mitochondria in spinal cords from ALS patients (Wiedemann *et al.*, 2002). Moreover, specific decreases in the activities of complexes II are observed in a mutated SOD transgenic model (Jung *et al.*, 2002). Furthermore, losses of complex IV activity are present in the *Wobbler* mouse (Xu *et al.*, 2001). It may be suggested that ALS samples presented a defect in the assembly of mitochondrial respiratory complexes, that would lead to changes in free radical production (Rana *et al.*, 2000; Sellem *et al.*, 2005). It may be also hypothesized that this scenario could contribute to a more reduced state of Fe-S clusters, leading to increased free radical efflux (Herrero and Barja, 2000). In this line, the amount of AIF, a bifunctional flavoprotein with NADH oxidase activity involved in mitochondrial respiration and caspase-independent apoptosis, was unchanged in spinal cords. Besides an ALS-induced increased apoptotic rate in this tissue (Oh *et al.*, 2006), AIF could be also considered as a part of an adaptation response to increased free radical production (Zhu *et al.*, 2003; Cande *et al.*, 2004) or to decreased respiratory activities. Changes in AIF are not evident in ALS samples when compared to data in the *in vitro* paradigm: AIF presenting increased non-nuclear staining in THA-treated slices suggests an important role of this protein in the response to excitotoxicity, that may be focus of future studies. Therefore, it could be suggested that increased free radical production, arising from complex I and III suboptimal assembly, together with unchanged or even increased AIF expression, contributes to protein oxidative damage specifically in spinal cords, being those changes absent in frontal cortex. Despite such an increased mitochondrial leak could lead to potentially extensive protein modifications, western-blot analyses revealed that there are specific targets for oxidative, glycoxidative and lipoxidative damage that will be the focus of future studies.

To summarize, the present data demonstrate that there is increased protein oxidative modification in spinal cords and frontal cortex from ALS cases, together with changes in lipid composition. Concerning cellular targets of those phenomena, we have demonstrated a motorneuron involvement, but it should be remarked that glial cells are the major contributors to protein mass in spinal cords. Therefore, it is feasible to assume that many of the changes observed here respond to changes in both (or mainly) glial cell and neuronal populations. In this line, it should be recalled the importance of glial support and trophic environment for motorneurons, so any given change to glial population could contribute to motorneuron loss. In spinal cords, where loss of motorneurons was evident, build up of oxidatively damaged proteins was linked to changes in mitochondrial respiratory complexes and to increased ubiquitination, potentially linked to impaired

proteasome function. More importantly, this was associated to changes in ER proteins suggesting the occurrence of ER stress. Since those changes were reproducible by an excitotoxic paradigm at an early stage, it can be suggested that excitotoxicity leads to increased protein oxidation, proteasomal dysfunction and ER stress in neuronal and non-neuronal cells, potentially contributing to motor-neuron death in ALS.

Supplementary material

Supplementary material is available at *Brain* online.

Acknowledgements

We are fully indebted to tissue donors and their families. We thank David Argiles for excellent technical assistance. We are deeply thankful to Dr Jesus Requena (from the Universidad de Santiago de Compostela, Spain) for providing us with GSA and AASA standards and to Dr Josep Esquerda for thoughtful discussion.

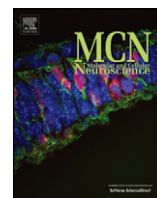
This study was supported in part by I+D grants from the Spanish Ministry of Education and Science (BFU2006-14495/BFI) and the Generalitat of Catalunya (2005 SGR00101) to R.P.; the Spanish Ministry of Health (FIS 04-0355, 05-2214 and 05-2241), Spanish Ministry of Education and Science (AGL2006-12433), the ALS Association (USA) and "La Caixa" Foundation to M.P.O. and E.D., E.I. (a predoctoral fellow from the Generalitat) and D.C.; and FIS grants PI04-0184 and PI05-1570, and support by the European Commission under the Sixth Framework Programme (BrainNet Europe II, LSHM-CT-2004-503039) to I.F. Supported by the COST B-35 Action.

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Calpain activation and CaMKIV reduction in spinal cords from hSOD1G93A mouse model



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ARTICLE INFO

Article history:

Received 24 October 2013

Revised 17 July 2014

Accepted 21 July 2014

Available online 22 July 2014

Keywords:

ALS

Neurodegeneration

Intracellular calcium

CaMKIV

Calpain

hSOD1G93A

ABSTRACT

Amyotrophic Lateral Sclerosis (ALS), a severe neurodegenerative disease, affects the upper and lower motor neurons in the brain and spinal cord. In some studies, ALS disease progression has been associated with an increase in calcium-dependent degeneration processes. Motoneurons are specifically vulnerable to sustained membrane depolarization and excessive elevation of intracellular calcium concentration. The present study analyzed intracellular events in embryonic motoneurons and adult spinal cords of the hSOD1G93A ALS mouse model. We observed activation of calpain, a calcium-dependent cysteine protease that degrades a variety of substrates, and a reduction in calcium-calmodulin dependent protein kinase type IV (CaMKIV) levels in protein extracts from spinal cords obtained at several time-points of hSOD1G93A mice disease progression. However, in cultured embryonic motoneurons these differences between controls and hSOD1G93A mutants are not evident. Our results support the hypothesis that age-dependent changes in calcium homeostasis and resulting events, e.g., calpain activation and CaMKIV processing, are involved in ALS pathogenesis.

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Introduction

Amyotrophic Lateral Sclerosis (ALS) is a fatal, adult-onset, neurodegenerative disease causing the degeneration of cranial and spinal cord motor neurons (MNs), which leads to muscle atrophy and paralysis. Numerous ALS studies have analyzed subgroups of familial cases originating from mutations in the SOD1 gene (Rosen et al., 1993). The precise mechanisms whereby mutant SOD1 is toxic to MNs are not defined. However, studies in mutant hSOD1 transgenic mice have revealed many pathogenic changes in degenerating MNs, including hyperexcitability, disturbed calcium homeostasis, SOD1 aggregation, and activation of cell death signals (Bento-Abreu et al., 2010; Cleveland and Rothstein, 2001; Pasinelli and Brown, 2006). Several of these pathogenic changes are related to calcium deregulation in neurons. Unfortunately,

whether these are primary or secondary events or represent compensatory mechanisms remains unknown.

MNs are specifically vulnerable to membrane depolarization and increased intracellular calcium concentration (Arakawa et al., 2002). Levels of intracellular calcium determine neuronal dependence on neurotrophic factors and susceptibility to cell death, although how calcium induces MN cell death is not fully understood. Diverse molecular mechanisms that lead to neuronal degeneration and death in response to excessive calcium influx are being elucidated, among them the activation of specific enzymes such as protein phosphatases, endonucleases, or proteases. One of these enzymes is calpain, the calcium-sensitive protease that mediates cell death when intracellular calcium is increased (Das et al., 2005).

Previous results from our group and others have shown that chronically depolarizing conditions induces cell death in mouse MNs through increased intracellular calcium and calpain activation (Gou-Fabregas et al., 2009; Kaiser et al., 2006). This protease can become overactivated under extreme conditions – for example, as a consequence of sustained elevation of cytosolic calcium levels, which in turn is associated with apoptotic or non-apoptotic cell death (Wang, 2000). In the central nervous system, calpain activation is related to neuronal damage in ischemia, stroke, and Alzheimer and Huntington diseases (Cowan et al., 2008; Shields et al., 2000; Yamashima, 2013). One of these calpain substrates is the calcium-calmodulin dependent protein kinase type IV (CaMKIV). This kinase is highly expressed in the nervous system and is

Abbreviations: ALS, Amyotrophic Lateral Sclerosis; MN, spinal cord motor neurons; hSOD1G93A, mutant human superoxide dismutase 1; CaMKIV, calcium-calmodulin dependent protein kinase IV; NTF, neurotrophic factor; BDNF, brain derived neurotrophic factor; GDNF, glial cell line-derived neurotrophic factor; CNTF, ciliary neurotrophic factor; CT-1, ciliary neurotrophic factor; HGF, hepatocyte growth factor; WT, wild type.

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involved in neuronal survival and development (Bok et al., 2007; Perez-Garcia et al., 2008; See et al., 2001). Under conditions of sustained calcium influx, CaMKIV and associated signaling molecules can be processed by activated calpain (McGinnis et al., 1998; Tremper-Wells and Vallano, 2005).

In the present study, we investigated the hypothesis that processes resulting from intracellular calcium increase, such as calpain activation and CaMKIV processing, are involved in ALS pathogenesis. We studied CaMKIV levels under culture conditions that are known to activate calpain protease activity in MNs. Results obtained indicate that membrane depolarization activates calpain and reduces CaMKIV protein level. We further analyzed calpain activation in cultured hSOD1G93A embryonic MNs and their vulnerability in response to membrane depolarization. No differences were found, compared to the control cultures. However, analysis of protein extracts from adult SOD1G93A mutant spinal cords revealed calpain activation and CaMKIV reduction, in support of our hypothesis.

Results

Effect of high-potassium medium on CaMKIV protein level in cultured mouse MNs

Addition of high potassium to the culture medium induces chronic depolarization of the neuronal plasma membrane, resulting in calcium influx and elevation of intracellular calcium concentration. Mouse spinal cord MNs are specifically vulnerable to this calcium increase and high-potassium treatment induces cell death. This cell death process is dependent on calpain activation (Gou-Fabregas et al., 2009). Under certain depolarizing conditions, calpain induces CaMKIV proteolysis (Tremper-Wells and Vallano, 2005), and CaMKIV is involved in neuronal survival (Hansen et al., 2003; Perez-Garcia et al., 2008; See et al., 2001).

To test whether membrane depolarization treatment induces changes in CaMKIV protein level, isolated MNs from E12.5 CD1 mouse embryos were cultured in the presence of neurotrophic factors with or without high potassium (see [Experimental methods](#) section). Three days after treatment, samples were collected and submitted to western blot. To determine calpain activation, we analyzed the presence of the calpain-specific 150/140 kDa α -fodrin fragment using an anti- α -fodrin antibody. As we reported previously (Gou-Fabregas et al., 2009), under depolarizing conditions the level of 140/150 kDa product was 1.7 times higher than observed in the NTF-treated control condition, indicating the activation of calpain. CaMKIV protein was also analyzed using an anti-CaMKIV antibody. The levels of CaMKIV protein in depolarized cultures were significantly lower than in controls (Fig. 1A). Together, these results suggest that depolarizing conditions in MNs induce an increase of calpain activity that can lead to CaMKIV proteolysis. Fodrin proteolysis and CaMKIV protein reduction are indicators of calcium dysregulation.

Effect of high-potassium treatment on cultured hSOD1G93A mutant MNs

In hSOD1 transgenic mice, intracellular calcium increase contributes to MN degeneration (Kaiser et al., 2006). High potassium treatment causes intracellular calcium increase and cell degeneration in cultured embryonic CD1 MNs. In order to establish whether there are differences between control and hSOD1 MNs, we decided to analyze the response of hSOD1-mutated MNs to depolarization. We obtained E12.5 embryos by crossing B6SJL-Tg (SOD1*G93A)1Gur/J (hSOD1G93A) mutants and B6SJL females. After genotyping, spinal cords from WT and hSOD1G93A mutants were dissected and MNs were isolated as described in the [Experimental methods](#) section. Cells were plated in 4-well dishes. Culture medium was supplemented with NTFs with or without 30 K. Three days after treatment, cell survival was evaluated. The percentage of surviving cells in 30 K conditions (WT and hSOD1G93A) was

significantly lower than in NTFs' controls ($51.1 \pm 5.5\%$ 30 K-treated WT and $44.8 \pm 4.6\%$ 30 K-treated hSOD1, $p < 0.005$; Fig. 1B). However, there were no significant survival differences between WT and hSOD1G93A cells under 30 K-treated conditions. This result shows that hSOD1G93A embryonic MNs are vulnerable to extracellular potassium increase in culture, but this vulnerability is comparable to cells from WT controls.

We also sought to analyze whether high-potassium treatment induces calpain activation and CaMKIV decrease. To this end, MNs were isolated from WT and hSOD1G93A mutants and cultured in the presence or absence of 30 K. Three days later, protein extracts were obtained and submitted to a western blot analysis using anti- α -fodrin and anti-CaMKIV antibodies. Results shown in Fig. 1C demonstrate an increase of 150/145 kDa-specific fodrin breakdown products and a reduction of CaMKIV protein levels in 30 K-treated hSOD1G93A MNs. Both parameters are also altered in the WT condition. These results together indicate that embryonic WT and hSOD1G93A mutant MNs show the same vulnerability in response to depolarizing conditions.

Fodrin cleavage and CaMKIV reduction in spinal cords from adult hSOD1G93A mice

Because isolated embryonic hSOD1G93A MNs did not show differences compared to WT embryonic MNs, we decided to analyze changes in calpain activity and CaMKIV protein level in adult spinal cords from hSOD1G93A mice. As described in the [Experimental methods](#) section, we obtained two sets of pooled protein extracts from spinal cord fragments, dissected from 30, 60, 90, and 120-day-old WT and hSOD1G93A mice. Protein extracts were obtained and submitted to western blot analysis using antibodies against α -fodrin or CaMKIV. We observed a significant increase of 150/145 kDa fodrin product in 90- and 120-day-old hSOD1G93A mutant samples compared to the WT condition (Fig. 2). The increase of fodrin products is time-dependent. Sixty-day-old samples show a slight but non-significant increase of 140/150 kDa product and no differences were observed in 30-day-old samples. The same protein extracts were probed using the CaMKIV antibody. Decreases in CaMKIV protein level are time-dependent. Accordingly, no differences were observed in 30-day-old samples, 60-day-old samples showed a slight but non-significant reduction, and 90-day-old and 120-day-old samples showed a significant reduction.

To determine whether calpain activation and CaMKIV measures differed by spinal cord section, 90-day-old WT or hSOD1G93A spinal cords were dissected in cervical or lumbar fragments and protein extracts were submitted to western blot. As observed in protein extracts obtained from the whole spinal cord, both cervical and lumbar hSOD1G93A samples showed increased fodrin products and reduced CaMKIV protein levels compared to WT controls (Fig. 3). However, there were no significant differences between cervical and lumbar samples, suggesting that these sections of the spinal cord undergo similar changes in fodrin and CaMKIV parameters at this period of disease evolution.

Discussion

The results obtained from the present work allow us to make two important contributions to the hSOD1G93A ALS mouse model. First, we report that embryonic cultured MNs did not differ from controls in their response to high-potassium treatment, and second, we propose that CaMKIV protective effects may be impaired during disease progression.

The increased presence of calpain-specific degradation products in protein extracts from adult spinal cords of SOD1 mutant mice indicates increased calpain activity. The observed calcium-dependent protease activation can be a consequence of either neuronal hyperexcitability or cytotoxic pathological conditions. We previously demonstrated that increased calpain activity induces MN cell death as a consequence of the specific vulnerability of these cells to high extracellular potassium

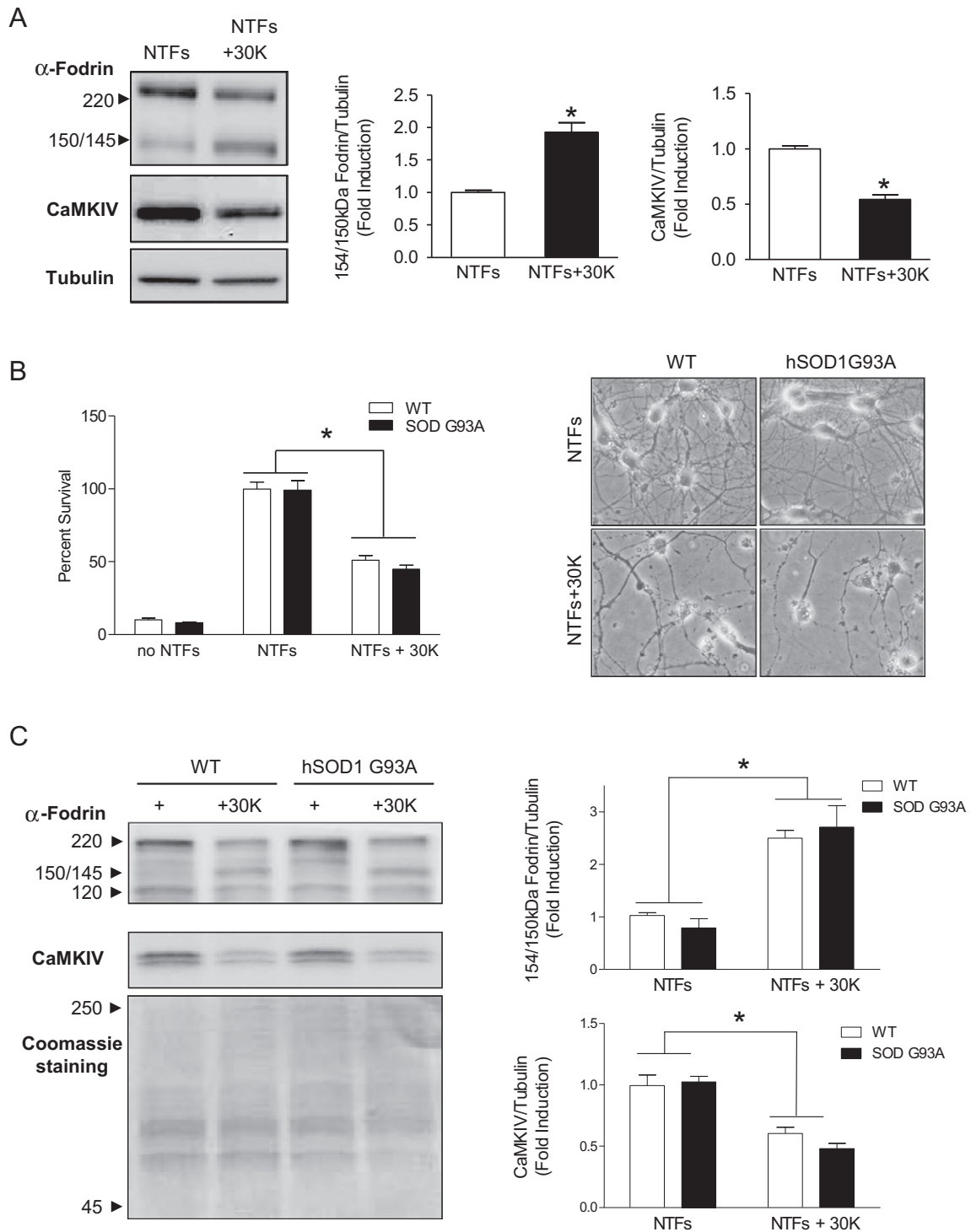


Fig. 1. Effect of 30 K treatment on embryonic MN survival, calpain-dependent α-fodrin cleavage, and CaMKIV protein level. MNs were cultured in the presence of NTFs (1 ng/mL BDNF; 10 ng/mL of GDNF, CNTF, CT-1, and HGF) or in the presence of NTFs plus 30 mM potassium (NTFs + 30 K). A) Total cell lysates of NTFs and NTFs + 30 K treated cultures were analyzed by western blot using anti-α-fodrin or CaMKIV antibodies. Membranes were re-blotted with α-tubulin antibody used as a loading control. Graphs represent the quantification of the 145/150 kDa band and CaMKIV from 3 or more independent experiments. Asterisk indicates significant differences between the 3 independent experiments using Student *t* test ($*p < 0.0007$ for 145/150 and $p < 0.0005$ for CaMKIV). B) The graph shows survival levels of MNs from WT or hSOD1G93A in the absence of NTFs or in the presence of NTFs with or without 30 K. Values are the mean of 3 independent wells for each condition \pm SEM (error bars) of a representative experiment repeated at least 3 times, with comparable results. Asterisk indicates significant differences between NTFs treatment in the presence or absence of 30 K of 3 independent experiments using two-way ANOVA test ($*p < 0.005$). Representative microscope images of WT and hSOD1G93A mouse MNs' cultures under control (NTFs) and high-potassium (NTFs + 30 K) conditions. C) Representative western blot images from protein extracts of embryonic WT or hSOD1G93A MN cultures using antibodies against α-fodrin and CaMKIV. Coomassie staining was used as a loading control. The graphs show relative protein quantification levels of the 145/150 kDa α-fodrin fragment and CaMKIV levels. Asterisk indicates significant differences between NTFs treatment in the presence or absence of 30 K of 3 independent experiments using two-way ANOVA test ($*p < 0.005$).

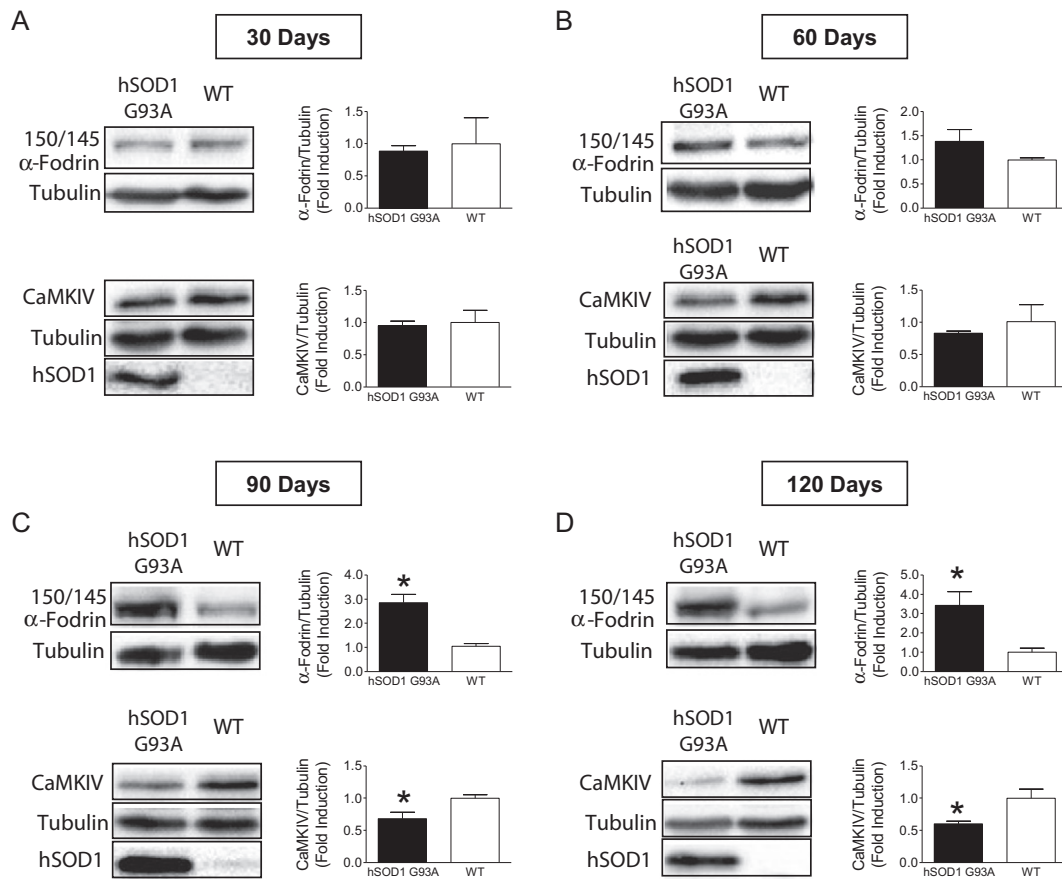


Fig. 2. Calpain-specific cleavage of α -fodrin and CaMKIV reduction in spinal cords from adult WT and SOD1G93A mice. Representative western blot images of protein extracts were obtained from pooled spinal cord fragments of WT or SOD1G93A transgenic mice. Each pool contains fragments of 5 spinal cords dissected from 30-, 60-, 90- or 120-day-old animals. Membranes were probed with an anti- α -fodrin antibody or anti-CaMKIV antibody and reprobed with an anti- α -tubulin antibody, used as a loading control. The graphs show the relative measures of the α -fodrin 145–150 kDa fragment or the CaMKIV levels from 3 separate experiments obtained from 3 independent WT or hSOD1G93A spinal cord pools. Asterisk indicates significant differences when comparing the data from the 3 independent experiments using Student *t* test ($*p < 0.05$).

concentration, which becomes elevated during neuronal activity; if uncorrected, this causes continued neuronal depolarization and hyperexcitability (Gou-Fabregas et al., 2009).

Although it is technically difficult to directly determine the potassium concentration in local MN compartments of the spinal cord, some information from mouse models is available. For example, in the SOD1 transgenic model, the glial inwardly rectifying potassium channels (Kir 4.1) are decreased in the brain and ventral horn of the spinal cord of SOD1 mutants (Kaiser et al., 2006). These observations strongly support that potassium accumulation in perineuronal compartments of the spinal cord is a likely mechanism of MN excitotoxicity in the SOD1 transgenic model of ALS. Clearance of potassium from the extracellular space (potassium spatial buffering) is considered an important function of astrocytes. A number of studies have suggested that astrocyte maintenance of extracellular potassium levels is mediated by potassium uptake through the Kir4.1 channels. Thus, the loss of these channels impairs perineuronal potassium homeostasis and may contribute to MN degeneration by excitotoxic mechanisms (Kaiser et al., 2006; Kofuji et al., 2000, 2002; Neusch et al., 2001). The consequence of extracellular potassium accumulation is continued membrane depolarization, which induces an increase in intracellular calcium concentration.

It is well-known that calpain regulates cell survival in response to calcium signals and can be over-activated under extreme conditions as a result of sustained elevation of cytosolic calcium levels (Das et al., 2005; Stifanese et al., 2010; Wang, 2000). Calpain protease has several substrates (Wang, 2000). One of them, α -fodrin, has been extensively used as a marker of calpain protease activity. The specific degradation products (150/145 kDa) of α -fodrin have been attributed to the

activation of calpain, whereas the 120 kDa fragment indicates caspase activation (Nath et al., 1996). Our previous work showed that sustained intracellular calcium increase causes calpain activation, elevation of 150/145 kDa fragments and MN cell death. This cell-death effect can be counteracted using calpain inhibitors or calpain gene silencing (Gou-Fabregas et al., 2009). Other calpain substrates have been related to the ALS pathology. It has been recently reported that calpain activation generates carboxy-terminal-cleaved TDP-43 fragments and causes mislocalization of TDP-43 in the MNs of a mouse model of ALS. The calpain-dependent TDP43 fragments have been found in the spinal cord and brain of ALS patients, supporting the crucial role of calpain-dependent cleavage of TDP43 in the ALS pathology (Yamashita et al., 2012).

Our results also demonstrate that CaMKIV protein levels are reduced in spinal cord protein extracts of adult SOD1 mutant mice. CaMKIV, a protein kinase involved in MN survival and a calpain substrate, has been reported to protect NSC34 MN-like cells from degeneration caused by transgenic SOD1 over-expression (Chiba et al., 2004). CaMKIV is also known to associate with the p85 subunit of PI 3-kinase and regulate PI 3-kinase/Akt pathway activity (Perez-Garcia et al., 2008), and a recent study reported that specific expression of constitutively active Akt3 in MNs prevents neuronal loss induced by hSOD1G93A (Peviani et al., 2013). A decade ago, Chiba and collaborators reported that activity-dependent neurotrophic factor protection (ADNF) against cell death caused by mutant SOD1 overexpression depends on CaMKIV and certain tyrosine kinase activity (Chiba et al., 2004). This suggests CaMKIV involvement in ALS pathogenesis through its role in regulating the PI 3-kinase/Akt survival pathway. Even though CaMKIV knockout mice

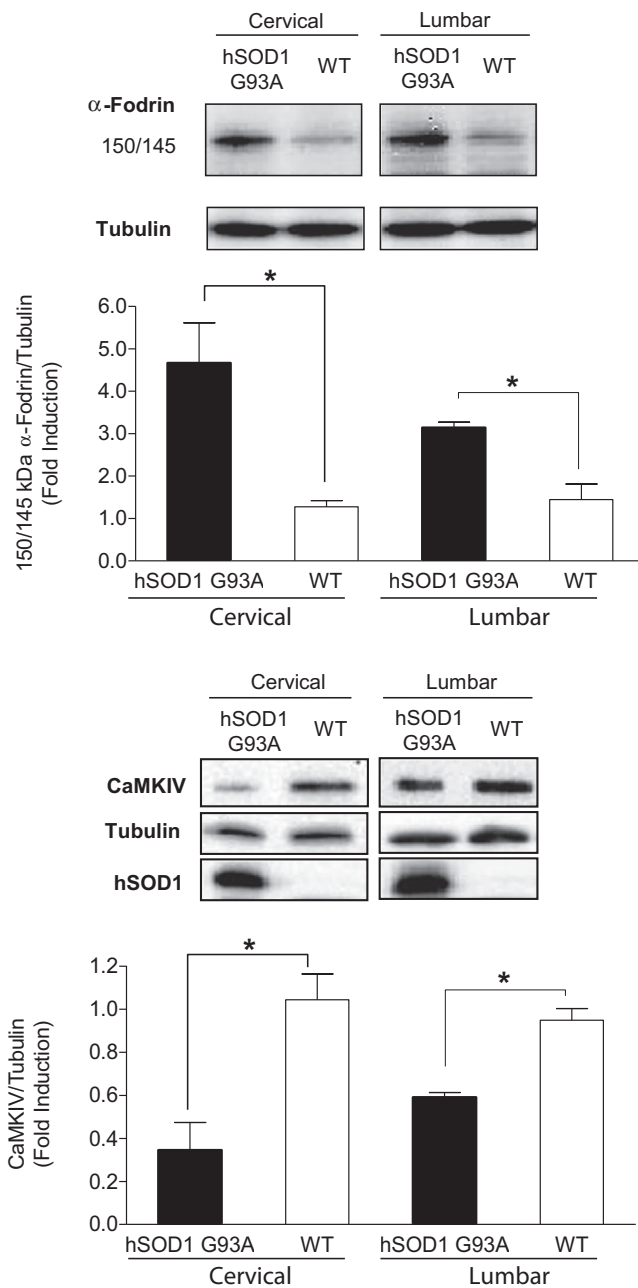


Fig. 3. α -Fodrin and CaMKIV levels in cranial and lumbar fragments of spinal cords of WT and hSOD1G93A mice. Representative western blot images of protein extracts obtained from pooled cervical or lumbar spinal cord fragments of WT or SOD1G93A transgenic mice. Each pool contains fragments of 5 spinal cords dissected from 90-day-old animals. Membranes were probed with an anti- α -fodrin antibody or anti-CaMKIV antibody and re-probed with an anti- α -tubulin antibody, used as a loading control. The graph shows the relative measures of the α -fodrin 145–150 kDa fragment or the CaMKIV levels from 2 separate experiments obtained from 2 independent WT or SOD1G93A spinal cord pools. Asterisk indicates significant differences when comparing the data from the 2 independent experiments using one-way ANOVA test ($*p < 0.05$).

do not show specific MN defects under healthy conditions (Ho et al., 2000; Ribar et al., 2000), under pathologic conditions it is probable that deficiency or reduced activity of the protein could exacerbate degeneration processes that result from excitotoxic mechanisms or mutant SOD1 over-expression.

Our results from *in vitro* studies showed no specific differences in embryonic hSOD1G93A MNs compared to embryonic WT cells. This observation suggests that cell vulnerability to high potassium treatment is not affected by mutant SOD1 overexpression in embryonic MNs. Cell

death, increased α -fodrin products and reduced CaMKIV were observed after high potassium treatment, but differences between embryonic hSOD1G93A MNs and control cells were not significant. However, significant differences were observed in proteins related to high calcium toxicity in spinal cords from symptomatic mice. Our results do not show whether these differences are located specifically in MNs, but do clearly demonstrate a deregulation of the level of these proteins, supporting the hypothesis that calcium homeostasis can be altered during disease progression (Grosskreutz et al., 2010; Kawamata and Manfredi, 2010). Further research is needed to determine whether CaMKIV reduction is directly caused by calpain activation in MNs and/or other spinal cord cells. The use of calpain inhibitors and a comparative analysis between events occurring in dorsal vs ventral spinal cord protein homogenates could provide valuable information.

Earlier theories suggested that MN degeneration during disease progression may be caused by alterations in the surrounding cells and MNs environment (Ilieva et al., 2009; Liao et al., 2012; Phatnani et al., 2013; Wang et al., 2011). This observation is further supported by the reduction of glial Kir4.1 channel observed in ALS, which contributes to developing an environment that is toxic to the MNs (Batavejic et al., 2012; Kaiser et al., 2006). Thus, modification of calcium homeostasis in ALS MNs and surrounding cells is also supported by calpain activation and CaMKIV reduction in the adult symptomatic SOD1 mutant.

In summary, our study demonstrates calpain activation and reduced levels of CaMKIV protein in damaged MNs. We report calpain activation – assessed as calpain-specific processing of the cytoskeleton substrate α -fodrin (145/150 kDa fragment) – and decreased CaMKIV levels after 30 K treatment in WT and hSOD1G93A mutant mouse MN cultures. Protein extracts of adult hSOD1G93A spinal cord analysis revealed similar signs of calcium dysregulation, increased calpain-processed substrates, and reduced CaMKIV levels. These observations suggest the role of intracellular calcium changes in ALS pathogenesis and of calpain and CaMKIV mediation in this process (Fig. 4). Therefore, calpain and CaMKIV can be considered therapeutic targets in future ALS intervention strategies.

Experimental methods

Animals

Care and use of rodents followed the Spanish Council on Animal Care guidelines and was approved by the University of Lleida Advisory Committee on Animal Services. Transgenic mice expressing high copy numbers of the mutated (glycine 93 to alanine) form of human SOD1 (hSOD1), B6SJL-Tg(SOD1*G93A)1Gur/J (hSOD1-G93A), were purchased from The Jackson Laboratories (Bar Harbor, Maine, USA). The colony was maintained by breeding male hemizygous carriers with non-transgenic B6SJL females. Offspring were identified by PCR and non-transgenic G93A littermates were used as wild-type (WT) controls. For PCR analysis, genomic DNA was extracted from mice tails (adults) or heads (embryos) by proteinase K overnight digestion or REExtract-N-Amp Tissue PCR Kit (Sigma), respectively. Primer pairs were the following: forward 5'-CTAGGCCACAGAATTGAAAGATCT-3' and reverse 5'-GTAGGTGAAATTCTAGCATCATCC-3', both of which amplify a product of 324 bp from the endogenous interleukin2 gene, used as positive control for DNA amplification, and forward 5'-CATCAGCCCTAATCCATCTGA-3' and reverse 5'-CGCGACTAACAAATCAAAGTGA-3', which amplify a product of 236 bp of exon4 from the hSOD1 gene within the transgene.

Spinal cords of 30, 60, 90, or 120-day-old genotyped mice were dissected and protein extracts were obtained. At the 90-day-old stage, hSOD1-G93A mutants show clinical symptoms. Protein extracts from 5 genotyped animals (hSOD1-G93A or WT) of each age were pooled and submitted to western blot using several antibodies. Two or three separate pools of hSOD1-G93A or WT protein extracts were analyzed.

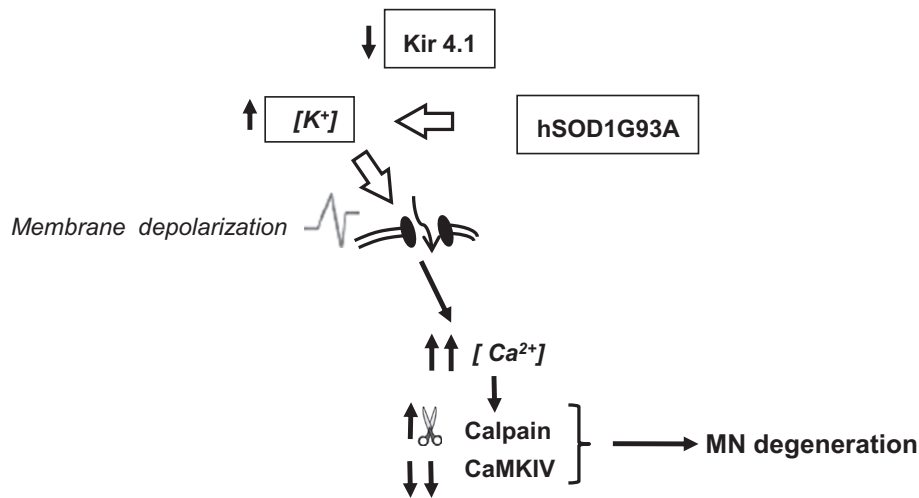


Fig. 4. Schematic model showing the proposed intracellular events of extracellular potassium increase and/or expression of mutated SOD1. Both mechanisms induce MN intracellular calcium overload, calpain activation, and reduction of CaMKIV protein levels. In ALS disease model, extracellular potassium increase can be a consequence of the reduction of the inward rectifying potassium channel, Kir 4.1. These mechanisms together or separately can contribute to MN hyperpolarization and degeneration.

Spinal cord MN isolation and culture

MN cultures were prepared from embryonic 12.5-day (E12.5) CD1 or transgenic mice spinal cord, essentially as described (Arce et al., 1999; Gou-Fabregas et al., 2009). After genotyping, WT and hSOD1-G93A embryos were submitted to spinal cord dissection and MN isolation following the same purification protocol. The isolated cells were collected in a tube containing culture medium and distributed in the tissue culture dishes. Enriched cultured MNs are clearly identified by morphological criteria (Fig. 1) and more than 80% of the cells are MNs identified by immunofluorescence using Islet-1/2 antibodies (Gou-Fabregas et al., 2009).

Isolated MNs were plated in 4-well tissue-culture dishes (Nunc, Thermo Fisher Scientific, Madrid, Spain) for survival experiments (1500 cells per well) and western blot (50,000 cells per well). Culture medium was NBMc (Neurobasal (Gibco, Invitrogen, Paisley, UK) supplemented with B27 (Gibco; Invitrogen), horse serum (2% v/v), L-glutamine (0.5 mM), and 2-mercaptoethanol (25 μ M)). Cells were plated with complete medium containing a cocktail of recombinant NTFs (1 ng/mL BDNF; 10 ng/mL GDNF, 10 ng/mL CNTF, 10 ng/mL CT-1, and 10 ng/mL HGF; Peprotech, London, UK).

Western blot analysis

Western blots were performed as described (Gou-Fabregas et al., 2009; Perez-Garcia et al., 2004). Total cell lysates were resolved in sodium dodecyl sulfate-polyacrylamide gels and transferred onto polyvinylidene difluoride Immobilon-P transfer-membrane filters (Millipore, Billerica, MA, USA) using an Amersham Biosciences (Piscataway, NJ, USA) semidry Trans-Blot. The membranes were blotted with anti-SOD1 antibody (1:2000) (Millipore, Billerica, MA, USA), anti-alpha-Fodrin antibody (1:2000) (Biomol International Inc., Exeter, UK), and anti-CaMKIV antibody (1:1000) (BD, Transduction Laboratories, Franklin Lakes, NJ, USA). To control the specific protein content per lane, membranes were reprobed with a monoclonal anti- α -tubulin antibody (Sigma) or Coomassie stain. Blots were developed using the Super Signal chemiluminescent substrate (Pierce, Rockford, IL, USA).

Statistical analysis

All experiments were performed at least 3 times. Values were expressed as mean \pm SEM. The data obtained from the independent experiments were used for statistical analysis. We used one-way or two-

way ANOVA to assess differences between treated and untreated groups and for transgenic and control cultures. If the ANOVA test was statistically significant, we performed post-hoc multiple comparisons using Bonferroni test; *p* values below 0.05 were considered statistically significant.

Acknowledgments

This work was supported by grants from the GENOME (Defining Targets for Therapeutics in SMA) to RMS; from the Instituto de Salud Carlos III, Fondo de Investigaciones Sanitarias [PI11-01047], Generalitat de Catalunya [SGR740], and Consolider-Ingenio 2010 [CSD2007-00020] to RMS. ORN holds a fellowship from the Comissionat de Universitats i Recerca, Departament d'Innovació, Universitats i Empresa de la Generalitat de Catalunya, and Fons Social Europeu. We thank Elaine Lilly, Ph.D. (Writer's First Aid), for the English language revision of the manuscript.

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