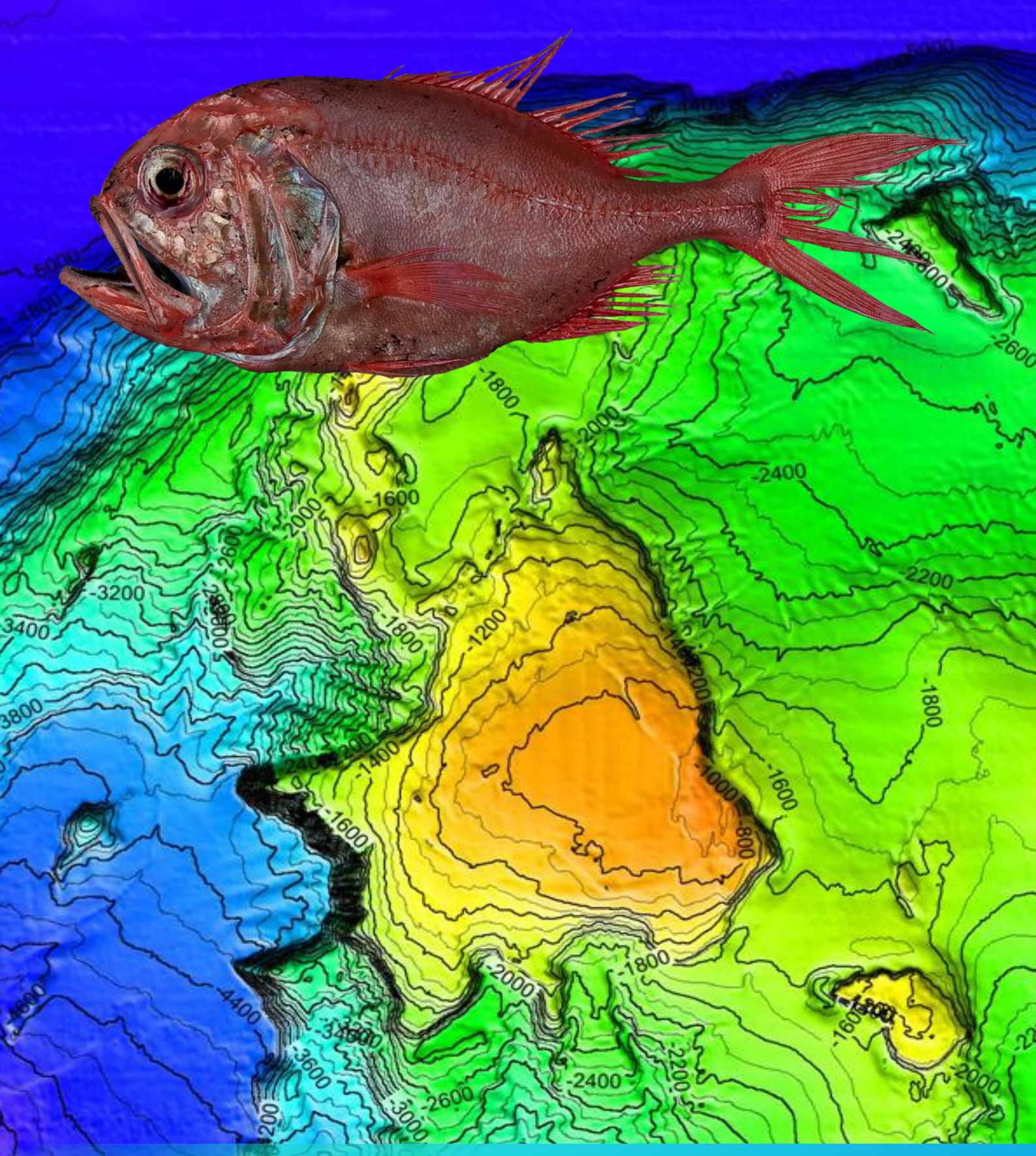

ICTIOFAUNA DEL BANCO DE GALICIA
COMPOSICIÓN TAXONÓMICA Y ASPECTOS BIOGEOGRÁFICOS

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ICTIOFAUNA DEL BANCO DE GALICIA: COMPOSICIÓN TAXONÓMICA Y ASPECTOS BIOGEOGRÁFICOS

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Los Doctores Alberto Serrano López, científico titular del Instituto Español de Oceanografía, Centro Oceanográfico de Santander y Alejandro de Carlos Villamarín, profesor titular en la Facultad de Biología de la Universidad de Vigo, en calidad de directores de esta Tesis Doctoral,

HACEN CONSTAR

que la presente memoria titulada "**Ictiofauna del banco de Galicia: composición taxonómica y aspectos biogeográficos**" para optar al grado de doctor por la Universidad de Vigo, fue realizada bajo nuestra dirección y cumple con las condiciones exigidas para su presentación, la cual autorizamos.

Y para que así conste y surta los efecto oportunos, firmamos la presente en Vigo, a 4 de marzo de 2016.

Fdo.: Dr. Alberto Serrano López

Fdo.: Dr. Alejandro de Carlos Villamarín

ÍNDICE

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2 MOTIVACIÓN E INTERÉS DEL ESTUDIO

La biodiversidad marina o diversidad biológica marina es el término que define la variedad de seres vivos que habitan el medio marino. Los océanos, con una extensión de 361 millones de km^2 (el 71% del planeta), son el lugar donde surgieron las primeras especies animales hace 640 millones de años, representan un espacio para la vida 300 veces superior al del sistema terrestre y constituyen el hábitat de millones de especies. Actualmente existen unas 275.000 especies de organismos marinos, pero se estima que aún quedan por descubrir alrededor de 1.400.000. Cada año se descubren unas 1.600 nuevas especies y se calcula que se necesitarán entre 250 y mil años para inventariar todas, con el riesgo que, para entonces, muchas puedan estar ya extinguidas.

Galicia presenta una alta biodiversidad biológica marina. Las condiciones oceanográficas y biogeográficas, junto con la extraordinaria variedad de hábitats costeros y oceánicos existentes configuran un medio marino muy complejo, con una flora y fauna marinas enormemente diversas.

El número de especies marinas en Galicia está aún por determinar. En aguas de la plataforma continental española se han descrito, hasta el momento, cerca de 1.000 especies vegetales y más de 7.500 animales. En cuanto a las especies de peces marinos, los últimos estudios establecen en 954 las especies de la península y Baleares y más de mil si sumamos las especies canarias.

Galicia cuenta con el ilustrado más destacado de la época en el ámbito de las ciencias marinas, José Andrés Cornide y Saavedra (A Coruña, 1734-Madrid, 1803), quien puede considerarse el padre de la ictiología en España. En 1788 publicó *Ensayo de una historia de los peces y otras producciones marinas de las costas de Galicia, arreglado al sistema del caballero Linneo*. En este trabajo se citan aproximadamente 65 especies, que constituyen el primer listado de peces marinos de Galicia. Con el paso de los años y las aportaciones de numerosos investigadores e instituciones, este número se ha incrementado notablemente hasta las 398 especies inventariadas en el 2010. Sin embargo, existe un claro desequilibrio entre el alto grado de conocimiento de la ictiofauna litoral y de plataforma y el escaso conocimiento que se tiene de la ictiofauna del talud, llanura abisal y montes submarinos.

Las profundidades marinas albergan uno de los mayores reservorios de la biodiversidad marina, pero también constituyen uno de los ecosistemas más

desconocidos, debido a las dificultades y el reto tecnológico que supone su estudio. Sólo los taludes continentales ocupan el 8,8 por ciento de la superficie mundial, frente al 7,5 por ciento de las plataformas continentales y los mares de aguas poco profundas. La ictiofauna marina profunda de Galicia, entendida como aquella que habita habitualmente a profundidades mayores de los 400 m, era escasamente conocida hasta hace relativamente poco tiempo. En 1996 el Instituto Español de Oceanografía de Vigo comienza un proyecto de prospección de especies comerciales en el talud de la plataforma gallega. Los resultados de este proyecto dan lugar a un amplio listado de especies, con aproximadamente 40 especies profundas nuevas para la ictiofauna gallega e incluso española. La montaña submarina del banco de Galicia, con su cima a 625 m de profundidad, constituye un hábitat profundo de características singulares. La elevada profundidad, presencia de sustratos duros, fuertes pendientes, topografía críptica, corrientes rápidas y variables, aguas oceánicas y aislamiento geográfico, hacen de los montes submarinos un hábitat único para los organismos.

La ictiofauna que habita los montes submarinos ha desarrollado características ecológicas y fisiológicas que les permiten explotar un ambiente de fuertes corrientes y grandes flujos de materia orgánica. Presentan adaptaciones morfológicas al medio, una longevidad alta, bajas tasas de crecimiento y reclutamientos altamente variables.

El banco de Galicia fue propuesto a la Comisión Europea como uno de los 10 nuevos Lugares de Importancia Comunitaria (LIC), para incrementar la protección de nuestros mares desde menos del 1% hasta más del 8%, en dirección al cumplimiento del compromiso internacional del Convenio de Diversidad Biológica de proteger el 10% de las regiones marinas del mundo.

Para proteger, primero es necesario conocer. Los estudios e investigaciones llevados a cabo en esta tesis doctoral forman parte del proyecto LIFE+ INDEMARES que han permitido finalmente la declaración del banco de Galicia como zona LIC (Decisión de Ejecución (UE) 2015/2373 de la Comisión de 26 de noviembre de 2015 por la que se adopta la novena lista actualizada de lugares de importancia comunitaria de la región biogeográfica atlántica).

3 OBJETIVOS

El objetivo general de esta tesis es determinar la composición faunística de peces que habitan el monte submarino del banco de Galicia y sus relaciones biogeográficas. Para ello se han planteado cinco objetivos específicos.

1. Listar las especies identificadas en el banco de Galicia, determinar la composición taxonómica y sus relaciones biogeográficas.
2. Determinar la composición de especies del género *Apristurus* (Pentanchidae) en el banco de Galicia.
3. Determinar la composición de especies de la familia Halosauridae (Notacanthiformes) en el banco de Galicia.
4. Determinar la composición de especies del género *Lepidion* (Moridae) en el banco de Galicia, sus relaciones interespecíficas y la descripción de hiperpigmentación melánica en ejemplares del género.
5. Determinar la composición de especies de la familia Bathygadidae (Gadiformes) en el banco de Galicia.

4 RESUMEN

La presente memoria doctoral viene a cubrir una parcela de conocimiento de la que se tiene poca información en la actualidad, como es la composición de la ictiofauna que habita los montes o montañas submarinas. El ser humano ha venido explorando y explotando los mares desde tiempos ancestrales, primero las playas y costas someras más cercanas, con el paso de los siglos, las amplias plataformas continentales y sólo recientemente el talud continental y las montañas submarinas. Desde este punto de vista cronológico, pues, las montañas submarinas, dada su inaccesibilidad y dificultades de explotación, han permanecido desconocidas y en buen estado de conservación hasta la actualidad, fuera de las fuertes presiones antrópicas costeras.

Un monte submarino es una elevación del fondo marino con una cumbre que no llega a la superficie. Si bien no hay una definición particular que sea mayoritariamente aceptada, una de las denominaciones más extendidas de monte submarino es aquella que establece que desde su base tiene una altitud de al menos 1.000 metros y no alcanza la superficie. Además de estas formaciones, existen otras miles de menor tamaño que son catalogadas como colinas o montículos, dependiendo de sus dimensiones, y que algunos autores consideran también que pueden desempeñar un papel importante en los ecosistemas de aguas profundas y oceánicas.

El origen de estas formaciones es en su mayoría volcánico, pero existe un pequeño porcentaje de origen continental. En este caso, las montañas submarinas surgen como consecuencia de la fractura de los continentes o por la colisión o empuje de las placas continentales.

El número estimado de montañas submarinos varía desde más de 100.000 mayores de 1000 m hasta más de 25 millones si reducimos su altura hasta los 100 m. En el océano Pacífico se contabilizan entre 30.000 y 50.000 montañas submarinas mayores de 1000 m, más de 800 en el océano Atlántico y un número indeterminado en el océano Índico. En la zona del Convenio Oslo-París (OSPAR), hay 104 montañas submarinas inventariadas, 74 dentro de la zona económica exclusiva nacional y sólo 30 fuera de ella, en alta mar.

El banco de Galicia es un monte submarino de origen no volcánico localizado en el margen continental de Galicia, a unos 200 km de la costa, en 42° 15′N y 43°N y 11° 30′W y 12° 15′W. El banco tiene una superficie de 1844 km^2 en su parte más superficial

y un contorno triangular, midiendo unos 75 km de largo por 58 km de ancho. Las profundidades a las que se encuentra el techo del banco de Galicia varían entre 625 m, en el sureste y 2000 m hacia el oeste.

El banco de Galicia es un monte submarino del tipo costero, perteneciente al grupo situado a lo largo de las costas ibéricas y africanas de la Región IV (bancos de Galicia, Ampere, Gorringe, Josephine y Seine), frente al grupo "offshore" del sur de Azores y dorsal medio atlántica de la Región V (Atlantis, Hyeres, Irving, Meteor y Plato). En el margen de Galicia se han identificado cinco plataformas marginales o montes submarinos que forman relieves tabulares discontinuos en el ascenso continental: Porto, Vigo, La Coruña, Finisterre y banco de Galicia.

El conocimiento de la existencia del banco de Galicia se remonta al año 1964, con la publicación de un estudio geomorfológico de la zona. A nivel pesquero, los primeros indicios de actividad tienen su origen a principio de la década de 1970, con varios barcos de diversos puertos gallegos equipados con palangres o volantas que capturaban primero especies demersales o bentopelágicas como la cherna (*Polyprion americanus*), tomás (*Epigonus telescopus*) o alfonsino (*Beryx splendens*) y más tarde especies epipelágicas como la palometa (*Brama brama*) y el pez espada (*Xiphias gladius*). La actividad pesquera se ha ido reduciendo gradualmente con el tiempo y ya a partir del año 2000 sólo algunos barcos faenaban de forma esporádica en la zona de estudio. La baja y ocasional actividad pesquera realizada sobre el banco con artes de pesca considerados poco destructivos (ausencia de arrastre) han permitido un alto grado de conservación de este ecosistema.

El banco de Galicia está bañado por tres capas de diferentes masas de agua de origen norteño y sureño: Masa de agua central del Atlántico NE europeo (East North Atlantic Central Water: ENACW), por debajo de las aguas superficiales y hasta los 500-600 m; Masa de agua mediterránea (Mediterranean Outflow Water: MOW) con dos núcleos situados a 800 y 1200 m y Masa de agua del Labrador (Labrador Sea Water: LSW), que tiene su centro sobre los 1800-1900 m. El relieve de las montañas submarinas interactúa con la circulación oceánica circundante con la consiguiente formación de giros o anillos ("meddies"), corrientes circulares (columnas de Taylor) y afloramientos locales, que causan incrementos locales de la producción primaria y secundaria por el ascenso de nutrientes y fenómenos de retención y acumulación de larvas y plancton, modificando las condiciones de oligotrofismo imperantes en el mar profundo.

El margen continental del oeste de Galicia se clasifica como un margen continental no volcánico, creado a partir de la propagación hacia el norte de la apertura del Océano Atlántico, hace aproximadamente 110 millones de años. Presenta una geomorfología formada por estructuras de bloques levantados y hundidos limitados por fallas normales con dirección NNW-SSE que están cruzadas por fallas NE-SO. El origen del banco de Galicia es probablemente tectónico, si bien ha sido modelado por los procesos sedimentarios dominantes durante los descensos del nivel del mar. El banco presenta pequeños relieves montañosos ("knolls"), crestas y canales, y dos valles rectilíneos de 40 m de relieve orientados en dirección NNW y que terminan abruptamente hacia las 850 m. La sedimentación en el flanco occidental del banco de Galicia posee la singularidad de presentar rasgos detríticos de importancia regional forzados climáticamente y asociados a procesos sedimentarios de talud continental.

Los peces, con unas 27.977 especies válidas, constituyen más de la mitad de especies conocidas de vertebrados, en comparación con las 26.734 de tetrápodos. La identificación de un ejemplar, consiste en adjudicarlo al grupo o taxón al que pertenece, de acuerdo con un modelo clasificatorio elaborado anteriormente. En los peces, los principales caracteres usados tradicionalmente para la identificación de especies son los atributos descriptivos, las medidas morfométricas (biometrías) y los caracteres merísticos. Existen, además, otros métodos utilizados más recientemente en la identificación de peces. Entre ellos está la identificación taxonómica con marcadores moleculares de ADN, que se ha ido instaurando con fuerza en los últimos años en la taxonomía moderna. El código de barras de ADN (barcoding) utiliza como región estándar la secuencia de una región de al menos 500 nucleótidos del extremo 5´ del gen mitocondrial citocromo c oxidasa I (COI), y para cuya comparación se dispone tanto de bases de datos de referencia (BOLD, Barcoding of life data) como generales (GenBank).

La información recogida en esta memoria doctoral es el resultado de numerosas campañas de investigación realizadas en el banco de Galicia desde 1980 hasta 2011, tanto de carácter exploratorio, con barcos de pesca comercial, como de investigación oceanográfico-pesquera, realizadas en buques oceanográficos. Aunque los objetivos y metodología de ambos tipos de campañas difieren ligeramente, el objetivo final es muy similar, conocer la composición de los organismos de la zona estudiada así como su distribución y su abundancia.

En el apartado 6.1 y anexo I de la presente memoria, se listan y comentan las 139 especies de 62 familias diferentes registradas en el banco de Galicia. La identificación y clasificación de peces se hizo principalmente con la metodología clásica, examinando los caracteres morfológicos descriptivos junto con las medidas biométricas y los caracteres merísticos que delimitan cada especie. En especies cuya identificación morfológica era más complicada o en aquellas en las que existe un interés taxonómico especial por su rareza o falta de estudios, se realizó también una identificación molecular con ayuda del código de barras de ADN.

De cada una de las especies listadas se aportan datos sobre su abundancia absoluta, tallas y profundidad, así como de su hábitat, distribución y el grado de amenaza existente sobre ella. Para algunas especies se aportan, además, los datos biométricos y recuentos merísticos que permitieron su identificación.

Como consecuencia de las artes de pesca utilizadas y de su selectividad interespecífica, la fauna bentopelágica es la mejor representada, si bien el listado recoge especies de toda la columna de agua: epipelágicas, mesopelágicas, batipelágicas, batidemersales y bentónicas. La familia mejor representada es Macrouridae, con nueve especies, seguida por Moridae, Stomiidae y Sternoptychidae con siete cada una. Las familias más abundantes son, Trachichthyidae y Moridae, debido a la gran cantidad de ejemplares capturados de *Hoplostethus mediterraneus* (Trachichthyidae), con 61.206 y de *Lepidion lepidion* (Moridae), con 41.585.

La mayor parte de las especies registradas son de aguas profundas, que viven habitualmente a más de 400 m de profundidad. Por sus características biológicas y ecológicas, los peces de las montañas submarinas son considerados como altamente vulnerables. Estas especies presentan elevada longevidad, crecimiento lento, baja fecundidad, madurez tardía y son muy vulnerables a las actividades humanas y cambios naturales en el ecosistema.

El estado de vulnerabilidad y conservación de cada especie se caracterizó a partir de dos listas globales (Unión Internacional para la Conservación de la Naturaleza, UICN y FishBase) y una regional (OSPAR). Debido a los diferentes criterios utilizados para estimar el estado de vulnerabilidad en cada lista, los resultados fueron muy diferentes. Sólo cinco especies (3%) fueron consideradas como amenazadas según OSPAR, nueve (6%) según UICN y 58 (42%) según FishBase. Este último es considerado el criterio más apropiado, al ser un estudio con un gran número de especies y contener la lista de UICN numerosas especies sin información. Del listado final hay que destacar el grupo

de los elasmobranquios, con 31 especies, de las cuales 19 (61%) se encontrarían amenazadas según FishBase.

Desde el punto de vista biogeográfico, el grupo de especies Atlánticas, que incluye especies profundas o mesopelágicas de amplia distribución, con 113 especies (81%), es el grupo más importante. Como consecuencia del carácter costero del banco de Galicia también es notoria la ausencia de endemismos, de manera que la práctica totalidad de especies registradas están presentes en aguas del Atlántico europeo.

Los resultados obtenidos en esta investigación muestran una elevada biodiversidad piscícola y un alto porcentaje de especies amenazadas, lo cual apoya la reciente declaración del banco Galicia como zona marina protegida.

En el apartado 6.2 y anexo II se identifican las especies del género *Apristurus* del banco de Galicia. Este género es considerado como uno de los más diversos y taxonómicamente confusos entre los elasmobranquios, debido a la gran cantidad de especies poco conocidas y a su semejanza morfológica. Los ejemplares de *Apristurus* fueron capturados en la campaña INDEMARES 2011, en los lances de mayor profundidad, entre 1460 y 1809 m. Los individuos fueron identificados combinando análisis morfológicos y moleculares. En total, fueron capturados 20 ejemplares, de los cuales 18 resultaron ser *Apristurus aphyodes*, uno *Apristurus melanoasper* y otro *Apristurus profundorum*. Esta última identificación constituye la cita más al norte registrada para la especie en el Atlántico nororiental.

A nivel morfológico *A. melanoasper* se distingue de las otras dos especies por tener el surco labial superior más largo que el inferior y un mayor número de válvulas espirales en el intestino. *Apristurus aphyodes* se diferencia de *A. profundorum* por tener un rostro ancho y corto (< 6% LT), y por una coloración más clara.

A nivel molecular, la identificación se realizó examinando el código de barras de ADN del gen mitocondrial COI en *A. profundorum* y *A. melanoasper* y parte de la secuencia del gen 16S rRNA en *A. aphyodes*, al no disponer de secuencias de COI de esta especie en las bases de datos de referencia. Las secuencias obtenidas se agruparon con las de referencia disponibles con un valor estadístico de remuestreo ("bootstrap″) del 99% para *A. profundorum y A. aphyodes* y del 95% para *A. melanoasper*, confirmando las identificaciones morfológicas previas.

En el apartado 6.3 se determina la composición de especies de la familia Halosauridae (Notacanthiformes) en el banco de Galicia. Se trata de una familia de peces marinos que cuenta actualmente con 16 especies distribuidas en las aguas

profundas y abisales de todo el planeta, entre 500 y 5000 m de profundidad, pero más habitualmente entre 1100 y 3300 m. Los ejemplares fueron identificados combinando análisis morfológicos y moleculares (código de barras de ADN).

Treinta y cinco ejemplares de seis especies de la familia Halosauridae fueron capturados en dos localidades diferentes del norte de España entre los años 2009 y 2011, 33 en el banco de Galicia y dos en el banco El Cachucho, en el Golfo de Vizcaya. En el primer sitio se identificaron 5 especies de 3 géneros distintos: *Halosauropsis macrochir, Halosaurus ovenii, Aldrovandia affinis, A. phalacra* y *A. oleosa* mientras que *H. johnsonianus* sólo apareció en el banco del Cachucho. Los registros de *A. oleosa* en el banco de Galicia constituyen la primera cita de esta especie en aguas atlánticas europeas y establecen un nuevo límite norte de distribución en el Atlántico este.

Morfológicamente, la ausencia de escamas en la parte superior de la cabeza distingue los ejemplares de *H. macrochir* de los del género *Halosaurus*, y la presencia de escamas en el hueso opercular los distingue del género *Aldrovandia*. Además, la distancia interorbital en *H. macrochir* es mayor que en las especies de *Halosaurus* o *Aldrovandia* (6.0-7.9 frente a 2.2-5.3% LGP). *H. ovenii* se diferencia de *H. johnsonianus* por tener más escamas en la línea lateral hasta el ano (61-67 frente a 57), más ciegos pilóricos (12-13 frente a 6-8) y menos branquiespinas en el primer arco branquial (12-13 frente a 17-18).

Entre las especies del género *Aldrovandia*, *A. affinis* se diferencia de *A. phalacra* y *A. oleosa* por una mayor longitud preoral del rostro, contenida 2-2,2 veces en la longitud del rostro (frente a 3-5,3) y menos branquiespinas en el primer arco branquial (13-15 frente a 20-25). *Aldrovandia phalacra* difiere de *A. oleosa* por tener más escamas en la línea lateral hasta el ano (26 frente a 20-22) y más radios en la aleta pectoral (14-15 frente a 9-12).

A nivel molecular, las 35 secuencias de COI se agruparon en seis clados diferentes que se correspondían con la asignación morfológica previa. Las diferencias existentes en la secuencia de nucleótidos de los códigos de barras entre individuos se cuantificaron en forma de distancia p o número de posiciones ocupadas por nucleótidos distintos en relación con el total de posiciones examinadas. El valor porcentual medio obtenido entre individuos de la misma especie fue 0,42% y entre individuos del mismo género 7,33%, un valor 17 veces superior. Además, el mayor valor de distancia obtenido entre individuos de una especie fue 0,8%, mientras que al comparar individuos de distintas especies del mismo género fue 3,3%, mostrando no sólo la ausencia de solapamiento

entre ambas medidas sino la existencia de un número significativo de diferencias en nucleótidos entre especie y género denominado "barcoding gap", que asegura la aplicabilidad del procedimiento de utilización del código de barras de ADN a la distinción de las especies que forman la familia Halosauridae.

En el apartado 6.4 y anexos III-1 y III-2 se estudian las especies del género *Lepidion* (Moridae) del banco de Galicia y su relación con las demás especies del género. Además, la hiperpigmentación melánica de un ejemplar de *L. lepidion* del banco confirma la presencia de esta anomalía cromática en especies del género.

El género *Lepidion* Swainson, 1838 (Moridae), está compuesto por nueve especies bentopelágicas que viven en el talud inferior y montes submarinos de los océanos Atlántico, Índico, Pacífico y del Mar Mediterráneo. En el banco de Galicia se identificaron dos especies, *L. eques* y *L. guentheri*. Para el estudio de las relaciones entre especies y la comprobación de la eficacia del código de barras de ADN en la identificación molecular de especies del género *Lepidion*, se obtuvieron 32 secuencias de nucleótidos de COI de individuos pertenecientes a cinco especies diferentes de *Lepidion*. Once de las secuencias procedían del banco de Galicia y el resto de diferentes zonas del Golfo de Vizcaya y del Atlántico suroeste, a las que se sumaron 26 secuencias de individuos del mismo género y diferentes especies procedentes de la base de datos BOLD. Como resultado, se compararon 58 códigos de barras de ADN pertenecientes a ocho de las nueve especies conocidas del género *Lepidion*. El alineamiento de las secuencias y su posterior comparación, mediante inferencia bayesiana, produjo un árbol consensuado en el cual las mismas se agruparon en siete clados distintos, con las secuencias de dos especies, *L. lepidion* y *L. eques*, formando parte del mismo agrupamiento, indicando una posible sinonimia. La distancia genética entre *L. eques* y *L. lepidion* varió entre 0 y 0,62 % (con un valor medio de 0,29%) similar al valor de la distancia media de todas las especies del género (0,27%) y muy por debajo del 2% establecido de manera general como valor mínimo de distancia para discriminar especies distintas. La distancia promedio entre pares de secuencias de distintas especies fue de 4,28%, 16 veces mayor que la promediada entre individuos de la misma especie, que fue de 0,27%. En este caso, las distancias entre secuencias se calcularon empleando el modelo de sustitución de nucleótidos de Kimura 2 parámetros, si bien los valores resultantes en el caso del gen COI, suelen ser similares a los que se obtienen calculando las distancias p.

A nivel morfológico, se analizaron comparativamente 36 ejemplares del Atlántico identificados previamente como *L. eques* y 20 del Mediterráneo, identificados previamente como *L. lepidion*. Los caracteres distintivos que separan a ambas especies según la bibliografía son el diámetro del ojo, contenido entre 3,1 y 3,6 veces en la cabeza en *L. lepidion* en vez de entre 2,6 y 3,1 veces en *L. eques* y el número de radios de la aleta anal, entre 48 y 51 en *L. lepidion* frente a entre 50 y 54 en *L. eques*. Nuestros resultados, sin embargo, muestran un gran solapamiento en los valores obtenidos de estas variables entre ambas especies, lo que eliminaría su validez como carácter taxonómico distintivo. El diámetro del ojo resultó estar contenido entre 2,8 y 3,6 veces en la cabeza en *L. lepidion* y entre 2,6 y 3.4 veces en *L. eques* y el número de radios de la anal fueron entre 45 y 51 en *L. lepidion* y entre 47 y 54 *en L. eques.* La biología de la especie, con huevos y primeras fases de desarrollo pelágicas y las corrientes dominantes tampoco sugieren barreras biogeográficas que interrumpan el flujo genético y delimiten dos especies distintas.

Los resultados de los análisis morfológicos y moleculares junto con la información biológica y oceanográfica sugieren que la especie endémica del Mediterráneo, *L. lepidion*, y la especie del Atlántico norte, *L. eques*, son en realidad la misma especie, por lo que *L. eques* es un sinónimo más moderno de *L. lepidion*.

En el apartado 6.4 y anexo III-2 se describen dos casos de hiperpigmentación melánica o melanosis encontrada en dos ejemplares de *L. lepidion* (antes *L. eques*) observados en el banco de Galicia y en el cañón de la Gaviera, en el Golfo de Vizcaya. La pigmentación normal de *L. lepidion* es uniformemente pálida, variando de un color pardo claro a un gris rosado, con las aletas algo más oscuras. Macroscópicamente, los ejemplares con melanosis presentan una coloración atípica con la piel cubierta con numerosas manchas oscuras e irregulares dispersas por la cabeza, el cuerpo y las aletas. Microscópicamente, la histología muestra una hiperplasia de los melanóforos dérmicos formando una capa gruesa y continua, paralela a la membrana basal. No se observaron bacterias, parásitos u hongos que pudieran ser los causantes indirectos de esta coloración. Sin embargo un trauma o herida fueron detectados tanto en el ejemplar de *L. lepidion* del banco de Galicia como en otro de *L. guentheri* del Golfo de Vizcaya publicado anteriormente, que podrían ser los desencadenantes originarios de la reacción hiperplásica. El mismo patrón de coloración puede ser observado en la figura de un ejemplar de *L. lepidion* del Mediterráneo que aparece en la publicación de Moreau en

1881, siendo esta cita la primera documentación que se tiene de melanosis en el género *Lepidion* y una de las primeras, si no la primera, en todos los peces.

En el apartado 6.5 y anexo IV, se analiza la composición de especies de la familia Bathygadidae (Gadiformes) presentes en el banco de Galicia. Bathygadinae era considerada tradicionalmente como una subfamilia de la familia Macrouridae, pero recientes estudios basados en evidencias morfológicas y genéticas la han elevado al rango de familia. Los batigádidos están ampliamente distribuidos, en zonas tropicales y subtropicales de todos los océanos, entre 100 y 3000 m de profundidad. Entre 2009 y 2011, se capturaron nueve ejemplares de esta familia en el banco de Galicia y dos en el cañón de Avilés. Los ejemplares fueron identificados combinando análisis morfológicos y moleculares (código de barras de ADN).

Se identificaron cuatro especies de batigádidos, tres en el banco de Galicia (*Gadomus dispar, G. longifilis y Bathygadus melanobranchus*) y una en el cañón de Avilés (*G. arcuatus*) que representa un nuevo límite norte de distribución de la especie en el Atlántico este. Morfológicamente, la ausencia de un barbillón en el extremo de la mandíbula inferior y de radios muy alargados en las aletas diferencia las especies del género *Bathygadus* de las del género *Gadomus*. *Gadomus arcuatus* tiene un número de radios en la pectoral mayor que las otras especies de *Gadomus* (25 frente a 16–21). *Gadomus longifilis* se diferencia de *G. dispar* por el número menor de radios en la aleta pectoral (16–17 frente a 19–21), mayor número de branquiespinas en arco inferior del primer arco branquial (29–31 frente a 19–21), mayor distancia interorbitaria (21,1–22.7 frente a 16,1–20.5 % longitud de la cabeza), menor longitud del barbillón (40,9–51,2 frente a 83,6–119,4 % longitud de la cabeza) y menor número de ciegos pilóricos (9–12 frente a más de 50).

A nivel molecular, las secuencias de nucleótidos correspondientes a los ejemplares de la misma especie fueron idénticas entre sí, dando lugar a una única secuencia o haplotipo representativo. La diversidad de nucleótidos global media encontrada al comparar los códigos de barras (medida como distancia p) fue 9,6%. La de género fue 5,6% para *Bathygadus* y 8% para *Gadomus*. La distancia media entre los dos géneros fue de 11,5%. La mayor divergencia encontrada ocurrió entre los haplotipos de *B. melanobranchus* y *G. arcuatus* (12,4%) mientras que los valores menores se dieron entre *B. antrodes* y *B. favosus* (5,1%).

5 INTRODUCCIÓN GENERAL

5.1 ÁREA DE ESTUDIO. EL BANCO DE GALICIA COMO MONTE SUBMARINO.

El término montaña o monte submarino se ha definido de muchas y diferentes maneras, pero no hay una definición particular que sea mayoritariamente aceptada. De manera general, un monte submarino es una elevación del fondo marino con una cumbre que no llega a la superficie. El origen geológico, la longitud vertical de la elevación y la forma y tamaño de la cumbre van a ser las características principales que definen un monte submarino según los distintos autores.

Una de las definiciones más extendidas de monte submarino lo describe como aquel que tiene desde su base una altitud de al menos 1.000 metros y no alcanza la superficie (Froese y Sampang, 2004; White y Mohn, 2004). Sin embargo, ninguna justificación ecológica parece apoyar éste límite tradicional (Pitcher y col., 2007; Wessel, 2007) y esta definición se ha modificado ampliamente en la bibliografía para satisfacer mejor las necesidades de diferentes disciplinas. Algunos autores reducen la altitud mínima hasta los 100 m (Staudigel y col., 2010; Morato y col., 2012) ya que los pequeños accidentes submarinos también pueden desempeñar un papel importante en los ecosistemas de aguas profundas y oceánicas (Koslow y col., 2001).

El origen de estas formaciones es en su mayoría volcánico (Wessel y col., 2010), pero existe un pequeño porcentaje de origen continental, que surgen como consecuencia de la fractura de los continentes o por la colisión o empuje de las placas continentales.

El número estimado de montes submarinos también varía, desde más de 100.000 mayores de 1000 m hasta más de 25 millones si reducimos su altura hasta los 100 m (Wessel y col., 2010). En el océano Pacífico se contabilizan entre 30.000 y 50.000 montes submarinos mayores de 1000 m, más de 800 en el Océano Atlántico y un número indeterminado en el Océano Índico (Rogers, 1994).

El número de montañas submarinas en el área OSPAR está aún sin calcular con exactitud. Sin embargo, según Kitchingman y col. (2007) existen al menos 325 grandes montañas submarinas, la mayor parte de ellas a lo largo de la dorsal atlántica y frente a las costas de Portugal, España y Reino Unido. De las 104 montañas submarinas en la base de datos de OSPAR, 74 se encuentran dentro de la zona económica exclusiva nacional y sólo 30 fuera de ella, en alta mar (Serrao y col., 2010).

El banco de Galicia (BG) es un monte submarino del tipo costero, perteneciente al grupo situado a lo largo de las costas ibéricas y africanas de la Región IV (BG, Ampere,

Gorringe, Josephine y Seine), frente al grupo *offshore* del sur de Azores y dorsal medio atlántica de la Región V (Atlantis, Hyeres, Irving, Meteor y Plato) (Surugiu y col., 2008). En el margen de Galicia se han identificado cinco plataformas marginales o montañas submarinas que forman relieves tabulares discontinuos en el ascenso continental: Porto, Vigo, La Coruña, Finisterre y BG (Vázquez y col., 2015).

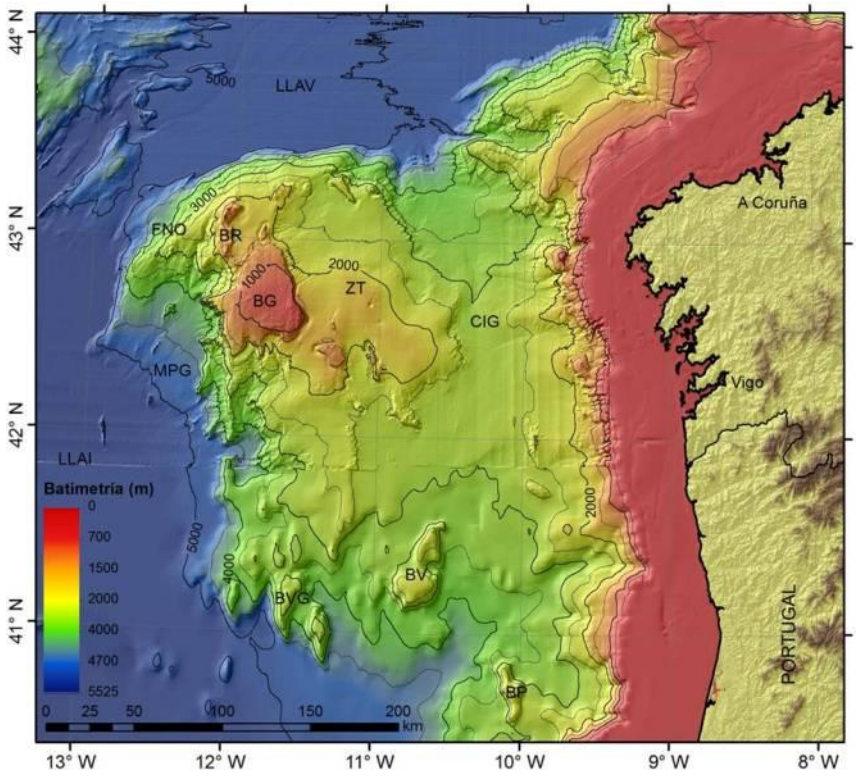

Figura 1. Margen continental de Galicia, en el que se localizan el banco de Galicia (BG) y otros rasgos geomorfológicos de la zona: los montes submarinos de Vasco da Gama (BVG), el banco de Vigo (BV), el banco de Porto (BP), la cuenca interior de Galicia (CIG), la zona de transición (ZT), el flanco noroeste (FNO), los montes Rucabado y García (BR), el margen profundo de Galicia (MPG), la llanura abisal de Vizcaya (LLAV) y la llanura abisal ibérica (LLAI). Fuente: Proyecto ZEE (batimetría de ecosonda multihaz) y Atlas Digital GEBCO.

El BG es un monte submarino profundo de origen no volcánico (Black y col., 1964) situado al noroeste de la península ibérica, entre 42° 15′N y 43°N y 11° 30′W y 12° 15′W, a 120 millas náuticas de la costa noroeste española, en la Región noratlántica (IXb2 del ICES), en la provincia biogeográfica Lusitánica de la Región IV de OSPAR (Francia y Península Ibérica) (Fig. 1). Su origen está relacionado con el proceso de rift continental Mesozoico que dio lugar a la apertura del océano Atlántico.

El BG (Fig. 2) tiene una superficie de 1844 km^2 en su parte más somera, con un contorno aproximadamente triangular, midiendo unos 75 km en dirección NNE-SSO,

por 58 km en dirección ONO-ESE (de la Torriente y col., 2014). Las profundidades a las que se encuentra el techo del BG varían entre 625 m, hacia el sureste, y 2000 m, hacia el oeste Hacia el este, el BG limita con una Zona de Transición que lo conecta con la Cuenca Interior de Galicia, también conocida como surco de Valle Inclán, que capta la mayoría de los sedimentos procedentes del continente. Hacia el norte y el noroeste, el BG limita con los bancos submarinos de El Rucabado y García, que a su vez conectan con un área de relieve escarpado, denominada Flanco Noroeste por Vázquez y col. (2008). Este Flanco Noroeste o escarpe de Galicia, lleva a la Llanura Abisal de Vizcaya; hacia el oeste y suroeste del BG, se encuentra el llamado Margen Profundo de Galicia (Murillas y col., 1990), una zona de transición entre la corteza continental adelgazada y la corteza oceánica de la llanura abisal ibérica.

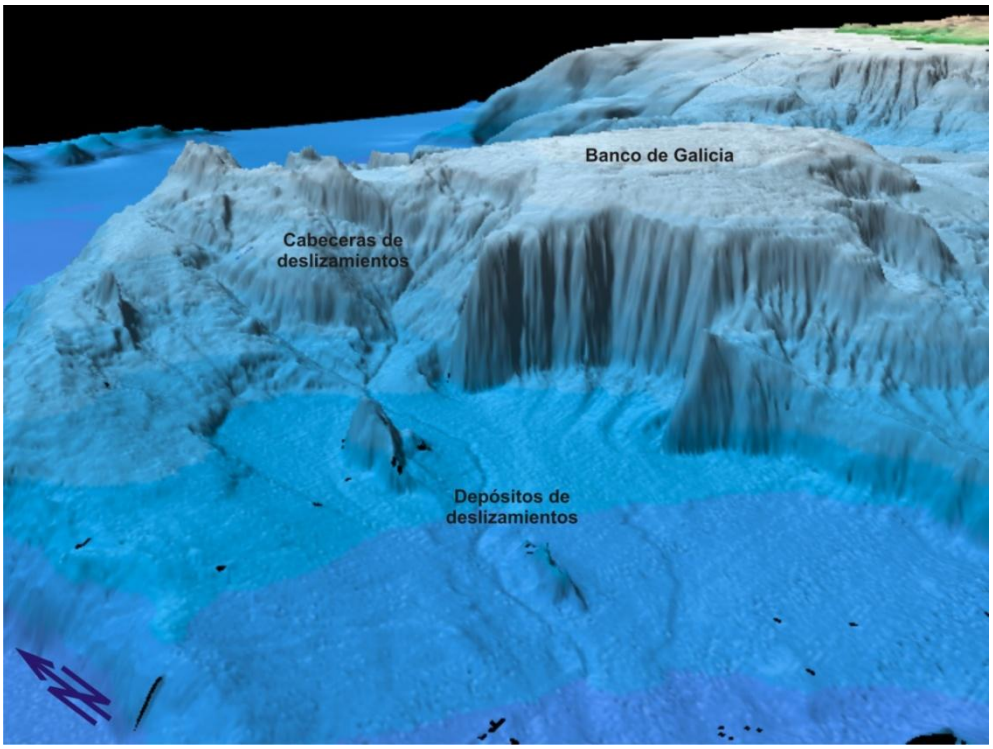

Figura 2. Modelo digital del banco de Galicia y sus alrededores. Fuente: IEO

La parte superior del BG es relativamente plana, a excepción de la parte más oriental que consiste en una serie de picos escarpados a lo largo de la vertiente oriental del banco. La parte plana está cubierta por una gruesa capa de exudado de foraminíferos planctónicos con un tamaño de grano medio de unas 190 micras y sólo el 0,2% de carbono orgánico (Flach y col., 2002). La superficie del sedimento se compone de

numerosas pequeñas ondulaciones actuales y de "megaripples" ocasionales de unos 50 cm de altura, lo que indica movilidad y altas velocidades actuales de los sedimentos.

Comunidades de corales de aguas frías como *Lophelia pertusa* y *Madrepora oculata* se encuentran en parches aislados cerca o encima de los "megaripples" (Somoza y col., 2014). El pico oriental del banco consiste en roca basáltica estéril sin apenas corales u otras formas de vida. La zona de transición entre la llanura de arena y las cumbres áridas está densamente cubierta por crinoideos móviles (Duineveld y col., 2004). El banco presenta también pequeños relieves montañosos ("knolls"), pequeñas crestas y canales, y dos valles rectilíneos en el sector sur. Estos valles tienen 40 m de relieve, están orientados en dirección NNO y su origen es probablemente tectónico, si bien han sido modelados por los procesos sedimentarios dominantes durante los descensos del nivel del mar (Black y col., 1964).

5.2 ANTECEDENTES

5.2.1 ANTECEDENTES EN LA EXPLOTACIÓN DE LOS RECURSOS

Existe poca información sobre la explotación de los recursos pesquero-marisqueros del BG. Dada la lejanía del banco de los principales puertos pesqueros gallegos, la carencia de cartas de la zona, las elevadas profundidades y el desconocimiento sobre la presencia y abundancia de especies comerciales, es de suponer una actividad pesquera relativamente reducida y reciente en el tiempo.

No se conoce con exactitud cuándo fue el primer momento que el sector pesquero tuvo conciencia de la existencia del BG. La principal fuente de información proviene de unos informes realizados sobre las primeras prospecciones de pesca promovidas por la Asociación Provincial de Armadores de Pesca Fresca de Pontevedra, realizadas en el banco con la ayuda científica del Instituto de Investigacións Mariñas (IIM-CSIC) (Pérez-Gándaras, 1980), donde se nombran varios barcos de diversos puertos gallegos con palangres o volantas. El primero de ellos, según dicho informe, fue el "Puerto de Burela", en 1971, con palangre de fondo. En 1975 se tiene constancia de la presencia de dos volanteros, el "Sirín" y el "Rodriguez Baz", con capturas de cherna (*Polyprion americanus*), tomás (*Epigonus telescopus*), alfonsino (*Beryx splendens*) y brótola de fango (*Phycis blennoides*). En 1979 se recoge la actividad de dos palangreros, el "Nuevo Golondrina", que capturó 140 cajas de palometa (*Brama brama*) y el "Monte Real", que hizo buenas capturas de pez espada (*Xiphias gladius*).

En 1980 ya había varios palangreros al pez espada, entre los que se nombran los "Hermanos Bahamonde", "Monte Real", "Peña Liceira", "Angel Mari" y "Playa de Celeiro", todos de la costa lucense. También se menciona algún intento de realizar arrastre de fondo en la zona. A partir de 1985 hay entre cuatro y cinco barcos dirigidos a la palometa roja (*Beryx* spp.), de tres a cuatro barcos que trabajan mediante la modalidad de palangre de fondo y uno con la modalidad de enmalle (Serrano y col., 2014). A final de la década de 1990 desaparece la pesquería de palangre de fondo dirigida a *Beryx* spp, y es sustituida por la de enmalle dirigida a rape (*Lophius* spp). Al mismo tiempo, comienza a desarrollarse una pesquería mediante palangre de fondo dirigida a tiburones de profundidad, principalmente *Centroscymnus coelolepis* y *Centrophorus squamosus*. En esta pesquería participan aproximadamente tres barcos, en función del año y de la época. A principios del 2000, unos siete barcos faenan de forma esporádica en la zona de estudio. Cuatro barcos dedicados a la modalidad de enmalle (miños y volantas), cuya especie objetivo es el rape, y tres dedicados a la pesca de los tiburones de profundidad mediante la modalidad de palangre de fondo. Existe también cierta actividad estacional en la pesquería de cacea dirigida al bonito (*Thunnus alalunga*) de manera casi específica.

Finalmente, la implementación en los últimos años de una legislación más restrictiva sobre los períodos de pesca (descanso semanal), las prohibiciones de la pesca de tiburones de profundidad (Reglamento Europeo 1262/2012) y del calado de las artes de enmalle a más de 600 m han contribuido a limitar la actividad pesquera en esta zona.

A nivel marisquero, la abundancia de cangrejo real *Chaceon affinis* fue también documentada en la misma serie de prospecciones (Pérez-Gándaras, 1980, 1981a,b). En dichos informes se mencionan unos rendimientos de 1,63 individuos/nasa y unas posibilidades de pesca para cuatro embarcaciones de 700 kg de cangrejo real por barco y día. Al final de la década de 1980 se descubre también la abundancia de este recurso en el talud de la plataforma gallega, entre 15 y 40 millas de la costa.

En 1990-1991, y durante distintos períodos, la por entonces denominada Consellería de Pesca, Marisqueo y Acuicultura (Xunta de Galicia) promueve la realización de campañas experimentales subvencionadas para la captura de cangrejo real. De todos los barcos que participaron en las campañas, tan solo uno de ellos, el "Madre Modesta" faenó en el BG entre 612-640 m (Ramonell y col., 1990). Las capturas declaradas por este barco fueron de 2594 individuos en 220 nasas, con unos rendimientos de 11,8 individuos/nasa, supuestamente con nasas grandes del tipo "nasa fanequeira".

Por lo visto anteriormente, podemos considerar la presión pesquera realizada sobre el banco como baja, con una actividad esporádica con artes de pesca considerados poco destructivos, principalmente enmalle y anzuelo, lo que ha permitido un alto grado de conservación de este ecosistema.

5.2.2 ANTECEDENTES EN LA INVESTIGACIÓN CIENTÍFICA

El BG ha siso objeto de interés en diversos y variados campos científicos. La primera referencia bibliográfica sobre la existencia del BG la encontramos en Black y col. (1964). Las primeras investigaciones llevadas a cabo en este entorno están dirigidas a estudios geomorfológicos de la corteza, en donde figuran por primera vez mapas batimétricos más o menos detallados (Sibuet y col., 1978; Vanney y col., 1979).

Los primeros estudios malacológicos surgen a raíz de las capturas accidentales de corales y gorgonias durante las primeras prospecciones pesqueras, sobre los cuales se encontraron adheridos diversas especies de moluscos. En un primer informe sobre la riqueza malacológica del banco (Rolán y Gándaras, 1980) se citan dos braquiópodos y 30 especies de moluscos gasterópodos y bivalvos. Este listado fue publicado posteriormente con ligeros cambios (Rolán y Pedrosa, 1981).

Posteriores campañas e investigaciones han permitido el descubrimiento de numerosas especies marinas, alguna de ellas nuevas para la ciencia. Algunos ejemplos son el monoplacóforo *Laevipilina rolani* (Warén y Bouchet, 1990), los solenogastros *Urgorria compostelana* (García-Alvarez y Salvini-Plawen, 2001), *Hemimenia cyclomyata*, *H. glandulosa*, *Neomenia oscari* y *N. simplex* (Salvini-Plawen, 2006), los crustáceos *Uroptychus cartesi* (Baba y Macpherson, 2012) y *Petalophthalmus papilloculatus* (San Vicente y col., 2014), la esponja carnívora *Chondrocladia robertballardi* (Cristobo y col., 2015) o el gasterópodo *Aforia serranoi* (Gofas y col., 2014), constituyendo en su conjunto una muestra de la importante biodiversidad que alberga el banco.

Las primeras investigaciones científico-pesqueras con objeto de evaluar la composición y abundancia de especies de interés pesquero en el BG tienen lugar por parte del ya mencionado IIM-CSIC en distintos períodos de 1980 y 1981. Los estudios fueron realizados a bordo de barcos de pesca de distintas modalidades (arrastre, palangre) y las especies más abundantes fueron el reloj mediterráneo (*Hoplostethus*

mediterraneus) con artes de arrastre y brótola de fango (*Phycis blennoides*), tomás (*Epigonus telescopus*), congrio (*Conger conger*) y mora (*Mora moro*, Fig. 3), aunque figura erróneamente como *Phycis phycis* en el informe original, con artes de anzuelo.

Figura 3. Varios ejemplares de mora (*Mora moro*) capturados en el banco de Galicia

En la década de 1990, el Instituto Español de Oceanografía (C.O de Vigo) realiza una serie de campañas experimentales primero con palangres (palangre de fondo y piedra-bola) en los años 1997-1998 y a continuación con arrastre de fondo, en los años 1998-1999. Las especies capturadas más abundantes fueron quelvacho (*Centrophorus squamosus*) y quelve (*Centrophorus granulosus*) con palangre de fondo, alfonsino (*Beryx splendens*) con palangre piedra-bola y reloj mediterráneo (*Hoplostethus mediterraneus*) con arrastre de fondo (Piñeiro y col., 2001).

El hundimiento del petrolero "Prestige" el 19 de noviembre de 2002, en una zona próxima al BG y a una profundidad de 3850 m, supuso la movilización multidisciplinar de todos los centros de investigación de Galicia, y la publicación de diversos trabajos sobre la geomorfología, polución marina y dinámica oceanográfica de la zona (Albaigés y col., 2006; Ercilla y Vilas, 2008).

Por último, el Instituto Español de Oceanografía (C.O de Santander), dentro de los proyectos ECOMARG e INDEMARES, realiza tres campañas oceanográficas entre los años 2009 y 2011, con el fin de recolectar datos que permitieran avanzar en el conocimiento del banco y del funcionamiento de la zona en su conjunto. Las especies de

peces recolectadas durante estas campañas van a constituir el material de partida de la presente tesis doctoral.

5.3 CARACTERÍSTICAS OCEANOGRÁFICAS

El margen occidental de la península Ibérica se encuentra en el extremo nororiental del giro subtropical. La circulación en este sector del Atlántico gira siguiendo el sentido de las agujas del reloj, como resultado de la acción de los vientos alisios y vientos del oeste, combinados con la fuerza de Coriolis, derivada de la acción de los márgenes continentales.

El BG está bañado por capas de diferentes masas de agua de origen norteño y sureño. Hasta tres masas de agua diferentes se pueden identificar en la zona (Cartes y col., 2014; Somoza y col., 2014) (Fig. 4).

- **Masa de agua central del Atlántico NE europeo (East North Atlantic Central Water: ENACW):** por debajo de las aguas superficiales y hasta los 500-600 m. Formada por subducción y mezcla invernal en la región entre el noreste de Azores y el margen occidental europeo (Pollard y Pu, 1985, González-Pola y col., 2005). Dentro de estas aguas se pueden distinguir dos subtipos de agua de origen y características termohalinas diferentes (Somoza y col., 2014). El subtipo subtropical ENACWt (T=12,2-18,5°C, S=35,66-36,75‰), cuyo origen se encuentra en un frente cerca de las Azores. El subtipo subpolar ENACWp está formado por agua más fría y menos salina que se forma en invierno en la parte este del Atlántico norte, sobre los 46°N, por enfriamiento y convención profunda (T=4-12°C y S=34,96-35.66‰).
- **Masa de agua mediterránea (Mediterranean Outflow Water: MOW)**: se forma en el Golfo de Cádiz a partir de la salida de agua profunda desde el mar Mediterráneo al océano Atlántico a través del estrecho de Gibraltar y progresa hacia el norte a lo largo del margen oeste ibérico. Esta agua relativamente densa, a su salida de la cuenca mediterránea, comienza a mezclarse con agua más fría y menos salina a medida que se desplaza, formando dos núcleos situados en 800 m (AMs, T=13ºC, S=36.4‰) y 1200 m (AMs, T=13ºC, S=36.4‰) (Daniault y col., 1994; Iorga y Lozier, 1999).

- **Masa de agua del Labrador (Labrador Sea Water: LSW)**: Capa más profunda. Proviene del noroeste y tiene su centro sobre los 1800-1900 m (Pingree, 1973; Johnson y col., 2005), con valores ya dados por Worthington y Wright (1970) de T=2.4ºC y S=34.92‰.

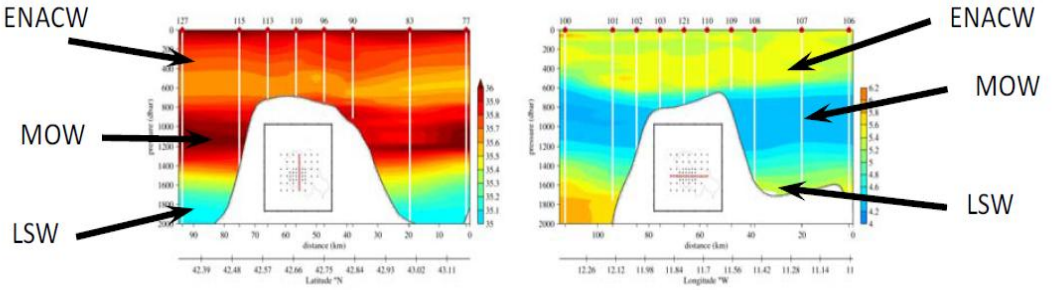

Figura 4. Capas de agua que bañan el BG mostrando una sección vertical de salinidad a lo largo de una sección meridional que cruza el eje principal del Banco en agosto de 2010 (izquierda) y oxígeno disuelto (ml/l) a lo largo de una sección zonal que cruza el eje principal del banco. Se muestran mapas con las isobatas de 1000 y 2000 m y las secciones (derecha). Proyecto VACLAN/COVACLAN- IEO.

Por debajo de estas masas de agua, se reconocen otras masas de agua profunda que no interactúan con la morfología del BG (Somoza y col., 2014).

El relieve de las montañas submarinas interactúa con la circulación oceánica modificando las condiciones de oligotrofismo imperantes en el mar profundo. La interrupción de las corrientes oceánicas, con la consiguiente formación de giros o anillos ("meddies"), corrientes circulares (columnas de Taylor) y afloramientos locales, son factores causantes de incrementos locales de la producción primaria y secundaria, fundamentalmente por el ascenso de nutrientes y fenómenos de retención y acumulación de larvas y plancton (Fock y col., 2002). La dinámica que se establece alrededor de los montes submarinos es la de un sistema altamente complejo de interacciones que depende de muchos procesos y características de éstos. La influencia de la estructura del monte depende de diversas variables topográficas (altura y extensión), profundidad de la cumbre, localización geográfica del monte (latitud y distancia a la plataforma continental) y pendiente.

White y Mohn (2004) y Lavelle y Mohn (2010) resumen los procesos físicos oceanográficos que se producen por la interacción entre las montañas submarinas y el

océano. En cuanto al BG, su impacto en la circulación en el Atlántico noreste ha sido reconocido en distintos estudios (Mazé y col., 1997; Coelho y col., 2002; Colas, 2003).

Las columnas de Taylor, los "meddies", la marea interna o los filamentos de afloramientos son algunos de estos fenómenos oceanográficos de mesoescala, responsables de la enorme riqueza existente en el BG (Serrano y col., 2014). El cambio de dirección de las corrientes marinas al chocar con el banco, producen las llamadas columnas de Taylor, que tienen como consecuencia giros sobre la cima y finalmente un enriquecimiento de las aguas que bañan el banco. La cima del banco está a una profundidad de 625 m próxima a donde se localiza la vena de agua mediterránea. La estratificación a esta profundidad favorece la intensificación de fenómenos como la marea interna. Asimismo, al nivel de la capa de agua mediterránea, existe en el área actividad de mesoescala, con vórtices conocidos como meddies. Estos meddies son generados cerca de la costa y en su desplazamiento mar adentro pueden interaccionar con el banco. Alvarez-Salgado y col. (2006) documentan una estructura ciclónica observada sobre el banco causada probablemente por una rama de la Iberian Poleward Current separada del talud en 42º N fluyendo al norte y oeste, que interactuaría con la corriente de Portugal que fluye al sur y al este, rodeando el flanco occidental del banco. De manera similar, la corriente mediterránea (MOW) se separa del talud, en aproximadamente 42ºN, en dos ramas, una que fluye al oeste del BG y otra fluye hacia el norte a lo largo del talud continental de la Península Ibérica (Mazé y col., 1997; Iorga y Lozier, 1999).

Otro fenómeno de mesoescala que puede influir en el banco es la generación de filamentos que exportan la producción del sistema de afloramiento hacia mar adentro y pueden alcanzar el banco.

5.4 MARCO GEOMORFOLÓGICO DEL BANCO DE GALICIA

El margen continental del oeste de Galicia se clasifica como no volcánico, creado a partir de la propagación hacia el norte de la apertura del océano Atlántico, hace aproximadamente 110 M.a. (Malod y col., 1993). Presenta una geomorfología formada por estructuras de bloques levantados y hundidos limitados por fallas. La región limita al norte con la llanura abisal de Vizcaya y al oeste con la llanura abisal Ibérica.

En este margen continental se diferencian, de este a oeste, cinco unidades fisiográficas (Fig. 5): (1) Plataforma continental, (2) Talud continental; (3) Cuenca

interior de Galicia, (4) Plataformas marginales y/o región de bancos submarinas, y (5) Ascenso continental o margen profundo de Galicia.

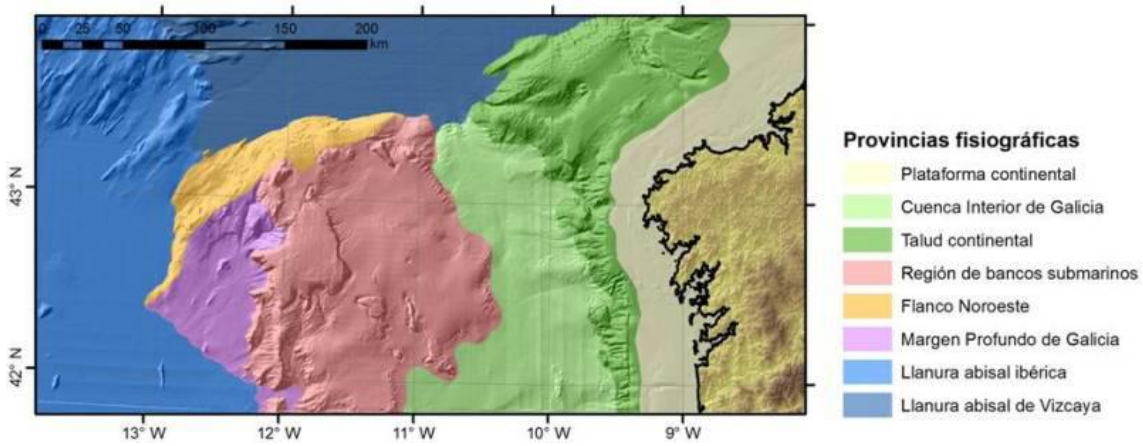

Figura 5. Provincias fisiográficas del margen continental del noroeste de Iberia según Serrano y col. (2014)

La plataforma continental es relativamente estrecha, con una anchura media de 35 km y su borde se sitúa a partir de 180-200 m de profundidad.

El talud continental presenta una anchura media de 22 km, con el límite inferior sobre los 2.500-3.000 m de profundidad. Está dividido en dos sectores, el talud superior, hasta los 1800 m de profundidad, con pendientes relativamente altas, y el talud inferior, hasta más allá de los 2500 m, con pendientes relativamente más suaves.

La cuenca interior de Galicia es una cuenca sedimentaria de grandes dimensiones (350 km de largo, 100 km de ancho, 3-4 km de profundidad) que recorre el margen oeste peninsular a partir de la plataforma continental gallega.

Las plataformas marginales y/o montañas submarinas forman relieves tabulares discontinuos en el ascenso continental. De norte a sur son los siguientes: banco de Galicia (~600 m de profundidad), Vigo (~2100 m de profundidad), Vasco da Gama (~1750 m de profundidad) y Porto (~2200 m profundidad) (Pinheiro y col., 1996).

El Ascenso continental o Cuenca profunda de Galicia, se extiende desde 4000 a 5300 m de profundidad y está caracterizado por una topografía suave interrumpida por la presencia de bancos geoestructurales.

En el marco geológico, el margen continental puede ser dividido en cinco áreas bien delimitadas: (1) la plataforma continental; (2) la Cuenca Interior de Galicia; (3) los Bancos Occidentales; (4) el Margen Profundo de Galicia y la Llanura Abisal de Iberia al

oeste; y (5) el Escarpe Septentrional de Galicia con la Llanura Abisal de Vizcaya al norte.

La plataforma continental presenta una cobertura sedimentaria delgada y numerosos afloramientos de rocas paleozoicas y mesozoicas. Se caracteriza por presentar una textura mixta, tanto siliciclástica como carbonatada, con una banda longitudinal de dirección N-S en la plataforma media compuesta por sedimentos limosos denominada cinturón fangoso de Galicia (Ares y col., 2008).

La Cuenca interior de Galicia presenta un encuadre estructural formado por fallas normales con dirección NNO-SSE cruzadas por fallas NE-SO (Boillot y col., 1988). El basamento continental está fracturado por fallas normales y fallas afectando a bloques estrechos (10-20 km) y alargados (60-100 km) basculados con dirección NE inclinadas ligeramente al E (Alonso y col., 2008).

Los Bancos Occidentales que separan la Cuenca Interior de Galicia de la zona profunda del margen se consideran como *horsts* tectónicos de la etapa extensional mesozoica y reactivados posteriormente durante la etapa compresiva cenozoica (Boillot y col., 1979).

El Margen gallego profundo se caracteriza por tratarse de un sistema sedimentario profundo estructurado en bloques basculados por procesos de extensión que da lugar a la formación de *horsts*, *grabens* y *semigrabens*.

El escarpe septentrional de Galicia constituye una zona compresiva cuyo basamento pertenece al dominio oceánico.

El origen del BG es probablemente tectónico si bien ha sido modelado por los procesos sedimentarios dominantes durante los descensos del nivel del mar (Black y col., 1964).

La sedimentación en el BG no tiene un origen continental, sino que procede de la propia columna de agua que cubre el monte submarino. Se trata, principalmente, de sedimentos marinos que proceden fundamentalmente de restos de conchas de pequeños organismos planctónicos y de otros depósitos procedentes de partículas removilizadas que son depositadas en estas zonas por corrientes submarinas profundas (de la Torriente y col., 2014).

5.5 TAXONOMÍA ÍCTICA Y NOMENCLATURA

Los peces constituyen más de la mitad del número total de las aproximadamente 54.711 especies conocidas de vertebrados. Hay descritas unas 27.977 especies válidas de peces, en comparación con las 26.734 de tetrápodos (Nelson, 2006).

La sistemática es el estudio de las relaciones y la clasificación de los organismos, que incluye las disciplinas de la nomenclatura y la taxonomía. La nomenclatura se ocupa de asignar nombres científicos a los organismos y la taxonomía es la ciencia de la descripción y la clasificación de los organismos, fundamental en la biología básica y aplicada (Guerra-García y col., 2008).

Clasificar es organizar en grupos o conjuntos a distintos elementos u organismos que comparten uno o más caracteres y que a su vez, pueden diferenciarse de los miembros de otros grupos. Identificar un ejemplar consiste en adjudicarlo al grupo o taxón al que pertenece, de acuerdo con un modelo clasificatorio elaborado con anterioridad (Lanteri y col., 2004).

La correcta identificación de las especies ícticas es la base de otras disciplinas de la biología básica como la ecología, biogeografía, biodiversidad, pero también de la biología aplicada, como biología pesquera, salud animal y humana, fraude alimentario, trazabilidad alimentaria, inspección pesquera, etc.

La taxonomía tradicional se basa en la descripción de los fenotipos (Boero, 2010), es decir, de los caracteres morfológicos visibles que diferencian a una especie de otra. La morfología es la disciplina de la zoología que estudia la forma, la estructura y el desarrollo de los organismos (Lloris, 2015). Los caracteres morfológicos son las partes observables o atributos de los organismos que constituyen la unidad del análisis sistemático (Gill y Mooi, 2002).

En los peces, los principales caracteres usados tradicionalmente para la identificación de especies son atributos descriptivos (Strauss y Bond, 1990), que hacen referencia a: caracteres morfológicos distintivos (por ejemplo la forma del cuerpo, número y tipo de radios de las aletas) (Fig. 6), medidas morfométricas (Fig. 7), que hacen referencia a variables numéricas continuas (por ejemplo la longitud de la cabeza en relación a la longitud del cuerpo) o caracteres merísticos, variaciones en el número de una estructura o parte de ella, y que hacen referencia a variables numéricas discretas (por ejemplo el número de radios blandos y espinosos de la aleta dorsal).

Cada especie tiene una serie de características bien definidas obtenidas a partir de un primer espécimen utilizado para realizar la descripción taxonómica, llamado espécimen tipo u holotipo. Los caracteres distintivos de varias especies constituyen una clave dicotómica, que consiste en un modelo o esquema que permite la determinación de distintas especies a través de la comparación de caracteres excluyentes (Lahitte y col., 1997).

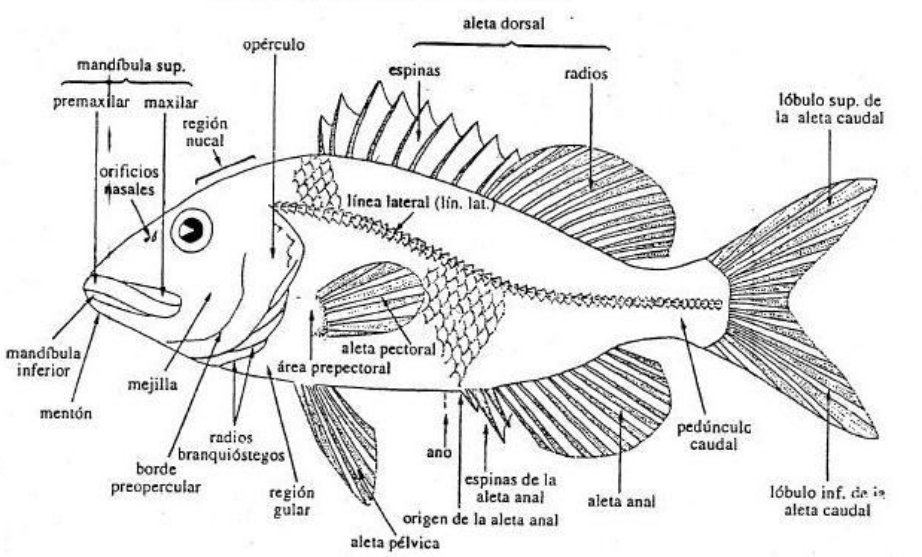

Figura 6. esquema básico de la anatomía de un pez mostrando las principales partes y estructuras de carácter taxonómico. Fuente: Ichthyology at the Florida Museum of Natural History (https://www.flmnh.ufl.edu)

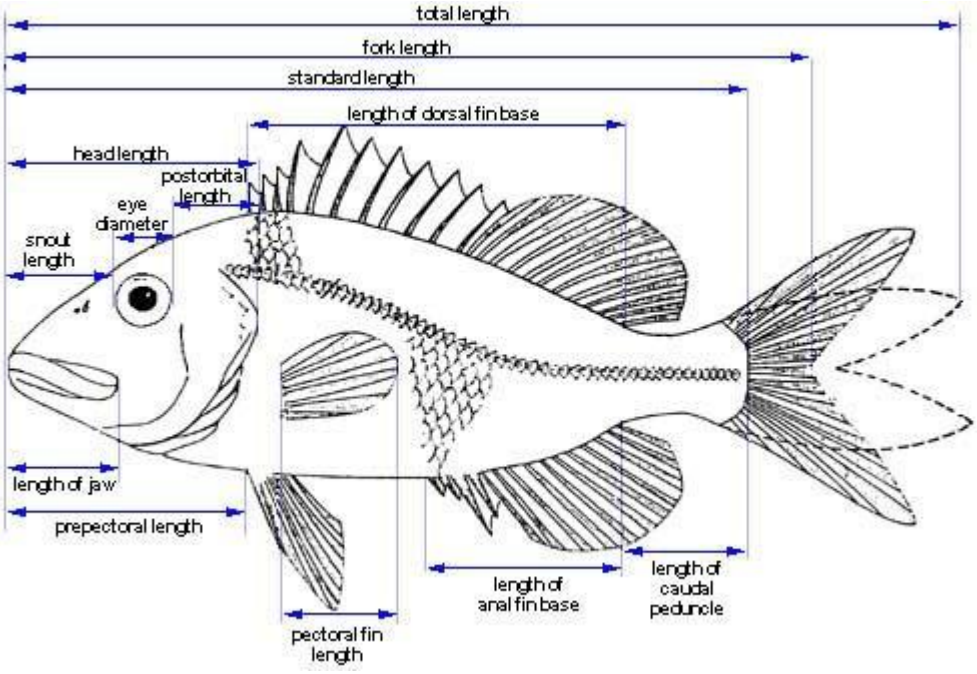

Figura 7. Algunas de las principales biometrías utilizadas en la identificación de peces. Fuente: Ichthyology at the Florida Museum of Natural History (https://www.flmnh.ufl.edu)

Además de la taxonomía clásica, basada principalmente en caracteres morfológicos externos, actualmente se utilizan otros métodos en la identificación de peces. En una reciente revisión, Fischer (2013) enumera hasta doce métodos distintos utilizados en la identificación de organismos acuáticos. Algunos de ellos son derivados de la aplicación de la taxonomía morfológica clásica, como por ejemplo la utilización de guías y claves de identificación, la utilización de colecciones de referencia o sistemas integrados de identificación online. Otros métodos son más novedosos, como IPez (Guisande y col., 2010) que consiste en un sistema automático de identificación de peces basado en un software de aprendizaje automático y que utiliza mediciones morfométricas de los ejemplares. Las estructuras duras, como los otolitos, con una morfología característica para cada especie, son utilizados en la identificación de peces teleósteos (Lombarte y col., 2006), con especial utilidad en la identificación de presas de los contenidos estomacales.

La identificación taxonómica con marcadores moleculares de ADN mitocondrial se ha ido instaurando en los últimos años con mucha fuerza en la taxonomía moderna. Teletchea (2009) enumera entre los más frecuentes citocromo b, 16S RNA, 12S RNA, 5S RNA, D-Loop, ATPasa, ATPasa 8, ND3/ND4 y COI. De todos ellos, citocromo c oxidasa I (COI) es el que cuenta actualmente con más arraigo y aceptación.

5.6 CÓDIGO DE BARRAS DE ADN

En 2003, investigadores de la Universidad Guelph en Ontario (Canadá), animaron a la comunidad científica implicada en el "Census of Marine Life" a la determinación de códigos de barras de ADN de los especímenes que se iban recolectando. El análisis de la secuencia de nucleótidos de un gen concreto previamente consensuado, con objeto de permitir la identificación de la especie a la que pertenece, pasó a denominarse "DNA barcoding" o examen de código de barras de ADN, por analogía con los códigos de barras UPC ("universal product code") de doce dígitos que sirven para la identificación de mercancías (Hebert y col., 2003 a,b).

El fundamento de la identificación mediante código de barras de ADN estaría en el hecho de que incluso una secuencia de ADN corta contiene información más que suficiente como para distinguir diez o incluso 100 millones de especies. Por ejemplo, un

segmento de 600 nucleótidos perteneciente a un gen codificante de proteína contiene 200 posiciones correspondientes a la tercera base de cada codón. Al tratarse de un gen proteico, en estas posiciones las sustituciones suelen ser neutrales desde el punto de vista selectivo, y las mutaciones se acumulan por el proceso aleatorio de la deriva génica. Incluso asumiendo que un grupo de organismos se encuentre sesgado al empleo de AT o GC en las terceras posiciones de los codones, seguirá habiendo dos posibles alternativas de base en 200 terceras posiciones distintas, es decir, $2^{200} = 10^{60}$ posibles secuencias distintas basadas tan sólo en los cambios que ocurran en la tercera posición de los codones. La prueba de que este principio es válido fue aportada mediante la comparación de secuencias del gen mitocondrial codificante de la subunidad I del enzima citocromo c oxidasa entre especies cercanas y entre diversos filos del reino animal (Hebert y col., 2003b).

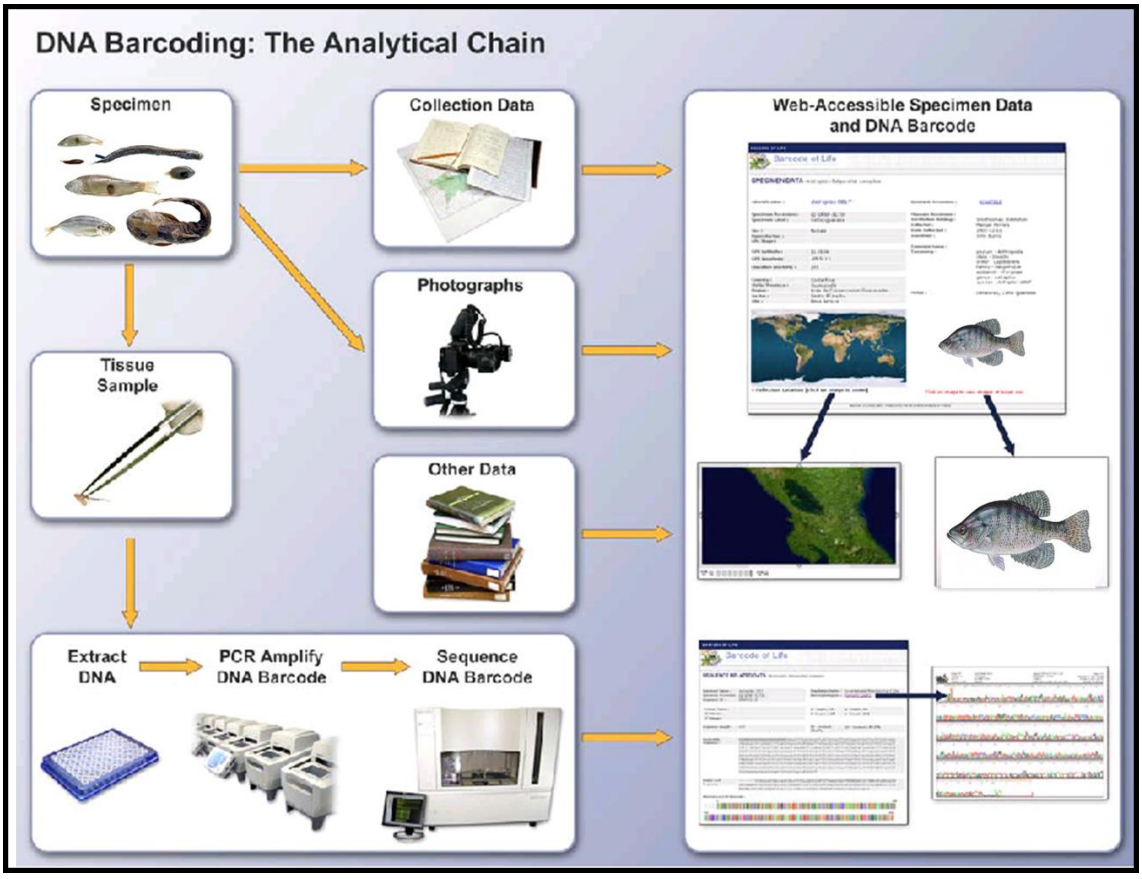

Figura 8. Cadena analítica de identificación de especies por código de barras de ADN. (https://paibiopai.wordpress.com)

Ya en 2003 se especulaba con que el "DNA barcoding" tendría el potencial de ser un método práctico para la identificación de los 10 millones de especies estimadas de eucariotas sobre la tierra. Como método uniformizado de identificación de especies, el examen del código de barras de ADN tendría amplias aplicaciones científicas, siendo de gran utilidad en biología de la conservación, incluyendo campañas de estudio de la biodiversidad. Podría ser incluso aplicado allí donde los métodos tradicionales no consiguieran ser resolutivos como, por ejemplo, en la identificación de puestas, embriones y formas inmaduras o en el análisis del contenido estomacal o de las excreciones, para la determinación de cadenas tróficas. Además de la facilitación de la identificación de especies, los códigos de barras de ADN ayudarían al análisis filogenético y a revelar la historia evolutiva de la vida sobre la tierra.

Un gen apropiado cuya secuencia de nucleótidos pueda servir como código de barras de ADN debe estar suficientemente conservado a lo largo del proceso evolutivo como para que su amplificación, por PCR, pueda realizarse con cebadores de rango amplio y, al mismo tiempo, debe divergir suficientemente como para permitir la discriminación entre especies. Cierto número de genes podrían cumplir con los requisitos exigidos (discriminación e identificación de especies, descubrimiento de especies nuevas y crípticas, reconstrucción de relaciones evolutivas entre especies y taxones superiores). La elección del gen mitocondrial codificantede la subunidad I del enzima citocromo c oxidasa (COI) está apoyada por numerosos resultados experimentales (Achurra y Erséus, 2013; Radulovici y col., 2010).

En algunos grupos taxonómicos, sin embargo, el código de barras de ADN no es eficiente. Los cnidarios (anémonas, corales y algunas medusas), por ejemplo, exhiben una diversidad de secuencia mitocondrial pequeña, tal vez por poseer un sistema adicional de reparación de mutaciones del ADN mitocondrial. En las plantas superiores, la secuencia de nucleótidos de COI es poco variable y, por lo tanto, no permite identificar especies. Tampoco se resuelven bien, mediante examen del código de barras de COI, las especies recién divergidas desde el punto de vista evolutivo y aquéllas surgidas mediante hibridación.

Los puntos esenciales de la iniciativa de examen del código de barras son (Fig. 8):

1) preservación del espécimen en etanol al 95% para facilitar el aislamiento del ADN.

2) amplificación y secuenciación del gen diana consensuado (COI).

3) depósito en una base de datos de las secuencias ligadas a los especímenes, incluyendo datos adicionales de los mismos.

El éxito del examen de códigos de barras de ADN depende de la conexión entre la secuencia de nucleótidos de COI a su correspondiente espécimen y sus datos asociados (recolector, confirmación taxonómica, fecha, referencia geográfica en forma de coordenadas, etc.).

Como secuencia de código de barras se utiliza el segmento 5´ del gen mitocondrial que codifica la subunidad I del enzima de citocromo c oxidasa, que se abrevia como COI-5P. Para su amplificación efectiva mediante reacción en cadena de la polimerasa (PCR) existen un conjunto de cebadores de rango amplio válidos para peces (Ivanova y cols., 2007).

Si bien inicialmente las secuencias de nucleótidos de código de barras de ADN generadas por la iniciativa "Census of Marine Life" se depositaban en el banco de secuencias generalista denominado GenBank (www.ncbi.nlm.nih.gov/genbank/), en la actualidad se dispone de una base de datos específica de secuencias COI-5P, denominada "Barcoding of Life Datasystems" (BOLD, www.boldsystems.org) (Ratnasingham y Hebert, 2007), que incluye 24.000 registros de elasmobranquios y 237.004 de actinopterigios (22 de febrero de 2016).

La identificación de especies se basa en la divergencia de las secuencias de nucleótidos COI-5 dentro y entre las especies (distancias intra e interespecificas). Idealmente se espera la aparición de un "gap" o una zona donde el valor superior de las distancias intra-específicas se encuentre alejado del valor inferior de las distancias inter-específicas, de manera que no exista un solapamiento entre estos dos valores.

FISH-BOL, la campaña de código de barras de ADN de peces, es una colaboración científica internacional que pretende crear una base de datos de referencia estandarizada que incluya los códigos de barras de ADN de todos los peces (Ward y cols., 2009). El análisis se dirige al examen de 648 pares de bases de la región 5´ del gen mitocondrial citocromo c oxidasa I (COI). En 2009 se habían recogido más de 5.000 especies, con una media de 5 códigos por especie, procedentes de sendos especímenes con identificaciones realizadas por expertos (especímenes de referencia o "voucher"). Hasta la fecha, los resultados indicaban que los códigos de barras separaban, aproximadamente, el 98% de las especies de peces marinos examinadas. Mediante taxonomía integrativa se pudo confirmar el estatus de especie nueva en el caso de varios especímenes con secuencias de códigos divergentes inicialmente adscritos a la misma

especie. En relación con las precauciones debidas ante el uso de códigos de barras para la discriminación entre especies, hay que decir que estas incluyen la hibridación, la radiación evolutiva reciente, la diferenciación regional de los códigos y de copias nucleares de los mismos. Los resultados indican que tales situaciones se han contemplado escasamente en la inmensa mayoría de las especies estudiadas.

En peces, el valor medio de las diferencias en la secuencia de nucleótidos de códigos de barras pertenecientes a ejemplares de la misma especie o distancia intraespecífica media es de 0,3% (Zhang y Hanner, 2011), aproximadamente dos posiciones de nucleótidos distintas en la secuencia del código de barras, y el límite para considerar especies diferentes está cuando la variación sobrepasa el valor de 2% (Ward y col., 2009). Sin embargo, no hay un patrón común para todas las especies y estos valores pueden variar y no ajustarse a estas cifras. Por otro lado, Hebert y col. (2004) proponen la "regla del 10x" como un indicador para la delimitación de especies, por el que dos individuos se marcan como especies diferentes si sus secuencias de nucleótidos COI-5P difieren al menos 10 veces más que la distancia intraespecífica media del grupo. Finalmente, el depósito de las secuencias en bases de datos de referencia (por ejemplo GenBank o Barcode of Life Data Systems, BOLD) va a permitir asignar con una alta probabilidad de acierto secuencias de procedencia desconocida a secuencias de organismos previamente descritos representadas por los especímenes "voucher".

La aparición de una técnica de identificación molecular universal ha generado mucha controversia sobre su validez y limitaciones (Ebach y Holdredge, 2005a,b; Ebach, 2011), pero su valor y eficacia sobre la morfología también han sido exaltados por otros (Miller, 2007; Packer y col., 2009). Sin embargo, en los últimos años el concepto de una taxonomía integrativa, no excluyente, se ha ido imponiendo (Dayrat, 2005; Kipling y col., 2005; Goldstein y col., 2010). El código de barras de ADN no excluye a la taxonomía clásica morfológica sino que la complementa y ambas son necesarias para la correcta identificación de las especies.

5.7 COMENTARIOS DEL DOCTORANDO

Si bien esta tesis está centrada en la ictiofauna del BG, se han incluido especies del mismo o similar nivel taxonómico capturadas fuera de esta área. La adicción de estas especies fue considerada necesaria debido a su alto interés científico y a que pueden servir como elementos comparativos y diferenciadores en la identificación de las

especies del BG, ya sea a nivel morfológico, pero sobre todo a nivel molecular, dada la escasez de secuencias del gen COI de peces de aguas profundas depositadas en las bases de datos de referencia, principalmente BOLD y GenBank. La exactitud de la identificación molecular va a depender, entre otros factores, del número total de secuencias que pertenecen a las especies identificadas y a taxones estrechamente relacionados depositadas en las bases de datos (Millar y col., 2011).

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6 COMPOSICIÓN TAXONÓMICA Y ASPECTOS BIOGEOGRÁFICOS DE LA ICTIOFAUNA DEL BANCO DE GALICIA

6.1 LISTADO FAUNÍSTICO DE LA ICTIOFAUNA DEL BANCO DE GALICIA: ESPECIES VULNERABLES Y ASPECTOS BIOGEOGRÁFICOS

Comparados con el océano circundante, los montes submarinos son ecosistemas altamente productivos y conocidos por su capacidad para soportar una gran biodiversidad, incluyendo comunidades biológicas especiales como los arrecifes de coral de aguas frías, abundantes recursos pesqueros, mamíferos, tortugas y aves marinas (Niklitschek y col., 2010). Son, por tanto, hábitats de incalculable valor, tanto ecológico como económico. Aunque la existencia de las montañas submarinas es conocida desde hace cientos de años, la falta de tecnología para su exploración ha retrasado los estudios biológicos exhaustivos hasta finales de 1950 (Hubbs, 1959). Aún hoy en día, con la tecnología ya desarrollada, apenas unos 200 montes submarinos han sido estudiados en profundidad (Secretariat of the Convention on Biological Diversity 2008), por lo que todavía es muy escaso el conocimiento detallado de los hábitats, especies y su distribución en estas montañas submarinas. El BG no es una excepción a esta regla general; su descubrimiento para la ciencia es relativamente reciente (Black y col. 1964) y los primeros estudios de los organismos que lo habitan datan de principios de 1980 (Rolán y Pedrosa, 1981).

La riqueza y diversidad ictiológica en las montañas submarinas no está bien documentada (Fig. 9). Aunque el número de las montañas submarinas investigadas es pequeño, cada vez es más evidente que las comunidades de peces que llevan asociadas muestran adaptaciones específicas a estos hábitats y representan una porción relativamente elevada y singular de la biodiversidad de peces (Morato y Clark 2007). Koslow y col. (2000) describen las comunidades de peces de las montañas submarinas como aquellas que tienen en común características morfológicas, ecológicas, biológicas y fisiológicas que les permiten explotar con éxito un entorno con mayores corrientes y flujo de materia orgánica que la mayoría de las profundidades marinas. Muchas especies presentan adaptaciones a las fuertes corrientes al tener un cuerpo aplastado y presentan además tasas metabólicas y de ingesta de alimentos relativamente altas.

Figura 9. Captura de un arte arrastre GOC en el banco de Galicia donde se puede observar en un primer plano un ejemplar de *Cataetyx laticeps*.

Algunas especies demersales forman agregaciones en las montañas submarinas y dada su abundancia y valor comercial son objeto de importantes pesquerías (Clark, 2009). Se han sugerido varias hipótesis sobre las grandes concentraciones de peces que se producen alrededor de las montañas submarinas. Según Rogers (1994), el aumento de las presas sobre las montañas submarinas es, a su vez, debido al aumento de la producción primaria por los efectos topográficos y las condiciones hidrográficas locales o por la migración diaria del plancton, que queda atrapados durante su descenso durante el día por los depredadores que viven en la cima del monte submarino.

Pitcher (2010), cita las ocho especies con mayores capturas a nivel global en las montañas submarinas: reloj anaranjado *Hoplostethus atlanticus*, alfonsino *Beryx splendens*, tomás *Epigonus telescopus*, escolar *Ruvettus pretiosus*, sable negro *Aphanopus carbo*, pez jabalí *Pseudopentaceros richardsoni*, granadero *Coryphaenoides armatus* y reloj pardo sureño *Pseudocyttus maculatus*. En estos entornos se observan también agregaciones de especies pelágicas, ya que funcionan como estaciones de descanso, alimentación, reproducción y como puntos de orientación de muchas especies pelágicas migratorias, entre las que figuran diversas especies de túnidos *Thunnus* spp.,

pez espada *Xiphias gladius*, marrajo *Isurus oxyrinchus* y marlín azul *Makaira nigricans* (Morato y col., 2008, 2010).

Figura 10. El reloj mediterráneo *Hoplostethus mediterraneus* resultó ser la especie más abundante en el banco de Galicia, muy frecuente en la zona más somera y sedimentaria (Fuente: IEO-INDEMARES).

En el monte submarino del BG se han identificado 139 especies de peces marinos (ver anexo I). El listado se basa en nueve campañas de prospección e investigación llevadas a cabo desde 1980 hasta 2011 con diferentes artes de pesca. Las especies se agrupan en 2 superclases, 3 clases, 20 órdenes, 62 familias y 113 géneros. Las familias más diversas son Macrouridae con 9 especies, seguida por Moridae, Stomiidae y Sternoptychidae con 7 especies cada una. Por especies, el trachíchtido *Hoplostethus mediterraneus* (Fig. 10) y el mórido *Lepidion lepidion* fueron las más abundantes.

Debido probablemente a la gran extensión del banco, las numerosas campañas realizadas y los diferentes métodos de muestreo, el BG, es uno de los montes submarinos de los que mejor se conoce su ictiofauna, en comparación con otros montes submarinos del Atlántico Norte. Las 139 especies identificadas suponen una cifra muy superior a las 40 especies de Gorringe (Abecasis y col., 2009), 78 especies de Sedlo (Menezes y col., 2012), 53 especies de Meteor (Mohn, 2010) o las 34 especies de Ampère (Christiansen y col., 2015), todos ellos situados en el entorno de las Azores.

A nivel biogeográfico, y teniendo en cuenta la totalidad de las especies de peces presentes en el BG, 113 especies (81,3%) pertenecen al grupo Atlántico y 17 especies se adscriben al grupo del Lusitánico (12,2%) (ver anexo I). Los resultados muestran una ictiofauna compuesta en su mayor parte por especies de aguas profundas de amplia distribución, similar a la del talud continental. La ausencia de especies endémicas en el BG apoya la tesis que contempla los montes submarinos como ecosistemas singulares, ricos en biodiversidad pero no aislados (Samadi y col. 2006; McClain, 2007).

Por sus características biológicas y ecológicas, los peces de los montes submarinos son considerados como altamente vulnerables (Morato y col., 2006). En vista de las tres bases de datos utilizadas para evaluar este criterio en el BG (OSPAR, UICN y FishBase), 9 especies (6%) fueron consideradas como vulnerables según la UICN, 5 especies (3%) según OSPAR y 58 (42%) según FishBase. Sin embargo, en los casos de datos no disponibles por la UICN o en estudios macro-ecológicos generales o con un gran número de especies, el uso de las categorías de FishBase parece ser la mejor opción (Strona y col. 2013). Por lo tanto, el 42% de las especies de peces registradas en el BG, deben ser considerados como especies amenazadas (ver anexo I).

Los resultados obtenidos, una alta biodiversidad de peces y un alto nivel de vulnerabilidad, apoyan la declaración del BG como Área Marina Protegida.

6.2 ESPECIES DEL GÉNERO *APRISTURUS* (ELASMOBRANCHII: PENTANCHIDAE) EN EL BANCO DE GALICIA

El género *Apristurus* (Garman, 1913) (Condríctios: Pentanchidae) constituye un grupo de tiburones de aguas profundas de amplia distribución, con 37 especies reconocidas hasta el momento (Froese y Pauly, 2016). Las especies de *Apristurus* se caracterizan por tener un cuerpo largo y delgado, rostro largo y aplanado, aleta anal grande y elevada, separada de la aleta caudal más baja por una escotadura y la ausencia de una cresta de dentículos dérmicos en el margen superior de la aleta caudal en la mayoría especies (Sato y col., 1999).

El género *Apristurus* estaba tradicionalmente incluido en la familia Scyliorhinidae, pero recientes estudios filogenéticos moleculares y morfológicos han resucitado la familia Pentanchidae, mostrando que la familia Scyliorhinidae era parafilética (Maisey, 1984; Winchell y col., 2004; Iglesias y col., 2005). Pentánchidos (es decir, géneros *Apristurus*, *Asymbolus*, *Bythaelurus*, *Cephalurus*, *Galeus*, *Halaelurus*, *Haploblepharus*, *Holohalaelurus*, *Parmaturus* y *Pentanchus*) difieren de esciliorhínidos sensu estricto (es decir, géneros *Atelomycterus*, *Aulohalaelurus*, *Cephaloscyllium*, *Poroderma*, *Schroederichthys* y *Scyliorhinus*) por la ausencia de las crestas supraorbitales en el condrocráneo (Compagno, 1988). El género *Apristurus* comprende un grupo de pintarrojas de aguas profundas y amplia distribución, que habitan los taludes continentales y elevaciones submarinas a profundidades de 500 hasta 2100 m en todos los océanos, excepto en aguas polares.

Figura 11. Vista dorsal de un ejemplar de *Apristurus aphyodes* Nakaya y Stehmann, 1998, especie de *Apristurus* más frecuente en el banco de Galicia (Foto: Antonio Punzón).

De las 89 especies de tiburones presentes en aguas europeas, 6 pertenecen al género *Apristurus* (George y Zidowitz, 2006). En aguas españolas, sólo *Apristurus laurussonii*, había sido descrita anteriormente, citada como *A. atlanticus* en las Islas Canarias (Iglésias y Nakaya, 2004).

Varios ejemplares del género *Apristurus* fueron capturados en el monte submarino del BG (NE Atlántico), entre 1460 y 1809 m profundidad, durante un estudio multidisciplinario llevado a cabo en 2011 en el marco del proyecto INDEMARES (ver anexo II). Los análisis morfométricos y moleculares permitieron la identificación de los 20 ejemplares capturados, de los cuales 18 fueron *Apristurus aphyodes* Nakaya y Stehmann, 1998 (Fig. 11), uno *A. profundorum* (Goode y Bean, 1896) y otro *A. melanoasper* Iglesias, Nakaya y Stehmann, 2004. Los resultados moleculares basados en la comparación de códigos de barras de ADN apoyan la identificación de *A. profundorum* y *A. melanoasper*, con valores estadísticos de re-muestreo del 99% y 95%, respectivamente. La identificación molecular de *A. aphyodes* se realizó utilizando un segmento de 499 nucleótidos del gen mitocondrial 16S. Estos son los primeros registros de *Apristurus* en aguas gallegas, lo cual extiende su área de distribución conocida y proporciona nueva información sobre diferentes aspectos biológicos y ecológicos de este complejo grupo taxonómico.

Nakaya y Sato (1999), basándose en caracteres morfológicos como la longitud del rostro, el número de válvulas espirales y la longitud de los surcos labiales, distinguen tres grupos de especies diferentes en el género *Apristurus* (i.e. *brunneus*, *longicephalus* y *spongiceps*). Más tarde, estos grupos fueron reconocidos como monofiléticos por inferencias morfológicas y moleculares (Sato, 2000; Iglésias y col., 2005).

A. aphyodes y *A. profundorum* están incluidos en el grupo *spongiceps*, que se caracteriza por tener entre 7 y 12 válvulas espirales en el intestino, el surco labial superior subigual o más corto que el inferior y canal sensorial supraorbital continuo. *A melanoasper*, sin embargo, está incluido en el grupo *brunneus*, que se caracteriza por tener entre 12 y 23 válvulas espirales en el intestino, el surco labial superior más largo que el inferior y canal sensorial supraorbital discontinuo.

El descubrimiento en el BG de 3 nuevas especies de *Apristurus*: *A. aphyodes*, *A. profundorum* y *A. melanoasper*, incrementa notablemente el número de especies de este género en aguas españolas y establece una nueva especie, *A. profundorum*, para aguas europeas, como muestra de la importancia ecológica del banco y su aporte al conocimiento de la biodiversidad ictiológica marina.

6.3 COMPOSICIÓN DE ESPECIES DE LA FAMILIA HALOSAURIDAE (NOTACANTHIFORMES) EN EL BANCO DE GALICIA

Introducción

Notacanthiformes Goodrich 1909, es un orden de peces de aguas profundas que contiene las familias Halosauridae (halosáuridos) y Notacanthidae (notacántidos o anguilas espinosas) (Zhang, 2011). Los peces notacantiformes se caracterizan por tener un cuerpo anguiliforme, rostro que sobresale visiblemente por delante de la boca, grandes nódulos de tejido conectivo insertados entre el arco pterigoideo y el maxilar, y aletas ventrales unidas en la línea media ventral del cuerpo (McDowell, 1973; Nelson, 2006; Wiley y Johnson, 2010).

Los halosáuridos son peces bentónicos o bentopelágicos que se encuentran en todos los océanos, desde el talud de la plataforma continental hasta las llanuras abisales y desde 500 hasta 5000 m de profundidad, pero más frecuentemente entre 1100 y 3300 m (Klimpel y col., 2008). Aunque raramente son capturados, probablemente sean frecuentes desde el talud inferior hasta las zonas abisales (Mceachran y Fechhelm, 1998). De hecho, *Halosauropsis macrochir* es una specie abundante en la dorsal Atlántica (Klimpel y col., 2008).

La familia Halosauridae contiene actualmente 16 especies distribuidas por todos los océanos y agrupadas en tres géneros: *Halosaurus* Johnson, 1863; *Halosauropsis* Collett, 1896 y *Aldrovandia* Goode & Bean, 1896 (Kamikawa y Stevenson, 2010; Eschmeyer, 2015). Su composición y distribución ha sido estudiada por diversos ictiólogos en diferentes áreas: Atlántico Centro-Occidental (Smith, 2003); Atlántico Noroccidental (McDowell, 1973); Atlántico Nororiental y mar Mediterráneo (Sulak, 1986a); sur de África (Sulak, 1986b); Pacífico centro-occidental (Smith, 1999); Australia (Williams y col., 1996) y mares del Sur (Gon, 1990).

En el Atlántico europeo, los halosáuridos están representados por cinco especies (Sulak, 1986a; Alcázar y col., 1992; Quéro y col., 2003): *Halosaurus johnsonianus* Vaillant 1888, *Halosaurus ovenii* Johnson 1864, *H. macrochir* (Günther, 1878), *Aldrovandia phalacra* (Vaillant, 1888) y *Aldrovandia affinis* (Günther, 1877).

Las diferencias existentes entre secuencias del gen mitocondrial COI de distintas especies pueden utilizarse como código de barras para facilitar la identificación de

especies, poner de manifiesto casos de expansión de especies conocidas, detectar especies previamente omitidas y permitir identificaciones allí donde los métodos tradicionales no pueden aplicarse (Hebert y col., 2003). El análisis se centra en una región de aproximadamente 650 pares de bases de una región del extremo 5´de este gen. Los beneficios resultantes de la simplificación de la identificación de especies se han probado de manera extensiva en peces marinos, para los que los códigos de barras han discriminado cerca del 98% de las especies previamente descritas (Ward y col., 2009). Pueden darse excepciones entre especies que han divergido recientemente o entre aquéllas que hibridan con regularidad. De manera alternativa, pequeñas diferencias entre los códigos de barras de especímenes atribuidos a distintas especies pueden indicar sinonimia, es decir, miembros de una única especie separados en taxones distintos, o especímenes mal identificados (Ward y col., 2009). El examen de códigos de barras de ADN se reconoce como una herramienta importante que puede ser aprovechada en la resolución de cuestiones taxonómicas en peces (Ward y col., 2005, 2009; Zemlak y col., 2009), basándose en el desarrollo de una base de datos de códigos de barras preparada a partir de especímenes de referencia identificados fehacientemente por taxónomos expertos (Federhen, 2011).

Material y Métodos

Recolección de muestras, identificación de especies y análisis morfológico

Los especímenes se capturaron en el transcurso de varias campañas oceanográficas realizadas entre 2009 y 2011 con objeto de investigar la estructura de las comunidades de profundidad en dos áreas de la costa española: el banco de Galicia y el banco El Cachucho (noreste del Océano Atlántico).

Todas las muestras fueron identificadas provisionalmente y, a continuación, congeladas a bordo. Una vez en el laboratorio, la identificación de los especímenes hasta el nivel de especie se llevó a cabo de acuerdo con McDowell (1973) y Sulak (1986a). Las biometrías, tomadas al mm inferior, y los caracteres merísticos, fueron determinados según McDowell (1973) y expresados como porcentaje de la longitud gnatoproctal (LGP), desde el extremo de la mandíbula inferior hasta la apertura anal.

Se tomaron muestras de tejido de los ejemplares descongelados que se conservaron en etanol al 95%. A continuación los especímenes se fijaron en formol al 10% y se conservaron en etanol al 70%. Los ejemplares de referencia se depositaron en el Museo de Historia Natural de la Universidad de Santiago de Compostela (MHNUSC, Santiago

de Compostela, España). Las fotografías de los especímenes utilizados en este estudio, así como los datos de secuencia de ADN están disponibles en el proyecto titulado "Barcoding of North Atlantic Notacanthiformes" (código NOTAC) en la Barcode of Life Database (BOLD).

Extracción de ADN, amplificación por PCR y secuenciación

El ADN total se purificó de 25 mg de tejido muscular tomado de cada espécimen, utilizando el protocolo de columna centrifugada del Tissue DNA Extraction Kit (Omega Biotek). Se amplificó por PCR la región de código de barras estándar del gen COI (aprox. 650 pb) utilizando los cócteles de cebadores para peces COI-1 y COI-3 (Ivanova y col., 2007). Se aplicaron las siguientes condiciones de reacción: desnaturalización inicial a 98 ºC durante 30 s seguida de 35 ciclos de 98 ºC durante 5 s, hibridación a 52 ºC durante 5 s y 72 ºC durante 10 s, con una extensión final a 72 ºC durante 1 min. La reacción en cadena de la polimerasa se llevó a cabo empleando la polimerasa de ADN Phire Green Hot Start II (Thermo Scientific); se empleó un volumen final de 50 µL de mezcla incluyendo tampón de reacción 1x, 200 µM de cada dNTP, 0.1 µM de cada cebador y 1 µL de enzima; se añadieron entre 50 ng y 100 ng de molde de ADN. Las bandas formadas por los amplicones de COI se visualizaron en geles de agarosa al 1,2% (Seakem LE Agarose) teñidos con bromuro de etidio y, a causa de la especificidad de los resultados, se purificaron directamente con ExoSAP-IT (USB) siguiendo las instrucciones del fabricante. Las reacciones de secuenciación de ADN se llevaron a cabo en los sentidos directo e inverso con los mismos cebadores de amplificación, en el caso de los amplicones obtenidos con el coctel COI-1, o los cebadores M13F (-21) y M13R (-27) (Ivanova y col. 2007) cuando los amplicones se obtuvieron con el coctel COI-3. Los productos resultantes se resolvieron en un analizador genético ABI 3130 y las secuencias consenso se obtuvieron tras ensamblar las señales obtenidas en ambos sentidos mediante SeqScape v2.5.

Alineamiento y análisis de las secuencias

Los análisis moleculares evolutivos de las secuencias de ADN se llevaron a cabo con la versión 6 del paquete informático MEGA (Tamura y col., 2013), del que se empleó la herramienta "Alignment Explorer" mediante el algoritmo MUSCLE (Edgar, 2004) para crear un alineamiento. Como estima de la divergencia genética se empleó el número de nucleótidos diferentes por sitio existentes entre dos secuencias de ADN (denominado

distancia *p*) (Nei y Kumar, 2000), y se aplicó para la comparación de pares de haplotipos en general y también entre individuos de la misma y de distintas especies.
El empleo de distancias *p* es más preciso cuando se comparan valores entre individuos del mismo género o especie y rinde tasas de identificación exitosas similares o mayores para árboles de "neighbour-joining" que la distancia K2P que, además, sobreestima las distancias genéticas (Srivathsan y Meier, 2012). Utilizando las 35 secuencias de COI de Halosauridae de las aguas atlánticas españolas, se construyó un diagrama de clados de Neighbor-Joining (NJ) (Saitou y Nei, 1987).

El porcentaje de árboles replicados en los cuales los taxones asociados se agruparon se calculó mediante un ensayo de muestreo tras 2000 réplicas (Felsenstein, 1985). El método de NJ demostró ser una herramienta útil para la el análisis de delimitación de especies, ya que produjo agrupaciones monofiléticas estadísticamente fiables, dado que todas las secuencias previamente identificadas a nivel de especie se agruparon representando, por lo tanto, a una única especie.

Resultados

Examen de los códigos de barras de ADN

En el presente estudio se han considerado 35 secuencias de código de barras de ADN de seis especies de peces de aguas atlánticas españolas pertenecientes a la familia Halosauridae (Tabla S1). Se creo un alineamiento de 657 posiciones de nucleótidos que, cuando fueron traducidas, dieron una secuencia de 219 aminoácidos en todos los casos. Cuando las posiciones de nucleótidos se compararon entre las 35 secuencias se encontraron un total de 477 sitos conservados y 180 variables, de los cuales 172 fueron informativos de parsimonia.

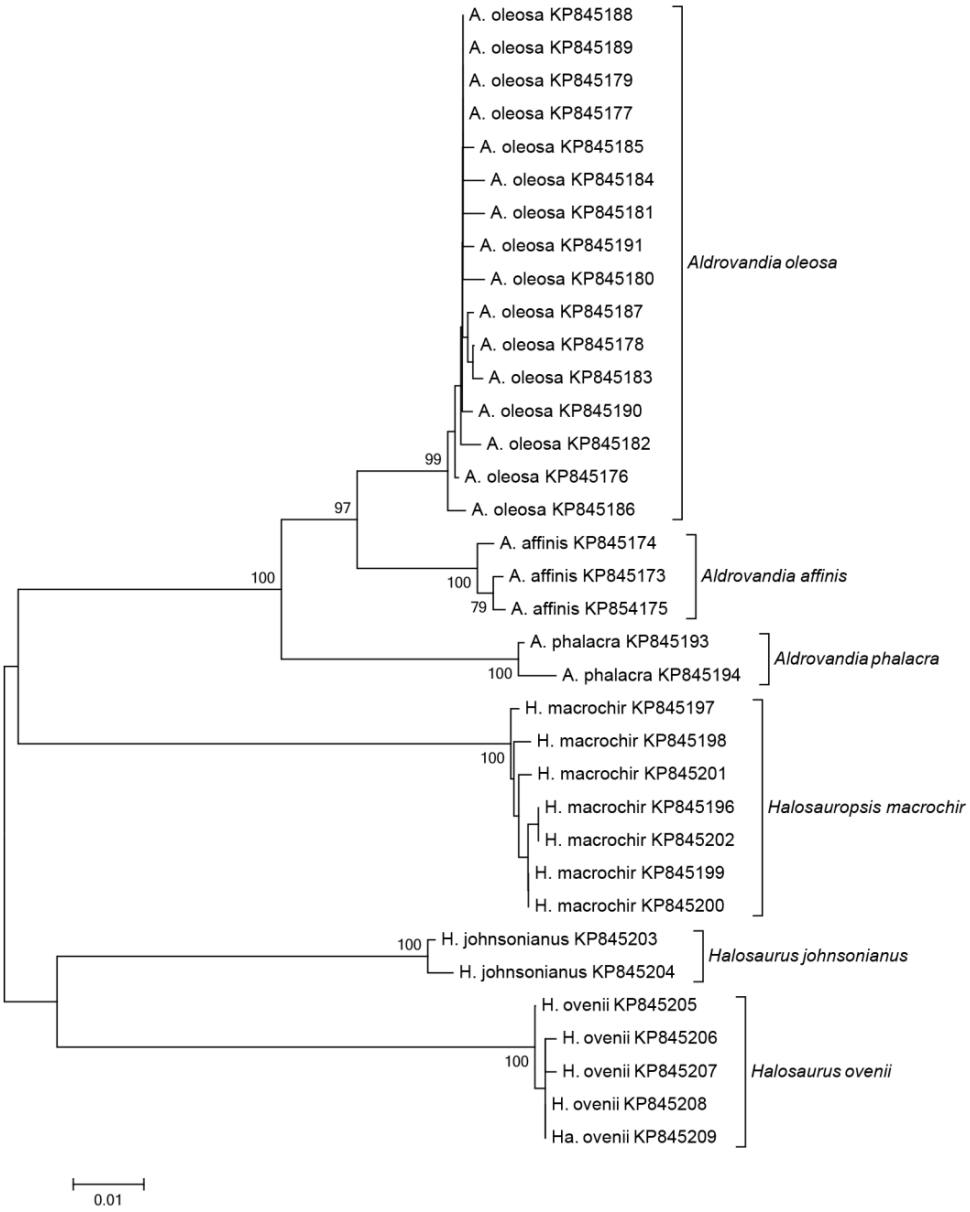

Figura 12. Diagrama de clados de Neighbor-Joining de secuencias del gen COI de Halosauridae del Atlántico del norte de España.

Los valores de distancia genética media entre las secuencias COI de este conjunto de datos medida entre los individuos de la misma especie y del mismo género fueron 0,42% y 7,33%, respectivamente, constituyendo una diferencia de 17 veces (Tabla 1). Es más, la distancia máxima entre individuos de la misma especie fue 0,8% y la distancia mínima entre individuos del mismo género fue 3,3%, de manera que los códigos separaron claramente ambas categorías taxonómicas entre los especímenes de Halosauridae del las aguas atlánticas españolas (Tabla 1).

Tabla 1. Distancias genéticas (% *p*-distancia) entre secuencias COI de ejemplares de Halosauridae del Atlántico del norte de España (el rango de valores se muestra entre paréntesis).

		Entre especies					
Especies (n)	Dentro especies	*A. affinis*	*A. oleosa*	*A. phalacra*	*H. macrochir*	*H. johnsonianus*	*H. ovenii*
A. affinis (3)	0,5 (0,3-0,8)						
A. oleosa (16)	0,4 (0-0,8)	3,7 (3,3-4,0)					
A. phalacra (2)	0,6	6,8 (6,4-7,2)	6,4 (5,8-6,8)				
H. macrochir (7)	0,3 (0-0,6)	14,2 (13,9-14,5)	13,7 (13,4-14,0)	14,4 (14,0-14,8)			
H. johnsonianus (2)	0,5	13,2 (13,1-13,2)	12,7 (12,3-13,1)	14,5 (14,3-14,6)	15,4 (14,9-15,8)		
H. ovenii (5)	0,2 (0-0,3)	14,6 (14,3-14,8)	14,5 (14,2-14,9)	15,1 (14,9-15,2)	13,4 (13,1-13,9)	12,4 (12,2-12,6)	

En el diagrama de clados de NJ resultante, 35 secuencias de COI de Halosauridae se agrupan en seis clados monofiléticos que reciben asignaciones a nivel de especie como *A. affinis*, *A. oleosa*, *A. phalacra*, *H. macrochir*, *H. ovenii* y *H. johnsonianus* (Fig. 12). La identidad de cada clado se confirmó también mediante la herramienta de búsqueda en línea BOLD IDS, empleando en cada caso una secuencia representativa de cada agrupamiento. Cada agrupamiento del diagrama se apoya en valores bajos de divergencia intraespecífica.

Descripción taxonómica

Familia HALOSAURIDAE

Género *Halosauropsis* Collett, 1896

***Halosauropsis macrochir* (Günther, 1878)**

Fig. 13.

Halosaurus macrochir (Günther, 1878): (251) 23. Estrecho de Gibraltar, estación Challenger 5, 1993 m profundidad. Lectotipo: BMNH 1887.12.7.237. McDowell, 1973: 74–87 (descripción, clave); Sulak, 1977: 11–12 (clave); Paulin y Moreland 1979: 268-270 (descripción); Sulak 1986a: 593–598 (descripción, clave); Machida y col. 1988 (descripción); Gon, 1990 (descripción); Smith 2003 (clave); Bergstad y col. 2012 (edad, crecimiento).

Figure 13. *Halosauropsis macrochir* del banco de Galicia (Atlántico noreste), MHNUSC 25009-5, 566 mm longitud total.

Tabla 2. Compaativa de los datos biométricos , merísticos y de sus proporciones respecto al cuerpo (%LGP) en los ejemplares de *Halosauropsis macrochir*.

Halosauropsis macrochir	MHNUSC 25009 (1-7)	McDowell (1973) N=8	Paulin y Moreland (1979) N=4	Filatova. (1985) N=84
Longitud Total (mm)	528-626	—	—	340-800
Longitud Preanal (mm)	214-258	—	—	—
Longitud Gnatoproctal (mm)	193-234	186-271	189-268	—
Como % LGP				
Longitud cabeza	34,6-37,8	—	—	—
Diámetro del ojo	3,7-4,6	4,2-5,4	—	—
Longitud preorbitaria	14,1-16,1	14,3-17,7	—	—
Longitud postorbitaria	15,2-17,6	—	—	—
Longitud interorbitaria	6,0-7,9	—	7,2-8,4	—
Longitud preoral del rostro	4,1-4,5	3,5-5,4	—	—
Longitud predorsal	70,4-75,6	—	—	—
Longitud base dorsal	12,0-14,1	—	—	—
Longitud aleta pectoral	26,4-31,1	—	—	—
Longitud preventral	68,3-71,2	—	—	—
Longitud aleta ventral	13,6-15,2	—	—	—
Altura del cuerpo	14,4-19,8	—	—	—
Caracteres merísticos				
Radios aleta dorsal	12-14	11-13	11-12	10-13
Radios aleta ventral	I+8-9	I+9	—	8-10
Radios aleta pectoral	10-13	12-13	12	10-14
ELL hasta el ano	30-32	26-32	—	—
ELL hasta el origen de la ventral	13-14	12-16	14	12-16
Escamas por encima de la LL	13-14	14-16	12-14	10-13
Radios branquiostegos	10-11	11-13	11-12	10-13
Branquiespinas	3+1+9-10	15-16	12-13	12-16
Ciegos pilóricos	8-12	10-12	11-12	7-13

Material examinado. MHNUSC 25009-1, 536 mm LT, 7 de agosto de 2011, banco de Galicia, 42º41.771'N—11º33.647'W, 1477 m; MHNUSC 25009-2, 528 mm LT, 8 de agosto de 2011, banco de Galicia; 42º43.536'N—11º28.128, 1751 m; MHNUSC 25009-3, 604 mm LT, 8 de agosto de 2011, banco de Galicia; 42º43.536'N—11º28.128; 1,751

m; MHNUSC 25009-4, 585 mm LT, 8 de agosto de 2011, banco de Galicia; 42º43.536'N—11º28.128, 1751 m; MHNUSC 25009-5, 566 mm LT, 29 de julio de 2011, banco de Galicia; 42º56.172'N—11º 55.816'W, 1545 m; MHNUSC 25009-6, 626 mm LT, 29 de julio de 2011, banco de Galicia, 42º56.172'N —11º 55.816'W, 1545 m; MHNUSC 25009-7, 579 mm LT, 29 de julio de 2011, banco de Galicia, 42º56.172'N—11º 55.816'W; 1545 m.

Descripción. Cuerpo anguiliforme, moderadamente comprimido y alargado, atenuándose hacia el pedúnculo caudal; parte superior del rostro sin escamas, opérculo con escamas; cabeza deprimida anteriormente, distancia interorbital ancha, contenida 4,8–6, 2 veces en la cabeza; origen de la dorsal ligeramente por detrás del origen de las ventrales; primer radio dorsal segmentado y de igual longitud que el segundo; aleta pectoral larga y estrecha, alcanzando al menos la base de la dorsal y contenida 1,2–1,3 veces en la cabeza; línea lateral pigmentada, formada por escamas de mayor tamaño que las del cuerpo; ciegos pilóricos largos, de color crema, dispuestos en una sóla fila. Las principales medidas morfométricas y caracteres merísticos se presentan en la Tabla 2.

Hábitat y Distribución. Bentopelágico, en el talud inferior y montañas submarinas, entre 1100 y 3300 m. Cosmopolita: Atlántico este, desde Irlanda hasta Mauritania y Sudáfrica; Atlántico central, a lo largo de la dorsal atlántica; Atlántico oeste, incluyendo Canadá hasta 25°N y sur de Brasil; Pacífico oeste, incluyendo Australia, Nueva Zelanda y Japón; y océano Índico occidental (Sulak, 1986a; Bergstad y col., 2012).

Género *Halosaurus* Johnson, 1864

***Halosaurus ovenii* Johnson, 1864**

Fig. 14.

Halosaurus ovenii Johnson, 1864: 406, Pl. 26 (fig. 1). Holotipo (único): BMNH 1863.12.12.1. McDowell, 1973: 56–66 (descripción, clave); Sulak, 1977: 11–12 (clave); Sulak, 1986a: 593–598 (descripción, clave); Sulak, 1986b (descripción, clave); Mceachran y Fechhelm 1998: 210-215 (descripción, clave); Smith, 2003 (clave).

Figure 14. *Halosaurus ovenii* del banco de Galicia (Atlántico noreste), MHNUSC 25010-2, 578 mm longitud total.

Material examinado. MHNUSC 25010-1, 538 mm LT, 4 de agosto de 2011, banco de Galicia, 42º41.771'N—11º33.647'W, 916 m; MHNUSC 25010-2, 578 mm LT, 29 de julio de 2009, banco de Galicia, 42º 73.58'N—11º73.580'W, 779 m; MHNUSC 25010-3, 516 mm LT, 29 de julio de 2009, banco de Galicia, 42º 73.58'N—011º73.580'W, 779 m; MHNUSC 25010-4, 517 mm LT, 29 de julio de 2009, banco de Galicia, 42º 73.58'N—011º73.580'W, 779 m; MHNUSC 25010-5, 523 mm LT, 27 de agosto de 2009, banco de Galicia, 42º 73.58'N—011º73.580'W, 779 m.

Descripción. Cuerpo anguiliforme, moderadamente comprimido y alargado, atenuándose hacia el pedúnculo caudal; parte superior y lados de la cabeza, hasta el extremo anterior de la mandíbula inferior, y opérculo, con escamas; rostro relativamente corto, contenido 2,4-2,6 veces en la cabeza; base de las ventrales anterior a la base de la dorsal; dientes palatinos dispuestos en la línea media del paladar; interior de la boca oscura con zonás pálidas características; escamas de la línea lateral (ELL) no pigmentadas y sólo ligeramente más grandes que las escamas del cuerpo; ciegos pilóricos pálidos. Las principales medidas morfométricas y caracteres merísticos se presentan en la Tabla 3.

Hábitat y Distribución. Especie bentopelágica, desde 440 hasta 2800 m de profundidad, pero más frecuentemente a profundidades menores de 800 m (D'Onghia y col., 2004). Presente a ambos lados del Atlántico y en el mar Mediterráneo. En el

Atlántico este se encuentra en el sur de Irlanda, golfo de Vizcaya, España, Portugal, islas de Madeira, Azores y Canarias y costa occidental de África, desde Marruecos hasta Sudáfrica (Quéro y col., 1994; Sulak, 1990; Bañón y col., 1997) y en el Atlántico oeste desde Nueva York hasta Colombia, incluyendo el golfo de México, mar Caribe y las Antillas (McEachran y Fechhelm, 1998; Saavedra-Díaz y col., 2004); sólo unos pocos registros en el mar Mediterráneo (Pais y col., 2009).

Tabla 3. Compaativa de los datos biométricos , merísticos y de sus proporciones respecto al cuerpo (%LGP) en los ejemplares de *Halosaurus ovenii*.

Halosaurus ovenii	MHNUSC 25010 (1-5)	McDowell (1973) N=26	Lloris, 1988 N=5	Pais y col., 2009 N=1
Longitud Total (mm)	516-578	—	194-296	470
Longitud Preanal (mm)	230-267	—	—	210
Longitud Gnatoproctal (mm)	212-246	93-180	—	
Como % LGP				
Longitud cabeza	27,2-29,2	—	—	26,7
Diámetro del ojo	3,8-4,4	—	—	4,4
Longitud preorbitaria	10,8-12,3	—	—	10,9
Longitud postorbitaria	11,8-13,2	—	—	—
Longitud interorbitaria	2,2-2,8	—	—	2,2
Longitud preoral del rostro	4,4-5,3	—	—	—
Longitud predorsal	68,2-74,2	—	—	67,6
Longitud base dorsal	7,6-8,5	—	—	—
Longitud aleta pectoral	16,6-20,3	—	—	—
Longitud preventral	59,6-64,8	—	—	—
Longitud aleta ventral	11,2-12,7	—	—	—
Altura del cuerpo	14,5-17,9	—	—	16,7
Caracteres merísticos				
Radios aleta dorsal	I+9-10	9-10	11	I+10
Radios aleta ventral	I+8-9	I+8-9	I+9	I+7
Radios aleta pectoral	I+15-17	I+13-16	14-16	I+14
ELL hasta el ano	61-67	59-68	—	66
ELL hasta el origen ventral	25-29	23-29	—	—
Escamas por encima de la LL	13-15	14-15	—	12-14
Radios branquiostegos	14	14-16	—	11-12
Branquiespinas	3+1+8-9	11-14	3+1+10	3+9
Ciegos pilóricos	12-13	12-20	±16	11

***Halosaurus johnsonianus* Vaillant, 1888**:Fig. 15.

Halosaurus johnsonianus Vaillant [L. L.] 1888: 181, Pl. 15 (figs. 2-2d). Oeste del Sahara, 23°50'N, 17°17'W, 1139 m profundidad. Lectotipo: MNHN 1885-0361. McDowell, 1973: 56-57 (clave); Harrisson, 1972: 254; Maul, 1976: 20 (descripción); Sulak 1986a: 593-598 (descripción, clave); Sulak, 1990: 131.

Figure 15. *Halosaurus johnsonianus* del banco El Cachucho (Atlántico noreste), MHNUSC 25013-2, 404 mm de longitud total.

Material examinado. MHNUSC 25013-1, 354 mm LT, 19 de julio de 2009, del banco El Cachucho; 43º55.22'N—4º47.92'W; 1198 m; MHNUSC 25013-2, 404 mm LT, 19 de julio de 2009, banco El Cachucho; 43º55.22'N—4º47.92'W; 1198 m.

Descripción. Cuerpo anguiliforme, moderadamente comprimido y alargado, atenuándose hacia el pedúnculo caudal; cuerpo muy delgado, mayor altura del cuerpo comprendida 2,8-3,1 veces en la longitud de la cabeza; parte superior y lados de la cabeza con escamas, hasta cerca del extremo del rostro; opérculo con escamas; escamas de la línea latera sólo algo más grandes que las del cuerpo y formando una banda oscura; branquiespinas más largas que las láminas branquiales opuestas; ciegos pilóricos cortos y de color negro. Las principales medidas morfométricas y caracteres merísticos se presentan en la Tabla 4.

Tabla 4. Compaativa de los datos biométricos , merísticos y de sus proporciones respecto al cuerpo (%LGP) en los ejemplares de *Halosaurus johnsonianus*.

Halosaurus johnsonianus	MHNUSC 25013 (1-2)		Maul, 1976 (N=1)	Sulak, 1986a
Longitud Total (mm)	354	404	294+	—
Longitud Preanal (mm)	140	165	—	—
Longitud Gnatoproctal (mm)	129	151	—	—
Como % LGP				
Longitud cabeza	34,1	29,4	—	—
Diámetro del ojo	2,3	3,1	—	—
Longitud preorbitaria	17,1	13,5	—	—
Longitud postorbitaria	15,5	12,9	—	—
Longitud interorbitaria	3,9	2,5	—	—
Longitud preoral del rostro	6,2	4,9	—	—
Longitud predorsal	72,9	67,5	—	—
Longitud base dorsal	7,8	8,6	—	—
Longitud aleta pectoral	15,5	15,3	—	—
Longitud preventral	62,8	62,0	—	—
Longitud aleta ventral	10,1	8,0	—	—
Altura del cuerpo	10,9	10,4	—	—
Caracteres merísticos				
Radios aleta dorsal	I+10	I+10	10	I+9-10
Radios aleta ventral	I+9	I+8	—	I+8
Radios aleta pectoral	I+12	I+12	—	I+15
ELL hasta el ano	57	57	—	51
ELL hasta el origen de la ventral	25	24	~27	—
Escamas por encima de la LL	11	11	—	—
Radios branquiostegos	14	14	—	—
Branquiespinas	3+1+14	3+1+13	4+1+13	+14
Ciegos pilóricos	8	6	—	4-9

Hábitat y Distribución. Bentopelágico, entre 680 y 2100 m de profundidad y 4-11ºC. Atlántico este, desde Porcupine Seabight, Portugal y sur de España hasta

Mauritania, incluyendo las islas Azores, Cabo Verde y Canarias (Maul, 1976; Sulak, 1990; Priede y col., 2010).

Genus *Aldrovandia* Goode & Bean, 1896

***Aldrovandia affinis* Günther 1877**

Fig. 16.

Halosaurus affinis, Günther 1877: 444. Sur de Japón, 34°N, 138°E, estación Challenger 235, 1033 m de profundidad. Sintipos: BMNH 1887.12.7.244-245 (2). McDowell, 1973: 91–101 (descripción, clave); Maul, 1976: 22 (descripción); Filatova, 1985: 27-29 (descripción), 33-34 (clave); Sulak, 1986a: 593–598 (descripción, clave); Mceachran y Fechhelm, 1998: 210-215 (descripción, clave); Smith, 2003 (clave).

Figure 16. *Aldrovandia affinis* del banco de Galicia (Atlántico noreste), MHNUSC 25011-2, 486 mm longitud total.

Material examinado. MHNUSC 25011-1, 423 mm LT, 7 de agosto de 2011, banco de Galicia; 42º56.172'N—11º55.816'W; 1545 m; MHNUSC 25011-2, 486 mm LT, 7 de agosto de 2011, banco de Galicia; 42º41.771'N—11º33.647; 1477 m; MHNUSC 25011-3, 442 mm LT, 2 de agosto de 2011, banco de Galicia; 42º56.172'N—11º55.816; 1545 m.

Tabla 5. Compaativa de los datos biométricos , merísticos y de sus proporciones respecto al cuerpo (%LGP) en los ejemplares de *Aldrovandia affinis*.

Aldrovandia affinis	MHNUSC 25011 (1-3)	McDowell, 1973	Paulin y Moreland, 1979	Filatova, 1985	Hsin-Ming y col., 2006
Longitud Total (mm)	423-486	—	—	—	—
Longitud Preanal (mm)	165-186	—	—	—	—
Longitud Gnatoproctal (mm)	146-163	—	—	—	—
Como % LGP					
Longitud cabeza	32,7-35,6	—	—	—	—
Diámetro del ojo	3,1-4,1	—	—	—	—
Longitud preorbitaria	13,7-16	—	—	—	—
Longitud postorbitaria	14,8-17,8	—	—	—	—
Longitud interorbitaria	3,7-4,1	—	—	—	—
Longitud preoral del rostro	6,2-8	—	—	—	—
Longitud predorsal	74,8-76	—	—	—	—
Longitud base dorsal	10,4-11	—	—	—	—
Longitud aleta pectoral	18,4-18,5	—	—	—	—
Longitud preventral	69,2-71,2	—	—	—	—
Longitud aleta ventral	10,4-13	—	—	—	—
Altura del cuerpo	11,6-15,4	—	—	—	—
Caracteres merísticos					
Radios aleta dorsal	I+11	11-13	12	10-12	10-12
Radios aleta ventral	I+8	7-9	9	8	8-9
Radios aleta pectoral	I+13	11-14	13	12	—
ELL hasta el ano	26-27	—	—	—	18-20
ELL hasta el origen de la ventral	13-15	13-17	18	12-14	—
Escamas por encima de la LL	11-15	13-16	11	10-12	—
Radios branquiostegos	10	—	10	10	10-11
Branquiespinas	3+1+9-11	—	—	12-16	14-16
Ciegos pilóricos	8-9	—	9	6-9	—

Descripción. Cuerpo anguiliforme, moderadamente comprimido y alargado, atenuándose hacia el pedúnculo caudal; parte superior de la cabeza y opérculo sin escamas; región preoral del rostro larga, contenida 2-2,2 veces en la longitud del rostro; primer radio de la dorsal muy corto, semejando una espina; aleta pectoral corta y ancha, bien separada del origen de la ventral; origen de la dorsal ligeramente por detrás de las ventrales; el grupo de dientes palatinos se junta en su línea media; ciegos pilóricos

negros y ano blanco. Las principales medidas morfométricas y caracteres merísticos se presentan en la Tabla 5.

Hábitat y Distribución. Bentopelágico, en la parte media e inferior del talud continental (700-2200 m), principalmente por encima de la isoterma de los 4° C. En latitudes tropicales y templadas de todos los océanos. Atlántico este, desde el golfo de Vizcaya, Madeira hasta el Sahara occidental y Sudáfrica; Atlántico oeste, desde Nueva Inglaterra hasta Florida, golfo de Mexico, islas del Caribe y América del Sur; Indo-Pacífico, en Zanzibar, Maldivas, Taiwán y Japón y en el Pacífico cemtro-oriental (Froese y Sampang, 2004;Yeh y col., 2006).

***Aldrovandia phalacra* (Vaillant 1888)**

Fig. 17.

Halosaurus phalacrus, Vaillant [L. L.] 1888: 185, Pl. 15 (fig. 3), 16 (figs. 1-1c). Marruecos, 1103-2190 m; Sudán, 1250-1435 m; Azores, 37°35'N, 29°26'W, 1442-2220 m. Lectotipo: MNHN 1885-0382. McDowell, 1973: 91–92 (clave), 105–114 (descripción); Filatova, 1985: 27-29 (descripción), 33-34 (clave); Sulak 1986a: 593–598 (descripción, clave); Sulak, 1986b: 196–197 (descripción, clave); Maul, 1976: 20-22 (descripción); Smith, 2003 (clave).

Figure 17. *Aldrovandia phalacra* del banco de Galicia (Atlántico noreste), MHNUSC 25014-2, 330 mm longitud total.

Material examinado. MHNUSC 25014-1, 190 mm LT, 7 de agosto de 2011, banco de Galicia; 42º41.771'N—011º33.647'W; 1536 m; MHNUSC 25012-2, 330 mm LT, 6 de agosto de 2011, banco de Galicia; 42º41.771'N—11º33.647'W; 1477 m.

Tabla 6. Compaativa de los datos biométricos , merísticos y de sus proporciones respecto al cuerpo (%LGP) en los ejemplares de *Aldrovandia phalacra*.

Aldrovandia phalacra	MHNUSC 25013 (1-2)		McDowell, 1973	Maul, 1976 N=10	Hsin-Ming y col., 2006
Longitud Total (mm)	190	330	—	—	—
Longitud Preanal (mm)	75	117	—	—	—
Longitud Gnatoproctal (mm)	70	114	—	—	—
Como % LGP					
Longitud cabeza	38.6	36.0	—	—	—
Diámetro del ojo	2.9	2.6	—	—	—
Longitud preorbitaria	20.0	16.7	—	—	—
Longitud postorbitaria	18.6	16.7	—	—	—
Longitud interorbitaria	4.3	4.4	—	—	—
Longitud preoral del rostro	4.3	4.4	—	—	—
Longitud predorsal	77.1	72.8	—	—	—
Longitud base dorsal	12.9	10.5	—	—	—
Longitud aleta pectoral	12.9	18.4	—	—	—
Longitud preventral	70.0	63.2	—	—	—
Longitud aleta ventral	12.9	11.4	—	—	—
Altura del cuerpo	14.3	14.9	—	—	—
Caracteres merísticos					
Radios aleta dorsal	I+10	I+11	10-12	8-11	11
Radios aleta ventral	I+8	I+8	I+7-8	—	8
Radios aleta pectoral	I+14	I+13	I+11-13	13-14	12-13
ELL hasta el ano	26	26	19-31	—	24-28
ELL hasta el origen de la ventral	12	13	9-16	—	10
Escamas por encima de la LL	13	12	11-12	—	11-13
Radios branquiostegos	10	13	10-14	—	10-11
Branquiespinas	6+1+18	6+1+17	19-24	20-22	24-25
Ciegos pilóricos	—	—	5-8	—	—

Descripción. Cuerpo anguiliforme, moderadamente comprimido y alargado, atenuándose hacia el pedúnculo caudal; parte superior del rostro y cabeza sin escamas, opérculo sin escamas; porción preoral del rostro corta, contenida 3,8 y 4,7 veces en la longitud de la cabeza; primer radio de la dorsal muy corto y vestigial; aletas pélvicas insertadas por delante del origen de la dorsal; grupos de dientes palatinos separados; ciegos pilóricos negros y apertura anal blanca rodeada de negro. Las principales medidas morfométricas y caracteres merísticos se presentan en la Tabla 6.

Hábitat y Distribución. Bentopelágico, entre 500 y 2300 m de profundidad. Principalmente en latitudes tropicales y templadas de todos los océanos. Atlántico este, desde el golfo de Vizcaya hasta Guinea y Sudáfrica; Atlántico oeste, desde Groenlandia, Nueva Inglaterra, EE.UU hasta Bahamas y sur de Brasil; Pacífico este, en Hawái y Chile (Froese y Sampang, 2004;Yeh y col., 2006).

***Aldrovandia oleosa* Sulak, 1977**

Fig. 18.

Aldrovandia oleosa Sulak, 1977:12, Figs. 1, 2 izquierda, 3 superior, 4 (A-C). Tongue-of-the-Ocean, Bahamas, 23°38.5'-23°40.3'N, 76°47.75'-76°45.1'W, 1324-1307 m profundidad. Holotipo: USNM 214590. Sulak, 1977: 11–20 (descripción, clave); Filatova, 1985: 32-34 (descripción, clave); Smith, 2003 (clave); Kamikawa y Stevenson, 2010 (descripción).

Figure 18. *Aldrovandia oleosa* del banco de Galicia (Atlántico noreste), MHNUSC 25012-8, 342 mm longitud total.

Material examinado. MHNUSC 25012-1, 226 mm LT, 7 de agosto de 2011, banco de Galicia; 42º56.172'N—11º55.816'W, 1545 m; MHNUSC 25012-2, 305 mm LT, 7 de

agosto de 2011, banco de Galicia, 42º56.172'N—11º55.816'W, 1545 m; MHNUSC 25012-3, 274 mm LT, 7 de agosto de 2011, banco de Galicia, 42º56.172'N—11º55.816'W, 1545 m; MHNUSC 25012-4, 317 mm LT, 7 de agosto de 2011, banco de Galicia, 42º56.172'N—11º55.816'W, 1545 m; MHNUSC 25012-5, 255 mm LT, 7 de agosto de 2011, banco de Galicia, 42º56.172'N—11º55.816'W, 1545 m; MHNUSC 25012-6, 269 mm LT, 7 de agosto de 2011, banco de Galicia, 42º41.771'N—011º33.647'W, 1477 m; MHNUSC 25012-7, 330 mm LT, 8 de agosto de 2011, banco de Galicia; 42º43.536'N—11º28.128'W; 1751 m depth; MHNUSC 25012-8, 342 mm LT, 8 de agosto de 2011, banco de Galicia, 42º43.536'N—11º28.128'W, 1751 m; MHNUSC 25012-9, 333 mm LT, 8 de agosto de 2011, banco de Galicia, 42º43.536'N—11º28.128'W, 1751 m; MHNUSC 25012-10, 347 mm LT, 8 de agosto de 2011, banco de Galicia, 42º43.536'N—11º28.128'W, 1751 m; MHNUSC 25012-11, 205 mm LT, 7 de agosto de 2011, banco de Galicia, 42º56.172'N—11º55.816'W,1545 m; MHNUSC 25012-12, 381 mm LT, 7 de agosto de 2011, banco de Galicia, 42º56.172'N—11º55.816'W, 1545 m; MHNUSC 25012-13, 352 mm LT, 7 de agosto de 2011, banco de Galicia, 42º56.172'N—11º55.816'W, 1545 m; MHNUSC 25012-14, 259 mm LT, 7 de agosto de 2011, banco de Galicia, 42º56.172'N—11º55.816'W, 1545 m; MHNUSC 25012-15, 397 mm LT, 7 de agosto de 2011, banco de Galicia, 42º56.172'N—11º55.816'W, 1545 m; MHNUSC 25012-16, 287 mm LT, 7 de agosto de 2011, banco de Galicia, 42º56.172'N—11º55.816'W, 1545 m.

Descripción. Cuerpo anguiliforme, moderadamente comprimido y alargado, atenuándose hacia el pedúnculo caudal; escamas ausentes en la parte superior de la cabeza y opérculo; longitud pre-oral muy corta, contenida de 3 a 5,3 veces en la longitud del rostro; los dientes palatinos separados de los pterigoideos por una distacia comprendida entre 0,7 y 1,7 veces su longitud; primer radio de la dorsal vestigial, muy corto; apertura anal blanca, rodeada por un anillo de tejido oscuro; ciegos pilóricos negros. Las principales medidas morfométricas y caracteres merísticos se presentan en la Tabla 7.

Hábitat y Distribución. Bentónico a bentopelágico, en el talud inferior y la parte superior abisal, entre 1100 y 3300 m de profundidad y principalmente entre las isotermas de 2 y 4ºC (Sulak, 1990). En latitudes tropicales y templadas de todos los océanos. Atlántico oeste, desde Canadá hasta Venezuela y las Guyanas; Atlántico este,

noroeste de África, Azores y golfo de Guinea (Sulak, 1977, 1990); océano Índico, desde el banco de Saya-de-Malaya hasta el East Indian Range (Filatova 1985) y Pacífico este, central y norte y aguas de Chile (Froese y Sampang, 2004; Kamikawa y Stevenson, 2010; Hanke y col., 2014).

Tabla 7. Compaativa de los datos biométricos , merísticos y de sus proporciones respecto al cuerpo (%LGP) en los ejemplares de *Aldrovandia oleosa*.

Aldrovandia oleosa	MHNUSC 25012 (1-16)	Sulak, 1977 N=8	Filatova, 1985 N=17
Longitud Total (mm)	205-397	—	100-300
Longitud Preanal (mm)	88-157	—	50-120
Longitud Gnatoproctal (mm)	78-143	—	—
Como % LGP			
Longitud cabeza	33,8-43,6	—	—
Diámetro del ojo	3,1-5,1	—	—
Longitud preorbitaria	15,5-19,2	—	—
Longitud postorbitaria	14,1-19,2	—	—
Longitud interorbitaria	3,8-5,3	—	—
Longitud preoral del rostro	3,3-5,8	—	—
Longitud predorsal	72,4-83,2	—	—
Longitud base dorsal	7,8-12,5	—	—
Longitud aleta pectoral	7,3-20,5	—	—
Longitud preventral	64,6-73,2	—	—
Longitud aleta ventral	4,4-11,9	—	—
Altura del cuerpo	11,3-17,6	—	—
Caracteres merísticos			
Radios aleta dorsal	I+9-11	10-11	9-10
Radios aleta ventral	I+8-9	I+8-9	8
Radios aleta pectoral	I+8-11	I+9-11	9-11
ELL hasta el ano	19-22 (9)	16-23	16-20
ELL hasta el origen de la ventral	10-11 (12)	—	8-10
Escamas por encima de la LL	10-11 (11)	—	10-11
Radios branquiostegos	9-11	9-11	9-10
Branquiespinas	4-6+1+15-17	19-23	17-19
Ciegos pilóricos	7-9	5-8	6-8

Clave de especies de la familia Halosauridae para el Atlántico este (adaptado de Smith, 2003)

1a. Parte superior de la cabeza con escamas, al menos hasta la altura de las narinas; escamas de la línea lateral ligeramente más grandes que las del cuerpo, 1 escama de la línea lateral por cada hilera transversal de escamas del cuerpo.....2

1b. Parte superior de la cabeza sin escamas; escamas de la línea lateral notablemente más grandes que las del cuerpo, 1 escama de la línea lateral por cada 2 a 3 hileras transversales de escamas del cuerpo 5

2a. Parte superior del interior de la boca de color oscuro pero que no se extiende por los lados hasta la arcada palatopterigoide; parte inferior del interior de la boca oscura, extendiéndose sólo ligeramente hasta la parte anterior de la lengua, con la parte más anterior de color claro; de 12 a 20 ciegos pilóricos.....*Halosaurus ovenii*

2b. Interior de la boca completamente oscura; de 4 a 12 ciegos pilóricos.....3

3a. Longitud de la cabeza aproximadamente 1/4 de la longitud preanal; de 8 a 12 ciegos pilóricos largos.....*Halosaurus guentheri*

3b. Longitud de la cabeza aproximadamente 1/3 de la longitud preanal; de 4 a 9 ciegos pilóricos cortos.....4

4a. 13-14 branquiespinas en el primer arco branquial, más largas que las láminas branquiales opuestas.....*Halosaurus johnsonianus*

4b. 7-12 branquiespinas en el primer arco branquial, más cortas que las láminas branquiales opuestas.....*Halosaurus attenuatus*

5a. Primer radio de la dorsal dividido y de igual longitud que el segundo; opérculo con escamas; ejemplares adultos con la línea lateral oscura; ciegos pilóricos claros y largos.....*Halosauropsis macrochir*

5b. Primer radio de la dorsal no dividido y mucho más corto que el segundo; opérculo sin escamas; línea lateral no pigmentada; ciegos pilóricos negros.....6

6a. Apertura anal azul oscura o negra rodeada de tejido claro.....7

6b. Apertura anal blanca rodeada de tejido oscuro.....8

7a. Escamas en la línea lateral contiguas; 1 escama de la línea lateral por cada dos escamas del cuerpo, 22 o 23 anteriores al ano; porción preoral del rostro muy larga, comprendida menos de 2 veces en la longitud del rostro .....*Aldrovandia rostrata*

7b. Escamas en la línea lateral no contiguas, separadas por las escamas del cuerpo; 1 escama de la línea lateral por cada 3 escamas del cuerpo, 18 a 20 anteriores al ano; porción preoral del rostro más corta, comprendida entre 2,25 y 2,5 veces en la longitud del rostro.....*Aldrovandia gracilis*

8a. Las bandas de dientes palatinos de los dos lados contactan en su parte media; de 13 a 15 branquiespinas en el primer arco branquial; porción preoral del rostro contenida

aproximadamente 2 veces en la longitud del rostro; origen de la dorsal sobre o muy ligeramente por detrás de de la base de las aletas ventrales.....*Aldrovandia affinis*
8b. Las bandas de dientes palatinos de los dos lados separados en su parte media; de 17 a 23 branquiespinas en el primer arco branquial; porción preoral del rostro contenida aproximadamente 3 veces en la longitud del rostro; origen de la dorsal claramente por detrás de de la base de las aletas ventrales 9
9a. De 24 a 28 escamas en la línea lateral anteriores al ano; dientes palatinos separados de los pterigoideos por menos de la mitad de su propia longitud; de 11 a 14 radios pectorales.....*Aldrovandia phalacra*
9b. De 16 a 23 escamas en la línea lateral anteriores al ano; dientes palatinos separados de los pterigoideos de 1 a 4 veces su propia longitud; de 8 a 11 radios pectorales.....*Aldrovandia oleosa*

Discusión

La medida de la longitud total en Halosauridae no es precisa, ya que muchos de los ejemplares tienen la parte final de su frágil cola rota o regenerada. Quizás por esta razón, hay muchas menos medidas biométricas que datos merísticos en la bibliografía ictiológica de la familia. Además, las medidas relativas vienen registradas de maneras diferentes, como porcentajes de la longitud rostro-ano (Kamikawa y Stevenson, 2010), de la longitud preanal (Filatova, 1985; Gon, 1990; Hsin-Ming y col., 2006), de la longitud predorsal (Maul, 1976) y de la longitud gnatoproctal (McDowell, 1973; Costa y Reiner, 1978; Paulin y Moreland, 1979; Machida y col., 1988). La ausencia de un criterio único en la toma de las biometrías dificulta la comparación entre las especies y la obtención de un rango de medidas relativas que sirvan como carácter distintivo en la identificación de especies de Halosauridae. Debido a esta carencia, los datos comparativos que se muestran en las tablas taxonómicas se basan principalmente en los caracteres merísticos (Tablas 2-7). La LGP parece ser la biometría más adecuada para expresar las medida relativas en los halosáuridos, debido a que tanto el rostro como la cola suelen estar dañados (McDowell, 1973). Por tanto, se recomienda utilizar la LGP como medida estándar para expresar las medidas relativas en los próximos estudios taxonómicos de la familia.

La ausencia de escamas en la parte superior de la cabeza distingue *H. macrochir* de las especies de *Halosaurus*, y la presencia de escamas en el opérculo los distingue

asimismo de las especies de *Aldrovandia* (Paulin y Moreland, 1979). *H. macrochir* difiere también de los otros halosáuridos citados en este trabajo por tener una longitud interiorbital mayor (6,0-7,9 frente a 2,2-5,3% LGP).

H. ovenii se diferencia de *H. johnsonianus* por tener mayor número de escamas en la línea lateral anteriores al ano (61-67 frente a 57), más ciegos pilóricos (12-13 frente a 6-8) y menos branquiespinas en el primer arco branquial (12-13 frente a 17-18).

Entre las especies de *Aldrovandia*, *A. affinis* difiere de las otras dos por tener un porción preoral más larga, contenida 2-2,2 veces en la longitud del rostro (frente a 3-5,3) y menos branquiespinas en el primer arco branquial (13-15 frente a 20-25). *A. phalacra* difiere de *A. oleosa* por tener mayor número de escamas en la línea lateral anteriores al ano (26 frente a 20-22) y más radios pectorales (14-15 frente a 9-12).

De manera general, los datos registrados de distribución latitudinal y en profundidad están en el rango de estudios anteriores. La excepción la constituye *A. oleosa*, cuyo anterior límite norte de distribución estaba en las Azores (Carneiro y col., 2014) y su presencia en el banco de Galicia constituye un nuevo límite norte de distribución en el Atlántico este.

Los caracteres merísticos y las medidas biométricas también coinciden con estudios anteriores, salvo alguna excepción. Según la bibliografía, el ojo de *H. johnsonianus* es grande, su diámetro horizontal es aproximadamente un 15% de la longitud de la cabeza (Vaillant, 1888), 1/6 de la longitud de la cabeza (Sulak, 1986a) o 7,3% de la longitud preanal (Maul, 1976). Sin embargo, nuestros ejemplares tenían los ojos más pequeños, 6,8 y 10,4% de la longitud de la cabeza o 2,1 y 3% de la longitud preanal, respectivamente. La presencia de dimorfismo sexual podría ser una posible explicación a estos resultados, pero el sexo no fue determinado y las biometrías de esta especie, incluidas el diámetro del ojo, están muy poco documentadas en la bibliografía.

En *A. oleosa*, los dientes palatinos están bien separados de los pterigoideos, de una a cuatro veces su propia longitud (Sulak, 1977; Kamikawa y Stevenson, 2010) pero sólo entre 0,7 y 1,7 veces en los ejemplares de Galicia. Esta separación relativa va a depender en gran medida de la longitud de la banda de dientes palatinos, que parecen ser mayores en nuestros ejemplares.

Machida y col. (1988) y Filatova (1985) documentan diferencias geográficas en los caracteres merísticos de *H. macrochir*. Nuestros resultados, sin embargo, muestran también diferencias similares en las otras especies examinadas (Tablas 2-7), que podrían estar por tanto dentro de las variaciones intraespecíficas normales que se dan en esta

familia. De hecho, la estructura genética poblacional de *H. macrochir* no muestra diferencia genéticas geográficas entre ejemplares del Atlántico norte y del Pacífico suroeste (David Barros-García comunicación personal).

Los valores de distancia de nucleótidos media entre los individuos de la misma especie (0,42%) y del mismo género (7,33%) (Tabla 1) están dentro de los valores habituales de los estudios de código de barras de peces (Costa y col., 2012; Lakra y col., 2011). La existencia de un claro "barcoding gap" hace de este procedimiento una herramienta muy útil para la identificación de especies de este grupo. Como muestra, el código de barras de ADN ha permitido la validación de las identificaciones taxonómicas de los halosáuridos del Atlántico del norte de España. Otra consecuencia de esta investigación es la incorporación de treinta y cinco nuevas secuencias de COI en los repositorios de referencia BOLDSYSTEMS y GenBank, aumentando el número de muestras de referencia o especímenes "voucher" y el conocimiento de estos peces relativamente raros. De hecho, este trabajo supone un aumento de un 49,3% en las secuencias depositadas en BOLDSYTEMS de las seis especies estudiadas (en mayo de 2015). Los códigos de barra de ADN incluyen las cinco especies representadas históricamente en el Atlántico europeo y la recién descubierta *A. oleosa,*como se discutió anteriormente. No se encontraron incongruencias cuando se compararon las identificaciones morfológicas y moleculares. La identificación morfológica apoya la identificación molecular y viceversa, reforzando así la identificación resultante. El incremento del número de códigos de barras disponibles de halosáuridos contribuirá en el futuro al desarrollo de estudios demográficos y filogenéticos. Esta investigación constituye un claro ejemplo de taxonomía integrativa (Dayrat, 2005) o de cómo la técnica del código de barras de ADN se ha integrado con éxito con el análisis morfológico tradicional en los estudios de sistemática de peces (Baldwin y Weigt, 2012;. Bañón y col., 2013).

Table S1. Ejemplares de Halosauridae utilizados en el presente estudio y secuencias incluidas en el análisis de código de barras de ADN.

No.	Identificación taxonómica	Región	BOLD Process ID	GenBank Acc. No.
1	*Aldrovandia affinis*	banco de Galicia	NOTAC014-15	KP845174
2	*Aldrovandia affinis*	banco de Galicia	NOTAC015-15	KP845175
3	*Aldrovandia affinis*	banco de Galicia	NOTAC016-15	KP845173
4	*Aldrovandia oleosa*	banco de Galicia	NOTAC017-15	KP845185
5	*Aldrovandia oleosa*	banco de Galicia	NOTAC018-15	KP845184
6	*Aldrovandia oleosa*	banco de Galicia	NOTAC019-15	KP845183
7	*Aldrovandia oleosa*	banco de Galicia	NOTAC020-15	KP845182
8	*Aldrovandia oleosa*	banco de Galicia	NOTAC021-15	KP845181
9	*Aldrovandia oleosa*	banco de Galicia	NOTAC022-15	KP845180
10	*Aldrovandia oleosa*	banco de Galicia	NOTAC023-15	KP845179
11	*Aldrovandia oleosa*	banco de Galicia	NOTAC024-15	KP845178
12	*Aldrovandia oleosa*	banco de Galicia	NOTAC025-15	KP845177
13	*Aldrovandia oleosa*	banco de Galicia	NOTAC026-15	KP845176
14	*Aldrovandia oleosa*	banco de Galicia	NOTAC027-15	KP845188
15	*Aldrovandia oleosa*	banco de Galicia	NOTAC028-15	KP845187
16	*Aldrovandia oleosa*	banco de Galicia	NOTAC029-15	KP845191
17	*Aldrovandia oleosa*	banco de Galicia	NOTAC030-15	KP845186
18	*Aldrovandia oleosa*	banco de Galicia	NOTAC031-15	KP845190
19	*Aldrovandia oleosa*	banco de Galicia	NOTAC032-15	KP845189
20	*Aldrovandia phalacra*	banco de Galicia	NOTAC068-15	KP845193
21	*Aldrovandia phalacra*	banco de Galicia	NOTAC069-15	KP845194
22	*Halosauropsis macrochir*	banco de Galicia	NOTAC001-15	KP845201
23	*Halosauropsis macrochir*	banco de Galicia	NOTAC002-15	KP845196
24	*Halosauropsis macrochir*	banco de Galicia	NOTAC003-15	KP845202
25	*Halosauropsis macrochir*	banco de Galicia	NOTAC004-15	KP845200
26	*Halosauropsis macrochir*	banco de Galicia	NOTAC005-15	KP845199
27	*Halosauropsis macrochir*	banco de Galicia	NOTAC006-15	KP845198
28	*Halosauropsis macrochir*	banco de Galicia	NOTAC007-15	KP845197
29	*Halosaurus johnsonianus*	banco El Cachucho	NOTAC033-15	KP845203
30	*Halosaurus johnsonianus*	banco El Cachucho	NOTAC034-15	KP845204
31	*Halosaurus ovenii*	banco de Galicia	NOTAC008-15	KP845208
32	*Halosaurus ovenii*	banco de Galicia	NOTAC009-15	KP845209
33	*Halosaurus ovenii*	banco de Galicia	NOTAC010-15	KP845206
34	*Halosaurus ovenii*	banco de Galicia	NOTAC011-15	KP845207
35	*Halosaurus ovenii*	banco de Galicia	NOTAC012-15	KP845205

6.4 COMPOSICIÓN DE ESPECIES Y CASOS DE HIPERPIGMENTACIÓN EN EL GÉNERO LEPIDION (GADIFORMES: MORIDAE) EN EL BANCO DE GALICIA.

El género *Lepidion* Swainson, 1838 (Moridae), contiene en la actualidad nueve especies bentopelágicas que viven en el talud inferior y montes submarinos de los océanos Atlántico, Índico y Pacífico y del mar Mediterráneo (Nakaya y col., 1980). En el Atlántico nordeste se han registrados tres especies: *Lepidion eques* (Günther 1887), *Lepidion guentheri* (Giglioli 1880) y *Lepidion schmidti* Svetovidov 1936 y dos en el Mediterráneo: *L. guentheri* y *Lepidion lepidion* (Risso, 1810) (Cohen, 1986; Quéro y col., 2003).

Las especies del género *Lepidion* se caracterizan por tener el cuerpo alargado; rostro redondeado, con la mandíbula superior prominente; barbillón presente en la mandíbula inferior; dos aletas dorsales separadas, el segundo radio de la primera aleta dorsal muy alargado; dientes viliformes en mandíbulas y vómer, ausentes en los palatinos; órgano luminoso ventral ausente (Templeman, 1970; Nakaya y col., 1980).

Para probar la eficacia de la identificación molecular entre las especies del género *Lepidion*, incluyendo ejemplares de *L. eques* y *L. guentheri* del BG (ver anexo III), se han examinado y comparado sus correspondientes códigos de barras de ADN. Se obtuvieron 32 secuencias de COI propias de cinco especies diferentes de *Lepidion*, a las que se sumaron 26 secuencias de otros proyectos presentes en el repositorio BOLD. Se compararon un total de 58 códigos de barras de ADN pertenecientes a ocho de las nueve especies conocidas de *Lepidion*. Las secuencias de COI fueron alineadas y, al ser comparadas mediante un método bayesiano, formaron siete clados distintos, con las secuencias de *L. lepidion* y *L. eques* agrupadas en el mismo clado. La distancia interespecífica promedio entre pares de secuencias, según el modelo de 2-parámetros de Kimura, fue de 4,28%, 16 veces mayor que la obtenida al comparar secuencias de la misma especie (media = 0,27%).

La distancia entre las secuencias de *L. eques* y *L. lepidion* varió entre 0 y 0,62 % (media = 0,29%), similar a la media intraespecífica de todas las especies del género (0,27%) y muy por debajo del 2% establecido de manera general como valor mínimo de distancia para discriminar especies distintas (Hebert y col., 2003, 2004).

Figura 19. Ejemplar de *L. eques* del banco de Galicia mostrando el radio alargado en la 1ª dorsal característico del género

Se recopilaron los principales caracteres distintivos del género y se realizó una revisión morfológica (biometría y merística) de *L. eques* y *L. lepidion* (ver anexo III) . El diámetro del ojo fue significativamente diferente entre *L. eques* y *L. lepidion* (P <0,001). El número de radios de la aleta anal osciló entre 45 y 51 en *L. lepidion* y de 47 a 54 en *L. eques*, pero sin diferencias significativas en los valores medios de esta variable (P = 0,07).

Según Günther (1887), *L. eques* se puede distinguir de *L. lepidion* por su ojo, comparativamente más grande y la cabeza más corta. Sin embargo el estatus de la especie Atlántica *L. eques* en relación con su congénere del Mediterráneo *L. lepidion* ha sido cuestionado desde principios del siglo XX (Collett, 1905; Roule, 1919). Finalmente, Templeman (1970) encuentra grandes semejanzas en la merística y las biometrías de ambas especies, indicando que podrían tener una relación subespecífica, pero, siguiendo un criterio de precaución, decide no cambiar su estatus.

Los resultados morfológicos muestran una gradación latitudinal descendente norte-sur en los caracteres merísticos analizados de *L. eques*, siendo los valores más al sur, del BG, similares a los de *L. lepidion* del Mediterráneo. Las diferencias morfológicas con carácter diagnóstico encontradas pueden ser en realidad los extremos de la variación latitudinal de la misma especie relacionadas probablemente con la temperatura del agua.

Las información biológica y oceanográfica también sugiere la ausencia de barreras biogeográficas que delimiten dos especies distintas en Atlántico y Mediterráneo. Los huevos y las primeras fases de desarrollo de los móridos son pelágicas (Cohen, 1986). Si bien los huevos de *Lepidion* están aun sin describir, la fase juvenil pelágica está descrita en varias especies como *L. eques* (Saemundsson, 1926; Koefoed, 1927), *L. lepidion* (Templeman, 1970) y *L. inosimae* (Okamoto y col. 2009). El estrecho de Gibraltar comunica ambos mares y se estima que alrededor del 59% de los peces del

Mediterráneo tienen un origen Atlántico (Psomadakis y col., 2012). Por otro lado, diversos estudios sugieren la existencia de dos venas de agua del Mediterráneo a ambos lados del BG (Ruiz-Villarreal y col., 2006) que podrían ser las responsables del flujo genético entre el Mediterráneo y el BG.

Los resultados de los análisis morfológicos y moleculares, junto con la información biológica y oceanográfica sugieren que la especie del Mediterráneo *L. lepidion* y la del Atlántico Norte *L. eques* son la misma especie, por lo que *L. eques* es un sinónimo más moderno de *L. lepidion*.

Muchas especies de peces, silvestres o cultivadas, pueden desarrollar anomalías en sus patrones de pigmentación. Estas anomalías incluyen principalmente el albinismo parcial o completo, melanosis, ambicoloración y xantocromía (Simon y col., 2009). Los individuos con melanosis o hiper-pigmentación melánica se caracterizan por un aumento de manchas oscuras o negras en la piel debido a un incremento en el depósito de melanina de localización ectópica (Lincoln y col., 1998). La melanosis es relativamente rara en la naturaleza y su presencia se relaciona con una respuesta inflamatoria crónica al daño de los tejidos por traumas físicos, patologías infecciosas, herencia genética, hibridación intergenérica o infestación parasitaria (Simon y col., 2009).

Figura 20. Ejemplar de *L. lepidion* del banco de Galicia con melanosis

Dos casos de hiperpigmentación melánica en ejemplares de *Lepidion lepidion* (antes *L. eques*) fueron registrados en el BG y el cañón de la Gaviera, en el golfo de Vizcaya (ver anexo III). Una búsqueda bibliográfica revela la presencia de esta anomalía

cromática en otros dos ejemplares del mismo género, el primero de ellos en un *L. lepidion* del Mediterráneo a finales del siglo XIX (Moreau, 1881).

Macroscópicamente, la hiperpigmentación se caracteriza por la presencia de numerosas manchas oscuras e irregulares sobre la cabeza, cuerpo y aletas. Microscópicamente, la melanosis se corresponde con una proliferación hiperplásica de melanóforos dérmicos. Aunque la causa de la proliferación hiperplásica de células pigmentadas no se pudo determinar, se propuso la posible acción de agentes etiológicos. Este trabajo es el primer estudio histopatológico de un ejemplar melánico del género *Lepidion*.

6.5 COMPOSICIÓN DE ESPECIES DE LA FAMILIA BATHYGADIDAE (OSTEÍCTIOS: GADIFORMES) EN EL BANCO DE GALICIA

La subfamilia Bathygadinae, considerada tradicionalmente dentro de la familia Macrouridae, es ahora elevada al rango de familia en base a estudios morfológicos y moleculares (Howes, 1989; Roa-Varón y Ortí, 2009). Los miembros de esta familia se caracterizan por tener un rostro redondeado; boca amplia, terminal y no protráctil; dientes pequeños, viliformes, dispuestos en bandas en ambas mandíbulas; barbillón largo, reducido o ausente; 7 radios branquiostegos; dos aletas dorsales, la segunda inmediatamente a continuación de la primera; radios de la dorsal más largos que los de la anal; branquiespinas numerosas, largas y delgadas en el primer arco branquial; primer arco branquial sin pliegues de la piel que conecten las regiones dorsal y ventral del arco con el opérculo; órgano luminosos ausente (Marshall y Iwamoto, 1973; Iwamoto y Graham, 2001). Los batigádidos presentan una amplia distribución por los océanos Atlántico, Índico y Pacífico oeste, principalmente en latitudes tropicales, subtropicales y templadas, entre 100 y 3000 m de profundidad. En el Atlántico oriental se han registrado siete especies de batigádidos: cuatro del género *Gadomus*: *G. dispar*, *G. longifilis*, *G. arcuatus* y *G. capensis* y tres del género *Bathygadus*: *B. melanobranchus*, *B. macrops* y *B. favosus* (Sobrino y col., 2012).

Figura 21. Detalle del ejemplar de *B. melanobranchus* capturado en el banco de Galicia.

Once ejemplares de cuatro especies de batigádidos (familia Bathygadidae) fueron capturados entre los años 2009 y 2011 en aguas del norte de España, nueve en el BG y dos en el cañón de Avilés (ver anexo IV). Las medidas morfométricas al milímetro inferior y los caracteres merísticos fueron tomados según Marshall e Iwamoto (1973). Los ejemplares fueron identificados como pertenecientes a los géneros *Gadomus* Regan, 1903 y *Bathygadus* Günther, 1878, incluyendo las siguientes especies: *Gadomus dispar* (Vaillant, 1888), *Gadomus longifilis* (Goode y Bean, 1885), *Gadomus arcuatus* (Goode y Bean, 1886) y *Bathygadus melanobranchus* Vaillant, 1888 (Fig. 21). Como resultado de este estudio, se establece un nuevo límite norte de distribución de *G. arcuatus* en el Atlántico noreste.

La identificación molecular de las especies de la familia Bathygadidae se ha explorado mediante el examen y la comparación de las secuencias de nucleótidos de los códigos de barras de ADN (ver anexo IV). Las secuencias correspondientes a los ejemplares de las mismas especies fueron idénticas, dando lugar a un único haplotipo por especie. La diversidad nucleotídica (distancia p) global media fue de 9,6%. La diversidad global media intragenérica fue de 5,6% en *Bathygadus* y de 8% en *Gadomus*. La distancia media entre los dos géneros fue de 11,5%. La mayor divergencia encontrada se dio entre secuencias de COI de *B. melanobranchus* y *G. arcuatus* (12,4%) mientras que los valores menores ocurrieron entre *B. antrodes* y *B. favosus* (5,1%).

La taxonomía integrativa se define como la ciencia que tiene por objetivo delimitar la diversidad de unidades de vida de maneras múltiples y complementarias (Dayrat, 2005). Para ello, el código de barras de ADN se ha ido implementando en la identificación de peces junto con los tradicionales análisis morfológicos (Bañón y col., 2014).

Los análisis realizados en la familia Bathygadidae no solo no muestran divergencias entre los resultados morfológicos y moleculares sino que éstos se refuerzan mutuamente, incrementando notablemente la fiabilidad de las identificaciones taxonómicas realizadas.

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7 CONCLUSIONES

1. La aplicación de la taxonomía integrativa, utilizando análisis complementarios morfológicos y moleculares (código de barras de ADN), resulta en identificaciones más fiables y veraces.
2. Por el número de especies identificadas, el banco de Galicia es una zona de alta biodiversidad ictiológica, superior al de las montañas submarinas más próximas del entorno de las Azores.
3. Las especies de aguas profundas ("deep water fishes"), que viven habitualmente a profundidades mayores de 400 m, constituyen la mayoría de las especies que componen el banco de Galicia.
4. El ochenta y uno por ciento de las especies de peces registradas en el banco de Galicia fueron registradas anteriormente en otras montañas submarinas y por tanto pueden ser categorizados como peces de montañas submarinas.
5. El setenta y uno por ciento de las especies de peces del banco de Galicia han sido citadas con anterioridad en el talud o plataforma de Galicia, pero la práctica totalidad de las especies ya habían sido registradas en aguas del Atlántico europeo, indicando la ausencia de especies endémicas en el banco de Galicia.
6. La mayoría de las especies fueron capturadas dentro del rango de presencia de corales de agua fría, entre 620 y 1125 m de profundidad, indicando una posible asociación que es preciso confirmar.
7. Se ha constatado que la actividad pesquera en el banco de Galicia ha sido escasa y ha ido disminuyen con el tiempo, ejercida principalmente con artes de pesca poco destructivos como volantas y palangres, lo que ha mantenido el ecosistema del banco de Galicia en un buen estado de conservación.
8. Especies como *Aldrovandia oleosa*, *Physiculus dalwigki*, *Pseudophychthys splendens* o *Gaidropsarus granti*, que tenían anteriormente su límite norte de distribución en el Atlántico este en las Azores, son citadas ahora en el banco de Galicia, pareciendo indicar una distribución a saltos ("stepping stones") utilizando las islas y montañas submarinas.
9. Los análisis morfológicos y moleculares junto con la información biológica y oceanográfica sugieren que la especie endémica del Mediterráneo *L. lepidion* y la

del Atlántico norte *L. eques* son en realidad la misma especie, por lo que *L. eques* es un sinónimo más moderno de *L. lepidion.*

10. La alta biodiversidad encontrada y porcentaje de especies vulnerables presentes en el banco de Galicia recomiendan su protección y ratifican su declaración como Lugar de Importancia Comunitaria (LIC) realizada recientemente por la Unión Europea (Ejecución UE 2015/2373 de la Comisión de 26 de noviembre de 2015).

ANEXO I

Bañón, R., J.C. Arronte, C. Rodríguez-Cabello, C.-G. Piñeiro, A. Punzón & A. Serrano. 2016. Commented checklist of marine fishes from the Galicia Bank seamount (NW Spain). Zootaxa. 4067 (3): 293–333

Abstract A commented checklist containing 139 species of marine fishes recorded at the Galician Bank seamount is presented. The list is based on nine prospecting and research surveys carried out from 1980 to 2011 with different fishing gears. The ichthyofauna list is diversified in 2 superclasses, 3 classes, 20 orders, 62 families and 113 genera. The largest family is Macrouridae, with 9 species, followed by Moridae, Stomiidae and Sternoptychidae with 7 species each. The trachichthyd *Hoplostethus mediterraneus* and the morid *Lepidion lepidion* were the most abundant species. Biogeographically, the Atlantic group, with 113 species (81.3%) is the best represented, followed by the Lusitanian one with 17 species (12.2%). Data on species abundance, as number of individuals caught, size and depth are reported. Habitat, distribution and vulnerability status are commented. Moreover, biometric data and meristic counts are also reported for several species. The results obtained showing a high fish biodiversity and a sensible number of threatened species, strongly support the future declaration of the Galicia Bank as a Marine Protected Area.

Introduction

Seamounts are typically defined as submarine mountains that rise at least 1000 m from the abyssal floor of the ocean but do not reach the surface. However, there is not a general accepted definition, having being extensively modified in the literature according to the author's disciplines (Staudigel *et al.* 2010). In fact, the Galicia Bank aside from a seamount, has been defined in many different ways, such as a structural high (Ercilla *et al.* 2006; Alonso *et al.* 2008), a submarine bank (Ruiz-Villareal *et al.* 2006) or a microplate (Sibuet *et al.* 2007). In the North East Atlantic, seamounts are defined according to the Oslo-Paris Convention (OSPAR) as undersea mountains of volcanic origin, with a crest that rises more than 1000 m above the surrounding seafloor (Howell *et al.* 2010).

The number of seamounts is difficult to estimate, but, according to the Census of Marine Life, there are potentially up to 100,000 seamounts over 1 km high and many more of smaller elevation. Seamounts biodiversity is still poorly understood on a global scale due to the lack of prospecting and exploratory surveys. Thus, very few seamounts have been studied so far; only about 350 seamounts have been sampled and less than 200 have been surveyed in any detail, many of them located in waters within national jurisdiction (Secretariat of the Convention on Biological Diversity 2008).

Available research results suggest that seamounts are often highly productive ecosystems known for their ability to support high biodiversity and special biological communities, including cold-water coral reefs, abundant fishery resources, marine mammals and seabirds (Johnston & Santillo 2004).

The Galicia Bank seamount was described for the first time by Black *et al.* (1964). The first biological study was on fossil benthonic foraminifera (Fisher 1969). The geophysical and geological studies were carried out focussing on its geodynamic origins, evolution and magnetic field (Black *et al.* 1964; Sibuet *et al.* 1978; Vanney *et al.* 1979).

Unfortunately, on 19 November 2002, the Galicia Bank gained international notoriety with the sinking of the ‘‘Prestige’’ oil tanker in the south-western part of the Bank. As a result of this environmental catastrophe, the area was the object of intensive and multidisciplinary studies, resulting in many scientific papers mainly related to marine pollution and geology (Albaigés *et al.* 2006; Ercilla & Vilas 2008).

The available biological information on the Galicia Bank showed a low benthic biomass dominated by filter feeders (Duineveld *et al.* 2004). The Bank is characterized by the presence of live and dead cold-water corals *Lophelia pertusa* and *Madrepora oculata*, both of high ecological importance (Bouchet & Metivier 1988; Somoza *et al.* 2014). The rest of the macrofauna is diverse and includes mainly corals (Scleractinia, Octocorallaires), mollusks (bivalves, gastropods, aplacophora), echinoderms (including some stalked crinoids and ophiuroids), polychaetes (Nereidae and Polynoidae) sponges (Demospongiae and Hexactinellida) and decapod crustaceans (decapods, euphausiids, peracarids, ostracods) (Rolán & Pedrosa 1981; Flach *et al.* 2002; Duineveld *et al.* 2004; Cristobo *et al.* 2010; Cartes *et al.* 2014)

Compared with the surrounding ocean waters, seamounts support a great diversity of fish species, which may form dense aggregations for spawning or feeding and are generally targeted by large-scale fisheries (Clark *et al.* 2006). The ichthyofauna of the Galicia Bank is not well known. The first records have been reported in the decade of 1980 in grey literature and since the late 1990's in scientific journals. The first compilation reported the presence of 86 fish species in this area: 70 teleosts, 11 sharks, 3 rays and 2 chimaeras (Piñeiro *et al.* 2001). However, these authors only provided the scientific name of 19 species**.** Bañón *et al.* (2010) included in a checklist of marine

fishes from Galician waters the ones captured until 2009 in the Galicia Bank, but without distinguishing between fishes captured in the continental shelf and in the Bank.

There is a need for large-scale management and conservation of deep-sea biodiversity and ecosystem function, including the establishment of networks of marine protected areas (MPAs) on the High Seas, including the seamounts (Clark *et al.* 2011). The Galicia Bank is one of the eleven areas proposed by the Spanish Ministry for Agriculture, Food and Environment (Ministerio de Agricultura, Alimentación y Medio Ambiente) to be designated, first as a special area of conservation (SAC) for species and habitats, under the Habitat Directive (Council Directive 92/43/EEC), and finally as part of the Natura 2000 network of MPAs in the North East Atlantic Ocean. In order to obtain the information required to fulfil the SAC proposal and begin conservation and management actions, the project LIFE+ "Inventory and designation of marine Natura 2000 areas in the Spanish sea (INDEMARES)" (EC contract INDEMARES-LIFE, 07/NAT/E/0007) was conducted (www.indemares.es). In addition, the Galicia Bank is one of the areas under evaluation in the habitat monitoring in the European Union's Marine Strategy Framework Directive (2008/56/CE). In both Habitats and Marine Strategy directives, the presence of vulnerable and threatened species listed on international conventions such as the Convention for the Protection of the Marine Environment of the North-East Atlantic (OSPAR) or the International Union for Conservation of Nature (IUCN), is one of the key factors in conservation actions.
The aim of this investigation is to present an updated and commented check list of the marine fishes currently known in the Galicia Bank and to briefly discuss the results obtained.

Material and Methods

Study area. The Galicia Bank is an isolated non-volcanic large seamount, located in the Northwestern of the Iberian Peninsula (North-east Atlantic), between 42° 15′N and 43°N and from 11° 30′W to 12° 15′W, at water depths from 625 to 1,800 m and approximately 125 nautical miles offshore the coast (Fig. 1). The Bank has an extension of about 2117 km^2 and shows a trapezoidal shape of 75 km wide in the NNE-SSO direction and 58 km length in the ONO-ESE direction mostly bounded by a steep scarp (Cristobo *et al.* 2014; Somoza *et al.* 2014). A peak in the Eastern zone of the bank comes within 625 m of the surface. To the North, Northwest it slopes very steeply from

approximately 1,000 m down to the abyssal plain at 5,000 m, and is separated from the Iberian continental margin by a 3000 m depth channel.

The Bank is part of the Galicia Bank region, an area of complex morphology, which is divided, from east to west, in five physiographic provinces: the Galicia Interior Basin, the Transitional Zone, the Galicia Bank, the Half-Graben province and the Deep Galicia Margin (Vázquez *et al.* 2008). The Galicia Bank is formed by series of narrow (10–20 km) and elongated (60–100 km) blocks tilted to the continent along normal faults oriented roughly N–S, interrupted and/or slightly displaced by NW–SE and ESE–WNW transverse faults (Díaz *et al.* 2007).

The Galicia Bank is under the influence of several thermohaline driven water masses flowing northwards. These mostly comprise the North Atlantic Central Water, at depths around 540 m, the Mediterranean Outflow Water, at around 1,490 m, the Labrador Sea influenced Deep Intermediate Water at around 2,155 m, the Lower North Atlantic Deep Water at around 3,450 m and the Lower Deep Water below this depth (Rey et al. 2008).

Sampling, species identification and morphological analysis. Ichthyological samplings were carried out during three distinct periods between 1980 and 2011 (Table 1). The samplings included both exploratory surveys, conducted by commercial vessels, and multidisciplinary scientific research surveys, conducted by oceanographic vessels. Both type of surveys aimed different objectives. The main purposes of the exploratory surveys were to evaluate the possibility of a long-term sustainable exploitation of the fisheries resources and also to obtain scientific information (Durán & Román 2000), whereas the main objective of the INDEMARES scientific surveys was to obtain information about habitats, species and the environmental conditions required for the Natura 2000/ SAC proposals.

The present checklist includes the compilation of all fish species recorded in each survey. However, the taxonomical list obtained during the exploratory surveys carried out during the decade of 1980 was partial and restricted to the main commercial species. Therefore, this information was only used to point out the presence of some epipelagic species reported in these surveys or as complementary information of some species poorly recorded in the other surveys.

Fish species were collected using many types of fishing gears, including commercial ones such as bottom trawl, pelagic and bottom longlines, "piedra-bola" longline and scientific sampling gears, mainly beam trawl (10 mm codend mesh size) and GOC73 otter trawl (20 mm codend mesh size).

TABLE 1. Summary of datasets used for this study.

Year	No. Surveys	Total days	Survey type	Gear	Acronym
1980	2	37	exploratory	multi-gear	—
1981	2	23	exploratory	multi-gear	—
1997	2	13	exploratory	longline	—
1998	1	5	exploratory	longline	—
1998	3	13	exploratory	bottom trawl	—
1999	9	35	exploratory	bottom trawl	—
2009	1	3	scientific	multi-gear	Ecomarg0709
2010	1	16	scientific	multi-gear	BanGal0810
2011	1	13	scientific	multi-gear	BanGal0811

Only specimens identified to species level have been included in the list. Fish species were identified according to published keys and guides, mainly Whitehead *et al.* (1986) and Quéro *et al.* (2003), but also following other specific guides and numerous scientific papers. The checklist is presented in the taxonomic sequence: superclass, class, order, family, genus and species. Quéro *et al.* (2003), Eschmeyer (2014) and Froese & Pauly (2014) were followed for the classification system order, the scientific nomenclature and the common names respectively.

For the majority of species listed, the total number of captured specimens, their size or size range, the mean length±SD (only in samples with N≥30), depth or depth range and the habitat and distribution data are reported. Size was generally reported as total length (TL) to the nearest cm or mm, with the exception of macrurids (family Macrouridae), where the preanal length (PAL) was measured. Habitat and distribution information has been compiled from Ebert & Stehman (2013) for elasmobranches and from Froese & Pauly (2014) and Whitehead *et al.* (1986) for teleosts. In addition, specific literature on several species was used when necessary.

Biometric data and meristic counts were also reported for several species. The total length, standard length and fork length data are expressed in millimeters and the rest of the measures as percentage of the standard length.

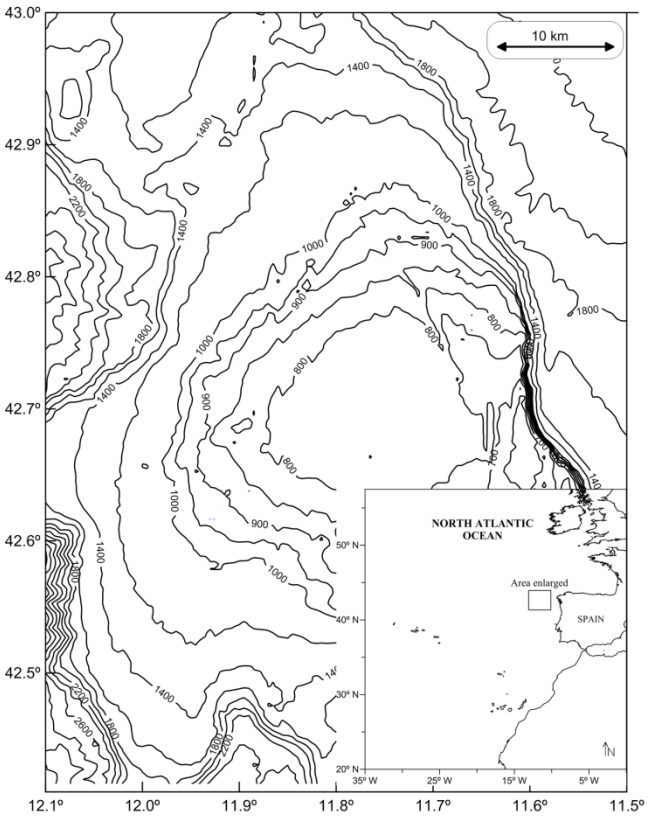

FIGURE 1. Map of the study area

The following abbreviations were used for morphometric and meristic characters: total length (TL), standard length (SL), Fork length (FL), Head length (HL), pre-orbital length (PO), Eye diameter (ED), Post orbital Length (POL), Inter-orbital width (IOW), barbel length (BL), pre-dorsal length, first, second (PD, PD1, PD2), pre-anal length (PA), dorsal fin base length, first, second (LD, LD1, LD2), anal fin base length (LA), pre-pectoral distance (PP), pre-ventral distance (PV), pectoral fin length (LP),ventral fin length (LV), maximum body height (H), number of rays in dorsal, first, second (D, 1D, 2D), pectoral (P), ventral (V), anal (A) and caudal (C) fins., total number of gillrakers on the first gill arch (Gr); number of scales on the lateral line (LL). For the nomenclature of photophores; ventral-anal (VAV); pectoral-pelvic (PV); lateral series (OA); ventral series posterior to anal fin origin (AC); isthmus-pectoral (IP); (IC); subpectoral (PVO); suprapectoral (PLO); thoracic (PO); supraventral (VLO); superanal (SAO); ventral (VO); anal (AO).

Biogeography and Vulnerability. The attribution of biogeographic affinity categories was adopted following Ellis *et al.* (2007): Boreal, Lusitanian (including Mediterranean species), Atlantic (including deep-water or mesopelagic species widely distributed) and African.

The vulnerability and conservation status of each fish species were compiled from two global Red List inventories, IUCN (IUCN 2014; Nieto *et al.* 2015) and FishBase (Froese & Pauly 2014) and one regional, OSPAR (OSPAR, 2014). According to IUCN criteria, species are consider threatened if they are categorized as critically endangered (CR), endangered (EN) or vulnerable (VU), and non-threatened if categorized as near threatened (NT), least concern (LC) or data deficient (DD). According to FishBase criteria (Cheung *et al.* 2005) species are considered to be threatened if they are categorized as very high vulnerability (VHV), high to very high vulnerability (HHV) and high vulnerability (HV) and non-threatened if categorized as moderate to high vulnerability (MHV), moderate vulnerability (MV), low to moderate vulnerability (LMV) and low vulnerability (LV). Species listed in the OSPAR list of threatened and/or declining species were considered as vulnerable (VU).

Results

SUPERCLASS GNATHOSTOMATA

CLASS CHONDRICHTHYES

ORDER HEXANCHIFORMES

Family Hexanchidae

Hexanchus griseus (Bonnaterre, 1788) — Bluntnose sixgill shark

14 specimens were caught at depths between 682 and 1,035 m. Length data were available for eight females from 130 to 355 cm and one male of 73 cm TL. Habitat and Distribution: deep-water demersal species inhabiting the outer continental shelves, upper continental slopes, insular shelves and slopes, and submarine canyons down to at least 2,500 m depth. Circumglobal in tropical and

temperate seas, including the Mediterranean, Baltic and North Seas and the Hawaiian Islands. Vulnerability: NT (IUCN), VHV (FishBase).

ORDER SQUALIFORMES

Family Centrophoridae

Centrophorus granulosus (Bloch & Schneider, 1801) — Gulper shark

218 specimens were caught at depths between 823 and 1,119 m. Length data were recorded for all specimens: two males of 115 cm TL and 216 females between 107 and 166 cm TL (145.4±12.4). The main biological data of the specimens of *C. granulosus* captured in Galician waters, including the Galicia Bank, were previously reported by Bañón *et al.* (2008). Habitat and Distribution: deep-water shark of the outer continental shelves and upper slopes at depths from 50 to 1,440 m. Widely distributed in all ocean basins except the Eastern Pacific. Vulnerability: CR (IUCN), VU (OSPAR), VHV (FishBase).

Centrophorus squamosus (Bonnaterre, 1788) — Leafscale gulper shark

1,329 specimens were caught at depths between 749 and 1119 m. Length data were available for 1,226 specimens, with males between 88 and 129 cm (110.9±4.1, N=1,015) and females between 96 and 144 cm (122.2±10.6, N=211) The main biological data relating to *C. squamosus* caught in Galician waters, including the Galicia Bank, were previously reported (Bañón *et al.* 2006a). Habitat and Distribution: deepwater gulper shark of the continental slopes from 229 to over 4,000 m depth, but rare above 1,000 m depth. Eastern Atlantic, Western North Atlantic (one record from Venezuela), Western Indian and Western Pacific Oceans. Vulnerability: EN (IUCN), VU (OSPAR), VHV (FishBase).

Deania calcea (Lowe, 1839) — Birdbeak dogfish

Prior to 2009 this species was classified erroneously together with *D. profundorum* and since them only 4 males, from 90 to 108 cm TL, were caught at depths between 851 and 916 m. Habitat and Distribution: outer continental and insular shelves and upper, middle, and lower slopes from 60 to 1,490 m

depth, but usually at depths between 400 and 900 m. Wide and patchy distribution in the Eastern Atlantic (Iceland to Southern Africa) and Pacific Oceans (Chile, Peru, Japan, southern Australia and New Zealand). Vulnerability: EN (IUCN), HHV (FishBase).

Deania profundorum (Smith & Radcliffe, 1912) — Arrowhead dogfish

Until 2009 this species was misidentified as *D. calcea*. It was correctly identified from 2009 based on morphological and molecular approaches (Sanjuán *et al.* 2012). 83 specimens were caught at depths between 749 and 1,079 m. Length data were available for 70 specimens ranging from 25 to 88 cm TL (61.8±17.6), with males between 27 and 76 cm TL (61.9±13.7, N=32) and females between 25 and 88 cm TL (61.8±20.4, N=38). Habitat and Distribution: bathydemersal with patchy distribution in Eastern Atlantic, Western Indian and Western Pacific Oceans from 275 to 1,785 m depth. Vulnerability: LC (IUCN), HHV (FishBase).

Deania hystricosa (Garman, 1906) — Rough longnose dogfish

4 specimens were caught between 766 and 909 m depth. Only one specimen was measured, a female of 100 cm TL. Habitat and Distribution: benthic and probably epibenthic of the upper and middle continental and insular slopes, at depths between 471 and 1,300 m. Patchily distributed in Eastern Atlantic and Western North Pacific. Vulnerability: DD (IUCN), HHV (FishBase).

Family Etmopteridae

Etmopterus spinax (Linnaeus, 1758) — Velvet belly lantern shark

2,951 specimens were caught at depths between 643 and 1,115 m. Length data were available for 1,156 specimens ranging from 13 to 49 cm TL (33.9±7.5), with males between 13 and 44 cm TL (31.6±6.3, N=446) and females between 13 and 49 cm TL (35.8±7.6, N=680). Habitat and Distribution: bathydemersal, found on the outer continental shelves and upper slopes at depths of 70–2,000 m, mostly between 200 and 500 m. Eastern Atlantic, from Iceland and Norway to Gabon, including the Azores and Cape Verde islands and Western Mediterranean Sea. Vulnerability: LC (IUCN), MHV (FishBase).

Etmopterus pusillus (Lowe, 1839) — Smooth lanternshark

33 specimens were caught at depths between 643 and 936 m. Length data were available for 21 specimens ranging from 33 to 47 cm TL, with males between 33 and 45 cm (N=15) and females between 33 and 47 cm (N=6). Habitat and Distribution: benthopelagic, on the continental slopes, on or near bottom at a depth of 274 to 1000 m or deeper (possibly up to 1998 m). Eastern Atlantic, Western Atlantic, Indian, Central and Western Pacific Oceans. Vulnerability: LC (IUCN), MV (FishBase).

Etmopterus princeps Collet, 1904 — Great lanternshark

25 specimens were caught at depths between 1,460 and 1,809 m. Length data were recorded for all specimens ranging from 18 to 64 cm TL, with males between 19 and 64 cm (N=11) and females between 18 and 60 cm (N=14). Habitat and Distribution: bathydemersal on the continental slopes and also lower rise from 350 to 4,500 m depth. Eastern North Atlantic, from Greenland and Iceland to Mauritania and possibly Sierra Leone and Western North Atlantic (Canada and USA). Vulnerability: DD (IUCN), MHV (FishBase).

Family Somniosidae

Centroscymnus coelolepis Barbosa du Bocage & de Brito Capello, 1864 — Portuguese dogfish.

318 specimens were caught at depths between 749 and 1,685 m. Length data were available for 306 specimens ranging from 78 to 120 cm TL (107.3±7.5), with males between 83 and 100 cm (91.8±3.3, N=34) and females between 78 and 120 cm (109.2±5.3, N=272). The main biological data of the specimens of *C. coelolepis* caught in Galician waters, including the Galicia Bank, was previously reported by Bañón *et al.* (2006a). Habitat and Distribution: bathydemersal, inhabits continental and insular slopes and abyssal plains, on or near the bottom at depths of 128-3,675 m, but mostly below 400 m depth. Widely distributed in the Atlantic, including Western Mediterranean Sea and Indian and Pacific Oceans. Vulnerability: EN (IUCN), HV (FishBase), VU (OSPAR).

Centroselachus crepidater (Barbosa du Bocage & de Brito Capello, 1864) — Longnose velvet dogfish.

14 specimens were caught at depths between 823 and 1,024 m. Length data were available for one male of 58 cm TL and 11 females between 74 and 88 cm TL. Habitat and Distribution: bathydemersal, occurs along upper continental and insular slopes on or near the bottom at depths of 200 to 1,500 m. Eastern Atlantic, from Iceland to South Africa and scattered distributed throughout the Indo–Pacific and Eastern South Pacific from off Chile. Vulnerability: LC (IUCN), VHV (FishBase).

Scymnodon ringens Barbosa du Bocage & de Brito Capello, 1864 — Knifetooth dogfish

366 specimens were caught at depths between 712 and 1,470 m. Length data were available for 185 specimens ranging from 25 to 110 cm TL (69.5±23.2), with males between 26 and 84 cm (53.3±14.3, N=46) and females between 25 and 110 cm (78±22.1, N=125). Habitat and Distribution: usually mesopelagic, although captured most often near the bottom at depths from 200 to 1,600 m. Eastern Atlantic: from Scotland to Mauritania, and Senegal. One specimen recorded in the South Pacific Ocean. Vulnerability: DD (IUCN), HV (FishBase).

FIGURE 2. *Oxynotus paradoxus*.

Somniosus rostratus (Risso, 1827) — Little sleeper shark

17 specimens were caught at depths between 822 and 1,119 m. Length data were recorded for all specimens ranging from 76 to 126 cm TL, with males between

76 and 106 cm (N=7) and females between 89 and 126 cm (N=10). Habitat and Distribution: outter continental shelves and upper slopes, occurring on or near the bottom at depths between 180 and 2,200 m. Eastern Atlantic: France, Portugal, and Madeira Islands, and the Western Mediterranean Sea. Western Central Atlantic: possibly off Cuba. Vulnerability: DD (IUCN), VHV (FishBase).

Family Oxynotidae

Oxynotus paradoxus Frade, 1929 — Sailfin roughshark (Fig. 2)

2 specimens were caught at depths between 866 and 877 m. Only one specimen of 32 cm TL was measured. Habitat and Distribution: continental slope at depths from 265 to 720 m. Endemic to the Eastern Atlantic, from Scotland and northern North Sea to Senegal and possibly southwards to the Gulf of Guinea region. Apparently absent from the Mediterranean Sea. Vulnerability: DD (IUCN), HV (FishBase).

Family Dalatiidae

Dalatias licha (Bonnaterre, 1788) — Kitefin shark

101 specimens were caught at depths between 731 and 1,115 m. Length data were available for 37 specimens ranging from 38 to 151 cm TL (117.1±31.8), with males between 38 and 122 cm (N=10) and females between 42 and 151 cm (N=26). Habitat and Distribution: deepwater, warm–temperate and tropical shark of the outer continental and insular shelves and slopes from 37 to at least 1800 m depth, but commonest below 200 m. North-east Atlantic from the north of the British Isles to the north-western coast of Africa, including Azores and Madeira Islands and the Mediterranean Sea. Western North Atlantic, central and Western Pacific, and Indian Oceans. Vulnerability: EN (IUCN), VHV (FishBase).

ORDER LAMNIFORMES

Family Pentanchidae

Galeus melastomus Rafinesque, 1810 —Blackmouth catshark

One female of 70 cm TL was caught at depths between 669 and 676 m. Habitat and Distribution: deepwater bottom shark found on the outer continental shelves and upper slopes, mainly between 200 and 500 m but occasionally up to 55 m and down to 2000 m. Eastern North Atlantic, from Norway to Senegal and throughout the Mediterranean Sea. Vulnerability: LC (IUCN), HV (FishBase).

FIGURE 3. *Galeus murinus.*

Galeus murinus (Collett, 1904) — Mouse catshark (Fig. 3)

18 specimens between 29 and 44 cm TL were caught at a depth range from 1,450 to 1,683 m, with males between 29-41 cm TL (N=5) and females between 31-44 cm (N=13). Habitat and Distribution: Iceland to the Faroe Islands, and recently it has been found off Scotland, the Hebrides Islands, Ireland, France, Spain, Morocco, and Western Sahara. Vulnerability: LC (IUCN), MHV (FishBase).

Apristurus aphyodes Nakaya & Stehmann, 1998 — No common name

18 specimens, 6 males ranging from 24 to 39 cm and 12 females from 22 to 37 cm TL, were caught at a depth range of 1,460–1,809 m. Habitat and Distribution: bathydemersal deepwater species known from continental slopes, on or near bottom at depths of 380 to 1,250 m. North Atlantic, from Iceland to the northern Bay of Biscay. The Galicia Bank records constitute the southern

limit in the distribution of this species (Rodríguez-Cabello *et al.* 2014). Vulnerability: DD (IUCN), HHV (FishBase).

Apristurus profundorum (Smith & Radcliffe, 1912) — Arrowhead dogfish

One female of 14 cm TL was caught at 1,459 m depth. Habitat and Distribution: deepwater shark found on the continental slopes at 1,100 to 1,830 m. Reported in the western North Atlantic, the mid-Atlantic Ridge and eastern North Atlantic (Mauritania). This record extends northwards the known distribution of this species in the Northeast Atlantic (Rodríguez-Cabello *et al.* 2014). Vulnerability: DD (IUCN), MHV (FishBase).

Apristurus melanoasper Iglesias, Nakaya and Stehmann, 2004 — Black roughscale catshark

One female of 25 cm TL was caught at 1,683 m depth. Habitat and Distribution: widely distributed but very patchy in the North Atlantic, Southeastern Atlantic (Namibia), Central Indian Ocean and south of Madagascar and in the Western South Pacific (Australia, New Zealand and New Caledonia). This record extends the known distribution of this species in the Northeast Atlantic (Rodríguez-Cabello *et al.* 2014). Vulnerability: DD (IUCN), MHV (FishBase).

Family Pseudotriakidae

Pseudotriakis microdon de Brito Capello, 1868 — False catshark

32 specimens were caught at depths between 823 and 1,119 m. Length data were recorded for all specimens ranging from 186 to 256 cm TL (224.1±21.2), with males between 186 and 220 cm (N=16) and females between 207 and 256 cm (N=16). Habitat and Distribution: continental and insular slopes at depths from 100 to 1,890 m; occasionally wandering onto continental shelves, even in shallow water. Sporadically recorded in all Oceans, with the exception of the South Atlantic and Eastern Pacific. Vulnerability: LC (IUCN), HHV (FishBase).

Family Carcharhinidae

Prionace glauca (Linnaeus, 1758) — Blue shark

5 females ranging between 75-113 cm TL were caught at depth unknown, during the hauling of bottom longline. In addition, 13 specimens were reported

during the exploratory surveys carried out on the 1980's. Habitat and Distribution: oceanic epipelagic and fringe-littoral shark, occurring from the surface to at least 350 m depth; deeper in warm temperate and subtropical waters. Circumglobal in temperate and tropical waters. Vulnerability: NT (IUCN), HHV (FishBase).

Isurus oxyrinchus Rafinesque, 1810 — Shortfin mako

Reported only during the exploratory surveys on the 1980's with length range from 125 to 245 cm TL. Habitat and Distribution: epipelagic, oceanic shark generally occurs in tropical and warm temperate seas off the continental shelf at depths of 120 to 240 m or even deeper. North Atlantic Ocean and scattered records in the Pacific and Western Indian Oceans. Vulnerability: VU (IUCN), VHV (FishBase).

ORDER RAJIFORMES

Family Rajidae

Dipturus batis (Linnaeus, 1758) — Blue skate

9 specimens were caught at depths between 729 and 896 m. Length data were available for five specimens ranging from 22 to 146 cm TL. Currently, this species is under taxonomic revision. According to Iglésias *et al.* (2010) *D. batis* is in fact a composite species and it was provisionally split into the smaller *D. sp. cf. flossada* and the much larger *D. sp. cf. intermedia*. Vulnerability: CR (IUCN), VHV (FishBase), VU (OSPAR).

Rajella bigelowi (Stehmann, 1978) — Bigelow's ray (Fig. 4)

Two specimens, one male of 53 cm and one female of 42 cm TL, were caught at depths between 1,450 and 1,683 m. Habitat and Distribution: demersal on several types of bottom substrate from 650 to up to 4,165 m depth. Eastern North Atlantic, from Greenland and Iceland to Mauritania. Vulnerability: LC (IUCN), MV (FishBase).

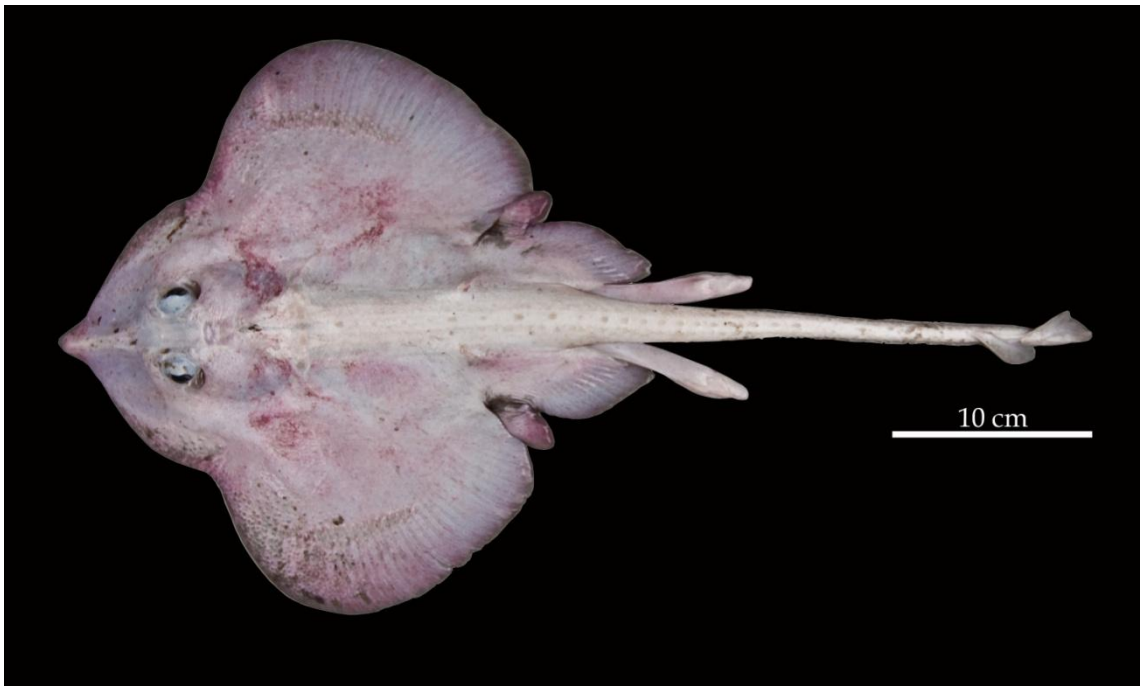

FIGURE 4. *Rajella bigelowi*.

Family Dasyatidae

Pteroplatytrygon violacea (Bonaparte, 1832) — Pelagic stingray

Two specimens, one male of 45 cm and one female of 109 cm TL, were caught at depth unknown, during the hauling of the bottom longline (Bañón *et al.* 1997). Habitat and Distribution: pelagic and oceanic, occurring from over the edge of continental and insular shelves into the open ocean at depths of 1–381 m usually in the upper 100 m depth. Tropical and subtropical seas, including Eastern Atlantic, Western Atlantic, East Pacific and North-Western Pacific (Japan and Taiwan). Vulnerability: LC (IUCN), HHV (FishBase).

CLASS HOLOCEPHALI

ORDER CHIMAERIFORMES

Family Chimaeridae

Chimaera monstrosa Linnaeus, 1758 — Rabbit fish

3 specimens were caught at depths between 877 and 1,323 m. Dubious identification specially after the capture of the cryptic species *C. opalescens* also in the Bank. Habitat and Distribution: bathydemersal to benthopelagic at depth range 40-1,000 m, generally between 300 and 500 m depth. Eastern Atlantic: northern Norway and Iceland, Skagerrak and Kattegat south to Morocco including western Mediterranean Sea (some isolated records from eastern part), Azores and Madeira Islands. Records from South Africa are questionable. Vulnerability: NT (IUCN), HHV (FishBase).

Chimaera opalescens Luchetti, Iglésias & Sellos, 2011 — Opal chimaera

4 specimens, 3 males of 10, 57 and 63 cm and one female of 64 cm TL, were caught at depths from 903 to 1,450 m. This species was recently described (Luchetti *et al.* 2011) and could probably be confused with *C. monstrosa* in previous surveys. Habitat and Distribution: Northeast Atlantic, along the slope to the west of the British Isles and France, from 900-1,400 m depth. Vulnerability: DD (IUCN), HV (FishBase).

Hydrolagus affinis (de Brito Capello, 1868) — Smalleyed rabbitfish

Three specimens, 2 females of 12 and 22 cm TL and one male of 24 cm, were caught at depths between 1,683 and 1,808 m. Habitat and Distribution: Found on continental slopes and down to deep-sea plains, reported up to 3,000 m. Occurs in North-Eastern Atlantic from the Rockall Trough along Ireland, northern Bay of Biscay and off Portugal down to 22º off NW Africa, Cape Verde and Azores. Vulnerability: LC (IUCN), HHV (FishBase).

CLASS ACTINOPTERYGII

ORDER NOTACANTHIFORMES

Family Halosauridae

Halosaurus ovenii Johnson, 1864 — No common name

12 specimens were caught at depths between 746 and 1,536 m. Length data were available for eight specimens ranging from 20 to 57 cm TL. Habitat and Distribution: both sides of the Atlantic Ocean, from Madeira, the Azores and

Canaries to Walvis Bay and the Gulf of Mexico, the Caribbean, the Antilles and the Mediterranean Sea. Vulnerability: DD (IUCN), MHV (FishBase).

FIGURE 5. *Halosauropsis macrochir*.

Halosauropsis macrochir (Günther, 1878) — Abyssal halosaur (Fig. 5)

7 specimens from 52 to 62 cm TL were caught at depths between 1,536 and 1,809 m. Habitat and Distribution: benthopelagic, 1,100-3,300 m. Antitropical distribution in Atlantic, Indian, and Pacific Oceans. Vulnerability: DD (IUCN), MHV (FishBase).

Aldrovandia affinis (Günther, 1877) — Gilbert's halosaurid fish

3 specimens from 42 to 48 cm TL were caught at depths between 1,477 and 1,545 m. Habitat and Distribution: benthopelagic, 730–2,200 m. Worldwide, known from all major oceans. Vulnerability: DD (IUCN), MHV (FishBase).

Aldrovandia phalacra (Vaillant 1888)— Hawaiian halosaurid fish

2 specimens of 19 and 33 cm TL were caught at a depth of 1,536 and 1,477 m respectively. Habitat and Distribution: Benthopelagic between 500-2,300 m depth. Circumglobal, mainly at tropical and temperate latitudes. Vulnerability: DD (IUCN), MV (FishBase).

Aldrovandia oleosa Sulak, 1977 — No common name

16 specimens from 20 to 39 cm TL were caught at depths between 1,477 and 1,751 m. Benthopelagic to benthic on the lower slope, continental rise and upper abyss, between 1,100 and 3,300 m depth and primarily between 2 and 4ºC isotherm. Circumglobal at tropical and temperate latitudes. in Atlantic, Indian, and Pacific Oceans. Vulnerability: DD (IUCN), MV (FishBase).

Family Notacanthidae

Notacanthus bonaparte Risso, 1840 — Shortfin spiny eel

656 specimens were caught at depths between 731 and 1685 m. Length data were available for 375 specimens ranging from 15 to 46 cm TL (31.3±6.5). Habitat and Distribution: bathypelagic between 487-2,000 m depth. Eastern Atlantic Ocean, Iceland, Faeroes, and from Ireland to Cape Blanc, Mauritania, and in the Western Mediterranean Sea. Vulnerability: DD (IUCN), LV (FishBase).

Polyacanthonotus rissoanus (De Filippi & Verany, 1857) — Smallmouth spiny eel

7 specimens between 21 and 43 cm TL were caught at depths between 1,536 snd 1,809 m. Habitat and Distribution: epibenthic anti-tropical on the continental slope, between 540-2,875 m with most records between 1,500-2,000 m depth. Eastern Atlantic, from Iceland to South Africa, including the Mediterranean Sea and Western Atlantic, from Davis Strait to Cape Hatteras and North Carolina in the USA. Vulnerability: DD (IUCN), MV (FishBase).

ORDER ANGUILLIFORMES

Family Synaphobranchidae

Synaphobranchus kaupii Johnson, 1862 — Kaup's arrowtooth eel

1,264 specimens were caught at depths between 711 and 1,809 m. Length data were available for 1,252 specimens ranging from 8 to 72 cm TL (21.8±11.4). Habitat and Distribution: demersal deep-sea fish between 120-4,800 m depth, usually 400-2,200 m. It is distributed in all the major ocean basins; the Atlantic, the Indian and the Pacific Oceans. In the Eastern North Atlantic it is recorded

from west of the Faroe Islands slope to the coast of northwest Africa. Vulnerability: LC (IUCN), MHV (FishBase).

Family Congridae

Conger conger (Linnaeus, 1758) — European conger

208 specimens were caught at depths between 643 and 914 m. Length data were available for 37 specimens ranging from 36 to 141 cm TL (73.8±33.3). Habitat and Distribution: benthic species living in rocky and sandy bottoms between 10 and 1,171 m. North-East Atlantic, from Norway and Iceland to Senegal, the Mediterranean and the western Black Seas. Vulnerability: DD (IUCN), VHV (FishBase).

Pseudophichthys splendens (Lea, 1913) — Purplemouthed conger

3 specimens, 1 adult of 31 cm TL and 2 juveniles of 12 and 15 cm TL, were recorded at depths between 887 and 1,041 m. Habitat and Distribution: bathydemersal species of amphi-Atlantic distribution, between 37 and 1,647 m depth. Off the Western Atlantic Ocean, from Canada (larval specimens) to Brazil, while off the Eastern Atlantic Ocean was recorded from Morocco, the Canary and Azores Islands and the Gulf of Guinea. These records constitute a northward range extension of their known distribution in the Eastern Atlantic (Bañón *et al.* 2011). Vulnerability: DD (IUCN), LMV (FishBase).

FIGURE 6. *Nessorhamphus ingolfianus.*

Family Derichthyidae

Nessorhamphus ingolfianus (Schmidt, 1912) — Duckbill oceanic eel (Fig. 6)

One specimen of 47 cm TL was caught at a depth of 1,470 m. Habitat and Distribution: bathypelagic, 0-1,800 m depth. Temperate, tropical and subtropical regions of Atlantic, Indian and Pacific Oceans. In the Eastern Atlantic it occurs from France to Morocco and off the Cape, South Africa. Vulnerability: DD (IUCN), MHV (FishBase).

Family Nemichthyidae

Nemichthys scolopaceus Richardson, 1848 — Slender snipe eel

14 specimens were caught at depths between 751 and 896 m. Length data were available for 11 specimens ranging from 60 to 111 cm TL. Habitat and Distribution: mesopelagic and oceanic, from the surface down to depths of 2,500 m, usually between 200-500 m depth. Worldwide in tropical and temperate seas. Vulnerability: DD (IUCN), MHV (FishBase).

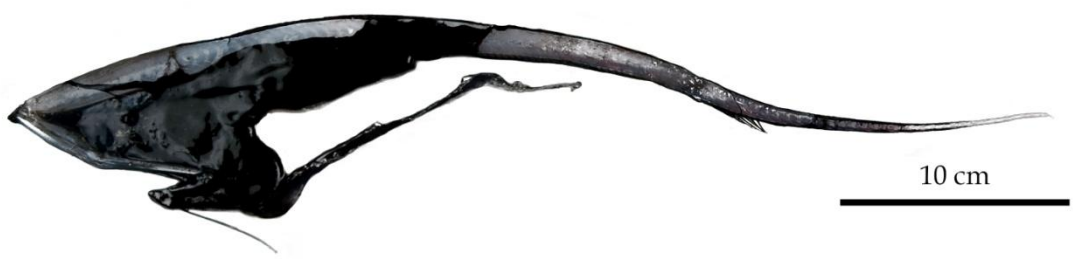

FIGURE 7. *Eurypharynx pelecanoides*.

Family Serrivomeridae

Serrivomer beanii Gill & Ryder, 1883 — Bean's sawtoothed eel

15 specimens were caught at depths between 726 and 1,750 m. Length data were available for 13 specimens ranging from 25 to 82 cm TL. Habitat and

Distribution: epibenthic-pelagic species distributed in the Atlantic and western Pacific Oceans. In the Eastern Atlantic it occurs from north to Iceland to South Africa. Vulnerability: DD (IUCN), MV (FishBase).

ORDER SACCOPHARYNGIFORMES

Family Eurypharyngidae

Eurypharynx pelecanoides Vaillant, 1882 — Pelican eel (Fig. 7)

3 specimens between 34 and 47 cm TL were caught at depths between 780-1,674 m. Habitat and Distribution: meso- to abyssopelagic and bathypelagic. Circumglobal in tropical and temperate waters. In the Atlantic Ocean it is recorded from off Iceland (65ºN) to 48ºS. Vulnerability: DD (IUCN), MHV (FishBase).

ORDER OSMERIFORMES

FIGURE 8. *Bathylagus euryops.*

Family Bathylagidae

Bathylagus euryops Goode & Bean, 1896 — Goiter blacksmelt (Fig. 8)

2 specimens of 19 and 20 cm TL were caught at depths between 1,685 and 1,750 m. Habitat and Distribution: meso-and bathy pelagic zones of the North Atlantic, sometimes in large aggregations, between 300 and 2,300 m depth. Western

Atlantic, as far north as Greenland, extending south to Bermuda and Eastern Atlantic, from Iceland to Portugal. Vulnerability: DD (IUCN), LMV (FishBase).

Family Alepocephalidae

Alepocephalus rostratus Risso, 1820 — Risso's smooth-head

72 specimens were caught at depths between 781 and 1,683 m. Length data were available for 51 specimens ranging from 18 to 65 cm TL (43.7±13.2). Habitat and Distribution: bathydemersal, over soft bottoms at about 300-3,600 m depth, usually at 300-1,600 m. Eastern Atlantic Ocean, from Iceland to Namibia and Western Mediterranean Sea. Vulnerability: DD (IUCN), HHV (FishBase).

Alepocephalus bairdii Goode & Bean, 1879 — Baird's smooth-head

1,895 specimens were caught at depths between 711 and 1,809 m. Length data were available for 1,228 specimens ranging from 13 to 89 cm TL (64.4±12.1). Biometry and meristic: 6 specimens 521-817 mm TL, 443-708 mm SL; HL: 23.8-28.3; PO: 4.5-5.1; POL: 14.4-17.4; ED: 4.6-7.0; IOW: 3.4-4.4; PD: 55.6-66.4; LD: 12.4-15.4; PA: 56.1-68.9; LA: 13.8-17.2, PP: 24.6-29.9; PV: 40.6-49.2; LP: 7.7-11.5; LV: 4.9-5.6; H: 17.8-20.5; D: 20-22; A: 21-24; P: 10-13; V: 8-9; Gr: 8-11+1+18-19; SLL: 61-64. Habitat and Distribution: bathydemersal over ooze and sand bottoms at a depth range of 365-2,500 m. Eastern Atlantic Ocean, from Greenland and Iceland southward to 17°N and Western Atlantic Ocean, from Greenland to Grand Banks and 29°52'N, 77°09'W. Vulnerability: DD (IUCN), HHV (FishBase).

Xenodermichthys copei (Gill, 1884) — Bluntsnout smooth-head

69 specimens were caught at depths between 735 and 1,640 m. Length data were available for 49 specimens ranging from 6 to 19 cm TL (14±2.8). Habitat and Distribution: mesopelagic to benthopelagic as adults, between 100-2,650 m, usually at 100-1,230 m depth. Widely distributed in the Atlantic, Eastern Pacific and Indian Oceans. Vulnerability: DD (IUCN), MV (FishBase).

Rouleina attrita (Vaillant, 1888) — Softskin smooth-head

248 specimens were caught at depths between 1,470 and 1,809 m. Length data were available for all specimens, ranging from 6 to 49 cm TL (25.4±9.6). Habitat and Distribution: bathypelagic at depth range 450-2,300 m.

Circumglobal, widely distributed in the Atlantic, most Indian submarine ridges, Subantarctic, North Pacific and tropical Western and Eastern Pacific Oceans. Vulnerability: DD (IUCN), MHV (FishBase).

Conocara macropterum (Vaillant, 1888) — Longfin smooth-head

41 specimens were caught at depths between 1,674 and 1,809 m. Length data were available for all specimens ranging from 17 to 39 cm TL (30.7±4.7). Habitat and Distribution: epibenthic at about 800-2,677 m depth, usually at 1,200-1,800 m. Known from widely scattered localities on both sides of the Atlantic Ocean, in Eastern Atlantic from 54°N to 45°S and in Western Atlantic in Bahamas, Gulf of Mexico and off Brazil. Vulnerability: DD (IUCN), MHV (FishBase).

ORDER STOMIIFORMES

Family Gonostomatidae

Gonostoma elongatum Günther, 1878 — Elongated bristlemouth fish

8 specimens were caught at depths between 740 and 916 m. Length data were available for 4 specimens ranging from 18 to 24 cm TL. Habitat and Distribution: meso- to bathypelagic, depth range 0-4,740 m, usually between 100-200 m and 500-800 m at night and 25-600 m and 1,250-1,500 m during the day. Worldwide distribution, in tropical and subtropical Atlantic, Indian and Pacific Oceans. In the Eastern Atlantic, from off Eastern Greenland, Iceland and Spain south to the Gulf of Guinea, being more common south of 40°N. Vulnerability: DD (IUCN), MV (FishBase).

Sigmops bathyphilus (Vaillant, 1884) — Spark anglemouth

3 specimens between 10 and 12 cm TL were caught at depths between 1,536 and 1,809 m. Habitat and Distribution: bathypelagic, juveniles and adults at 700-3,000 m with marked stratification of size with depth. Temperate and subtropical latitudes of the Atlantic, Pacific and Eastern Indian Oceans. Scattered records from 65°'N to Namibia and South Africa in the Eastern Atlantic. Vulnerability: DD (IUCN), MV (FishBase).

Cyclothone pallida Brauer, 1902 — Tan bristlemouth

1 specimen of 6 cm TL was caught at a depth of 1,674 m. Habitat and Distribution: oceanic, meso- to bathypelagic, at a depth range of 16-4,663 m, usually 600-1,800 m. Worldwide distribution, in tropical and subtropical Atlantic, Indian and Pacific Oceans. Vulnerability: DD (IUCN), MV (FishBase).

Family Sternoptychidae

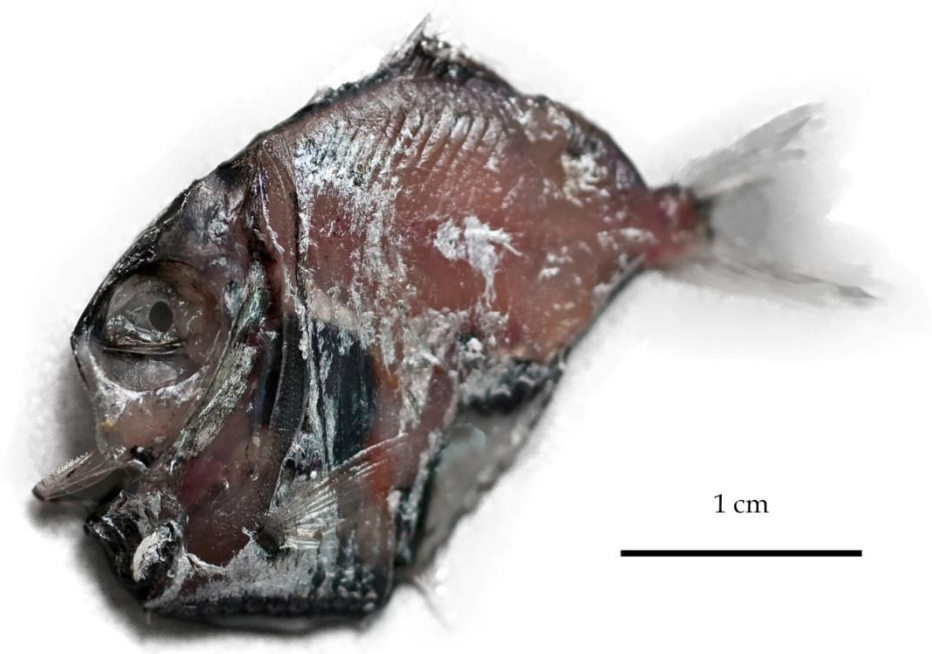

FIGURE 9. *Sternoptyx diaphana*.

Sternoptyx diaphana Hermann, 1781 — Diaphanous hatchet fish (Fig. 9)

One specimen of 4 cm TL was caught at a depth of 771 m. Habitat and Distribution: bathypelagic, oceanodromous at depth range 400-3,676 m, usually 500-800 m. Mainly in tropical regions of Atlantic, Pacific and Indian Oceans. Scattered records southwest of Ireland and also from Spain to Angola in the Eastern Atlantic. Vulnerability: DD (IUCN), LV (FishBase).

Argyropelecus hemigymnus Cocco, 1829 — Half-naked hatchetfish

23 specimens were caught at depths between 765 and 1,460 m. Length data were available for 22 specimens ranging from 2 to 4 cm TL. Habitat and Distribution: oceanic and mesopelagic, from 100 to 4,054 m depth, mainly at 250-650 m.

Worldwide distribution in tropical and subtropical waters of all oceans. Vulnerability: LC (IUCN), LV (FishBase).

Argyropelecus olfersii (Cuvier, 1829) — No common name

5 specimens were caught at depths between 771 and 1,674 m. Length data were available for 4 specimens ranging from 9 to 11 cm TL. Habitat and Distribution: oceanic, mesopelagic with adults and juveniles at 200-800 m during daylight and from 100 (sometimes shallower) to 600 m at night. Restricted in the North-East Atlantic Ocean between 35°N and 65°N, probably with a bipolar distribution, and in the Southern Pacific Ocean between 30˚ S and 50˚S from Chile to New Zealand. Vulnerability: DD (IUCN), LV (FishBase).

Argyropelecus aculeatus Valenciennes, 1850 — Lovely hatchetfish

1 specimen of 8 cm TL was caught at a depth of 791m. Habitat and Distribution: oceanic and mesopelagic species at 100-600 m depth, concentrated at 300-600 m during daylight and 100-300 at night. Atlantic Ocean, essentially absent from the tropical Atlantic; Pacific from north of New Guinea to Japan and off eastern Australia and Chile and central Indian Ocean from about 10°S to 40°S. Vulnerability: DD (IUCN), LMV (FishBase).

Argyropelecus gigas Norman, 1930 — Hatchetfish

124 specimens between 6-11 cm TL were caught by bottom trawl during 1998's surveys. They were identified as *A. gigas*, but we consider this identification, at least in part, as dubious. The size of the specimens, which is larger in *A gigas*, was used in the first surveys as one important criterion to differentiate *Argyropelecus* species. However, in posterior surveys, we found a similar size range in *A. olfersii*. Habitat and Distribution: bathypelagic at depth range 300-1,000 m, usually 400-600 m. Circumglobal, except North-Eastern Pacific Ocean. Vulnerability: DD (IUCN), LMV (FishBase).

Maurolicus muelleri (Gmelin, 1789) — Pearlsides

1 specimen of 5 cm TL was caught at a depth of 1,094 m. Habitat and Distribution: mesopelagic, abundant near continental shelf-slope breaks and seamounts and rare in the open ocean. It was found to depths of at least 1,524 m, migrating in the water column at depths of 150-250 m during daylight and to about 50 m at night. Tropical, subtropical, subarctic, and subantarctic waters of

the Pacific and Atlantic Oceans and the Mediterranean Sea. In the Eastern Atlantic it occurs from Iceland and Norway to Senegal and also from Democratic Republic of the Congo to Namibia. Vulnerability: DD (IUCN), LV (FishBase).

FIGURE 10. *Valenciennellus tripunctulatus*.

Valenciennellus tripunctulatus (Esmark, 1871) — Constellationfish (Fig. 10)

1 specimen was caught at 790 m depth. Biometry and meristic: 34 mm TL, 29 mm SL. Photophores: VAV: 5; PV: 15; OA: 4; AC: 3+3+3+2+4; IP: 3+4. Habitat and Distribution: oceanic and mesopelagic, between 100 and 700 m depth, with marked stratification of size with depth. Worldwide in tropical and temperate waters. Scattered records from the eastern Atlantic, in Iceland, Ireland, and from Portugal to Namibia and in the Mediterranean Sea. Vulnerability: DD (IUCN), LV (FishBase).

Family Phosichthyidae

Polymetme corythaeola (Alcock, 1898) — Rendezvous fish

124 specimens were caught at depths between 720 and 896 m. Length data were available for 82 specimens ranging from 10 to 21 cm TL (16.8±2.7). Habitat and Distribution: benthopelagic off continental and island slopes and seamounts in the Atlantic, Eastern Pacific and Indo-West Pacific Oceans. Vulnerability: DD (IUCN), LV (FishBase).

Family Stomiidae

Stomias boa (Risso, 1810) — Scaly dragonfish

7 specimens were caught at depths between 728 and 914 m. Length data were available for 5 specimens ranging from 18 to 35 cm TL. Habitat and Distribution: meso- to bathypelagic at depth range 200-1,500 m, but may migrate to near-surface waters at night. Atlantic, Southeast Pacific and sub-Antarctic region of the Indian Oceans and Western Mediterranean Sea. Vulnerability: DD (IUCN), MV (FishBase).

Chauliodus sloani Bloch & Schneider, 1801 — Sloane's viperfish

56 specimens were caught at depths between 715 and 1,685 m. Length data were available for 42 specimens ranging from 6 to 35 cm TL (23.3±7.1). Habitat and Distribution: bathypelagic, depth range 400-2,800 m. Cosmopolitan in temperate and tropical zones of all oceans, from about 63° N to 50° S and in the Mediterranean Sea. Vulnerability: DD (IUCN), MV (FishBase).

FIGURE 11. *Photostomias guernei*.

Photostomias guernei Collett, 1889 — Loosejaw (Fig. 11)

4 specimens were caught at depths between 847 and 866 m. Length data were available for 3 specimens ranging from 10 to 12 cm TL. Biometry and meristic:

107 mm TL, 99 mm SL; HL: 18.2; PO: 3.0; POL: 13.1; ED: 2.0; IOL: 4.0; PD: 84.8; LD: 12.1; PA: 83.8; LA: 13.1; PV: 46.5; LV: 42.4; H: 12.1; D: 22;A: 27. Photophores: OA: 37; IC: 55. Habitat and Distribution: mesopelagic during daylight to epipelagic at night, at depth range 1,138–3,100 m. Amphiatlantic, in temperate and northern subtropical waters of the North Atlantic. Kenaley & Hartel (2005) reported this species south to 3º58'N in the Eastern Atlantic, but Quéro *et al.* (2003) recorded this species in Portugal and south of Spain. The specimens captured in the Galicia Bank could constitute a new northern limit for this specie in the Eastern Atlantic. Vulnerability: DD (IUCN), LV (FishBase).

Melanostomias bartonbeani Parr, 1927 — Scaleless black dragonfish

1 specimen was caught at a depth of 877 m. Biometry and meristic: 187 mm TL, 169 mm SL; HL: 14.2; BL: 18.9; H: 9.5; D: 13;A: 18; P: 5; V: 7. Photophores: PV: 24. Habitat and Distribution: Meso- to bathypelagic at depth range 25-2,000 m. Nearly cosmopolitan in tropical and subtropical oceanic waters, apparently absent from the Eastern Indian and Western Central Pacific Oceans. In the Eastern Atlantic from 56°N to south of Guinea Bissau and also from Namibia to South Africa. Vulnerability: DD (IUCN), MV (FishBase).

Flagellostomias boureei (Zugmayer, 1913) — Longbarb dragonfish

1 specimen was caught at depths between 768 and 786 m. Biometry and meristic: 216 mm TL; 208 mm SL; HL: 13.0; PO: 4.3; POL: 5.8; ED: 2.9; IOL: 2.9; BL: 29.8 (broken); PD: 87.5; LD: 8.2; PA: 83.7; LA: 13.9; PV: 13.5; PD: 83.7; LV: 13.5; LP: H: 9.6; D: 13;A: 28; P: 10; V: 12. Habitat and Distribution: meso- to bathypelagic at depth range 0-3,000 m. Circumglobal in tropical through temperate seas. In the Eastern Atlantic from 58ºN to 40° S. Vulnerability: DD (IUCN), MV (FishBase).

Malacosteus niger Ayres, 1848 — Stoplight loosejaw

6 specimens were caught at depths between 739 and 1,683 m. Length data were available for 3 specimens ranging from 12 to 15 cm TL. Biometry and meristic: 140 mm TL; 130 mm SL; HL: 30.0; PO: 3.1; POL: 22.3; ED: 4.6; PD: 79.2; LD: 14.6; PA: 80.8; LA: 14.6; H: 17.7; D: 17; A: 19; P: 3; V: 6. Habitat and Distribution: meso- to bathypelagic at depth range 500-3,886 m, usually 915-1,830 m. It has been suggested that this species does not undergo substantial diel

vertical migration and remains below 500 m depth. Widely distributed in all oceans, mainly between 66ºN and 30ºS; unknown in the Mediterranean Sea. Vulnerability: DD (IUCN), LMV (FishBase).

Borostomias antarcticus (Lönnberg, 1905) — Snaggletooth

1 specimen of 21 cm TL was caught at a depth of 870-896 m. Habitat and Distribution: species widely distributed in all oceans. Vulnerability: DD (IUCN), MV (FishBase).

ORDER AULOPIFORMES

Family Ipnopidae

Bathypterois dubius Vaillant, 1888 — Spiderfish

29 specimens were caught at depths between 773 and 1,809 m. Length data were available for 22 specimens between 7 and 23 cm TL. Habitat and Distribution: bathydemersal at depth range 260-2,800 m, usually at 2,100-2,300 m. Eastern Atlantic Ocean from the British Isles to Sierra Leone, Azores and the Mediterranean Sea; one record from the western North Atlantic Ocean. Vulnerability: DD (IUCN), MHV (FishBase).

Family Paralepididae

FIGURE 12. *Arctozenus risso*.

Arctozenus risso (Bonaparte, 1840) — Ribbon barracudina (Fig. 12)

1 specimen was caught at a depth of 1.100 m. Biometry and meristic: 168 mm TL, 159 mm SL; HL: 21.4; PO: 10.7; POL: 7.5; ED: 3.1; IOW: 1.9; PD: 66.7; LD: 2.5; PA: 83.0; LA: 14.5; PP: 22.6; PV: 70.4; LP: 8.2; LV: 3.8; H: 6.9; D: 10; A: 32; V: 8. Habitat and Distribution: pseudoceanic and meso- to bathypelagic at depth range 0-2,200 m, usually 200-1,000 m. Circumglobal including the Mediterranean Sea. Vulnerability: DD (IUCN), LMV (FishBase).

Magnisudis atlantica (Krøyer, 1868) — Duckbill barracudina

2 specimens of 21 and 42 cm TL were caught at a depth of 764 and 892 respectively. Habitat and Distribution: oceanic, meso- and bathypelagic at depth range 0-5,499 m. Circumglobal in warm to cold temperate seas but not present in eastern tropical Pacific Ocaena. Vulnerability: DD (IUCN), MHV (FishBase).

Family Bathysauridae

FIGURE 13. *Bathysaurus ferox*.

Bathysaurus ferox Günther, 1878 — Deep-sea lizardfish (Fig. 13)

1 specimen of 31 cm TL was caught at a depth of 1,685 m. Habitat and Distribution: bathydemersal, depth range 600-3,500 m, usually 1,000-2,500 m. Atlantic and Indo-West Pacific. In the Eastern Atlantic Ocean, from Iceland to Guinea and also off South Africa. Vulnerability: DD (IUCN), MHV (FishBase).

ORDER MYCTOPHIFORMES

Family Neoscopelidae

Neoscopelus macrolepidotus Johnson, 1863 — Large-scaled lantern fish

2 specimens of 20 and 21 cm TL were caught at depths of 757 and 780 m respectively. Biometry and meristic: 219 mm TL, 178 mm SL; HL: 28.7; PO: 7.9; POL: 16.3; ED: 4.5; IOW: 6.7; PD: 42.7; LD: 12.9; PA: 74.2; LA: 11.8; LP: 27.0; LV: 15.2; H: 22.5; D: 13;A: 12; P: 19; V: 8; Gr: 3+8. Habitat and Distribution: bathypelagic, non-migratory, over continental and island slopes at depth range 300-1,180 m. Circumglobal in tropical through subtropical seas, but not in most parts of the Indian Ocean. In the Eastern Atlantic, from the Bay of Biscay to Western Sahara and also in Namibia. Vulnerability: DD (IUCN), MV (FishBase).

FIGURE 14. *Neoscopelus microchir*.

Neoscopelus microchir Matsubara, 1943 — Shortfin neoscopelid (Fig. 14)

287 specimens were caught at depths between 729 and 896 m. Length data were available for 176 specimens ranging from 18 to 37 cm TL (27.4±3.9). The main biometric and meristic data for this species and area were previously reported by Bañón *et al.* (2002). Habitat and Distribution: Atlantic and Indo-West Pacific Oceans. In the Eastern Atlantic Ocean, from the Galicia Bank to Morocco and South Africa: DD (IUCN), MV (FishBase).

Family Myctophidae

Myctophum punctatum Rafinesque, 1810 — Spotted lanternfish

1 specimen of 9 cm TL was caught at a depth of 749 m. Habitat and Distribution: high-oceanic, mesopelagic at depth range 0-1,000 m; nyctoepipelagic at the surface and down to 125 m and between 225-1,000 m during the day. North Atlantic Ocean, from 69ºN to 15ºN and in the Mediterranean Sea. Vulnerability: DD (IUCN), LMV (FishBase).

Benthosema glaciale (Reinhardt, 1837) — Glacier lantern fish

3 specimens were caught at depths between 790 and 796 m. Habitat and Distribution: pelagic-oceanic, non-migratory, at depth range 0-1,407 m, usually 300-400 m. North Atlantic Ocean, between 81°N - 11°N and 76°W - 29°E. In the Eastern Atlantic Ocean, from Greenland to Guinea and in the Mediterranean Sea. Vulnerability: DD (IUCN), LMV (FishBase).

FIGURE 15. *Electrona rissoi*.

Ceratoscopelus maderensis (Lowe, 1839) — No common name

1 specimen of 8 cm TL was caught at 1,079 m depth. Habitat and Distribution: mesopelagic and high-oceanic species, between 12-1,500 m depth, 650-700 m during the day and between 51-250 m at night. Temperate-subtropical Atlantic Ocean and in the Mediterranean Sea. In the eastern Atlantic Ocean, from about

57° N to the Mauritanian upwelling area. Vulnerability: DD (IUCN), LMV (FishBase).

Electrona rissoi (Cocco, 1829) — Electric lantern fish (Fig. 15)

2 specimens of 6 and 7 cm TL were caught at a depth of 762 and 782 m respectively. Biometry and meristic: 62 mm TL, 57 mm SL; HL: 36.8; PO: 7.0; POL: 15.8; ED: 14.0; IOW: 5.3; PD: 50.9; LD: 15.8; PA: 63.2; LA: 26.3, LP: 24.6; LV: 15.8; H: 29.8; D: 13; A: 19; P: 16; V: 9; Gr: 9+19. Photophores: PVO: 2; PLO: 1; PO: 5; VLO: 1; SAO: 3;VO: 4; AO: 11. Habitat and Distribution: high-oceanic and mesopelagic. Disjunct, circumtropical, in warm latitudes of Atlantic, Indian and Pacific Oceans and in the Mediterranean Sea. Vulnerability: DD (IUCN), LV (FishBase).

Lampadena speculigera Goode & Bean, 1896 — Mirror lanternfish

1 specimen of 10 cm TL was caught at depths between 755 and 759 m. Habitat and Distribution: oceanic and mesopelagic, depth range 0-1,000 m, between 475-950 m during the day and between 60-750 m at night. North Atlantic Ocean and southern circumglobal, between 66°N - 48°S. Vulnerability: DD (IUCN), MV (FishBase).

Notoscopelus kroeyeri (Malm, 1861) — Lancet fish

3 specimens between 12 and 14 cm TL were caught at depths between 749 and 766 m. Habitat and Distribution: epi- to bathypelagic and high-oceanic, from 325 to deeper than 1,000 m during the day and at surface and down to 125 m during the night. North Atlantic Ocean, between the Arctic Circle and 37°N in the east and between 60°N and 40°N in the west. Vulnerability: DD (IUCN), MV (FishBase).

ORDER GADIFORMES

Family Macrouridae

Trachyrincus scabrus (Rafinesque, 1810) — Roughsnout grenadier

69 specimens were caught at depths between 711 and 1,101 m. Length data were available for 17 specimens ranging from 2.5 to 20 cm PAL. Habitat and Distribution: bathydemersal at depth range 300-1,700 m. North Atlantic Ocean

and the Mediterranean Sea. In the eastern Atlantic, from Scotland to South Africa. Vulnerability: DD (IUCN), LMV (FishBase).

Hymenocephalus italicus Giglioli, 1884 — Glasshead grenadier

56 specimens were caught at depths between 731 and 868 m. Length data were available for 16 specimens ranging from 3 to 5.5 cm PAL. Habitat and Distribution: benthopelagic at depth range 100-1,400 m. Atlantic and Western Indian Oceans and in the Mediterranean Sea. In the eastern Atlantic Ocean, from the Gulf of Biscay to Angola and South Africa. Vulnerability: DD (IUCN), LMV (FishBase).

Coelorinchus caelorinchus (Risso, 1810) — Hollowsnout grenadier

9 specimens were caught at depths between 749 and 1,041 m. Length data were available for 7 specimens ranging from 1 to 10 cm PAL. Habitat and Distribution: benthopelagic at depth range 90-1,250 m, usually 200-500. North Atlantic Ocean and the Mediterranean Sea. In the eastern Atlantic Ocean, from Iceland and Faroe islands to Mauritania. Vulnerability: DD (IUCN), HV (FishBase).

Coelorinchus labiatus (Koelher, 1896) — Spearsnouted grenadier

117 specimens were caught at depths between 1,094 and 1,809 m. Length data were available for 117 specimens ranging from 8.5 to 18 cm PAL (12.3±2.2). Habitat and Distribution: bathydemersal at depth range 460-2,220 m. North Atlantic Ocean and the Mediterranean Sea. In the eastern Atlantic, from Iceland to Mauritania. Vulnerability: DD (IUCN), MHV (FishBase).

Coryphaenoides rupestris Gunnerus, 1765 — Roundhead rat-tail

34 specimens were caught at depths between 720 and 1,536 m. Length data were available for 13 specimens ranging from 5 to 13 cm PAL. Habitat and Distribution: bathypelagic at depth range 180-2,600 m, in continental, island, and seamount slopes. North Atlantic Ocean, from Iceland and Norway to western Sahara in the eastern Atlantic Ocean. Vulnerability: EN (IUCN), HHV (FishBase).

Coryphaenoides guentheri (Vaillant, 1888) — Günther's grenadier

40 specimens were caught at depths between 1,470 and 1,809 m. Length data were available for 40 specimens ranging from 3 to 13 cm PAL (8.1±2.1). Biometry and meristic: 320 mm TL, 316 mm SL; HL: 16.5; PO: 4.4; POL: 7.6; ED: 4.4; IOW: 3.8; BL: 1.6; PD1: 20.3; PD2: 34.8; LD1: 4.7; LD2: 65.2; PA: 28.2; LA: 71.8; PP: 19.3; PV: 19.6; LP: 12.3; LV: 8.2; H: 12.7; D1: II+9; P: 22; V: 7; Gr: 2+6. Habitat and Distribution: bathydemersal at depth range 831-2,830 m. North Atlantic Ocean and Mediterranean Sea. In the eastern Atlantic Ocean, from Iceland and Denmark Strait to Mauritania and Gabon. Vulnerability: DD (IUCN), MHV (FishBase).

Coryphaenoides mediterraneus (Giglioli, 1893) — Mediterranean grenadier

10 specimens were caught at depths between 1,470 and 1,809 m. Length data were available for all specimens ranging from 3.5 to 17.5 cm PAL. Habitat and Distribution: bathypelagic at depth range 883-4,262 m. North Atlantic Ocean and in the Mediterranean Sea. In the eastern Atlantic Ocean, from Iceland and west Scotland to Mauritania. Vulnerability: DD (IUCN), HV (FishBase).

Malacocephalus laevis (Lowe, 1843) — Rough rat-tail

924 specimens were caught at depths between 709 and 916 m. Length data were available for 378 specimens ranging from 3 to 12 cm PAL (6.7±1.7). Habitat and Distribution: bathydemersal at depth range 200-1,000 m, usually 300-750 m. Atlantic and Indo-west-central Pacific Oceans. In the eastern Atlantic Ocean, from Iceland and Faroe islands to South Africa. Vulnerability: DD (IUCN), HV (FishBase).

Nezumia aequalis (Günther, 1878) — Common Atlantic grenadier

3,645 specimens were caught at depths between 737 and 1,470 m. Length data were available for 544 specimens ranging from 1 to 9 cm PAL (4.3±1.3). Habitat and Distribution: benthopelagic at depth range 200-2,320 m, usually 200-1,000 m. North Atlantic Ocean and the Mediterranean Sea. In the eastern Atlantic, from the Faroe Bank Channel to northern Angola. Vulnerability: DD (IUCN), MV (FishBase).

Family Bathygadidae

Gadomus longifilis (Goode & Bean, 1885) — Treadfin grenadier

3 specimens ranging from 27 to 29 cm TL were caught at depths between 1,450 and 1,683 m (Bañón *et al.*, 2013a). Habitat and Distribution: benthopelagic, between 520 and 2,165 m depth. Amphi-Atlantic in tropical and subtropical North Atlantic Ocean. In Western Atlantic, from Greenland to the Gulf of Mexico and Caribbean Sea and from the northwest of Spain to the Gulf of Guinea in the Eastern Atlantic. Vulnerability: DD (IUCN), MV (FishBase).

Gadomus dispar (Vaillant, 1888) — No common name

6 specimens ranging from 17 to 36 cm TL were caught at depths between 764 and 1,051 m (Bañón *et al.* 2013a). Habitat and Distribution: benthopelagic between 548 and 1,543 m depth. Amphi-Atlantic distribution in tropical and subtropical North Atlantic Ocean. In Western Atlantic, from Norfolk Canyon to the Caribbean Sea and in Eastern Atlantic from the Cantabrian Sea to Mauritania and Guinea-Bissau. Vulnerability: DD (IUCN), MHV (FishBase).

FIGURE 16. *Guttigadus latifrons*.

Bathygadus melanobranchus Vaillant, 1888 — Vaillant's grenadier

One specimen of 37 cm TL was caught at depths between 1,185 and 1,187 m (Bañón *et al.* 2013a). Habitat and Distribution: benthopelagic at depths between 450 and 2,650 m, but generally from 700 to 1,400 m. Amphi-Atlantic distribution, in tropical and subtropical latitudes. In the Eastern Atlantic, from

the Irish continental slope to Senegal and Gabon. Vulnerability: DD (IUCN), MHV (FishBase).

Family Moridae

Guttigadus latifrons (Holt & Byrne, 1908) — No common name (Fig. 16)

4 specimens ranging 11-13 cm TL were caught at depths between 791 and 851 m. Biometry and meristic: 129 mm TL; 118 mm SL; HL: 23.7; PO: 5.1; POL: 11.0; ED: 7.6; IOW: 8.5; BL: 2.5; PD1: 24.6; PD2: 28.8; LD1: 3.4; LD2: 58.5; PA: 29.7; LA: 58.5; LP: 15.3; LV: 22.0; H: 22.0; D1: 5;D2: 72; A: 68; P: 22; V: 3; Gr: 7+16. Habitat and Distribution: bathydemersal between 770-1,875 m depth. Eastern and Southwestern Atlantic Ocean, Western Indian Ocean and in the Mediterranean Sea. In the Eastern Atlantic, from Ireland and Island to the Azores islands and the Galicia Bank. Vulnerability: DD (IUCN), MV (FishBase).

Halargyreus johnsonii Günther, 1862 — Slender codling

207 specimens were caught at depths between 731 and 1,685 m. Length data were available for 137 specimens ranging from 9 to 45 cm TL (29.7±9.6). Habitat and Distribution: bathypelagic, antitropical at depth range 450-3,000 m. North Atlantic, South Atlantic, South-west Pacific, and South-east Pacific Oceans. Patchy distribution in subarctic and subantarctic waters. Vulnerability: DD (IUCN), HV (FishBase).

Physiculus dalwigki Kaup, 1858 — Black codling

One specimen of 26 cm TL was caught at depths between 731-738m m (Bañón *et al.* 2002). Habitat and Distribution: benthopelagic at depth range 100-738 m. Eastern Atlantic: Galicia Bank, Great Meteor Bank, Madeira and south along the African coast to about 25°N and in Western Mediterranean Sea. Vulnerability: DD (IUCN), MV (FishBase).

Mora moro (Risso, 1810) — Common mora

6,596 specimens were caught at depths between 709 and 1,323 m. Length data were available for 1,310 specimens ranging from 13 to 67 cm TL (47.9 ±9.3), with males between 25 and 55 cm (45.7 ±4.0, N=431) and females between 35 and 65 cm (54.8 ±4.5, N=490). Habitat and Distribution: bathypelagic; depth

range 400-2,500 usually 400-1,000 m. Wide distribution along the Atlantic, Pacific and Indian Oceans and in the Western Mediterranean Sea. In the Eastern Atlantic, from Iceland and Faeroes to Cape Bojador, West Africa, and including Azores Islands and Madeira archipelago. Vulnerability: DD (IUCN), HV (FishBase).

Lepidion lepidion (Risso, 1810) — Mediterranean codling

41,585 specimens were caught at depths between 709 and 1,323 m. Length data were available for 3,196 specimens ranging from 11 to 53 cm TL (26±5.2). Following a recent revision of the genus, the Atlantic *L. eques* has been proposed as a junior synonym of the Mediterranean *L. lepidion* (Bañón *et al.* 2013b). Habitat and Distribution: benthopelagic, depth range 127-1,880 m, usually 500-900 m. North Atlantic Ocean and the Mediterranean Sea. Vulnerability: LC (IUCN), MHV (FishBase).

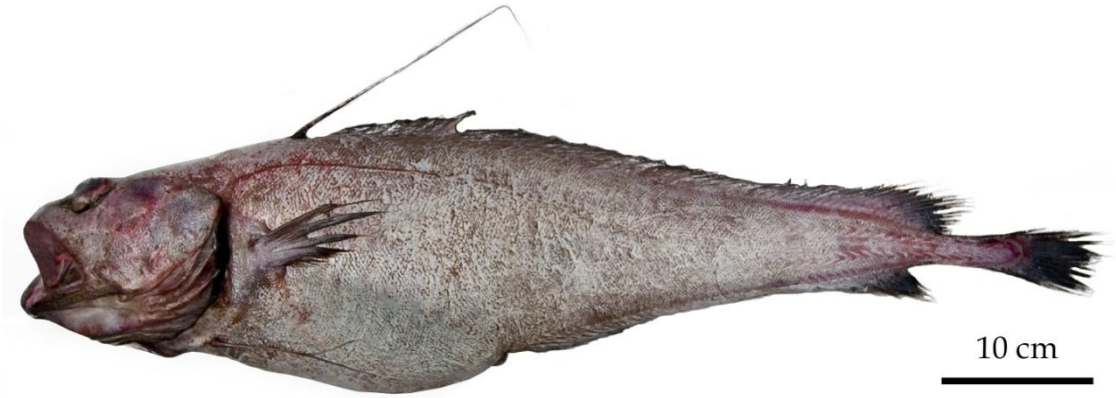

FIGURE 17. *Lepidion guentheri*.

Lepidion guentheri (Giglioli, 1880) — No common name (Fig. 17)

One specimen was caught at a depth of 1,536 m. Biometry and meristic: 697 mm TL; 632 mm SL; HL: 22.2; PO: 5.7; POL: 12.3; ED: 4.1; IOW: 5.1; PD1:25.3; PD2: 29.3; LD1: 2.5; LD2: 62.8; PA: 48.3; LA: 62.8, PV: 19.3; PP: 24.4; LP: 13.9; LV: 30.4; H: 23.1; 1D: 5; 2D: 56; P: 21; V: 6; A:50; Gr: 6+16. Habitat and Distribution: benthopelagic between 750 and 2,196 m depth. North-

eastern Atlantic, in west of Ireland, west and north coasts of Spain, north coast of Portugal, the Azores, Madeira, Canary Islands and the Mid-Atlantic Ridge and in Western Mediterranean Sea. Vulnerability: DD (IUCN), HHV (FishBase).

Antimora rostrata (Günther, 1878) — Blue antimora

One specimen of 16 cm TL was caught at a depth of 1,750 m. Habitat and Distribution: bathypelagic at depth range 350-3,000 m, usually 1,300-2,500 m. Circumglobal, except North Pacific. In the Eastern Atlantic, from Iceland to South Africa. Vulnerability: DD (IUCN), HHV (FishBase).

Family Melanonidae

Melanonus zugmayeri Norman, 1930 — Arrowtail

38 specimens were caught at depths between 773 and 1,470 m. Length data were available for 28 specimens ranging from 13 to 28 cm TL. Habitat and Distribution: oceanic and bathypelagic at depth range 0-3,000 m. Circumglobal in tropical and subtropical seas. Vulnerability: DD (IUCN), LV (FishBase).

Family Gadidae

Micromesistius poutassou (Risso, 1827) — Blue whiting

165 specimens were caught at depths between 709 and 892 m. Length data were available for 102 specimens ranging from 12 to 40 cm TL (29.2±4.7). Habitat and Distribution: oceanic and bathypelagic at depth range 150-3,000 m, usually 300-400 m. Northeast Atlantic, from 26ºN to 82ºN, with smaller populations in the Northwest Atlantic and the Mediterranean Sea. Vulnerability: DD (IUCN), LMV (FishBase).

Family Lotidae

Gaidropsarus granti (Regan, 1903) — Azores rockling

2 specimens of 33 and 17 cm TL were caught at depths of 782 and 866 m respectively (Bañón *et al.* 2002, 2010). Habitat and Distribution: demersal from 20 to over 800 m depth. Eastern Atlantic, in the Galicia Bank, Canary and the Azores Islands and in the Eastern Mediterranean Sea. Vulnerability: DD (IUCN), MV (FishBase).

Family Phycidae

Phycis blennoides (Brünnich, 1768) — Greater forkbeard

560 specimens were caught at depths between 709 and 952 m. Length data were available for 111 specimens ranging from 20 to 79 cm TL (38.6±16.1). Habitat and Distribution: benthopelagic over sandy and muddy bottoms at depth range 10-1,047 m, usually 100-450 m, with juveniles more coastal, over the continental shelf while adults migrate along the slope. Eastern Atlantic, from Norway and Iceland to Mauritania and in the Mediterranean Sea. Vulnerability: DD (IUCN), HV (FishBase).

Family Merluccidae

Merluccius merluccius (Linnaeus, 1758) — European hake

One specimen, a female of 61 cm TL was caught at a depth of 795 m. Habitat and Distribution: demersal to benthopelagic over sandy and muddy bottoms at depth range 30-1,075 m, usually 50-370 m. Eastern Atlantic, from Norway and Iceland to Mauritania and in the Mediterranean Sea. Vulnerability: DD (IUCN), HV (FishBase).

ORDER OPHIDIIFORMES

FIGURE 18. *Cataetyx alleni*.

Family Bythitidae

Cataetyx alleni (Byrne, 1906) — No common name (Fig. 18)

29 specimens were caught at depths between 755 and 916 m. Length data were available for 20 specimens ranging from 9 to 15 cm TL. Habitat and Distribution: bathydemersal, depth range 480-1,851 m, usually below 600 m. Eastern Atlantic, from the South-west Ireland to Portugal and Western Mediterranean Sea. Vulnerability: DD (IUCN), LV (FishBase).

Cataetyx laticeps Koefoed, 1927 — No common name

2 specimens of 72 and 82 cm TL were caught at depths of 1,683 and 1,685 m respectively. Habitat and Distribution: bathydemersal or benthopelagic at depth range 500-2,830. North Atlantic Ocean and the Mediterranean Sea. In the Eastern Atlantic, from Iceland, scattered localities around the British Isles, France, Azores, and along the coast of West Africa to the Cape of Good Hope. Vulnerability: DD (IUCN), HV (FishBase).

Family Ophididae

FIGURE 19. *Spectrunculus grandis*.

Spectrunculus grandis (Günther, 1877) — Pudgy cuskeel (Fig. 19)

One specimen of 55 cm TL was caught at a depth of 1,809 m. Habitat and Distribution: bathydemersal; depth range 800-4,300 m, usually 2,000-3,000 m.

Widely distributed in all oceans, between 57°N and 59°S. Vulnerability: DD (IUCN), HHV (FishBase).

ORDER LOPHIIFORMES

Family Lophiidae

Lophius piscatorius Linnaeus, 1758 — Anglerfish

137 specimens were caught at depths between 709 and 916 m. Length data were available for 41 specimens ranging from 17 to 97 cm TL (75.8±14.8) with males between 64 and 92 cm (N=8) and females between 67 and 97 cm (N=10). Habitat and Distribution: bathydemersal on sandy, muddy, gravelly and occasionally rocky bottoms, at depths from 20 to 2,600 m. Eastern Atlantic, from Iceland and south-western Barents Sea to Mauritania, including the Mediterranean and Black Sea. Vulnerability: DD (IUCN), HHV (FishBase).

Family Chaunacidae

Chaunax pictus Lowe, 1846 — Pink frogmouth

63 specimens were caught at depths between 726 and 940 m. Length data were available for 40 specimens ranging from 12 to 41 cm TL (23.6±7.1). Habitat and Distribution: bathydemersal on continental shelves, slopes and seamounts at depth range 200-978 m. Circumglobal in tropical to temperate waters, although Ho & Last (2013) limited its presence to the Atlantic Ocean. Vulnerability: DD (IUCN), LMV (FishBase).

Family Linophrynidae

Linophryne coronata Parr, 1927 — Deep-sea anglerfish

One female of 223 mm TL with attached parasitic male of 29 mm TL was caught at depths between 762 and 764 m (Bañón *et al.* 2006b). Habitat and Distribution: meso- to bathypelagic, depth range 0-1,500 m. Scattered records in the Atlantic and Eastern North Pacific Oceans. Vulnerability: DD (IUCN), LV (FishBase).

ORDER BERYCIFORMES

Family Trachichthyidae

Hoplostethus mediterraneus Cuvier, 1829 — Mediterranean slimehead

61,206 specimens were caught at depths between 737 and 1,187 m. Length data were available for 9,177 specimens ranging from 7 to 36 cm TL (21.5±3.4). Habitat and Distribution: benthopelagic at depth range 100-1175 m, usually 500-800 m. Northeastern Atlantic, Indian and South Pacific Oceans and in Mediterranean Sea. In the Eastern Atlantic, from Ireland to South Africa. Vulnerability: DD (IUCN), HV (FishBase).

Hoplostethus cadenati Quéro, 1974 — Black slimehead

47 specimens were caught between 777 and 940 m depth. Length data were available for 22 specimens ranging from 20 to 29 cm TL. Biometry and meristic: 272 and 237 mm TL; 210 and 184 mm SL; HL: 38.1 and 38.6; PO: 9.0 and 10.9; POL: 18.1 and 17.9; ED: 11.0 and 9.8; PD:41.9 and 41.8; LD: 37.1 and 38.0; PA: 65.2 and 64.1; LA: 17.6 and 18.5, LP: 33.3 and 32.6; LV: 21.0 and 19.0; H: 41.4 and 44.6; D: VI+13 and V+14; A:III+10; P: 17; V: I+5 and I+6; Gr: 5+17. Habitat and Distribution: bathypelagic, living near the bottom from 70 to at least 1,000 m depth, usually 200-700 m. Eastern Atlantic and Western Indian Oceans. In the eastern Atlantic, from northwest Ireland, northwest Spain and along the northwest coast of Africa between 27°30'N and 10°10'N and from 1°26'S to 26'14°S. Vulnerability: DD (IUCN), HV (FishBase).

Hoplostethus atlanticus Collett, 1889 — Orange roughy

3 specimens of 21, 24 and 31 cm TL were caught at depths between 1,470 and 1,685 m. Habitat and Distribution: bathypelagic, inhabits deep, cold waters over steep continental slopes, ocean ridges and seamounts, sometimes in dense aggregations, from 180 to 1,809 m depth, usually 400-900 m. Atlantic and Indo-West Pacific Oceans but not in the eastern Pacific. In the Eastern Atlantic, from Iceland to Morocco and from Namibia to South Africa. Vulnerability: VU (IUCN, OSPAR), HHV (FishBase).

Family Diretmidae

Diretmichthys parini (Post & Quéro, 1981) — Parin's spiny fin (Fig. 20)

Two specimens were caught at depths between 780 and 1,315 m. Biometry and meristic: 241 and 266 mm TL; 195 and 211 mm SL; HL: 35.9 and 36.5; PO: 6.7 and 9.5; POL: 15.9 and 11.4; ED: 13.3 and 16.1; IOW: 4.6 and 5.2; PD:42.1 and

43.1; LD: 42.1 and 43.1; PA: 60.0 and 61.6; LA: 42.1 and 32.2, LP: 27.2 and 27.5; LV: 28.7 and 29.9; H: 45.6 and 46.0; D: 27 and 29; P: I+17; V: I+6; A: 21 and 23; Gr: 6+1+12. Habitat and distribution: tropical, subtropical and moderate latitudes of the Atlantic, Pacific and Indian Oceans at depths ranging from to 270 to more than 2000 m, with juveniles from epipelagic to mesopelagic zone and adults collected close to the bottom (Arronte & Heredia 2006). Vulnerability: DD (IUCN), LMV (FishBase).

FIGURE 20. *Diretmichthys parini*.

Diretmus argenteus Johnson, 1864 — Silver spinyfin

Five specimens were caught at depths between 777 and 940 m. Two specimens were 6 and 26 cm TL respectively. Habitat and distribution: bathypelagic at depth range 0-2,000 m, usually 500-700 m. Circumglobal in temperate and tropical seas. In the Eastern Atlantic, from Iceland and British Isles to South Africa including the Canary and Ascension Islands. Vulnerability: DD (IUCN), LV (FishBase).

Family Berycidae

Beryx splendens Lowe, 1834 — Splendid alfonsino

1,968 specimens were caught at depths between 643 and 914 m. Length data were available for 698 specimens ranging from 21 to 48 cm TL (36.5±4.4). Habitat and Distribution: benthopelagic on continental shelves and slopes, seamounts, and oceanic ridges in a depth range from 25 to 1,300 m, usually 200-800 m. Circumglobal distribution, in temperate to tropical waters excluding the North-eastern Pacific. In the Eastern Atlantic, from Ireland to South Africa. Vulnerability: DD (IUCN), HV (FishBase).

Beryx decadactylus Cuvier, 1829 — Beryx

18 specimens were caught at depths between 643 and 877 m. Length data were available for 11 specimens ranging from 44 to 58 cm TL. Length data available during the exploratory surveys carried out in the 1980's was from 24 to 59 cm TL, but the total number of individuals caught was not reported. Habitat and Distribution: benthopelagic with a world-wide distribution, occurring in tropical, subtropical and some temperate areas of the Atlantic, Pacific and Indian Oceans, and in the Western Mediterranean Sea. In the Eastern Atlantic, from Greenland, Iceland and Norway to Western Sahara and South Africa. Vulnerability: DD (IUCN), HHV (FishBase).

Family Oreosomatidae

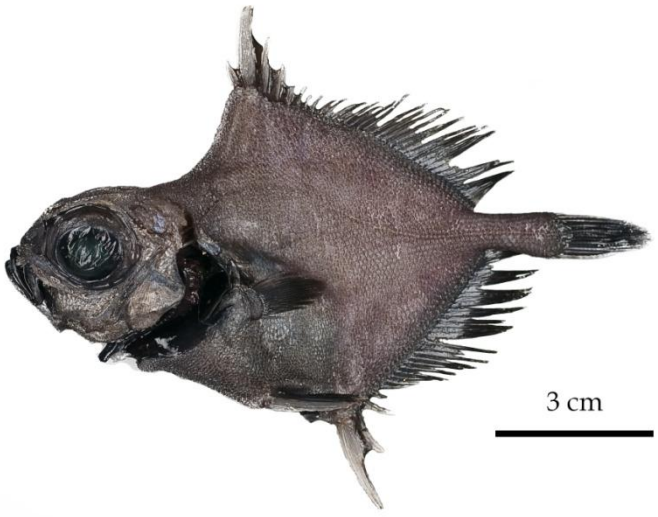

FIGURE 21. *Neocyttus helgae*.

Neocyttus helgae (Holt & Byrne, 1908) — False boarfish (Fig. 21)

One specimen was caught at depths between 1,410 and 1,427 m. Biometry and meristic: 119 mm TL; 100 mm SL; HL: 35.0; PO: 9.0; POL: 7.0; ED: 19.0; IOW: 12.0; PD: 45.0; LD: 50.0; PA: 48.0; LA: 37.0; PP: 40.0; PV: 39.0; LP: 15.0; LV: 15.0; H: 51.0; D: VII+33; A: IV+31; P: 19; V: I+6; Gr: 5+18; SLL: 80. Habitat and Distribution: bathypelagic species along the outer continental shelf insular slope and seamounts, strongly associated with habitats of high currents, ripple marks, slopes, reefs of rocks and gorgonians, at depths from 850 to 1,700 m. Northeast Atlantic, from Iceland to Madeira and Western North Atlantic. Vulnerability: DD (IUCN), HV (FishBase).

ORDER SYNGNATHIFORMES

Family Syngnathidae

Entelurus aequoreus (Linnaeus, 1758) — Snake pipefish

34 specimens between 11 and 35 cm TL were caught over seabed depths of 766-866 m, probably during the hauling of the bottom trawl. Habitat and Distribution: coastal or oceanic pelagic species. Eastern Atlantic Ocean, from the Azores to Iceland and Norway, including the Baltic Sea. Vulnerability: DD (IUCN), LMV (FishBase).

ORDER SCORPAENIFORMES

Family Sebastidae

Helicolenus dactylopterus (Delaroche, 1809) — Blackbelly rosefish

2 specimens were caught at depths between 704 and 869 m. Only one individual of 37 cm TL was measured. Habitat and Distribution: bathydemersal in soft bottom areas of the continental shelf and upper slope, at depth range 50-1,100 m, usually 150-600 m. Western Atlantic, from Canada to Venezuela and Eastern Atlantic, from Iceland and Norway to South Africa and in the Mediterranean Sea. Vulnerability: DD (IUCN), MHV (FishBase).

Trachyscorpia cristulata echinata (Koehler, 1896) — Spiny scorpionfish

1,105 specimens were caught at depths between 709 and 1,323 m. Length data were available for 267 specimens ranging from 12 to 50 cm TL (37.4±8.7). Biometry and meristic: 4 specimens, 392-506 mm TL, 336-418 mm SL; HL: 43.6-47.1; PO: 11.2-14.4; POL: 23.2-24.5; ED: 8.9-10.1; IOW: 4.7-5.5; PD: 33.5-41.1; LD: 46.7-50.3; PA: 68.7-74.2; LA: 11.2-13.2; PP: 42.9-44.3; PV: 39.3-41.8; LP: 21.3-24.9; LV: 14.4-17.6; H: 29.9-32.5; D: XII+9; A: III+5; P: 20-21; V: I+5; Gr: 6+12-13. Habitat and Distribution: bathydemersal on muddy and sandy bottoms between 200 and 2,500 m. Eastern Atlantic, from Ireland to Senegal, Mid-Atlantic Ridge and in the Mediterranean Sea. Vulnerability: DD (IUCN), HHV (FishBase).

Family Liparidae

Paraliparis hystrix Merrett, 1983 — No common name

One specimen of 4 cm TL was caught at a depth of 928 m. Habitat and Distribution: bathydemersal at depth range 250-1,150 m. North-East Atlantic, west of the British Isles and probably in North-West Atlantic. Vulnerability: DD (IUCN), LMV (FishBase).

ORDER PERCIFORMES

Family Polyprionidae

Polyprion americanus (Bloch & Schneider, 1801) — Wreckfish

12 specimens were caught at depths between 645 and 740 m. Length data were available for 2 specimens of 119 and 120 cm TL. Length data during the exploratory surveys carried out on the 1980's was to 132 cm for males and to 142 cm for females, but the total number of individuals caught was not reported. The presence of this species associated with floating objects has also been reported. At least one specimen of 51 cm TL was caught in the surface of the Galicia Bank during the 1980's surveys. Habitat and Distribution: pelagic (juveniles) to demersal (adults), above rocky and muddy/sandy bottoms in continental, oceanic island slopes and seamounts, from 40 to1,000 m, usually from 100 to 200 m. Circumglobal, including the Mediterranean Sea, mostly in

temperate and subtropical latitudes. In the Eastern Atlantic, from Norway to South Africa. Vulnerability: DD (IUCN), VHV (FishBase).

Family Epigonidae

Epigonus telescopus (Risso, 1810) — Bulls-eye

2,757 specimens were caught at depths between 643 and 1.323 m. Length data were available for 1,372 specimens ranging from 15 to 77 cm TL (42.3±10.4). Habitat and Distribution: pelagic (juveniles) to bathydemersal or benthopelagic (adults) on soft bottoms, between 75 and 1,200 m depth, usually at 300-800 m. Atlantic and Indo-West Pacific Oceans and in the Mediterranean Sea. In the Eastern Atlantic it has an antitropical distribution, occurring from Iceland to the Canary Islands and reappearing along the western coast of South Africa. Vulnerability: DD (IUCN), HHV (FishBase).

Epigonus denticulatus Dieuzeide, 1950 — Pencil cardinal

One specimen of 16 cm TL was caught at a depth of 847 m. The species is probably more abundant that it appears, having been confused with juveniles of *E. telescopus*. Habitat and Distribution: bathydemersal, inhabiting the continental slope from 200 to 830 m depth, although it occurs usually between 300 and 600 m. Circumglobal in warm seas, including the Mediterranean Sea. In the Eastern North Atlantic, it is extended from the Bay of Biscay to the west coast of Africa. Vulnerability: DD (IUCN), LMV (FishBase).

Family Carangidae

Trachurus trachurus (Linnaeus, 1758) —Atlantic horse mackerel

One specimen of 6 cm TL was caught over seabed depth of 771 m, probably during the hauling of the bottom trawl. Habitat and Distribution: pelagic-neritic usually over sandy bottom, at depth range 0-1,050 m, usually 100 -200 m. Eastern Atlantic, from Norway to South Africa, round the coast to Maputo and in the Mediterranean Sea. Vulnerability: DD (IUCN), HV (FishBase).

Family Coryphaenidae

Coryphaena equiselis Linnaeus, 1758 — Pompano dolphinfish

One specimen was caught over seabed depths of 804-859 m, probably during the hauling of the bottom longline. Biometry and meristic: 455 mm TL; 344 mm SL; FL: 104.7; HL: 23.5; PO: 8.4; POL: 11.0; ED: 4.9; IOW: 8.1; PD: 14.0; LD: 78.2; PA: 53.2; LA: 38.4, LP: 15.4; LV: 15.4; H: 27.0; D: 54; A: 25; P: 19; V: 5; Gr: 0+1+9. Habitat and Distribution: pelagic and oceanic species but may enter coastal waters. Worldwide in tropical and subtropical seas. Vulnerability: LC (IUCN), LMV (FishBase).

Family Bramidae

Brama brama (Bonnaterre, 1788) — Atlantic pomfret

Reported only during the exploratory surveys carried out in the 1980's. Length data of 994 specimens from 34 to 46 cm TL. Habitat and Distribution: pelagic-oceanic at depths between 0-800 m, usually 0-550 m. Worldwide in the Atlantic, Pacific and Indian Oceans in tropical, temperate, and sometimes cold waters. In the Eastern Atlantic, from Norway to South Africa. Vulnerability: DD (IUCN), HHV (FishBase).

Pterycombus brama Fries, 1837 — Atlantic fanfish

One specimen of unknown size but a weight of 750 g was caught over seabed depth of 778-804 m, probably during the hauling of the bottom longline. This species was also recorded during the exploratory surveys carried out in the 1980's, with length sizes between 34 and 41 cm TL, but the total number of individuals caught was not reported. Habitat and Distribution: pelagic-oceanic at depth range 25-400 m. North Atlantic Ocean and Mediterranean Sea. In the eastern Atlantic, from Iceland, British Isles and Norway to the Gulf of Guinea. Vulnerability: DD (IUCN), MHV (FishBase).

Taractes asper Lowe, 1843 — Rough pomfret

One specimen of 35 cm TL was caught over seabed depth of 685 m, probably during the hauling of the bottom longline. Habitat and Distribution: pelagic-oceanic at depth range 1-140 m. Circumglobal, antiequatorial, in tropical to temperate waters of Pacific, Indian and Atlantic Oceans. In the Eastern Atlantic, from Iceland and northern Norway to Madeira. Vulnerability: DD (IUCN), HV (FishBase).

Family Chiasmodontidae

Chiasmodon niger Johnson, 1864 — Black swallower

Two specimens, one of them measuring 15 cm TL, were caught at depths between 786 and 857 m. Habitat and Distribution: meso- to bathypelagic species between 150 and 3,900 m, specimens larger than 45 mm usually between 730-1,900 m. Distributed throughout the tropical and temperate eastern and western North Atlantic Ocean and the Gulf of Mexico, from 95ºW to 5ºE and 46ºN to 5ºS. Vulnerability: DD (IUCN), LV (FishBase).

Family Blenniidae

FIGURE 22. *Blennius ocellaris*.

Blennius ocellaris Linnaeus, 1758 — Butterfly blenny (Fig. 22)

One specimen of 13 cm TL was caught at depths between 762 and 799 m. Habitat and Distribution: demersal at a depth range 10-400 m. North-eastern Atlantic, from the English Channel to Morocco, also known from the Mediterranean and Black Sea. Vulnerability: DD (IUCN), LMV (FishBase).

Family Gempylidae

Nesiarchus nasutus Johnson, 1862 — Black gemfish

One specimen of 46 cm TL was caught at depths between 731-739 m. Habitat and Distribution: larvae and juveniles are epipelagic to mesopelagic and adults benthopelagic to mesopelagic at depth range 200-1,200 m. Dwell on the continental slope or underwater rises, migrating to midwater at night. Worldwide distributed in tropical and subtropical seas except in the Eastern Pacific and northern Indian Oceans. In the eastern Atlantic it occurs from Iceland and Norway to the Gulf of Guinea. Vulnerability: DD (IUCN), HHV (FishBase).

Ruvettus pretiosus Cocco, 1833 — Oilfish

One specimen was caught at depths between 658-768 m. Biometry and meristic: 958 mm TL; 810 mm SL; FL: 105.4; HL: 26.4; PO: 9.4; POL: 12.6; ED: 4.8; IOW: 6.2; PD: 23.7; LD: 65.4; PA: 68.3; LA: 20.4, LP: 19.4; LV: 8.3; H: 19.1; D: XIV+17+2'; A: I+16+2'; P: 15; V: I+5; Gr: 6+1+9. Habitat and Distribution: benthopelagic at continental slopes, around oceanic islands and submarine rises at depth range 100-800 m, usually 200-400 m. Widely distributed throughout the tropical and temperate waters of the world's oceans. Vulnerability: DD (IUCN), VHV (FishBase).

Family Trichiuridae

Aphanopus carbo Lowe, 1839 — Black scabbardfish

21 specimens were caught at depths between between 720 and 1,094 m. Length data were available for 17 specimens ranging from 35 to 136 cm TL. All specimens were identified as *A. carbo*. However, this species can be easily confused with the sympatric *A. intermedius*. Thus, the presence of the latter species in the catches cannot be ruled out. Habitat and Distribution: bathypelagic at depth range 200-1,700 m, usually 700-1,300 m. It is present at both sides of the North Atlantic Ocean, at least between 69ºN and 26ºN. In the eastern Atlantic Ocean it occurs from the strait of Denmark to Western Sahara, including the Canaries Islands and the Madeira Archipelago and numerous submarine banks and seamounts. Vulnerability: DD (IUCN), HHV (FishBase).

Benthodesmus simonyi (Steindachner, 1891) — Simony's frostfish

36 specimens were caught at depths between 652 and 877 m. Length data were available for 20 specimens ranging from 73 to 117 cm TL. Habitat and Distribution: benthopelagic and oceanic at depth range 200-900 m. Distributed on the continental slope and underwater rises; juveniles are mesopelagic. Both sides of the North Atlantic, off Newfoundland (Canada), Bermuda, New England (USA), Middle Atlantic Ridges, Iceland, Norway, Portugal, Madeira, and Canary Islands. Vulnerability: DD (IUCN), HV (FishBase).

Familly Centrolophidae

Centrolophus niger (Gmelin, 1789) — Blackfish

13 specimens were caught at depths between 735 and 868 m. Length data were available for 11 specimens ranging from 46 to 89 cm TL. Habitat and Distribution: oceanic, epipelagic or mesopelagic species with juveniles occurring in surface waters; depth range 40-1,050 m, usually 300-700 m. Circumglobal, including the western Baltic Sea, North Sea and the Mediterranean Sea, but absent in the northern Pacific Ocean. Vulnerability: DD (IUCN), VHV (FishBase).

Schedophilus medusophagus (Cocco, 1839) — Cornish blackfish

One specimen of 56 cm TL was caught at 766 m depth. Habitat and Distribution: mesopelagic species between 3 and 900 m depth. Present in temperate waters of the North Atlantic Ocean and Western Mediterranean Sea. In the Eastern Atlantic Ocean it occurs from Iceland and Ireland to Morocco, including the Azores and Madeira Islands. Vulnerability: DD (IUCN), MV (FishBase).

Familly Xiphiidae

Xiphias gladius Linnaeus, 1758 — Swordfish

This species was reported only during the exploratory surveys on the 1980's. Length data from 190 to 322 cm TL, but the number of individuals were not reported. Habitat and Distribution: pelagic-oceanic species preferring temperatures from 18°C to 22°C at depths ranging between 0-800 m, usually 0-550 m. Worldwide distributed in the Atlantic, Pacific, and Indian Oceans in tropical, temperate, and sometimes cold waters. Vulnerability: LC (IUCN), HHV (FishBase).

ORDER PLEURONECTIFORMES

Family Soleidae

Bathysolea profundicola (Vaillant, 1888) — Deepwater sole

19 specimens were caught at depths between 731 and 868 m. Length data were available for 8 specimens ranging from 17 to 23 cm TL. Habitat and Distribution: bathypelagic, between 200 and 1,350 m depth. Eastern Atlantic, from southern Ireland to Angola and the Mediterranean Sea. Vulnerability: DD (IUCN), LV (FishBase).

Discussion

The present checklist includes 139 species of marine fishes from the Galician Bank that represent 14.6 % of the 955 species listed for the European Atlantic waters by Quéro *et al.* (2003). Biogeographically, the Atlantic group is the most important (113 species, 81.3%), followed by the Lusitanian (17 species, 12.2%), the Boreal (6 species, 4.3%), the African (2 species. 1.4%) and the Macaronesian group (1 species, 0.7%).

The diversity in species composition and their relative abundance are dependent on the sampling effort, the type of fishing gears employed and the gear efficiencies. Thus, commercial bottom trawl gears operating over the shallower sedimentary areas of the Galicia Bank recorded both the highest species richness and abundance values.

The pelagic fish species are presumably underestimated. The abundance and composition of mesopelagic fishes, mainly lantern fishes (Myctophidae) and cyclothonids (Gonostomatidae), are probably underestimated because there was no specific sampling protocol aimed to these groups and many of the specimens caught were damaged during the trawling and could not be identified to species level. Likewise, the epipelagic fishes were only sampled during the exploratory surveys carried out in the 1980´s, with surface longline. The recorded species were captured either during these exploratory surveys (e.g. *X. gladius, I. oxyrhinchus*) or accidentally during the hauling of the bottom gears (e.g. *C. equiselis, P. violacea*).

Despite all these factors, the resulting list constitutes a good representation of the fish fauna inhabiting the Galicia Bank, which includes species of demersal and benthic domains and the three vertical oceanic zones (epi-, meso- and bathypelagic zones).

The ecology of seamounts is mainly determined by oceanographic, ecological and fisheries factors (Pitcher 2008). According to this, among the oceanographic factors, the summit peak depth and the proximity to the continental shelf seem to be the most evident geographic features that could explain, in first instance, the fish fauna composition of the Bank.

Seamounts can be classified, according to the water depth that the summit reaches in shallow seamounts, reaching the euphotic zone, intermediate seamounts, with summits below the euphotic zone but within the upper 400 m layer and deep seamounts with peaks below 400 m depth (White & Mohn 2004). The Galicia Bank, with a summit at 625 m of depth, can be classified as a deep seamount and its fish fauna is mainly constituted by deep-water fishes, which can be defined as fishes that spend most of the time at depths exceeding 400 m deep (Gordon 2001). Most of the 62 families of fishes occurring in the Galicia Bank, including the most speciose such as Macrouridae, Centrophoridae, Moridae and Alepocephalidae and many others such as Bathygadidae and Halosauridae, are typical components of the deep fish fauna (Table 2). This is also in agreement with the definition of seamount fishes, which are mostly deep-sea fishes with occasional visitors from the epipelagic realm or from the continental shelf or slope (Froese & Sampang 2004).

Globally, macrourids, scorpaenids, morids, squalids, alepocephalids and serranids are reported to be the most diverse families among seamount fishes while scorpaenids, morids, serranids, macrourids, and squalids are the most abundant ones (Wilson & Kaufmann 1987). In the case of the Galicia Bank, Macrouridae, with 9 species, is the most diverse family followed by Moridae, Stomiidae and Sternoptychidae with 7 species, whereas Trachichthyidae and Moridae are the most abundant with 61,257 and 48,395 specimens respectively. This is due to the higher abundance of the trachichthyd *H. mediterraneus* (61,206 individuals) and the morid *L. lepidion* (41,585 individuals).

Seamount fishes are also defined as fish that have been reported as occurring on seamounts (Morato *et al.* 2004). The number of seamount fishes occurring worldwide has been increasing from 450 species (Wilson & Kaufman 1987) to 795 species (Morato *et al*. 2006). A comparison between our results and the latter checklist showed that

80.6% (112 out of 139) of species recorded in the Galicia Bank can be considered as seamount fishes. An updated list of seamount fishes would probably increase this high percentage.

TABLE 2. Families, species number and percentage of fishes in the Galicia Bank

Family	No. species	Fauna (%)	Family	No. species	Fauna (%)
Chimaeridae	3	2.2	Macrouridae	9	6.5
Hexanchidae	1	0.7	Bathygadidae	3	2.2
Centrophoridae	5	3.6	Moridae	7	5.0
Etmopteridae	3	2.2	Melanonidae	1	0.7
Somniosidae	4	2.9	Gadidae	1	0.7
Oxynotidae	1	0.7	Lotidae	2	1.4
Dalatiidae	1	0.7	Phycidae	1	0.7
Pentanchidae	5	3.6	Merluccidae	1	0.7
Pseudotriakidae	1	0.7	Bythitidae	3	2.2
Carcharhinidae	2	1.4	Lophiidae	1	0.7
Rajidae	2	1.4	Chaunacidae	1	0.7
Dasyatidae	1	0.7	Linophrynidae	1	0.7
Halosauridae	5	3.6	Trachichthyidae	3	2.2
Notacanthidae	2	1.4	Diretmidae	2	1.4
Synaphobranchidae	1	0.7	Berycidae	2	1.4
Congridae	2	1.4	Oreosomatidae	1	0.7
Derichthydae	1	0.7	Syngnathidae	1	0.7
Nemichthyidae	1	0.7	Sebastidae	2	1.4
Serrivomeridae	1	0.7	Liparidae	1	0.7
Eurypharyngidae	1	0.7	Polyprionidae	1	0.7
Bathylagidae	1	0.7	Epigonidae	2	1.4
Alepocephalidae	5	3.6	Carangidae	1	0.7
Gonostomatidae	3	2.2	Coryphaenidae	1	0.7
Sternoptychidae	7	5.0	Bramidae	2	1.4
Phosichthyidae	1	0.7	Chiasmodontidae	1	0.7
Stomiidae	7	5.0	Blenniidae	1	0.7
Ipnopidae	1	0.7	Gempylidae	2	1.4
Paralepididae	2	1.4	Trichiuridae	2	1.4
Bathysauridae	1	0.7	Centrolophidae	2	1.4
Neoscopelidae	2	1.4	Xiphiidae	1	0.7
Myctophidae	6	4.3	Soleidae	1	0.7

According to Pitcher (2008), the proximity or distance of the seamount to the continental shelf is another important factor affecting the fish fauna composition. This feature was one of the main factors explaining the biological variability of Seamounts in the New Zealand region (Rowden *et al.* 2005). In the North-eastern Atlantic, the Galicia Bank is considered a coastal seamount, together with the Ampere, Gorringe, Josephine and Seine Banks, in contrast with oceanic seamounts, including the Atlantis, Hyeres,

Irving, Meteor and Plato Banks, located offshore (Gofas 2007; Surugiu *et al*. 2008). Nevertheless, some results on inter-seamount invertebrate faunal similarity highlight the separation of the Galicia Bank due to its isolated northern position and deep plateau (Surugiu *et al*. 2008).

Of the 139 fish species reported in this paper, 99 (71.2%) have been also reported in the continental shelf and slope of Galician waters whereas the remaining 40 species (28.8%) are exclusive of the Galicia Bank. This difference could be mainly ascribed to a relative more intensive sampling of the Galicia Bank compared to the deep-water areas of the Galician coast. In fact, all of the fish species captured in the Galicia Bank have been also reported in other areas of the North-eastern Atlantic, indicating the lack of endemic species in the Bank.

Seamounts have been frequently described as biological islands harbouring unique or characteristic fauna with high rates of endemism. However many of these characterizations have been questioned in the last years (McClain 2007) and the levels of endemic species on seamounts may vary between individual seamounts, regions and taxa, and may, in some cases, be limited to species with a low dispersal ability (Secretariat of the Convention on Biological Diversity 2008). A recent study suggest that seamount fish faunas are not unique to seamounts but are, in fact, similar to the fauna inhabiting the surrounding region (Lundsten *et al.*, 2009), which is in agreement with our results.

Among the ecological factors pointed out by Pitcher (2008), the presence of corals was related with the presence and abundance of seamount fishes. Corals provide an important source of three dimensional structures in the predominantly sedimentary habitats of deeper waters, acting as refuge habitat for many fish species (Söffker *et al.* 2011). Many fishes show spatial co-occurrence with deep-water corals and fish catches have been found to be higher in and around deep-water coral reefs (Clark *et al.* 2006). Studies on *Lophelia* coral reefs in the Northeast Atlantic have recorded the presence of 25 fish species (Costello *et al.* 2005). In the case of the Galicia Bank, the main areas of cold-water coral mounds and reefs have been identified between 620 and 1,125 m depth (Somoza *et al.* 2014). Although the relationships among fishes and corals in the Galicia Bank was not analysed, most of the fish species (about 100) were captured within this range of depth, which seems to indicate a positive relationship between corals and the presence and abundance of fishes. Moreover, *N. helgae* and *G. latifrons*, two fish

species particularly associated with coral reef habitats off Ireland (Söffker *et al.* 2011), were also present in the Bank.

Seamount communities are highly vulnerable to impacts from fisheries and recovery from fishing impacts is a lengthy process (Schlacher *et al.* 2010). Thus, the fishing activity is another feature to be considered when evaluating the conservation status of seamounts in relation to threats (Pitcher 2008). Evidences of fishing activity in the Galicia Bank were observed by the presence of derelict fishing gears, mainly gill nets. The first fishing activities in the area were reported in 1971, initially with bottom longlines and some years later with bottom gillnets (volantas) targeting *L. piscatorius*, *P. americanus*, *E. telescopus*, *Beryx splendens* and *P. blennoides*. In the late 1970's and early 1980's a fishery with pelagic longline targeting *X. gladius* and *B. brama* was developed. During the 1990's, there was also some fishing activity targeting deep-water sharks with bottom longline. Some attempts to fish by bottom trawling were also recorded in the area. However, the scarcity of sedimentary areas suitable for trawling combined with the low catch rate of commercial species and the high presence of corals discouraged the development of this fishery.

During the last years, the fishing activity in the Galicia Bank has been greatly reduced because of several aspects such as the great distance from homeports together with the prohibition of fishing during weekends since 2002, the scarcity of high value species and the zero catches for deep-water sharks set by the European Union since 2010. Nowadays, only 3 vessels are sporadically moving to the Bank targeting *L. piscatorius* with gillnet. Thus, and in general terms, the fishing activity carried out in the Bank has been low and has progressively decreased. This low level of fishing activity, specially the absence of bottom trawl, has preserved the benthic environment of the Galicia Bank in a relatively good state, with well-preserved deep-sea biotopes of conservation importance such as coral communities.

Regarding the occurrence of singular fish species, the presence of *B. ocellaris* in the Bank at 762-799 m depth set a new deep record for the species. *B. ocellaris* is a demersal species usually distributed between 10 and 400 m depth that typically closes its life-cycle in coastal waters without apparent dependence on seamounts. However, this species has been recently captured in the Concepción Bank seamount, at 390 m

depth (IEO 2013). Both findings confirm the presence of *B. ocellaris* not only in the continental or island shelves but also in coastal seamounts located near these areas.

TABLE 3. Species list to be threatened according to the OSPAR list of threatened and/or declining species (www.ospar.org), IUCN red list of threatened species (www.iucnredlist.org) and FishBase (www.fishbase.org). Abbreviations: critically endangered (CR), vulnerable (VU), very high vulnerability (VHV), high to very high vulnerability (HHV) and high vulnerability (HV).

Family	Species	OSPAR	IUCN	FishBase
Hexanchidae	*Hexanchus griseus*	—	—	**VHV**
Pentanchidae	*Galeus melastomus*	—	—	**HV**
Pentanchidae	*Apristurus aphyodes*	—	—	**HHV**
Pseudotriakidae	*Pseudotriakis microdon*	—	—	**HHV**
Carcharhinidae	*Isurus oxyrhinchus*	—	**VU**	**VHV**
Carcharhinidae	*Prionace glauca*	—	—	**HHV**
Dalatiidae	*Dalatias licha*	—	**EN**	**VHV**
Somniosidae	*Centroscymnus coelolepis*	**VU**	**EN**	**HV**
Somniosidae	*Centroselachus crepidater*	—	—	**VHV**
Somniosidae	*Somniosus rostratus*	—	—	**VHV**
Somniosidae	*Scymnodon ringens*	—	—	**HV**
Oxynotidae	*Oxynotus paradoxus*	—	—	**HV**
Centrophoridae	*Centrophorus granulosus*	**VU**	**CR**	**VHV**
Centrophoridae	*Centrophorus squamosus*	**VU**	**EN**	**VHV**
Centrophoridae	*Deania calcea*	—	**EN**	**HHV**
Centrophoridae	*Deania hystricosa*	—	—	**HHV**
Centrophoridae	*Deania profundorum*	—	—	**HHV**
Rajidae	*Dipturus batis*	**VU**	**CR**	**VHV**
Dasyatidae	*Pteroplatitrygon violacea*	—	—	**HHV**
Chimaeridae	*Chimaera monstrosa*	—	—	**HHV**
Chimaeridae	*Chimaera opalescens*	—	—	**HV**
Chimaeridae	*Hydrolagus affinis*	—	—	**HHV**
Congridae	*Conger conger*	—	—	**VHV**
Polyprionidae	*Polyprion americanus*	—	—	**VHV**
Gempylidae	*Ruvettus pretiosus*	—	—	**VHV**

Centrolophidae	*Centrolophus niger*	—	—	**VHV**
Alepocephalidae	*Alepocephalus bairdii*	—	—	**HHV**
Alepocephalidae	*Alepocephalus rostratus*	—	—	**HHV**
Macrouridae	*Coryphaenoides rupestris*	—	**EN**	**HHV**
Moridae	*Lepidion guentheri*	—	—	**HHV**
Moridae	*Antimora rostrata*	—	—	**HHV**
Ophididae	*Spectrunculus grandis*	—	—	**HHV**
Lophiidae	*Lophius piscatorius*	—	—	**HHV**
Trachichthyidae	*Hoplostethus atlanticus*	**VU**	**VU**	**HHV**
Berycidae	*Beryx decadactylus*	—	—	**HHV**
Sebastidae	*Trachyscorpia cristulata*	—	—	**HHV**
Epigonidae	*Epigonus telescopus*	—	—	**HHV**
Bramidae	*Brama brama*	—	—	**HHV**
Gempylidae	*Nesiarchus nasutus*	—	—	**HHV**
Trichiuridae	*Aphanopus carbo*	—	—	**HHV**
Xiphiidae	*Xiphias gladius*	—	—	**HHV**
Alepocephalidae	*Roulenia atrita*	—	—	**HV**
Macrouridae	*Coelorhynchus coelorhynchus*	—	—	**HV**
Macrouridae	*Coryphaenoides mediterraneus*	—	—	**HV**
Macrouridae	*Malacocephalus laevis*	—	—	**HV**
Moridae	*Halargyreus johnsonii*	—	—	**HV**
Moridae	*Mora moro*	—	—	**HV**
Phycidae	*Phycis blennoides*	—	—	**HV**
Merluccidae	*Merluccius merluccius*	—	—	**HV**
Bythitidae	*Cataetyx laticeps*	—	—	**HV**
Trachichthyidae	*Hoplostethus cadenati*	—	—	**HV**
Trachichthyidae	*Hoplostethus mediterraneus*	—	—	**HV**
Berycidae	*Beryx splendens*	—	—	**HV**
Oreosomatidae	*Neocyttus helgae*	—	—	**HV**
Carangidae	*Trachurus trachurus*	—	—	**HV**
Bramidae	*Taractes asper*	—	—	**HV**
Trichiuridae	*Benthodesmus simonyi*	—	—	**HV**

The presence in seamounts of unusual species, scarcely known on the continental shelf, has been related to the hypothesis that seamounts and islands are used as "stepping stones" for the transoceanic dispersal of species (Wilson & Kaufmann 1987). Examples of this could be the cases of *N. helgae* (Moore *et al.* 2008) or *P. dalwigki* (Bañón *et al.* 2002), but also of several species such as *P. splendens, G. granti, A. oleosa* and *N. microchir,* which have a northward eastern Atlantic distribution along the Canary and Azores Islands and the Galicia Bank (Bañón *et al.* 2011).

During the last two decades, there has been an internationally concern in order to protect the deep-sea ecosystems. Thus, the concept of 'Ecologically or Biologically Significant Marine Areas' (EBSAs) has been proposed to identify open ocean and deep-sea habitats in need of protection (Clark *et al.* 2014). According to this, seamounts are considered as EBSAs due to their importance as refuge locations for threatened, endangered and declining species. Seamount fishes, particularly seamount-aggregating fishes, have a higher intrinsic vulnerability than other groups of fishes due to a longer lifespan, later sexual maturation, slower growth and lower natural mortality (Morato *et al.* 2004).

Based on life history and ecological characteristics, several authors have placed the seamount fishes at the extreme end of the vulnerability spectrum. Morato *et al.* (2006) indicated that seamount species were more at risk than species that did not occur on seamounts, and that aggregating species were even more vulnerable. Considering the three databases (OSPAR, IUCN and FishBase) used to evaluate this criterion, 9 species (6%) were considered as threatened according to IUCN, 5 species (3%) according to OSPAR and 58 (42%) according to FishBase (Table 3). These differences are mainly due to the different criteria used to estimate the vulnerability. OSPAR criteria are based on the global and regional importance and on the presence of rare, sensitive, declining and key stone species. Those of the IUCN are inferred from several parameters mainly focusing on species population dynamics, which are not available for most of the listed species (data deficient), whereas FishBase provides vulnerability values for fish mainly based on fish life-history traits. Vulnerability data provided by FishBase are uncorrelated with those provided by IUCN, but both should be used together in studies dealing with fish conservation (Strona 2014). However, whenever data from IUCN are not available or in general macro-ecological studies focusing on large sets of species, the use of FishBase vulnerability data appears to be the best option (Strona *et al.* 2013).

Thus, 42% of the fish species recorded in the Galicia Bank should be considered as threatened species. In addition, the high fish biodiversity composed mainly of deep-water species, and their high vulnerability should be strong reasons to declare the Galicia Bank as a MPA by the Spanish government.

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Anexo II

Rodríguez-Cabello, C., Pérez, M. & **Bañón, R.** 2014. Occurrence of *Apristurus* species in the Galicia Bank Seamount (NE Atlantic). Journal of Applied Ichthyology, 30 (5): 906-915.

SUMMARY

The aim of this study was to identify some *Apristurus* species combining morphometric and genetic tools. Several specimens of the genus *Apristurus* were caught on the Galicia Bank Seamount (NE Atlantic), between 1,460 and 1,809 m depth, during a multidisciplinary survey carried out in 2011 within the framework of the INDEMARES Project. Morphometric and genetic analyses were conducted to aid the identification of the specimens collected. A total of 20 specimens were identified, of which 18 corresponded to *Apristurus aphyodes* (Nakaya & Stehmann, 1998), one to *A. profundorum* (Goode & Bean, 1896) and one to *A. melanoasper* Iglesias, Nakaya and Stehmann, 2004. Genetic results based on mtDNA COI sequences (682–690 bp fragment of the COI gene) support the identification of *A. profundorum* and *A. melanoasper*, with a bootstrap of 99% and 96% respectively. The identification of *A. aphyodes* was also performed using a 499 bp fragment of the 16S mitochondrial gene. These are the first records of *Apristurus* species from Galician waters, which extend the known distribution area of these species and provide more information about different biological and ecological aspects of this complex taxonomic group.

INTRODUCTION

The genus *Apristurus* (Garman, 1913), is one of the largest genera of living catsharks, with 37 species currently recognised as valid, and 55 nominal species (Froese & Pauly, 2011). It previously belonged to the family Scyliorhinidae, but was recently included in the family Pentanchidae, based on molecular and morphological phylogenetic studies that showed that the family Scyliorhinidae was paraphyletic (Maisey, 1984; Winchell et al., 2004; Iglesias et al., 2005). The resurrected family Pentachidae differs from the Scyliorhinidae by the absence of supraorbital crests on the chondocranium (Compagno, 1988; Iglesias et al., 2005).

Apristurus species inhabit the continental slopes and submarine elevations at depths of 400–2,000 m in all marine waters, except for the Polar regions (Compagno, 1984; Ebert & Stehmann, 2013). The Pacific Ocean accounts for the greatest number of species (n=24), followed by the Atlantic (n=10) and the Indian Ocean (n=4). One of these species, *A. australis* Sato, Nakaya & Yorozu, 2008

occurs in the Indian and Pacific coasts. Six species of *Apristurus* are known from the North Atlantic i.e., *A. laurussonii* (Saemundsson, 1922) (= *A. maderensis* Cadenat & Maul, 1966; = *A. atlanticus* (Koefoed, 1927), *A. microps* (Gilchrist, 1922), *A. manis* (Springer, 1979), *A. aphyodes* Nakaya & Stehmann, 1998 (= *A.atlanticus* Compagno, 1984), *A. profundorum* (Goode and Bean, 1896) and *A. melanoasper* Iglésias, Nakaya & Stehmann, 2004 (Iglesias et al., 2004). From Galician waters, catsharks are represented by five species (*Galeus atlanticus*, *G. melastomus*, *G. murinus*, *Scyliorhinus canicula* and *S. stellaris*), none of them from the genus *Apristurus* (Bañón et al., 2010). However, only *G. murinus* has been caught on the Galicia Bank Seamount, the other four species were found on the continental shelf and slope.

The genus *Apristurus* is considered one of the most diverse and taxonomically confusing genera among living sharks, in part due to the large number of poorly known species (Nakaya et al., 2008a). Taxonomic revisions of *Apristurus* have been previously carried out (Springer, 1979; Nakaya, 1991; Nakaya & Sato, 1998, 1999; Iglesias et al., 2005). Despite all these revisions, taxonomic confusion still exists, because many species are homogeneous in morphology and available material is lacking for many species (Iglesias & Nakaya, 2004).

Galicia Bank (GB) is a large seamount located 120 miles offshore from the west coast of Galicia (North Spain). The top of the Bank is at 600 m depth and reaches 4,000 m on its deepest side. It has a length of 50 km in the E–W direction and 90 km in the N–S axis (Figure 1). This region comprises part of an Environment Ministry (2004) proposal to make an inventory of the biodiversity in the Spanish seas through the identification of valuable areas for the Natura 2000 Network. The last surveys conducted in this area within this framework contributed to increase the number of species that inhabit these waters and confirmed the high biodiversity in the Galicia Bank. Although only scattered records have been published to date in this area (Bañon et al., 2011; Sanjuan et al., 2012, a complete list of the fish fauna found in the Galician Bank is now being processed.

Previous information on elasmobranch species present in the Galicia Bank is limited. Piñeiro et al. (2001), reported 11 sharks for this area based on experimental and commercial surveys, although they only provided the scientific name of six species. In addition, biological and taxonomic studies of other deep-water sharks,

mainly belonging to the family Centrophoridae, were also carried out (Casas et al., 2001; Bañón et al., 2008).

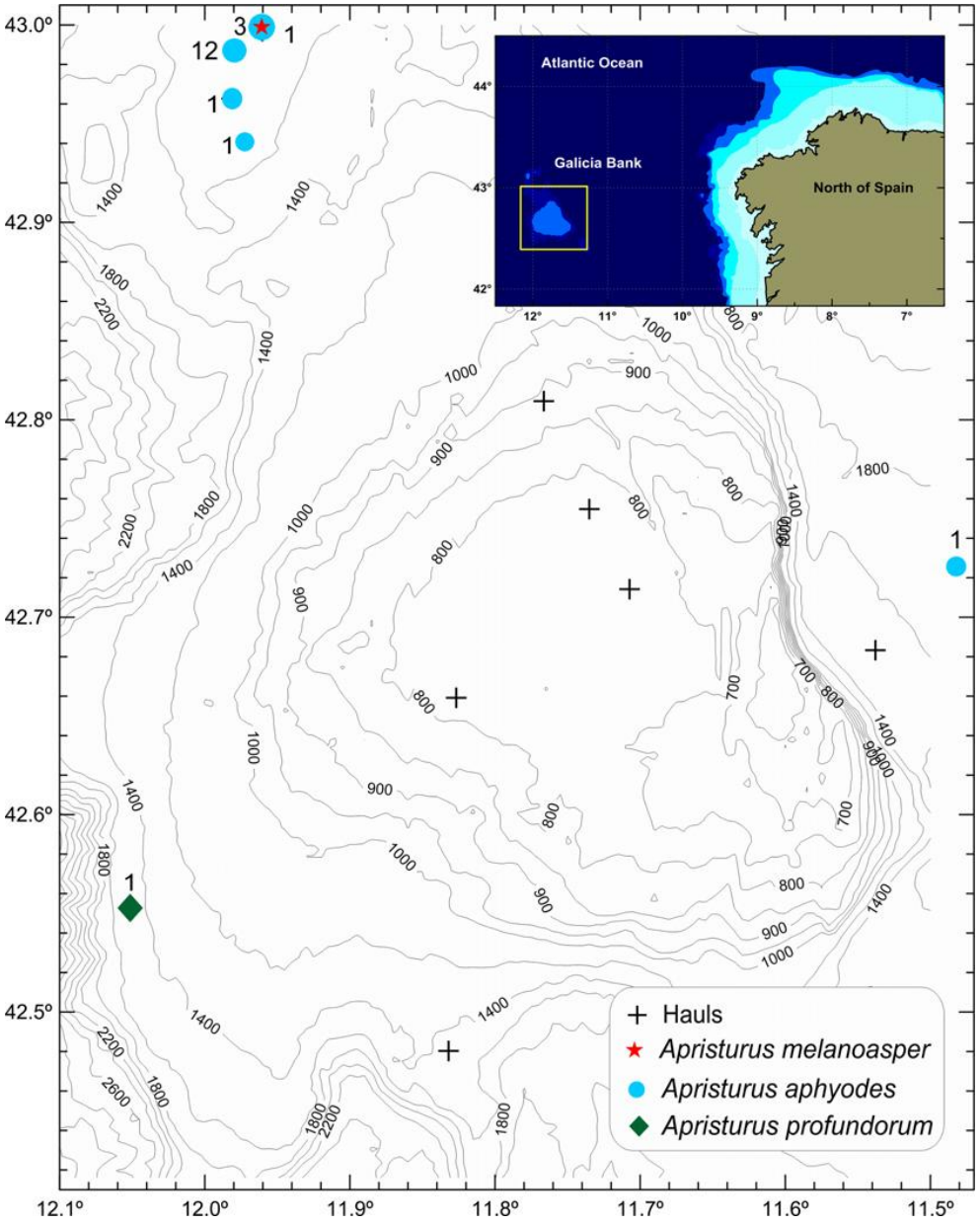

Fig. 1. Location of Galicia Bank and spatial distribution of *Apristurus* species caught in the study area. Figures on left and above the circles indicate number of specimens caught at each sample site.

The incorporation of molecular DNA techniques has provided new tools to aid the identification and classification of elasmobranch species (Ward et al., 2008, Vélez-Zuazo & Argnarsson, 2011, Dugdeon et al., 2012). With respect to the genus *Apristurus*, several molecular studies dealing with phylogeny and evolution,

conservation or diversity have been performed (Winchell et al., 2004; Iglesias et al., 2005; Naylor et al., 2012). Nevertheless, genetic and morphological techniques have their own limitations and therefore, the integration of both methodologies is recommended (White & Last, 2012).

The aim of this study was to identify the *Apristurus* species caught in Galicia Bank seamount combining morphometric and genetic tools, to increase the knowledge of this complex taxonomic group.

MATERIAL AND METHODS

Study area

Apristurus species were caught during a multidisciplinary survey carried out in the Galicia Bank in July 2011 within the framework of the INDEMARES project (Figure 1). Almost all the specimens were caught using a bottom trawl net (GOG-73) with a mesh size of 10 mm and haul duration of 30 min. Only one specimen was caught using a beam trawl (3.5 m width, 10 mm mesh size) during a 15 min trawl and another one with an Arcachon type suprabenthic sledge, aimed at colleting small fauna from different water layers adjacent to the sea floor. The sea floor was dredged for 2 min, at a speed of 2 knots (for more information about the different gears used in these surveys visit www.ecomarg.net).

During this survey, a total of 20 hauls were performed, nine using the bottom trawl net and eleven with the beam trawl at depths ranging from 700 to 1,809 m. *Apristurus* species were recorded in five of these hauls at depths ranging from 1,459 to 1,809 m. (Table 1, Figure 1). Thirteen trawls were additionally carried out with the suprabenthic sledge. The location and depth corresponded to the position recorded at the end of the tow when the gear left the sea floor. *Apristurus* species were identified according to several fish faunas and revisions of this genus (Compagno, 1984; Whitehead, 1984; Iglésias et al., 2004; Iglesias, 2013; Nakaya & Sato, 1999; Nakaya & Stehmann, 1998; Quéro et al., 2003; Springer, 1979; Ebert & Stehmann, 2013).

Muscle samples were removed from thawed individuals and stored in 96% ethanol. The specimens where then fixed in 10% formalin, prior to their storage in 70% ethanol. Specimens were stored in the IEO fish collection at the Oceanographic Centre of Santander (Table 2). Photographs of the specimens and the DNA sequence

data are public available in the Barcode of Life Data Base (BOLD) with the DOI: dx.doi.org/10.5883/DS-IEOBG10.

Table 1. Data of the specimens caught and sampled. Gear GOC = bottom trawl net, BT= beam trawl. % O.M.= organic matter percentage. Q50 = type of sediment: FS = fine sand, VFS = very fine sand, MS = medium sand.

Survey_Haul	Species	Total catch		N° sample	Length range (cm)	GEAR	Location		DEPTH (m)	T (°C)	S (‰)	% O.M.	Q50 (phi)	% Particle size			Type of sediment
		N°	W (g)				LAT	LON						> 500 µ	62-500 µ	< 62 µ	
BG1_G2	*Apristurus aphyodes*	3	144	3	24.7-26.0	GOC	43.0026	11.5748	1683	5.65	35.2715	1.10	2.36	6.432	90.849	2.718	FS
BG1_G2	*Apristurus melanoasper*	1	38	1	25.0	GOC	43.0027	11.5749	1684	5.66	35.2716	1.11	2.37	6.433	90.850	2.719	FS
BG1_G5	*Apristurus aphyodes*	1	14	0	15.7	GOC	42.5871	11.5871	1674	5.65	35.2715	1.11	2.36	6.432	90.850	2.719	FS
BG1_G9	*Apristurus aphyodes*	12	888	10	22.7-39.7	GOC	43.0004	11.5830	1685	5.66	35.2715	1.12	2.36	6.433	90.850	2.720	FS
BG1_G10	*Apristurus aphyodes*	1	264	1	37.7	GOC	42.4414	11.2635	1809	6.36	35.3824	3.24	3.80	2.411	51.280	46.309	VFS
BG1_V7	*Apristurus profundorum*	1	14	1	14.6	BT	42.3314	12.0301	1459	7.45	35.5777	1.91	1.68	15.261	81.962	2.774	MS
BG1_T5	*Apristurus aphyodes*	1	10	0	14.0	TS	42.3315	12.0302	1460	7.46	35.5778	1.91	1.68	15.262	81.963	2.775	MS

Morphological analysis

Morphometric measurements followed Nakaya et al., (2008a). All measurements were made point-to-point to the nearest mm. Values are expressed as a percentage of the total length (LT). Meristic characters for teeth and dermal denticles were also recorded and spiral valves counted for some specimens to confirm the group identification. Dermal denticles (n=20) were randomly taken from the dorsolateral side of the body below the first dorsal fin and mean crown length was recorded with a binocular micrometer.

Similarity between morphometric characters was calculated using the Bray-Curtis index (Clarke & Warwick, 2001) and the resulting dendrogram was obtained with the group average clustering algorithm using PRIMER software. The student's t-test was applied to examine differences in morphometric measurements between sexes in *A. aphyodes* specimens.

Genetic analysis. DNA isolation, amplification and sequencing

Total genomic DNA was extracted from ethanol-preserved muscle tissue using the FENOSALT method (Pérez & Presa, 2011). Cytochrome oxidase I (COI) is a reliable species tag and DNA barcoding can deliver species-level identifications (Ward et al., 2009). A total of sixteen COI DNA sequences were obtained from three different species of *Apristurus* caught in the Galicia Bank: *A. aphyodes* (14 sequences), *A. melanoasper* (1 sequence) and *A. profundorum* (1 sequence). A 682–690 bp fragment of the COI gene was amplified and sequenced using the primer pair FishF2 and FishR2 (Ward et al., 2005). Amplifications were carried out in a Mastercycler thermocycler gradient (Eppendorf). The PCR program consisted of 5 min at 95ºC, the.n 35 cycles of 95ºC for 30 s, 50ºC for 1 min, 72ºC for 1 min and a final extension of 10 min at 72ºC. The PCR amplification mixture of 25 µL contained between 10 and 20 ng purified DNA, 10 pmol each primer, 0.2 mM of dNTPs, 1.5 mM MgCl2, 1 U BioTaq DNA Polymerase (Bioline), and 2.5 µL of 10× reaction buffer. The data set was completed with available *Apristurus* COI sequences totalizing a complete data set of 71 sequences from twelve species.

In the case of *A. aphyodes*, COI failed to identify the sample species because there were not available public COI sequences to conduct a barcoding comparative identification. In this case, only 16S rRNA gene sequences were available (Iglesias et al., 2004). Therefore, 16S rRNA gene was sequenced in four specimens

(BG11G2ASP1, BG11G10AAP1, BG11G9AAP2, BG11G2ASP3) and the data set was completed with twelve sequences available in Genbank (AY462154-AY462157, AY462162- AY462166 and AF358916) (Fig.2). A 427 bp fragment of the 16S mitochondrial gene was also amplified by polymerase chain reaction (PCR) using two primers: 16S-RA (5´-CGCCTGTTTATCAAAAACAT-3´) and 16S-RB (5´-CCGGTCTGAACTCAGATCACGT-3´) (Palumbi et al. 1991). The PCR program consisted of 10 min at 95ºC, then 35 cycles of 95ºC for 1 min, 55ºC for 45 s, 72ºC for 1 min and a final extension of 10 min at 72ºC. Each PCR reaction had a total volume of 20 µL, containing between 10 and 20 ng of purified DNA, 2.5 µL of 10× NH4 Reaction Buffer (160 mM (NH4)2SO4, 670 mM Tris–HCl, pH 8.8), 1.5 µL of 8 mM pre-mixed dNTPs, 1.5 mM of MgCl2, 15 pmol of each primer, and 1 U of BioTaq DNA polymerase (Bioline).

PCR products were cleaned before the sequencing reaction using Exo-Sap (USB) according to the manufacturer's protocol. The purified fragments were directly sequenced on both DNA strands with the same primer pair used for PCR amplification. Sequencing was performed in an ABI Prism 3100 capilar sequencer using the BigDye Terminator Cycle Sequencing Standard (Applied Biosystems).

The final haplotypes were derived from the alignment of the forward and reverse sequences obtained from each individual, using CHROMAS software (http://www.technelysium.com.au/chromas.html). All *Apristurus* spp. public sequences available in the BOLD database as well as 13 sequences obtained in the present study were aligned and edited using the software Bioedit version 7.0.9.0 (Hall, 1999). The analysis involved 68 nucleotide sequences with a total of 468 positions in the final dataset. Evolutionary analyses were conducted using MEGA5 (Tamura et al., 2011). The bootstrap consensus tree based on COI sequences was inferred from 1,000 replicates (Felsenstein, 1985) using the Neighbour-Joining method (Saitou & Nei, 1987). The evolutionary distances were computed using the Maximum Composite Likelihood method (Tamura & Kumar, 2004). Branches corresponding to partitions reproduced in less than 50% bootstrap replicates were collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1,000 replicates) is shown next to the branches (Felsenstein, 1985). All positions containing gaps and missing data were eliminated.

The molecular identification of the *Apristurus* species was made using i) the identification engine provided in the Barcode of Life Data Systems (BOLD) based

on the COI sequences and, ii) a phylogenetic tree was inferred to assign unknown sequences to species using the FINS method as described in Pérez & Presa, (2008) and iii) the 16S sequences obtained from specimens; BG11G2ASP1, BG11G10AAP1, BG11G9AAP2, BG11G2ASP3 were compared to those found in GenBank using the Basic Local Alignment Search Tool algorithm (BLAST, Zhang et al., 2000). Sequences are available online under the Genbank accession numbers (Table 2).

Table 2. *Apristurus* species used in the present study with their respective codes: Sample identification, Genbank accession numbers, Voucher collection

Species	Survey_Haul	Sex	Length (mm)	Sample Identification	GenBank Accession numbers		Collection Voucher IEO
					COI	16 S	
Apristurus aphyodes	BG1_G2	Male	259	BG11G2ASP1	KJ202061	KJ170696	IEOST2011_1_426_A
Apristurus aphyodes	BG1_G2	Female	260	BG11G2ASP3	KJ202062	KJ170698	IEOST2011_1_426_B
Apristurus aphyodes	BG1_G2	Female	247	BG11G2ASP4	KJ202063		
Apristurus aphyodes	BG1_G5	Female	157	BG11G5ASP1	KJ202064		
Apristurus aphyodes	BG1_G9	Male	397	BG11G9AAP1	KJ202065		IEOST2011_1_426_C
Apristurus aphyodes	BG1_G9	Female	282	BG11G9AAP2	KJ202066	KJ170697	IEOST2011_1_426_D
Apristurus aphyodes	BG1_G9	Female	260	BG11G9AAP3	KJ202067		IEOST2011_1_426_E
Apristurus aphyodes	BG1_G9	Female	261	BG11G9AAP4	KJ202068		IEOST2011_1_426_F
Apristurus aphyodes	BG1_G9	Male	249	BG11G9AAP5	KJ202069		IEOST2011_1_426_G
Apristurus aphyodes	BG1_G9	Female	242	BG11G9AAP6	KJ202070		IEOST2011_1_426_H
Apristurus aphyodes	BG1_G9	Male	252	BG11G9RF1	KJ202071		
Apristurus aphyodes	BG1_G9	Male	294	BG11G9RF2	KJ202072		
Apristurus aphyodes	BG1_G10	Female	377	BG11G10AAP 1	KJ202073	KJ170695	IEOST2011_1_426_K
Apristurus aphyodes	BG1_T5	Female	140	BG11T5ASP1	KJ202074		
Apristurus profundorum	BG1_V7	Female	146	BG11V7ASP1	KJ202075		IEOST2011_1_437_A
Apristurus melanoasper	BG1_G2	Female	250	BG11G2ASP2	KJ202076		IEOST2011_1_436_A

RESULTS

Apristurus aphyodes Nakaya and Stehman, 1998.

Material examined. *Apristurus aphyodes* (see Table 2).

A total of 18 specimens were collected: six males ranging from 24.4–39.7 cm and 12 females from 22.7–37.7 cm TL at a depth range of 1,460–1,809 m (Table 1). The

majority of specimens were caught in the bottom grounds of fine sand and low organic matter content, however, two specimens were also caught in medium and very fine sand sediment. The bottom temperature ranged from 5.65–7.46ºC and salinity between 35.27–35.57‰.

Description. Upper labial furrow shorter than lower one, large eyes with horizontal diameter 1.9 to 2.5 times inter-orbital width, sub-equal size of dorsal fins, anterior position of first dorsal fin with origin above frontal half of pelvic base, widely spaced pectoral and pelvic fins with distance between their origins equaling head length, 9 to 11 spiral valves in the intestine and uniform whitish coloration.
Morphometric mean values were compared between males and females (Table 1_Supp.) and significant differences were found in several characters: eye length, head length, prebranchial length, preoral length, size of nostrils, pectoral and pelvic lengths and distance to first dorsal fin. However, in both cases, all the specimens sampled were juveniles. A comparison of the main morphometric measurements of the specimens described in this study to the paratypes is shown in Table 2_Supp.

Habitat and distribution. This species is widely distributed in the eastern North Atlantic, from Iceland to the northern Bay of Biscay (Nakaya & Stehmann, 1998), thus, these records extend its distribution further towards the south 42º N.

Genetic results. Sixteen COI sequences (GenBank accession numbers KJ202061-KJ202076) and four 16S sequences were obtained (GenBank accession numbers KJ170695-KJ170698). The inferred phylogenetic tree based on obtained COI sequences (Figure 2) clustered the 14 sequences together in the same group with a bootstrap support of 99% (Fig. 3). The COI sequence of this species was not available in the Genbank and BOLD databases, thus comparative identification was not possible. However, the analysis of 16S gene sequences, carried out on four specimens (BG11G2ASP1, BG11G10AAP1, BG11G9AAP2, BG11G2ASP3) and subsequently compared with the sequences available in BLAST submitted by Iglésias et al., (2004), allowed us to confirm that these samples corresponded to *A. aphyodes*. The phylogenetic tree using the 16S sequences of *A. aphyodes* is shown (Figure 3). All sequences were grouped with AF358916 sequence corresponding to *A. aphyodes*, with a bootstrap support of 100%.

***Apristurus profundorum* (Goode & Bean, 1896).**

Material examined. *Apristurus profundorum* (05/08/2011, 42.3315'N–12.0302'W, 1,460 m, 146 mm ♀ BG11V7ASP1). Only a female of 14.6 cm TL and 14.0 g weight was caught at 1,459 m depth on medium sand sediment with a bottom temperature and salinity of 7.45ºC and 35.57‰, respectively (Table 1). Morphometric measurements are given in Table 1_Supp.

Description. Upper labial furrows sub-equal or shorter than lower, snout moderately long and broad, preoral snout about 9% of total length. Eyes rather small, diameter about 3% of total length and 2.9 to 4.0 times in interorbital width. Mouth moderately long, large, and broadly arched; mouth and labial furrows extending well in front of eyes (Figure 4a). Caudal fin fairly broad, with a well-developed crest of enlarged denticles on dorsal caudal fin margin, with crest denticles directed obliquely downwards (Figure 4b). Lateral trunk denticles of body with crowns partly erect, giving skin surface (Figure 4c). Pectoral fins rather small, anterior margins about 11% of total length; inner margins fairly long, about half length of pectoral fin bases. Interspace between pectoral and pelvic fin bases moderately long, slightly less than prespiracular length and about 15% of total length. Pelvic fins high and broadly rounded. Interdorsal space slightly greater than first dorsal fin base. First dorsal fin about as large as second, bases about equally long. Spiral valve counts 10. Origin of first dorsal fin slightly behind pelvic fin mid bases (Figure 4d).

A comparison of some morphometric measurements of this specimen and the holotype according to Murray & Hjort (1932) is shown in Table 3_Supp.

Habitat and distribution. This species have been reported in the western North Atlantic (Kiraly et al., 2003; Moore et al., 2003), the mid-Atlantic Ridge (Gushchin & Kukuev, 1981) and eastern North Atlantic (Mauritania) (Compagno, 1984; Ebert & Stehmann, 2013). This is the first record from Galician waters, which extends the distribution of this species to the north in the Northeast Atlantic.

Genetic results. The COI sequence obtained from specimen BG11V7ASP1 (GenBank Accession No KJ202075) clustered together with the available sequences

of *A. profundorum* with a bootstrap support of 99% (Figure 2). The number of base substitutions per site between sequences is shown in Table 5_Supp.

***Apristurus melanoasper* Iglesias, Nakaya and Stehmann, 2004.**

Material examined. *Apristurus melanoasper* (28/07/2011, 43.0026'N–11.5748'W, 1,683 m, 250 mm ♀ BG11G2ASP2). One female of 25.0 cm TL and 37.8 g weight was caught at 1,683 m depth on fine sand sediment at 5.66ºC bottom temperature and 35.27‰ salinity (Table 1). Morphometric measurements are shown in Table 1_Supp.

Description. Upper labial furrows longer than the lower ones; first dorsal fin only slightly smaller than the second dorsal fin originating from above anterior third to the middle of the pelvic fin base; second dorsal fin insertion just before level of anal fin insertion; body uniformly black, slightly brownish in larger specimens; interorbital space 1.9 to 3.5 times eye horizontal diameter; abdomen between pectoral fin tip and pelvic fin origin 1.3 to 2.5 times pectoral fin width; spiral valve counts 19 to 23; large dermal denticles giving a rough texture to the skin, (the width ranges from 0.3 to 0.7 mm).

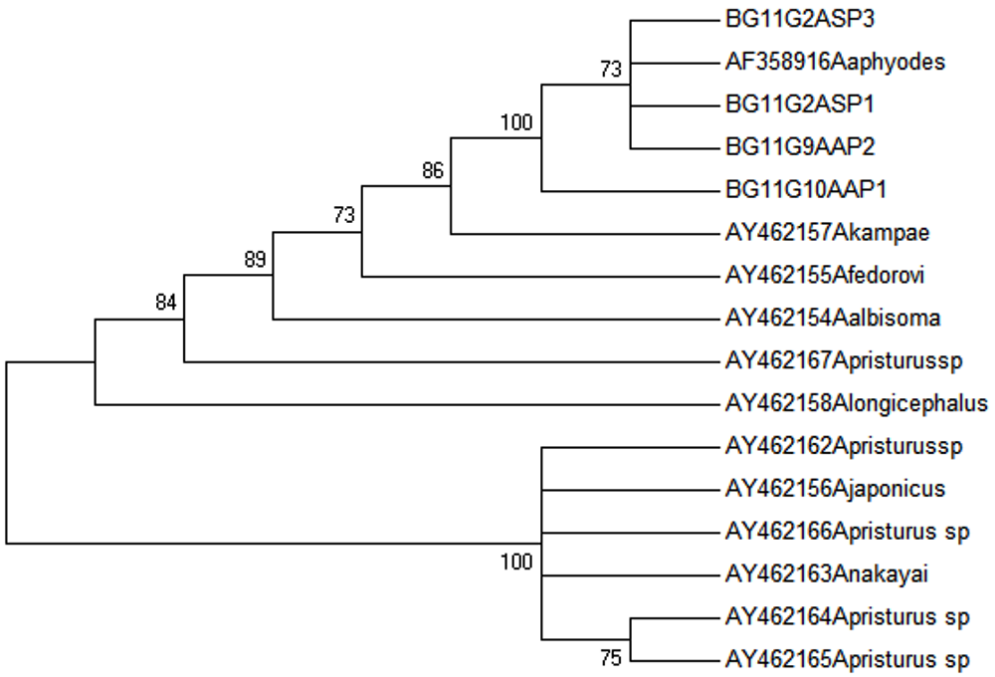

Fig. 2. Neighbor-Joining tree based on a 499 bp fragment of the 16S mitochondrial gene. Bootstrap values greater than 50 shown near the respective branches

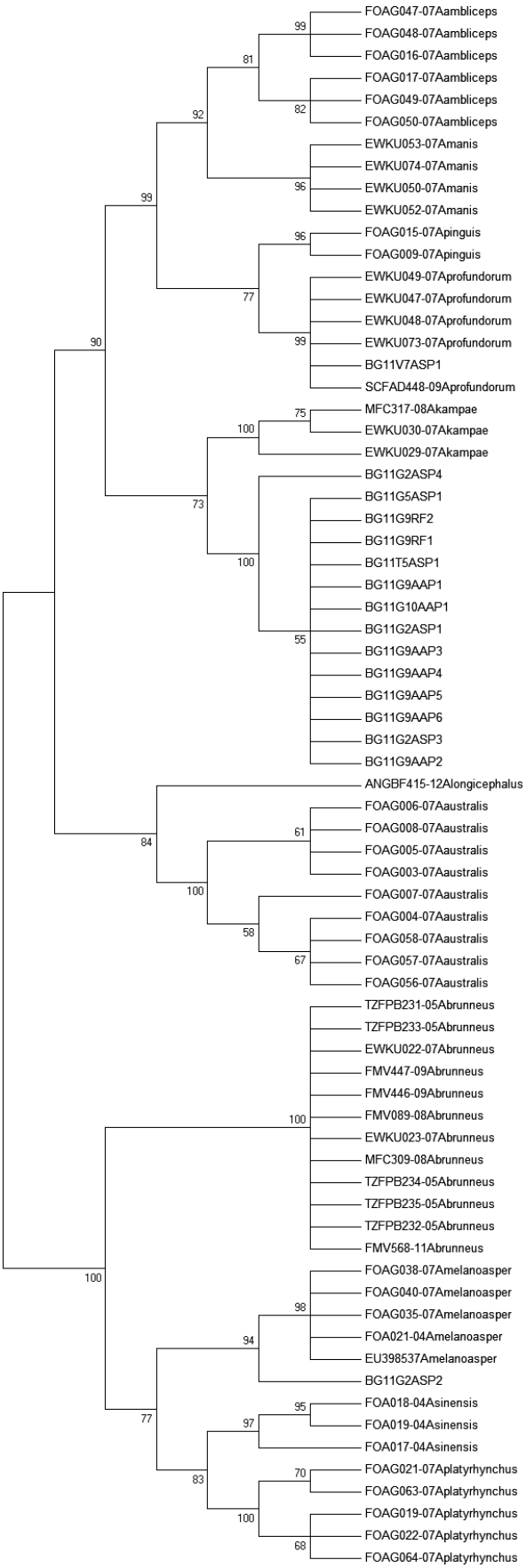

Fig. 3. Neighbor-Joining tree based on COI using Maximum Composite Likelihood distances. Bootstrap values greater than 50 shown near the respective branches.

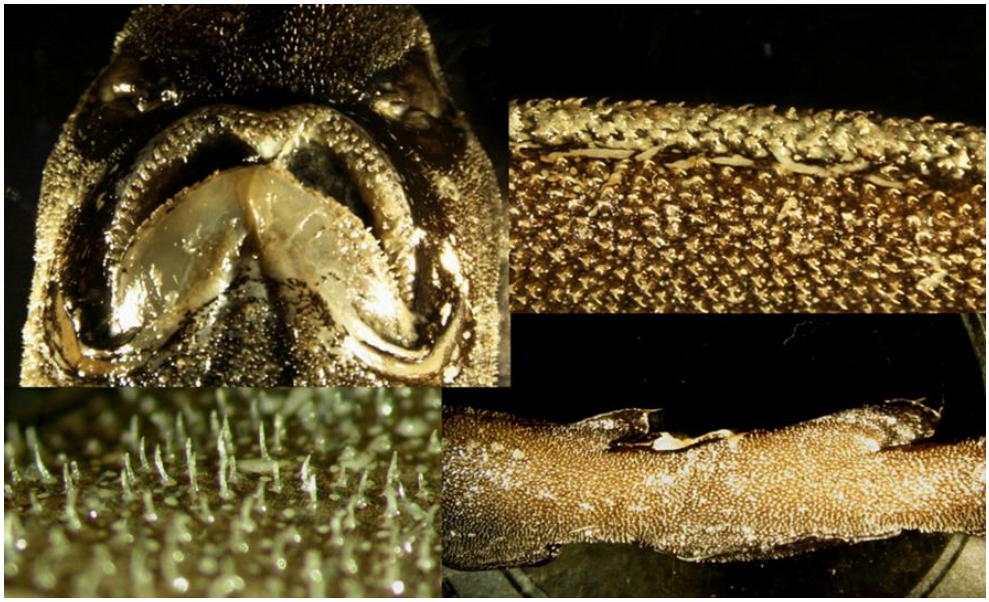

Fig. 4. Morphological characters of *Apristurus profundorum*. (a) Labial furrows, mouth shape and nostrils; (b) Dermal denticles on dorsal caudal fin; (c) Dermal denticles on lateral dorsal body; and (d) Dorsal and ventral fins.

A comparison of the main morphometric measurements followed Iglesias et al., (2004) based on all their specimens (n=53) and the one described in this study is shown in Table 4_Supp.

Habitat and distribution. This species is widely distributed but very patchy in the North Atlantic: northeastern U.S.A, France, Ireland and British Isles (Hartel et al. 2008; Iglesias et al., 2004; Moore et al., 2003). It also occurs in the Southeastern Atlantic (Namibia), in the Central Indian Ocean and south of Madagascar and in the western South Pacific (Australia, New Zealand and New Caledonia). This record extends the known distribution of this species in the Northeast Atlantic.

Genetic results. One COI sequence was obtained (GenBank Accession KJ202076) which is clustered within the *A. melanoasper* group with a bootstrap support of 95% (Figure 2). The number of base substitutions per site between sequences is shown in Table 5_Supp. The analysis involved 13 nucleotide sequences and was conducted using the Maximum Composite Likelihood model (Tamura & Kumar, 2004). There were a total of 592 positions in the final dataset because all positions containing gaps were eliminated. All the distance values between BG11V7ASP1 and

BG11G2ASP2 with the rest of sequences are compatible with the distances between species.

DISCUSSION

Apristurus aphyodes Nakaya & Stehman, 1998.

The comparison of the main morphometric measurements between the paratype specimens described in the original paper of Nakaya & Stehmann (1998) and those caught in the Galicia Bank (Table 2_Supp.) indicated that nearly all the measurements were within the reported range with the exception of four. The upper labial furrow, according to Nakaya & Stehmann (1998) was 2.6–3.8 (%TL) versus 4.2–4.4 in this study. The first and second dorsal fin base lengths were smaller in the specimens described in GB (6.0–7.6 and 6.1–7.5 respectively, versus 5.6–5.9 and 5.8–6.1) as well as the caudal peduncle height (4.0–4.8 versus 3.6–3.7). The maximum length recorded for this species is 55 cm in Rockall Trough (Moore et al., 2013). The largest specimens caught in GB measured 39.7 and 37.7 cm, a male and female respectively. Therefore, according to Nakaya & Stehmann (1998), who reported that this species attained full maturity at 47 cm length and Moore et al., (2013) reporting L50=51.6 cm and L50=49.5 cm for male and female respectively, all the individuals caught in this study area were juveniles.

Regarding other characters described for this species, the *A. aphyodes* examined in this study confirmed: the presence of dermal denticles tricuspid; denticles on dorsal margin of caudal fin closely packed but no enlargement in size and not forming a crest and teeth small in upper and lower jaws with frequently five cuspids (three cuspid in adults and two or three more lateral cuspids in small specimens). Table 6 summarizes the differences found among all the specimens examined, which could be attributed to size or individual variation.

The identification made using 16S sequences allowed us to confirm that 11 samples corresponded to *A. aphyodes*. The genetic distances (Table 5_Supp.) also indicate the homogeneity among them with values near zero.

Apristurus profundorum (Goode & Bean, 1896)

The specimen collected in the Galicia Bank matched the general description of this species; however, slight differences in some of the proportions of the main

characters described have been found (Table 3_Supp.), which might be due in part to the small size of the specimen caught.

The maximum length reported for this species is 74.5 cm (Kiraly et al., 2003). According to these authors, the holotype was collected in Hudson Canyon instead of Delaware Bay (North West Atlantic). Further records have been reported in nearby waters (Moore et al., 2003; Hartel et al., 2008) and in the Mid-Atlantic Ridge (Gushchin & Kukuev, 1981). The only known records that exist in the Northeastern Atlantic (Mauritania) need to be confirmed (Huveneers & Duffy, 2004). Thus, this record extends the distribution of this species to the East Atlantic.

The BG11V7ASP1 COI sequence perfectly matches the *A. profundorum* available sequences. All methods used to confirm this authentication, support this species identification.

Apristurus melanoasper Iglesias, Nakaya and Stehmann, 2004

The specimen caught in GB matched all the characters previously described. However, the dermal denticles that characterize this species and give its common English name did not appear large at all (0.32 ± 0.03 mm), compared to the dermal denticles of *A. aphyodes* of a similar size (0.36 ± 0.03 mm). This suggests that this character might not be as evident in small specimens. A comparison of the main morphometric measurements of this individual with those described by Iglesias et al., (2004) is shown in Table 4_Supp.

This species was first described in 2004 in Northeast Atlantic waters (Lorien Bank) at 1,243–1,260 m depth (Iglesias et al., 2004). However, some specimens from Northwest Atlantic waters (North America) were also identified as *A. melanoasper*. According to these authors, no significant differences were observed for proportional measurements between European specimens and American ones. The most significant difference found was in the size of the dermal denticles (0.3–0.7 mm), which were larger in European specimens. In 2008, this species was also encountered in the South Pacific, Indian and South Atlantic Oceans at depths of 880–1,275 m (Nakaya et al., 2008b). The diagnosis was similar and the dermal denticles were within the range of North Atlantic populations (0.3–0.7 mm) but were more similar in size to American specimens. In a recently study, Naylor et al., (2012) questioned the classification of some specimens examined from Australia

and New Zealand based on a genetic approach and provisionally gave them the designation *Apristurus cf. melanoasper*.

The genetic results based on COI allowed including this specimen (BG11G2ASP2) with a bootstrap support of 95% within the *A. melanoasper* group. The sequences accessible in the BOLD database corresponded to specimens caught in Australia, and this might be the reason why all the sequences available for this species clustered together with a 95% of bootstrap support and our sequence was not among them. More sequences similar to that obtained for BG11G2ASP2 specimen could clarify this situation. The BLAST comparison showed a maximum identity value of 99% with *A. melanoasper*.

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SUPLEMENTARY TABLES

Table 1 Supplement. Morphometric characters of *Apristurus* species (% TL) caught in the Galicia Bank. *A. aphyodes* values grouped by sex and respective mean and standard deviation (± SD) included. Values of t-test included; characters significantly different ($p<0.05$) are marked (*).

Morphometriccharacter	*A. prof.*	*A.melan.*	*A. aphyodes*				Significantly different
	Female	Female	Male (n=6)	Female (n=8)	t-value	p	p<0.05
1. Total length (cm)	14.6	25.0	28.3 ± 5.9	27.0 ± 4.6			
2. PreD2-insertion	63.0	69.2	67.3 ± 1.4	67.4 ± 1.3	-0.054	0.958	
3. PreD2-origin	56.8	60.4	61.7 ± 1.3	61.8 ± 1.4	-0.083	0.935	
4. PreD1-insertion	47.9	54.4	53.2 ± 1.4	54.7 ± 1.0	-2.454	0.030	*
5. PreD1-origin	45.2	49.2	47.3 ± 1.0	49.0 ± 1.0	-3.162	0.008	*
6. PreP1 length	22.6	22.4	23.1 ± 1.0	25.1 ± 0.7	-4.533	0.001	*
7. PreP2 length	38.4	43.6	43.2 ± 0.8	44.6 ± 0.6	-3.626	0.003	*
8. Pre-ventlength	44.5	48.0	46.4 ± 0.7	48.1 ± 1.0	-3.429	0.005	*
9. Preanal fin length	50.7	55.6	54.5 ± 1.6	55.2 ± 1.4	-0.858	0.408	
10. Precaudallength	64.4	70.8	68.1 ± 0.9	68.7 ± 1.0	-0.981	0.346	
11. PG1= Prebranchiallength	16.4	18.0	18.8 ± 0.6	19.8 ± 0.6	-2.967	0.012	*
12. Pre-spiracularlength	14.4	14.6	14.8 ± 0.9	15.7 ± 0.8	-1.800	0.097	
13. POB= Preorbitallength	10.3	10.8	10.4 ± 0.8	11.0 ± 0.9	-1.504	0.158	
14. Pre-outernostril	4.1	4.6	4.9 ± 0.6	5.6 ± 0.6	-2.226	0.046	*
15. Pre-innernostril	5.8	8.0	7.8 ± 0.5	8.3 ± 0.4	-2.245	0.044	*
16. POR= Pre-oral length	5.5	9.2	8.4 ± 0.4	9.1 ± 0.5	-2.589	0.024	*
17. HDL= Head length	21.2	22.0	23.6 ± 0.6	24.3 ± 0.5	-2.251	0.044	*
18. Head height (5º gill)	8.2	7.4	7.5 ± 0.9	7.8 ± 1.1	-0.555	0.589	
19. Head width (mouthcorners)	11.0	8.4	11.1 ± 0.7	11.3 ± 0.6	-0.416	0.685	
20. Head width (max.)	11.6	12.8	11.8 ± 0.7	12.2 ± 0.7	-1.098	0.294	
21. Mouthwidth MOW	11.0	8.0	9.8 ± 1.0	9.1 ± 1.0	1.209	0.250	
22. Mouthlength MOL	7.5	4.2	4.9 ± 0.7	5.3 ± 0.5	-1.439	0.176	
23. Internarialwidth(	5.1	4.0	4.1 ± 0.2	4.4 ± 0.4	-1.657	0.123	
24. Upper labial furrowlength	2.7	3.0	2.8 ± 0.5	3.0 ± 0.7	-0.748	0.469	
25. lower labial furrowlength	5.1	2.4	4.2 ± 0.6	4.2 ± 0.5	0.075	0.942	
26. Orbiteyelength	2.7	3.4	3.5 ± 0.5	3.9 ± 0.4	-1.575	0.141	
27. Orbitheightlength	2.4	1.8	1.4 ± 0.2	1.8 ± 0.3	-2.589	0.024	*
28. Oblique length of nostrils	3.8	4.6	3.0 ± 0.3	3.5 ± 0.4	-2.149	0.053	
29. Nostri-mouthspace	1.2	2.0	1.6 ± 0.3	1.8 ± 0.4	-1.126	0.282	
30. INO= Interorbitalwidth	9.2	7.8	7.2 ± 0.6	7.6 ± 0.4	-1.587	0.139	
31. 1º gillheight	2.1	2.0	2.1 ± 0.9	2.4 ± 0.7	-0.728	0.480	
32. 3º gillheight	2.7	2.0	2.5 ± 0.8	2.8 ± 0.3	-0.982	0.346	
33. 5º gillheight	2.1	1.6	2.3 ± 0.8	2.4 ± 0.3	-0.471	0.646	
34. Interdorsalspace	6.8	8.0	8.2 ± 1.3	7.8 ± 0.7	0.771	0.456	
35. D1-D2 origins	11.0	14.8	14.3 ± 0.8	13.8 ± 0.9	0.961	0.355	
36. D1-D2 insertions	14.4	14.4	14.4 ± 1.1	13.7 ± 1.0	1.173	0.263	
37. P1-P2 space	11.3	16.4	13.9 ± 0.6	13.1 ± 1.5	1.252	0.234	
38. P1 tip to P2 origin	8.9	12.4	8.5 ± 1.0	7.7 ± 1.5	1.059	0.311	
39. P1-P2 origins	16.1	21.2	19.5 ± 1.0	19.7 ± 1.5	-0.168	0.870	
40. P1-P2 insertions	17.1	23.2	19.2 ± 1.9	18.7 ± 1.9	0.440	0.668	
41. P2- Anal space	4.8	4.0	4.7 ± 1.3	4.4 ± 0.6	0.619	0.547	
42. P2- anal origins	10.6	11.2	12.1 ± 0.9	12.2 ± 1.0	-0.046	0.964	
43. D1 length	6.2	8.4	8.6 ± 1.1	9.3 ± 0.5	-1.647	0.125	
44. D1 base length	4.8	6.0	5.6 ± 0.4	5.9 ± 0.6	-1.110	0.289	
45. D1 height	2.1	2.4	2.5 ± 0.3	2.6 ± 0.2	-0.307	0.764	

46. D1 free lobelength	2.7	2.8	4.0 ± 0.5	3.8 ± 0.3	0.921	0.375
47. D2 length	7.9	8.4	9.3 ± 0.8	9.8 ± 0.4	-1.597	0.136
48. D2 base length	5.5	5.2	5.8 ± 0.3	6.1 ± 0.3	-1.973	0.072
49. D2 height	2.7	3.0	2.9 ± 0.4	3.0 ± 0.3	-0.661	0.521
50. D2 free lobe	3.4	3.8	4.3 ± 0.7	4.3 ± 0.2	-0.265	0.796
51. P1 base length	5.8	6.4	6.5 ± 0.5	6.3 ± 0.4	0.830	0.422
52. P1 anterior margin	6.2	8.4	10.7 ± 0.6	10.0 ± 0.8	1.617	0.132
53. P1 posterior margin	5.8	4.8	5.0 ± 0.3	5.4 ± 0.7	-1.139	0.277
54. P1 innermargin	3.1	5.6	5.9 ± 0.4	6.1 ± 0.5	-0.698	0.499
55. P1 width	4.8	6.2	6.2 ± 0.6	6.1 ± 0.6	0.484	0.637
56. P2 anterior margin	3.8	5.6	4.7 ± 1.0	5.1 ± 1.1	-0.875	0.399
57. P2 length	6.8	8.4	8.7 ± 0.6	8.3 ± 0.7	0.842	0.416
58. P2 base	6.2	5.6	5.6 ± 1.4	5.3 ± 1.2	0.557	0.588
59. P2 posterior margin	3.8	3.6	4.5 ± 0.9	4.6 ± 0.8	-0.125	0.903
60. P2 innermargin	1.4	1.8	3.1 ± 0.5	2.5 ± 0.6	1.858	0.088
61. Anal base length (ceratotr.)	13.7	13.6	12.3 ± 1.4	12.6 ± 0.3	-0.696	0.500
62. Anal base length (muscle)	14.4	14.8	12.9 ± 2.0	14.3 ± 1.8	-1.348	0.203
63. Anal anterior margin	7.2	8.8	9.4 ± 1.2	8.9 ± 1.4	0.605	0.556
64. Anal posterior margin	7.9	6.8	6.3 ± 1.3	6.0 ± 0.5	0.622	0.546
65. Anal height	2.1	3.8	4.4 ± 0.6	4.5 ± 1.0	-0.207	0.839
66. Anal innermargin	0.2	0.2	1.5 ± 0.4	1.3 ± 0.6	0.645	0.531
67. Caudal peduncleheight	4.1	4.0	3.6 ± 0.5	3.7 ± 0.4	-0.665	0.519
68. Caudal length CDM	36.3	30.0	31.4 ± 1.0	31.1 ± 1.7	0.427	0.677
69. Caudal height	6.8	6.6	7.0 ± 0.7	7.1 ± 0.9	-0.208	0.839
70. Caudal ventral margin	13.7	10.8	8.9 ± 0.7	9.5 ± 1.3	-1.074	0.304
71. Caudal postventralmargin	13.7	15.2	17.6 ± 1.1	16.8 ± 1.0	1.285	0.223
72. Caudal terminal lobeheight	2.4	2.8	2.1 ± 0.3	2.4 ± 0.4	-1.887	0.084
73. Caudal terminal lobelength	6.2	5.6	5.1 ± 0.9	5.2 ± 0.3	-0.311	0.761

Table 2 Supplement. Comparison of some morphometric measurements between selected paratypes of *A. aphyodes* (Nakaya and Stehmann, 1998) and specimens from this study. Values expressed as percentage of total length.

Morphometric character	Present study (N=14, M=6; F=8)		Nakaya&Stehmann (N=20, M=10; F=10)	
	Mean	SD	Min	Max
1. Total length (cm)	27.5	± 5.03	20.9	54.0
3. PreD2-origin	61.8	± 1.27	59.4	67.2
5. PreD1-origin	48.3	± 1.24	44.4	52.6
6. PreP1 length	24.3	± 1.32	22.2	25.0
9. Preanal fin length	54.9	± 1.41	50.6	60.8
10. Precaudallength	68.4	± 1.08	66.8	72.9
11. PG1= Prebranchiallength	19.4	± 0.82	19.1	22.5
13. POB= Preorbitallength	10.7	± 0.80	9.9	12.7
14. Pre-outernostril	5.3	± 0.67	4.0	6.4
16. POR= Pre-oral length	8.8	± 0.53	7.7	9.8
17. HDL= Head length	24.0	± 0.76	23.5	25.8
19. Head width (mouthcorners)	11.2	± 0.91	10.4	13.5
21. Mouthwidth MOW	9.4	± 1.03	8.4	11.0
23. Internarialwidth	4.3	± 0.36	4.0	4.7
24. Upper labial furrowlength	2.9	± 0.55	1.8	3.1
25. lower labial furrowlength	4.2	± 0.66	2.6	3.8
26. Orbiteyelength	3.7	± 0.42	3.0	3.5
28. Oblique length of nostrils	3.3	± 0.52	2.7	3.6
30. INO= Interorbitalwidth	7.5	± 0.47	6.6	8.2
31. 1º gillheight	2.2	± 0.69	1.6	2.7
32. 3º gillheight	2.6	± 0.54	1.8	3.2
33. 5º gillheight	2.3	± 0.51	1.3	2.3
34. Interdorsalspace	8.0	± 0.89	5.8	8.8
35. D1-D2 origins	14.0	± 0.79	12.6	15.7
37. P1-P2 space	13.4	± 1.38	11.2	18.3
39. P1-P2 origins	19.6	± 1.23	18.3	25.3
44. D1 base length	5.7	± 0.48	6.0	7.6
45. D1 height	2.5	± 0.22	2.2	3.3
48. D2 base length	5.9	± 0.37	6.1	7.5
49. D2 height	3.0	± 0.32	2.8	3.5
52. P1 anterior margin	10.3	± 0.84	8.5	12.2
57. P2 length	8.5	± 0.63	8.0	11.0
62. Anal base length (muscle)	13.7	± 1.82	12.5	14.5
65. Anal height	4.4	± 0.81	3.7	6.1
67. Caudal pedunclehеight	3.6	± 0.42	4.0	4.8
68. Caudal length CDM	31.2	± 1.33	26.7	33.6

Table 3 Supplement. Comparison of some morphometric measurementsfrom *A. profundorum* holotype (Goode & Bean, 1896), based on original description of Murray & Hjort (1932) (B) and the specimen caught in Galicia Bank following the character description of Nakaya et al. (2008) (A). In both cases values are expressed as percentage of total length.

Morphometric character description		This study	Goode&Bean 1896
A) Nakayaet al., 2008	B) Murray &Hjort, 1932		
Total length (cm)	Total length (cm)	14.6	52.0
Sex	Sex	Female	Male
PreD1-insertion	Snout to 1st dorsal fin	47.9	50.2
Pre-vent length	Snout to ventral fin	44.5	43.8
Preanal fin length	Snout to anal fin	50.7	58.6
Preorbital length	Length of snout	10.3	11.0
Pre-oral length	Distance from tip snout to upper jaw	5.5	8.7
Head length (HL)	Head length	21.2	24.2
HL-Prebranchial length	Distance 1ª to 5º branchial slit	4.8	4.6
Mouth width	Mouth width	11.0	8.5
Internarial width	Distance between nasal cavities	5.1	4.3
Orbit eye length	Horizontal diameter of eye	2.7	3.1
Nostril-mouth space	Nasal cavity to upper jaw	1.2	2.2
Interorbital width	Interorbital space	9.2	8.7
3º gill height	Height of 3rdbranchial slit	2.7	2.0
Interdorsal space	Distance between 1st and 2nd dorsal fins	6.8	8.7
D1 base length	Basis of 1st dorsal	4.8	6.3
D2 base length	Basis of 2st dorsal	5.5	6.3
Pelvic base length	Ventral fin basis	6.2	8.7
Anal base length	Basis of anal fin	13.7	12.4

Table 4 Supplement.Comparison of main morphometric measurements, *A. melanoasper*, based on Iglesias et al. (2004) study and the single specimen caught in Galicia Bank. Values expressed as percentage oftotal length. Numbers in brackets refer to the corresponding morphometric character description (see Table 2) based on Nakaya et al. (2008).

Morphometric character	Iglesias et al., 2004 (N=53, M=36; F=17)		Present study
	Mean	SD	N=1
Snout tip to D_2 origin (3)	64.1	± 1.9	60.4
Snout tip to D_1 origin (5)	49.2	± 1.5	49.2
Snout tip to P_2 origin (7)	45.6	± 1.8	43.6
Snouttipto cloaca (8)	50.3	± 1.5	48.0
Snout tip to anal origin (9)	56.8	± 1.9	55.6
Snout tip to 1st gill opening (11)	18.2	± 1.7	18.0
Snouttiptoeye (13)	9.7	± 1.2	10.8
Snout tip to anterior nostril (14)	4.1	± 0.4	4.6
Snout tip to posterior nostril (15)	6.8	± 0.8	8.0
Snouttiptomouth (16)	8.6	± 1.0	9.2
Snout tip to 5th gill opening (17)	21.9	± 1.5	22.0
Head width (20)	11.0	± 1.1	12,8
Mouthwidth (21)	7.9	± 0.8	8.0
Internarialspace (23)	3.6	± 0.4	4.0
Lengthupper labial furrow (24)	3.5	± 0.3	3.0
Lengthlower labial furrow (25)	2.2	± 0.3	2.4
Eye horizontal diameter (26)	3.0	± 0.3	3.4
Nostrildiameter (28)	3.5	± 0.5	4.6
Distance between nostril and mouth (29)	2,0	± 0.3	2.0
Interorbitalspace (30)	6.8	± 0.7	7.8
Length 1stgillopening (31)	1.4	± 0.2	2.0
Length 3rd gillopening (32)	1.5	± 0.3	2.0
Length 5thgillopening (33)	1.3	± 0.2	1.6
Distancebetween D bases (34)	8.5	± 0.9	8.0
Distancebetween D insertions (36)	14.7	± 0.7	14.4
Distance between P insertion and V origin (37)	17.5	± 2.1	16.4
Distance between P tip and V origin (38)	12.4	± 1.9	12.4
Distance between P and V origins (39)	24.5	± 1.9	21.2
Distance between V and A insertions	18.3	± 1.2	19.2
Distance between V insertion and A origin (37)	4.4	± 1.0	4.0
1st D overalllength (43)	10.1	± 0.8	8.4
1st D height (45)	2.5	± 0.3	2.4
2nd D overalllength (47)	9.7	± 0.5	8.4
2nd D height (49)	2.8	± 0.2	3.0
P1 anterior marginlength (52)	11.5	± 1,0	8.4
Pectoral width (55)	6.8	± 0.6	6.2
Ventral overalllength (57)	10	± 0.8	8.4
Anal base length (62)	14.4	± 0.9	14.8
Caudal peduncleheight (67)	4.3	± 0.2	4.0
Caudal lowermargin (68)	29.3	± 1.5	30.0

Table 5 Supplement. Estimates of evolutionary divergence between sequences obtained by Maximum Composite Likelihood method (below diagonal). Standard error estimates were obtained by 1,000 bootstrap replicates (above diagonal).

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1.BG11V7ASP1		0.023	0.023	0.023	0.023	0.023	0.023	0.023	0.023	0.023	0.049	0.023	0.023	0.021	0.021	0.026
2.BG11G5ASP1	0.086		0.002	0.002	0.003	0.002	0.002	0.002	0.002	0.002	0.053	0.002	0.002	0.002	0.002	0.008
3.BG11T5ASP1	0.084	0.002		0.000	0.002	0.002	0.000	0.000	0.000	0.000	0.053	0.000	0.000	0.002	0.002	0.008
4.BG11G9AAP1	0.084	0.002	0.000		0.002	0.002	0.000	0.000	0.000	0.000	0.053	0.000	0.000	0.002	0.002	0.008
5.BG11G10AAP1	0.082	0.003	0.002	0.002		0.002	0.002	0.002	0.002	0.002	0.053	0.002	0.002	0.002	0.002	0.009
6.BG11G2ASP1	0.085	0.003	0.002	0.002	0.003		0.002	0.002	0.002	0.002	0.052	0.002	0.002	0.002	0.000	0.009
7.BG11G9AAP3	0.084	0.002	0.000	0.000	0.002	0.002		0.000	0.000	0.000	0.053	0.000	0.000	0.002	0.002	0.008
8.BG11G9AAP4	0.084	0.002	0.000	0.000	0.002	0.002	0.000			0.000	0.053	0.000	0.000	0.002	0.002	0.008
9.BG11G9AAP5	0.084	0.002	0.000	0.000	0.002	0.002	0.000	0.000		0.000	0.053	0.000	0.000	0.002	0.002	0.008
10.BG11G9AAP6	0.084	0.002	0.000	0.000	0.002	0.002	0.000	0.000	0.000		0.053	0.000	0.000	0.002	0.002	0.008
11.BG11G2ASP2	0.199	0.202	0.200	0.200	0.197	0.200	0.200	0.200	0.200	0.200		0.053	0.053	0.048	0.047	0.056
12.BG11G2ASP3	0.084	0.002	0.000	0.000	0.002	0.002	0.000	0.000	0.000	0.000	0.200		0.000	0.002	0.002	0.008
13.BG11G9AAP2	0.084	0.002	0.000	0.000	0.002	0.002	0.000	0.000	0.000	0.000	0.200	0.000		0.002	0.002	0.008
14. BG11G9RF2	0.081	0.002	0.002	0.002	0.003	0.003	0.002	0.002	0.002	0.002	0.175	0.002	0.002		0.002	0.008
15. BG11GPRF1	0.079	0.003	0.002	0.002	0.003	0.000	0.002	0.002	0.002	0.002	0.173	0.002	0.002	0.003		0.009
16. BG11G2ASP4	0.101	0.028	0.030	0.030	0.031	0.031	0.030	0.030	0.030	0.030	0.206	0.030	0.030	0.030	0.031	

ANEXO III-1

Bañón, R., Arronte, J.C., Vázquez-Dorado, S., del Río J.L. & de Carlos, A. 2013. DNA barcoding of the genus *Lepidion* (Gadiformes: Moridae) with recognition of *Lepidion eques* as a junior synonym of *Lepidion lepidion*. Molecular Ecology Resources, 13: 189–199.

Abstract

DNA sequences of cytochrome *c* oxidase I gene (COI) from *Lepidion spp*. were employed to test the efficiency of species identification. A sample of 32 individuals from 5 *Lepidion* species was sequenced and combined with 26 sequences from other BOLD projects. As a result, 58 *Lepidion* DNA sequences of the COI gene belonging to eight of the nine recognized *Lepidion* species were analysed. Sequences were aligned and formed seven clades in a Bayesian phylogenetic tree, where *Lepidion lepidion* and *Lepidion eques* grouped jointly. The Kimura 2-parameter genetic distances, among congeners were, on average, 4.28%, 16 times greater than among conspecifics (0.27%). The main diagnostic meristic data of *Lepidion spp*. were compiled and a detailed morphological revision of the congeneric species *L. eques* and *L. lepidion* was made. The eye diameter was significantly different between *L. eques* and *L. lepidion* ($p < 0.001$). The number of anal fin rays ranged from 45 to 51 in *L. lepidion* and from 47 to 54 in *L. eques*, but no significant differences were obtained in the mean values of this variable ($p = 0.07$). According to the morphological and genetic analyses, the results strongly suggest that the Mediterranean codling *L. lepidion* and the North Atlantic codling *L. eques* are conspecific, making *L. eques* a junior synonym of *L. lepidion*.

Introduction

The morid cod family Moridae, as currently recognized, comprises 18 genera and about 110 species (Okamoto *et al*. 2007). The family Moridae was proposed on the basis of the unique swim bladder connection with the auditory capsules (Svetovidov 1937). Currently, the family is defined by the following four characters: a swim bladder-auditory capsule connection, a caudal skeleton with four or five hypurals and X-Y bones, a joined first neural spine and distinctive otoliths (Okamoto *et al*. 2007).

The genus *Lepidion* Swainson, 1838, as currently recognized, contains nine benthopelagic species, living on the continental slope and lower rise of the Atlantic, Indian and Pacific Oceans and the Mediterranean Sea. The list of nominal species within this genus includes: *Lepidion capensis* Gilchrist, 1922, the Patagonian codling *Lepidion ensiferus* (Günther, 1887), the North Atlantic codling *Lepidion eques* (Günther, 1887), *Lepidion guentheri* (Giglioli, 1880), the morid cod *Lepidion inosimae* (Günther, 1887), the Mediterranean codling *Lepidion lepidion* (Risso, 1810), the small-headed cod *Lepidion microcephalus* Cowper, 1956, *Lepidion natalensis* Gilchrist, 1922 and the Schmidt's cod *Lepidion schmidti* Svetovidov, 1936.

The genus *Lepidion* is characterized by an elongated and compressed body covered by cycloid scales, which also cover the head and the bases of the fins; a short blunt snout profile; the maxilla extending to vertical below the eye; a barbel on the chin; fine teeth in bands on both jaws; two dorsal fins narrowly separated; a first dorsal fin with a minute first ray and a filamentous, elongated second ray; a single and deeply indented anal fin; sub truncated caudal and narrow ventral fins, with the two uppermost rays long and filamentous; the anus located at about the midpoint of the body and no ventral luminous organ (Cowper 1956; Okamoto *et al*. 2009).

The description of *Lepidion* species is incomplete, based only on a few specimens or on reiterated descriptions of earlier authors. Some taxonomic inaccuracies and uncertainties still persist. Cohen *et al*. (1990) pointed out that there might be a dozen or more species whereas Paulin (1983), based on morphological similarities, suggested a reduction in the number of the nominal species to six or seven.

Revisions of the genus *Lepidion* from the North Atlantic (Templeman 1970a,b) and the Northwest Pacific Oceans (Nakaya *et al*. 1980) have been made previously. The taxonomy and distribution of *L. guentheri* (Bañón *et al*. 2010) and *L. schmidti* (Arronte *et al*. 2011), two poorly known species from the Northeast Atlantic, have recently been updated. The first study of early life stages of the genus was carried out with the morphological description of a pelagic juvenile of *L. inosimae* from the north east of Japan (Okamoto *et al*. 2009).

Interrelationships within and among morid genera still remain unsolved (Howes 1991). Based on the examination of otoliths, morids have been split into three natural groups, which possibly represent a basis for their division at the subfamily level, named ‘‘Mora”, “Pseudophycis” and ‘‘Physiculus,” plus a series of *incertae sedis* genera (Fitch & Baker 1972). In this classification, the genus *Lepidion* was grouped with the genera *Mora*, *Halargyreus* and *Antimora*, within the “Mora” group. Later on, the establishment of phylogenetic relationships among gadiform families, based on nuclear and mitochondrial data, confirmed the existence of the ‘‘Mora” group as including *Antimora*, *Lepidion* and *Halargyreus* (Roa-Varón & Ortí 2009); the genus *Mora* was excluded from this study because no samples were available.

Differences among COI mitochondrial gene sequences from distinct species can be used as a barcode (Hebert *et al*. 2003) in order to facilitate identification of species, highlight cases of range expansion for known species, flag previously overlooked species and enable identifications where traditional methods cannot be applied (Ward *et*

al. 2009). The analysis is focused on approximately 650 base pairs at the 5´end of the COI gene and the benefits in facilitating species identifications have been extensively proved for marine fish. Exceptions may occur among some species that diverged very recently or hybridise regularly. Alternatively, low barcode differences between specimens attributed to different species may indicate synonymy, i.e. single species incorrectly split into separate taxa, or misidentified specimens (Ward *et al*. 2009).

Although the DNA barcoding technique has been applied to address the characterisation of many species of fish, data from morid cods are scarce in ichthiological literature. DNA barcoding reveals the existence of a deep divergence among individuals of the slender codling *Halargyreus johnsonii* Günther, 1862 but little distinction between the congeneric violet cod *Antimora rostrata* (Günther, 1878) and the longfin cod *Antimora microlepis* Bean, 1890, suggesting that both species could be the same (Smith *et al*. 2011). A similar analysis of the common red cod *Pseudophycis bachus* (Forster, 1801) showed the presence of potentially cryptic species on either side of the Tasman Sea (Smith *et al*. 2008). As far as we know, there has not yet been a comprehensive initiative to barcode the genus *Lepidion*. So far, only COI sequences belonging to two species of this genus, *L. microcephalus* and *L. schmidti*, have been used to illustrate the phylogenetic relationships among other genera from the family Moridae (Smith *et al*. 2008, 2011).

The number and distribution of species belonging to the Moridae family still needs to be determined, and this task could be assisted by constructing a molecular phylogeny including additional specimens from the North Atlantic and Pacific Oceans (Smith *et al*. 2011). The relatively high number of species included in the genus *Lepidion* and the scarcity of specimens point to the need for a worldwide revision of the genus (Chiu *et al*. 1990).

The aim of the current paper is to revise the traditional and morphological specific composition of the genus *Lepidion* using the DNA barcoding method. The appearance of unreported distribution areas for some species of the genus is also inferred from the results of this analysis.

Materials and methods

Sample collection, species identification and morphological analysis

Table 1 List of specimens with collection details and voucher numbers

Species	Date	Location	Sample ID	BOLD specimen no.	GenBank accession no.
L. lepidion	February 2008	Balearic Basin W Mediterranean	LPJ001	MORID007-12	JX437993
			LPJ002	MORID008-12	JX437992
			LPJ003	MORID009-12	JX437991
			LPJ004	MORID010-12	JX437990
			LPJ005	MORID011-12	JX437998
			LPJ006	MORID012-12	JX437989
			LPJ007	MORID013-12	JX437994
			LPJ008	MORID014-12	JX437995
			LPJ009	MORID015-12	JX437996
			LPJ010	MORID016-12	JX437997
L. eques	August 2010	Galician Bank NE Atlantic	LPS001	MORID017-12	JX437983
			LPS002	MORID018-12	JX437982
			LPS003	MORID019-12	JX437981
			LPS004	MORID020-12	JX437980
			LPS005	MORID021-12	JX437979
			LPS006	MORID022-12	JX437978
			LPS007	MORID023-12	JX437977
			LPS008	MORID024-12	JX437976
			LPS009	MORID025-12	JX437975
			LPS010	MORID026-12	JX437974
	July 2010	Avilés Canyon NE Atlantic	LPS011	MORID027-12	JX437973
			LPS012	MORID028-12	JX437972
			LPS013	MORID029-12	JX437971
			LPS014	MORID030-12	JX437986
			LPS015	MORID031-12	JX437985
			LPS016	MORID032-12	JX437984
L. guentheri	August 2007	Gulf of Biscay NE Atlantic	LPH001	MORID001-12	JX437987
	August 2011	Galician Bank NE Atlantic	LPH002	MORID003-12	JX437988
L. schmidti	August 2007	Gulf of Biscay NE Atlantic	LPT001	MORID002-12	JX437999
L. ensiferus	December 2007	SE Atlantic	LPE001	MORID004-12	JX437969
			LPE002	MORID005-12	JX437970
			LPE003	MORID006-12	JX437968

Between 2007 and 2011, a total of 62 specimens belonging to five species of *Lepidion* were collected by commercial and research vessels at diverse localities in the Atlantic Ocean and the Mediterranean Sea (Table 1). All specimens were tentatively identified and frozen on board. Once in the laboratory, positive identifications were made according to Cohen (1986a), Templeman (1970 a,b) and Meléndez and Pequeño (1999). Due to their morphological similarities, identifications of *L. eques* and *L. lepidion* were mainly based on their catch area, Atlantic and Mediterranean, respectively. Muscle samples from 32 thawed individuals were stored in 90% ethanol

and the specimens were then fixed in 10% formalin, prior to their storage in 70% ethanol. Voucher specimens were deposited in the Centro de Experimentación Pesquera del Gobierno del Principado de Asturias, (Gijón, Spain) and in the Museo de Historia Natural da Universidade de Santiago de Compostela, (Santiago de Compostela, Spain). Photographs of specimens used in this study and DNA sequence data are available in the project entitled 'Barcoding of the genus *Lepidion'* (code MORID) on the Barcode of Life database (BOLD) at http://www. boldsystems.org.

The morphological analysis included measurements recorded to the nearest mm and meristic characters were determined according to Templeman (1970a,b). Differences in the two main distinctive characters, the eye diameter (as percentage of the head length) and the number of the anal fin rays between *L. eques* and *L. lepidion* were tested with general linear models (GLM) in R (R Development Core Team, 2011). In addition, differences in these two variables were investigated between the different locations of *L. eques* with GLM. For the eye diameter, only data from the present study were used, whereas for the analysis of anal fin rays, data from Templeman (1970a,b) were also included.

DNA extraction, PCR amplification and sequencing

DNA was extracted from samples of muscle tissues taken from reference specimens by means of the DNA Blood and Tissue Extraction Kit from QIAGEN. The standard 5´ barcoding region of COI (ca. 650 bp) was amplified by PCR using ExTaq DNA polymerase (TaKaRa) and primers LCOI1490 and HCOI2198 (Folmer et al. 1994) with reaction conditions as follows: 3 min at 94 ºC; 35 cycles of 30 s at 94 ºC, 45 s at 55 ºC, 1 min at 72 ºC, with a final extension of 7 min at 72 ºC. The PCR products were visualised on 1.5% agarose gels (Seakem LE Agarose, Cambrex) stained with ethidium bromide. They were then purified with ExoSAP-IT (USB) following the manufacturer's instructions. Each product was sequenced in the direct and reverse senses using the same primers and the BigDye Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems). Sequencing reactions were resolved on an ABI 3130 Genetic Analyzer and the consensus sequences were implemented with SeqScape v2.5.

Genetic relationships analyses

The evolutionary distances were calculated using the Kimura 2-parameter (K2P) model (Kimura 1980). The 58 sequences from the different species of the genus *Lepidion*, together with an outgroup sequence from *Halargyreus johnsonii* (BW1674_EU8) were employed to perform an alignment using MEGA5 (Tamura *et al*. 2011). To select the nucleotide substitution model that best fit the sequence data under the Bayesian criterion, ModelTest v2.4 (Posada & Crandall 1998) was used. Phylogenetic relationships were explored with the neighbour-joining method using the HKI+I nucleotide substitution model (Hasegawa *et al*. 1985) with MEGA5. To estimate the reliability of the constructed phylogenetic tree, a non-parametric bootstrap analysis (Felsenstein 1985) was carried out using 1000 replicates. The Bayesian phylogenetic analysis using the HKI+I nucleotide substitution model was conducted with the program MrBayes 3.2 (Ronquist & Huelsenbeck 2003). Four simultaneous Markov chains Monte Carlo (MCMC) were run for one million generations, saving the current tree every 1000 generations. A 50% majority-rule consensus tree was created with a burn-in value of 1000 (i.e. the first 1000 trees were discarded). The phylogenetic tree was edited using the program TreeGraph 2 (Stöver & Müller 2010).

Results

Genetics

A total of 32 COI DNA sequences were obtained from different species of the genus *Lepidion*: *L. ensiferus* (3 sequences), *L. eques* (16 sequences), *L. guentheri* (2 sequences), *L. lepidion* (10 sequences) and *L. schmidti* (1 sequence). A further 26 barcodes were obtained from the BOLD database: *L. capensis* (5 sequences), *L. ensiferus* (3 sequences), *L. inosimae* (3 sequences), *L. microcephalus* (8 sequences) and *L. schmidti* (7 sequences). A complete dataset of 58 sequences from 8 of the 9 currently recognized species with a uniform length of 651 positions was obtained. Unfortunately, samples of *L. natalensis* were not available for analysis.

A Bayesian tree derived from *Lepidion* COI sequences showed seven well-supported DNA clades among the sampled species (Fig. 1). All assemblages of conspecific individuals were grouped in separate clades with high bootstrap and posterior probability values, with the exception of *L. eques* and *L. lepidion*, which were grouped together. Molecular analysis of the COI gene showed that some samples that had previously been identified as a species by morphological similarities actually had a

higher genetic similarity with other species. This occurred in the case of one sequence of *L. inosimae*, which clustered with *L. guentheri* sequences, one *L. schmidti* that grouped with *L. inosimae* sequences, and four *L. microcephalus* relocated with the *L. ensiferus* sequences.

Distance matrices for intra- and interspecific variation among COI sequences for the species of *Lepidion* are provided in Table 2. The genetic distance using the K2P model over all sequence pairs within and between species and their ranges are shown. Because of the existence of sufficient difference between intraspecific and interspecific genetic distance values, DNA barcoding was able to assign every *Lepidion* individual to a particular species. The average intraspecific genetic distance was 0.27% and the average genetic distance among *Lepidion* species rose to 4.28%. The lowest distance occurred between *L. ensiferus* and *L. capensis* (1.89%) and the highest between *L. eques* and *L. microcephalus* (6.29%). The small distance value observed between *L. eques* and *L. lepidion* (0.29%) constituted an exception. Overall, the average of genetic distances among congeners was 16-fold higher than among conspecifics.

Morphology and meristic traits

A bibliographic compilation of the main meristic characters of the nominal species of the genus *Lepidion* is presented in Table 3. Most of the species show an extensive overlap in the magnitude of the meristic variables analyzed. A comparison of the morphometric measurements and meristic features of *L. eques* from Atlantic waters and *L. lepidion* from the Mediterranean Sea is given in the Table 4. Significant differences were found in mean eye diameter between both species ($n = 92$, $F = 36.12$, $p < 0.001$). However, the comparison of the anal fin rays counts between *L. eques* and *L. lepidion* resulted in non significant differences ($p = 0.07$). In *L. eques*, significant differences were found in eye diameter between specimens from the Galician Bank and the Aviles Canyon ($n = 36$, $F = 4.71$, $p = 0.037$). No significant differences were found, however, in the number of anal fin rays between the five locations analysed ($p = 0.711$).

The frequency distribution of three meristic characters from both species in the Mediterranean Sea and from different areas of Atlantic Ocean is given in Table 5. The previous known ranges of most of the characters measured were enlarged for both species. In addition, an overlap of all measurements and counts was found and a

latitudinal gradient in the meristic data of *L. eques* from Atlantic waters was also apparent.

Discussion

According to present knowledge, the species of the genus *Lepidion* have, in general terms, moderate distribution areas (Table 1), and none of the *Lepidion* species has a worldwide distribution. Conversely, many deep-water fish species have very broad global distributions (Grey 1956). In this sense, it has previously been stated that a worldwide revision of *Lepidion* might reduce the number of species belonging to this genus (Paulin 1983).

Analysis of COI sequences can reveal differentiation at fine taxonomic levels in a wide diversity of taxonomic groups. In marine fish, around 98% of the species tested to date can be distinguished by COI barcodes (Ward *et al*. 2009). The typical divergence for COI sequences found in marine fish is characterized by low intraspecific (<0.5%) and higher intra-generic values (>4%) (Smith *et al*. 2011), although these values may vary among taxa. The low average intraspecific genetic distance within the genus *Lepidion* (0.27%) is in accordance with most of the values previously found in fish species. The same parameter in all projects of the Fish Barcode of Life campaign (FISH-BOL) initiative (http://www.fishbol.org), which includes nearly 50,000 sequences obtained from over 7,000 species, was 0.3% (Zhang & Hanner 2011). The average conspecific distance between fifty-one shark specimens from the Egyptian Mediterranean was 0.35% (Moftah *et al*. 2011). Similar values were attained from the study of 229 DNA sequences of fish from Japan (0.3%) (Zhang & Hanner 2011) and from 321 sequences belonging to 121 species of fish from China (0.319%) (Zhang 2011).

The fact that the DNA sequences of specimens identified as *L. lepidion* clustered tightly together with those identified as *L. eques* constituted the most interesting result. Specimens of *L. lepidion* and *L. eques* showed very low interspecific divergences, averaging 0.29%. This is typical of differentiation within a single species (Ward *et al*. 2005), suggesting that the 26 sequences analysed belong to the same species.

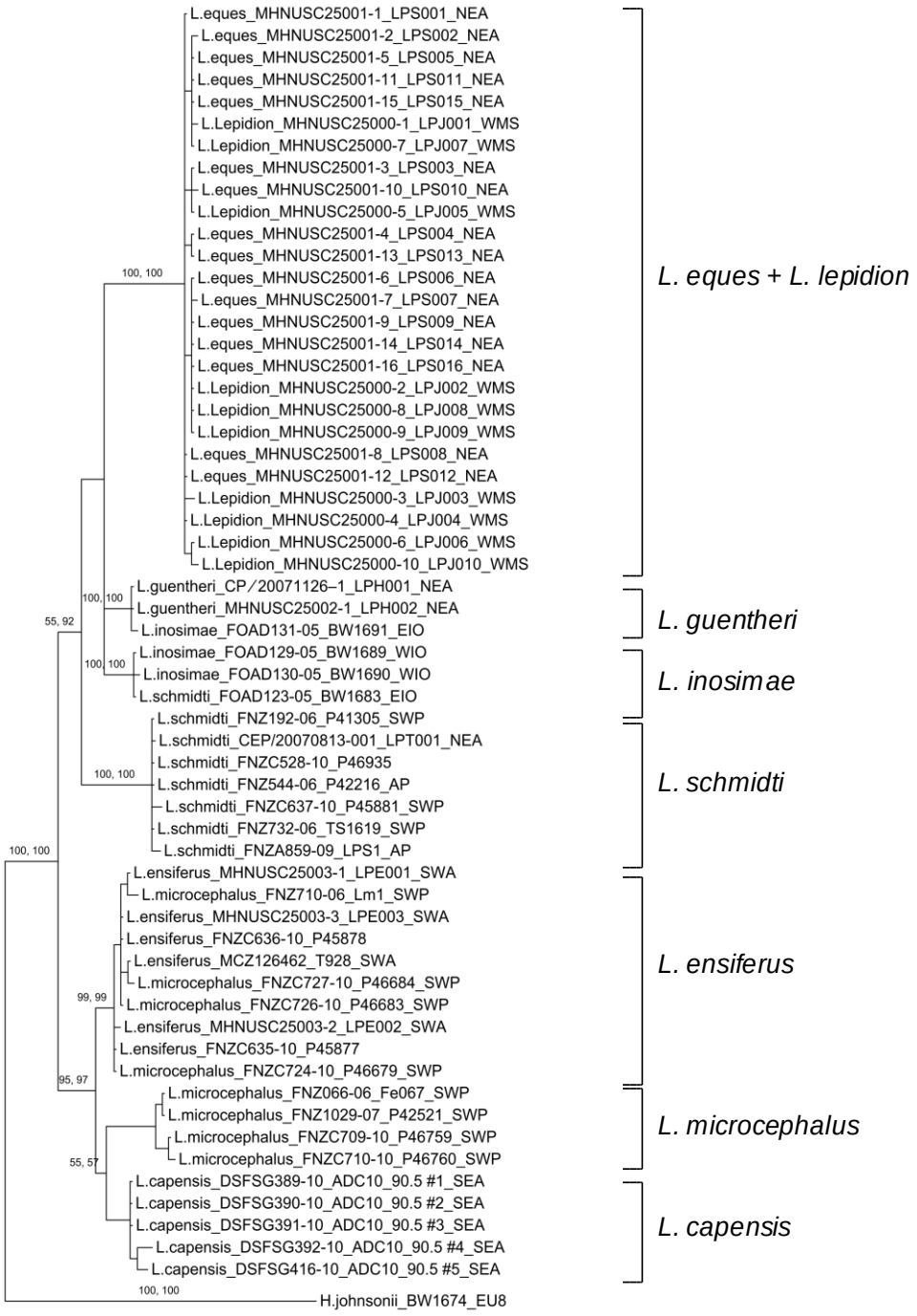

Fig. 1 Bayesian phylogenetic tree of Lepidion sp. COI sequences based on the HKI+I nucleotide substitution model. For each specimen a code followed by a location abbreviation (SWA, Southwest Atlantic; SEA, Southeast Atlantic; NEA, Northeast Atlantic; WMS, Western Mediterranean; SWP, Southwest Pacific; AP, Antarctic Pacific; EIO, Eastern Indian Ocean; WIO, Western Indian Ocean) was given. Additional voucher specimens were deposited in the Museum of New Zealand Te Papa Tongarewa (FNZC), National Institute of Water and Atmospheric Research (FNZ), CSIRO, Australian National Fish Collection (FOAD) and South African Institute for Aquatic Biodiversity (DSFSG). The tree has been rooted with the morid outgroup Halargyreus johnsonii (BW1674_EU8). Numbers at main nodes are

bootstrap percentages after 1000 replicates, based on genetic distances and Bayesian posterior probability values.

Table 2 Estimates of genetic distance over sequence pairs within and between *Lepidion* species using the Kimura 2-parameter model of nucleotide substitution.

		Between species						
Species (n)	**Within species**	*L. capensis*	*L. ensiferus*	*L. eques*	*L. guentheri*	*L. inosimae*	*L. lepidion*	*L. microcephalus*
L. capensis (5)	**0.40** (0-0.77)							
L. ensiferus (10)	**0.31** (0.15-0.77)	**1.89** (1.56-2.51)						
L. eques (16)	**0.26** (0-0.46)	**5.39** (4.18-6.16)	**4.82** (4.30-5.48)					
L. guentheri (3)	**0.10** (0-0.15)	**3.86** (3.64-4.29)	**3.69** (3.48-3.80)	**3.99** (3.81-4.30)				
L. inosimae (3)	**0.10** (0-0.15)	**4.19** (3.98-4.47)	**3.77** (3.48-4.14)	**4.02** (3.82-4.32)	**1.98** (1.87-2.19)			
L. lepidion (10)	**0.33** (0.15-0.62)	**5.42** (4.98-6.19)	**4.86** (4.47-5.48)	**0.29** (0-0.62)	**4.03** (3.81-4.30)	**4.04** (3.82-4.32)		
L. microcephalus (4)	**0.39** (0-0.62)	**2.70** (2.51-3.16)	**2.50** (2.19-2.99)	**6.29** (6.00-6.85)	**5.14** (4.97-5.46)	**5.21** (4.97-5.47)	**6.26** (6.00-6.85)	
L. schmidti (7)	**0.23** (0-0.46)	**4.53** (4.15-5.15)	**4.78** (4.31-5.15)	**5.90** (5.49-6.53)	**3.62** (3.48-3.97)	**4.51** (4.31-4.98)	**5.98** (5.66-6.70)	**6.18** (5.83-6.68)

Table 3 Bibliographic compilation of the main meristic characters of nominal species of the genus *Lepidion*.

Meristic: D2 second dorsal fin rays, A anal fin rays, GR gill rakers, P pectoral fin rays

Distribution: M Mediterranean, NA North Atlantic, NP North Pacific, OA off South Africa, SA South Atlantic, SP South Pacific

Species	D2	A	GR	P	Distribution	Source
L. inosimae	55–60	48–55	3–5 + 8–12 (11-17)	21-23	NP, SP	Nakaya et al (1980); Paulin (1984) ; Paulin and Roberts (1997)
L. guentheri	51–58	46–53	4-6 + 16–19 (20-25)	19-22	NA, M	Templeman (1970); Cohen (1986a) ; Bañón et al (2010)
L. schmidti	46–51	36–45	3–6 + 7–15 (10-21)	21-24	NA, NP, SP	Nakaya et al (1980); Paulin (1984, 1990); Arronte et al (2011)
L. capensis	50–56	43–49	4–5 + 9–13 (13-18)	20-24	OA, SA	Cohen (1986b); Lloris (1986); Trunov (1992)
L. ensiferus	50–56	42–49	5–6 + 9–13 (14-19)	23-24	SA	Nakamura (1986); Cohen et al (1990); Meléndez and Pequeño (1999)
L. natalensis	54–59	48-52	4–5 + 12–15 (16-20)	21-23	OA, SA	Cohen (1986b); Trunov (1992)
L. eques	55–60	50–54	5–6 + 13–16 (18-22)	21-25	NA	Templeman (1970); Cohen (1986a)
L. lepidion	54–59	48–51	5–6 + 13–16 (18-22)	21-24	M	Templeman (1970); Cohen (1986a)
L. microcephalus	49-56	40-46	3–5 + 8–15 (11-20)	17-23	SP	Cowper (1956); Paulin (1983, 1990)

Table 4 Comparison between measurements and meristic features of *L. eques* from Atlantic waters and *L. lepidion* from the Mediterranean Sea.

	L. eques				*L. lepidion*			
Character	Range	n	mean	SD	Range	n	mean	SD
Total Length (mm)	170-355	36			135-217	20		
As %HL								
Eye diameter	29.0-37.8	36	34.1	2.2	27.6-35.3	20	30.7	1.8
Preorbital length	20.8-28.6	36	23.8	2.0	17.6-25.0	20	22.8	1.9
Postorbital length	38.8-44.7	36	42.2	1.3	44.4-51.3	20	46.5	1.6
Interorbital length	15.4-21.9	36	19.0	1.7	17.8-25.8	20	20.6	2.1
Barbel length	11.3-19.4	36	15.6	1.9	14.6-22.6	19	19.0	2.5
As %SL								
Head length	19.4-23.9	36	21.9	1.0	21.2-25.3	20	23.6	1.1
2nd Predorsal length	23-27	36	25.1	1.1	26.1-29.3	20	28.1	0.9
2nd Dorsal base length	63.5-68.8	36	65.8	1.5	61.1-65.9	20	63.5	1.3
Anal base length	43.2-51.2	36	48.0	1.7	43.4-48.8	20	46.2	1.6
Caudal peduncle length	2.4-5.9	36	4.4	0.7	2.9-7.0	20	4.4	1.0
Pectoral length	12.6-17.5	36	15.3	1.2	9.7-17.4	17	14.4	2.2
Ventral length	10.2-14.8	36	12.9	1.1	9.1-19.8	20	15.9	2.5
Body depth	14.5-23.4	36	19.1	2.4	15.7-22.8	20	18.8	2.1
Meristic features								
1st Dorsal fin rays	4-5	36	4.4	0.5	4–5	20	4.7	0.4
2nd Dorsal fin rays	51-59	36	55.9	1.9	53-57	20	55.1	1.2
Anal fin rays	47-54	36	50.2	1.6	45-51	20	48	1.5
Ventral fin rays	7-8	36	7.8	0.4	7–8	20	7.8	0.4
Pectoral fin rays	19-24	36	22	1.0	20-23	20	21.8	0.7
Gill rakers	18-21	36	19.6	1.0	18-23	20	20.1	1.1

In marine fish species, interspecific variation in terms of genetic distance is generally much higher than intraspecific variation, such that COI sequences may help to discriminate among species. The interspecific genetic distance within the genus *Lepidion* was 4.28%. The lowest average divergence between pairs of congeneric species were 1.89% (range 1.56-2.51) for *L. ensiferus* and *L. capensis* and 1.98% (range 1.87-2.19) for *L. guentheri* and *L. inosimae*. These values were slightly lower than the 2% suggested as the minimal genetic distance value demanded for species discrimination (Hebert *et al*. 2003, 2004). However, as pointed out by Ferguson (2002), interspecific levels of divergence are variable among taxa, and a generalized 2% rule cannot be applied to all species. Congeneric pairs in groups with normal rates of mitochondrial evolution that show less than 2% divergence probably reflect short histories of reproductive isolation. Some additional cases of low divergence may simply be artefacts generated by flawed identifications, but other cases of congruence will undoubtedly reflect mitochondrial introgression (Hebert *et al.* 2003). In fact, *circa* 15%

of more than 5,000 barcoded fish species have congeneric distances <2.8% and 3.4% have distances <1%, indicating clearly that, there is no absolute distance value that can be employed as a hard criterion so that values above indicate interspecific divergence, while those below are intraspecific (Ward *et al*. 2009). Thus, divergence averages of 1.11% were obtained within the genus *Thunnus*, 4.17% within the genus *Squalus* (Ward *et al*. 2005) and 15.742% within genera of marine fishes from China (Zhang 2011). These differences among genera probably reflect the average age of species divergence, although within genera some species would be older than others (Ward *et al*. 2005).

Overall, the average genetic distance among congeneric species was 16-fold higher than that of individuals within species. As a consequence of the variability within genera, this metric also showed a great variability among taxa. The congeneric genetic distance in all projects registered in the FISH-BOL database, containing over 7,000 species, is at least 30-fold higher than the conspecific one (Zhang & Hanner 2011). In ornamental fishes, the average genetic distance between congeneric species was approximately 26-fold higher than the within species variation (Steinke *et al*. 2009). In coral reef fish larvae of the families Acanthuridae and Holocentridae, the divergence among congeneric species was, on average, 20 to 87-fold higher than the divergence between conspecific sequences (Hubert *et al*. 2010).

The *L. schmidti* haplotype from the NE Atlantic Ocean clustered together with the haplotypes from the Pacific Ocean. This molecular coincidence reaffirms the presence of *L. schmidti* in both oceans, as previously confirmed in a recent morphological study (Arronte *et al*. 2011). The only *L. guentheri* haplotype from the NE Atlantic Ocean clustered together with one haplotype of *L. inosimae* (FOAD131-05|BW-1691 EIO) from the South Pacific Ocean, considered here as a misidentification of *L. guentheri*. The possible presence of *L. guentheri* in the South Pacific Ocean suggests an Atlantic-Pacific distribution for this species, similar to *L. schmidti*, although this issue needs to be confirmed in future taxonomic studies.

The three haplotypes of *L. ensiferus* from the SE Atlantic Ocean clustered together with *L. ensiferus* haplotypes from the same geographic area, but also with four haplotypes of *L. microcephalus* from the SW Pacific Ocean, which were considered as misidentifications. This fact could extend the known distribution area of *L. ensiferus* to the SW Pacific Ocean.

Table 5 Comparison of three meristic characters of *L. eques* and *L. lepidion* from different geographical areas, including data from Templeman (1970a,b) denoted by an asterisk.

Species	**Area**	**2nd Dorsal fin**	**Range**	**n**	**mean**	**SD**
L. eques	NW Atlantic*		55-60	15	57.67	1.45
	Faroe Channel*		55-60	11	57.55	1.44
	W Ireland*		56-58	12	56.75	0.75
	Aviles canyon		53-59	10	56.6	1.9
	Galician Bank		51-58	26	55.6	1.8
	All areas		51-60	74	56.65	1.74
L. lepidion	Mediterranean*		54-59	13	55.31	1.65
	Balearic basin		53-57	20	55.1	1.2
	All areas		53-59	33	55.18	1.38
		Anal fin	**Range**	**n**	**mean**	**SD**
L. eques	NW Atlantic*		51-54	14	52.57	0.76
	Faroe Channel*		50-54	11	52.45	1.57
	W Ireland*		50-53	12	52.25	0.97
	Aviles canyon		49-54	10	51.2	1.6
	Galician Bank		47-53	26	49.8	1.4
	All areas		47-54	73	51.32	1.77
L. lepidion	Mediterranean*		48-51	13	49.54	1.05
	Balearic basin		45-51	20	48	1.5
	All areas		45-51	33	48.6	1.61
		Pectoral fin	**Range**	**n**	**mean**	**SD**
L. eques	NW Atlantic*		21-25	15	22.93	0.96
	Faroe Channel*		22-25	11	23	0.89
	W Ireland*		22-24	12	22.75	0.87
	Aviles canyon		21-23	10	22.3	0.67
	Galician Bank		19-24	26	21.9	1.1
	All areas		19-25	74	22.46	1.06
L. lepidion	Mediterranean*		21-24	13	22.38	0.77
	Balearic basin		20-23	20	21.8	0.7
	All areas		20-24	33	22.06	0.79

The presence of this species is well documented in the SW Atlantic Ocean, the sub-Antarctic islands of the Indian Ocean and the SE Pacific Ocean (Chiu *et al*. 1990; Meléndez & Pequeño 1999; Reyes *et al*. 2009). Therefore, it is probable that *L. ensiferus* has a circumglobal distribution in the Southern Hemisphere, and *L. ensiferus* and *L. microcephalus* are probably two sympatric species in the SW Pacific Ocean.

Morphological identification of the *Lepidion* species requires the examination of a number of features, which usually exhibit overlapping ranges, making accurate identification difficult and producing some taxonomical confusion. There is need for both a worldwide revision of the genus and a global identification key. In these cases, the natural tendency of fish taxonomists is to consult regional checklists as an aid to identification, although only a small number of species are usually included. However,

if the real distribution of the *Lepidion* species is broader than currently known, this could be a major source of potential misidentifications. For example, this seems to be the case with *L. schmidti*, a species originally described from the Pacific Ocean (Svetovidov 1936), erroneously misidentified as *L. guentheri* in the Northeast Atlantic Ocean (Forster 1968), tentatively identified two years later as correct by Templeman (1970a,b) and only recently confirmed in the latter area (Arronte *et al*. 2011). This could also be the reason for the misidentifications of *Lepidion spp*. found in the BOLD database.

The DNA barcoding results suggest the synonymy of *L. eques* and *L. lepidion*. Morphologically, the taxonomic similarity between these two species has been previously pointed out by several authors (Collett 1905, Roule 1919, Norman 1935, Grey 1956 & Raimbault 1963). In his revision of the genus, Templeman (1970a,b) stated that, in view of the great resemblances and the overlapping of meristic and mostly of the morphometric character values, both species could be considered to have a subspecific rather than a specific relationship, although, he concluded that it would be unwise to make *L. eques* a synonym of *L. lepidion.*

These taxonomic uncertainties were not taken into account in subsequent ichthyological publications (Cohen 1986a, Cohen *et al*. 1990), where *L. lepidion* and *L. eques* were still considered valid and separate species.

In the literature both species of *Lepidion* have usually been separated on the basis of the eye diameter in the head length, 3.1 to 3.6 times in *L. lepidion* and 2.6 to 3.1 times in *L. eques* and by anal fin rays counts, 48-51 in *L. lepidion* and 50-54 in *L.eques* (Cohen 1986a, Cohen *et al*. 1990). Our summary of comparative morphological and meristic data (Table 4) extends, and for most characters overlaps previously published ranges of values, invalidating them as specific diagnostic characters. For example, eye diameter is contained 2.8-3.6 times in the head in *L. lepidion* and 2.6-3.4 in *L. eques* and the number of anal fin rays are 45-51 in *L. lepidion* and 47-54 in *L. eques*. Significant differences in those two morphometric variables analysed were only found in the mean eye diameter. A significant latitudinal variation in this variable was also obtained in *L. eques*. This may reflect that the observed interspecific differences might be due to a location effect rather than to a species effect. Templeman (1970a) considered that the morphological differences found between both species may be related to the warmer and possibly also to the saltier environment of the Mediterranean Sea compared with the North Atlantic Ocean. Likewise, according to our results, it is clear the presence of a

latitudinal gradient in the meristic counts of *L. eques* within the North Atlantic Ocean (Table 5). The minimum average counts of the three meristic characters analysed were found in the southern North Atlantic Ocean (Galician Bank), gradually increased further northward. Moreover, these southern values are quite similar to the ones of the Mediterranean *L. lepidion*.

Although geographical variation of morphometric and meristic characters is well known in many fish species, they are poorly described for the genus *Lepidion*. Barlow (1961) noted that lower meristic counts were generally found in lower latitudes compared with higher latitudes. The *Lepidion* data followed the same trend, which could explain the meristic differences found between the Atlantic and Mediterranean specimens, which was erroneously used in the past to separate both species The number of counts in a given meristic character is susceptible to the effects of both the developmental stage and environmental factors, especially temperature variation with latitude (Morris 1977). In previous studies of *L. eques*, an area lying to the west of Ireland was the lowest latitude sampled (Templeman 1970a,b). Thus, in spite of suspicions about the morphological similarities between *L. eques* and *L. lepidion*, the results did not show the overlapping of characters caused by a latitudinal variation in *L. eques* entirely. As Barlow (1961) pointed out, it is essential for the progress of systematic ichthyology that the nature of the morphological variation in fishes is properly understood.

Results from historical hydrographical cruises and climatological studies suggest the existence of two veins of Mediterranean water in the NW of Spain, one on the slope between the Galician Bank and the Iberian coast and the other recirculating to the west of the Galician Bank (Ruiz-Villareal *et al*. 2006). The meristic similarities found between the Mediterranean *L. lepidion* and the Atlantic *L. eques* on the Galician Bank could be the result of both the environmental conditions of the Mediterranean water and the possibility of gene flow between these two remote areas.

The COI DNA sequencing along with the morphological and meristic analysis strongly suggests that there are no specific differences between the Atlantic *L. eques* and the Mediterranean *L. lepidion*. Therefore, we propose *L. eques* as a junior synonym of *L. lepidion*.

There has been a long controversy in the scientific community among advocates of classical morphological and modern molecular taxonomic identification for a long time (Ebach & Holdrege 2005). We agree with DeSalle *et al*. (2005), that genomic

information should be an active component of modern taxonomy, but DNA sequencing should not be the sole source of information retrieval. In this context, the combination of molecular and morphological data has become more frequent in more recent fish taxonomic studies. The combination of these two types of analyses provides more solid and reliable results, reducing the possibility of erroneous conclusions. Moreover, in our opinion, DNA barcoding represents an extraordinary resource for the development of new taxonomic hypotheses, which should be confirmed by reference to previously published and/or future ichthyological studies.

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Table S1 Biometric and meristic raw data of *L. eques* and *L. lepidion* used in the morphological analysis.

	Lepidion lepidion Balearic Basin						
BIOMETRIC	L (mm)	L (mm)	L (mm)	L (mm)	L (mm)	L (mm)	L (mm)
Total length	154	140	168	181	207	156	205
Standard length	144	132	157	167	190	143	189
Head length	35	32	38	39	48	33	46
Snout length	8	7	9	9	11	8	11
Postorbital length	16	15	17	18	22	15	21
Eye diameter	11	10	12	12	15	10	14
Interorbital length	8	6	8	7	9	7	9
$Predorsal_1$ length	34	31	40	39	45	35	46
$Predorsal_2$ length	39	36	46	46	53	41	53
$Dorsal_1$ base length	2	3	3	4	5	3	5
$Dorsal_2$ base length	94	85	98	107	119	90	119
Maxilla length	15	16	18	19	21	16	22
Anal base length	69	60	75	75	89	62	89
Pectoral length	–	16	23	–	33	17	29
Ventral length	19	12	25	25	33	23	27
Preanal length	60	58	68	74	79	65	80
Caudal peduncle Length	7	6	7	7	12	10	9
Minimum height of caudal peduncle	3	2	3	3	3	2	3
Body depth	26	22	26	34	36	26	39
Body width	12	10	14	16	24	14	18
MERISTIC							
First dorsal rays	4	4	5	5	4	5	5
Second dorsal rays	56	57	54	57	55	54	54
Anal rays	51	49	47	51	48	47	48
Pectoral rays	20	22	20	22	22	22	21
Ventral rays	7	7	8	7	8	8	8
Branchiostegal rays	7	7	7	7	7	7	7
Gillrakers in first arch	6+15	5+15	6+15	6+13	6+15	5+16	5+13

Lepidion lepidion Balearic Basin

BIOMETRIC	L (mm)	L (mm)	L (mm)	L (mm)	L (mm)	L (mm)	L (mm)
Total length	178	136	183	217	199	211	180
Standard length	167	134	175	202	184	196	162
Head length	41	32	42	45	45	48	40
Snout length	10	7	10	11	11	12	9
Postorbital length	19	15	19	20	21	22	18
Eye diameter	12	10	13	14	13	14	13
Interorbital length	8	6	9	9	8	9	9
$Predorsal_1$ length	41	33	45	50	46	49	40
$Predorsal_2$ length	49	38	51	57	53	56	46
$Dorsal_1$ base length	4	3	4	5	4	5	4
$Dorsal_2$ base length	105	85	107	128	116	123	101
Maxilla length	19	14	20	21	20	22	18
Anal base length	74	62	77	93	85	89	72
Pectoral length	23	17	17	30	23	20*	23
Ventral length	27	23	21	31	30	29	32
Preanal length	75	57	77	82	80	85	70
Caudal peduncle Length	7	7	8	8	8	9	7
Minimum height of caudal peduncle	3	2	3	3	3	4	3
Body depth	36	24	36	46	38	43	28
Body width	16	12	14	21	18	26	17
MERISTIC							
First dorsal rays	5	5	4	4	5	5	5
Second dorsal rays	56	56	54	55	55	54	54
Anal rays	48	47	49	45	48	46	48
Pectoral rays	22	22	23	22	22	22	22
Ventral rays	8	8	8	8	8	8	8
Branchiostegal rays	7	7	7	7	7	7	7
Gillrakers in first arch	6+14	5+14	6+15	5+15	6+14	6+14	6+17

Lepidion lepidion Balearic Basin

BIOMETRIC	L (mm)	L (mm)	L (mm)	L (mm)	L (mm)	L (mm)
Total length	171	159	172	145	157	135
Standard length	159	146	162	138	145	127
Head length	34	31	39	31	34	29
Snout length	6	7	8	6	8	7
Postorbital length	16	15	18	16	16	14
Eye diameter	12	9	13	9	10	8
Interorbital length	8	8	8	7	7	6
$Predorsal_1$ length	36	34	38	30	35	31
$Predorsal_2$ length	43	39	45	36	41	37
$Dorsal_1$ base length	4	4	4	4	4	3
$Dorsal_2$ base length	104	96	101	91	92	81
Maxilla length	14	14	15	12	13	11
Anal base length	77	70	76	65	65	62
Pectoral length	22	24	26	24	22	22
Ventral length	24	26	31	26	26	22
Preanal length	65	63	69	55	62	52
Caudal peduncle Length	5	5	7	4	5	4
Minimum height of caudal peduncle	3	2	3	3	2	2
Body depth	28	24	29	23	29	20
Body width	17	17	16	14	14	12
MERISTIC						
First dorsal rays	5	5	5	5	5	5
Second dorsal rays	57	56	54	56	55	53
Anal rays	50	48	47	49	45	49
Pectoral rays	22	22	22	22	23	22
Ventral rays	8	8	8	8	8	7
Branchiostegal rays	7	7	7	7	7	7
Gillrakers in first arch	6+15	6+13	6+13	6+14	6+14	6+14

Lepidion eques Galician Bank

BIOMETRIC	L (mm)	L (mm)	L (mm)	L (mm)	L (mm)	L (mm)	L (mm)
Total length	267	311	283	329	322	273	336
Standard length	245	291	265	308	296	255	312
Head length	56	64	58	68	67	61	72
Snout length	13	16	13	19	17	13	19
Postorbital length	24	27	24	28	28	27	30
Eye diameter	19	21	21	21	22	21	23
Interorbital length	12	14	11	13	14	12	14
$Predorsal_1$ length	50	63	53	69	63	60	70
$Predorsal_2$ length	60	74	65	78	72	67	78
$Dorsal_1$ base length	7	7	6	6	7	5	6
$Dorsal_2$ base length	164	188	174	199	197	163	205
Maxilla length	17	28	24	26	26	22	28
Anal base length	119	128	124	133	141	118	147
Pectoral length	37	51	43	48	46	40	52
Ventral length	29	39	33	44	41	32	42
Preanal length	100	123	109	134	121	106	124
Caudal peduncle Length	12	16	15	15	15	11	15
Minimum height of caudal peduncle	5	5	5	5	5	5	6
Body depth	49	58	59	61	66	52	70
Body width	28	38	31	36	37	31	37
MERISTIC							
First dorsal rays	4	4	4	4	4	4	4
Second dorsal rays	58	57	51	55	54	54	55
Anal rays	53	50	51	49	50	48	49
Pectoral rays	23	23	24	23	21	19	22
Ventral rays	7	7	8	7	7	8	7
Branchiostegal rays	7	7	7	7	7	7	7
Gillrakers in first arch	5+15	5+14	6+15	5+15	6+15	5+14	5+13

Lepidion eques Galician Bank

BIOMETRIC	L (mm)	L (mm)	L (mm)	L (mm)	L (mm)	L (mm)	L (mm)
Total length	355	282	279	296	290	332	304
Standard length	330	256	259	271	269	305	285
Head length	77	56	58	58	62	71	62
Snout length	22	12	13	15	17	19	15
Postorbital length	33	24	25	24	27	29	27
Eye diameter	23	20	20	19	18	23	20
Interorbital length	15	12	11	12	13	13	12
$Predorsal_1$ length	80	51	60	54	60	71	61
$Predorsal_2$ length	87	59	69	63	70	82	72
$Dorsal_1$ base length	5	6	6	6	6	7	6
$Dorsal_2$ base length	211	175	167	182	172	196	184
Maxilla length	34	23	26	24	27	31	28
Anal base length	149	128	126	130	128	142	136
Pectoral length	51	44	42	43	42	48	45
Ventral length	36	33	37	34	37	45	42
Preanal length	141	101	102	107	115	129	114
Caudal peduncle Length	18	10	12	13	12	15	13
Minimum height of caudal peduncle	6	5	5	5	5	6	5
Body depth	65	60	55	53	61	65	52
Body width	42	35	28	30	31	41	31
MERISTIC							
First dorsal rays	4	4	4	5	4	4	4
Second dorsal rays	57	56	56	58	57	53	56
Anal rays	49	49	51	49	48	49	50
Pectoral rays	21	23	23	22	21	22	21
Ventral rays	7	8	8	8	7	7	7
Branchiostegal rays	7	7	7	7	7	7	7
Gillrakers in first arch	6+14	6+15	6+15	5+13	6+14	5+13	5+13

Lepidion eques Galician Bank

BIOMETRIC	L (mm)	L (mm)	L (mm)	L (mm)	L (mm)	L (mm)	L (mm)
Total length	219	227	210	255	229	290	239
Standard length	199	210	194	236	211	268	217
Head length	42	47	38	53	46	57	48
Snout length	10	12	8	13	11	14	10
Postorbital length	18	20	16	23	20	24	21
Eye diameter	14	15	14	17	17	19	17
Interorbital length	7	9	8	9	9	11	9
$Predorsal_1$ length	41	43	41	50	49	58	48
$Predorsal_2$ length	47	53	48	61	57	66	55
$Dorsal_1$ base length	4	4	4	5	4	5	4
$Dorsal_2$ base length	132	137	127	152	134	180	142
Maxilla length	19	21	18	22	22	26	21
Anal base length	97	97	96	114	102	131	106
Pectoral length	26	33	28	35	31	37	32
Ventral length	23	27	27	32	28	34	28
Preanal length	76	84	75	94	85	109	87
Caudal peduncle Length	10	11	7	11	9	12	10
Minimum height of caudal peduncle	3	3	3	4	4	5	4
Body depth	35	42	33	43	44	55	35
Body width	19	23	16	26	22	31	20
MERISTIC							
First dorsal rays	4	4	5	5	4	5	5
Second dorsal rays	55	54	56	57	58	57	56
Anal rays	49	47	52	50	49	51	50
Pectoral rays	20	20	23	22	22	22	23
Ventral rays	8	8	8	8	8	8	8
Branchiostegal rays	7	7	7	7	7	7	7
Gillrakers in first arch	6+14	5+15	6+14	6+15	5+15	5+13	5+15

Lepidion eques Galician Bank

BIOMETRIC	L (mm)	L (mm)	L (mm)	L (mm)	L (mm)
Total length	254	194	205	248	261
Standard length	234	183	189	231	245
Head length	52	37	40	52	53
Snout length	13	8	9	12	12
Postorbital length	21	15	17	23	22
Eye diameter	18	14	14	17	19
Interorbital length	8	7	7	11	9
$Predorsal_1$ length	50	36	39	52	53
$Predorsal_2$ length	58	42	45	58	61
$Dorsal_1$ base length	5	4	4	5	5
$Dorsal_2$ base length	156	123	128	155	162
Maxilla length	23	18	18	23	23
Anal base length	116	89	94	116	118
Pectoral length	34	23	25	36	33
Ventral length	32	21	23	31	30
Preanal length	93	70	74	90	95
Caudal peduncle Length	11	9	9	10	12
Minimum height of caudal peduncle	4	3	3	4	4
Body depth	47	33	37	48	52
Body width	26	14	17	26	30
MERISTIC					
First dorsal rays	5	5	5	5	5
Second dorsal rays	52	56	57	55	57
Anal rays	52	49	52	49	49
Pectoral rays	22	22	22	21	22
Ventral rays	8	8	8	8	8
Branchiostegal rays	7	7	7	7	7
Gillrakers in first arch	6+13	5+15	6+15	5+15	5+13

Lepidion eques Aviles canyon

BIOMETRIC	L (mm)	L (mm)	L (mm)	L (mm)	L (mm)	L (mm)	L (mm)
Total length	230	272	238	230	265	275	235
Standard length	215	250	220	209	244	254	219
Head length	45	55	47	43	54	54	49
Snout length	11	12	10	10	12	12	12
Postorbital length	19	23	21	18	22	22	19
Eye diameter	15	20	16	15	20	20	18
Interorbital length	8	9	8	7	10	10	9
$Predorsal_1$ length	48	56	49	47	51	56	50
$Predorsal_2$ length	57	65	56	52	60	60	57
$Dorsal_1$ base length	5	5	4	4	5	6	6
$Dorsal_2$ base length	137	172	145	138	165	171	142
Maxilla length	17	23	20	20	27	24	21
Anal base length	107	120	103	104	125	121	105
Pectoral length	31	42	35	33	40	41	33
Ventral length	22	36	24	25	31	32	30
Preanal length	82	100	93	82	93	105	90
Caudal peduncle Length	9	10	9	8	9	9	9
Minimum height of caudal peduncle	3	3	3	3	4	4	4
Body depth	33	47	34	34	45	42	36
Body width	19	26	22	19	25	29	21
MERISTIC							
First dorsal rays	4	4	5	5	4	5	5
Second dorsal rays	57	56	58	59	58	53	54
Anal rays	51	51	51	54	53	52	49
Pectoral rays	21	22	23	22	23	22	22
Ventral rays	8	8	8	8	8	8	8
Branchiostegal rays	7	7	7	7	7	7	7
Gillrakers in first arch	5+13	5+14	6+15	5+14	6+14	5+14	6+15

Lepidion eques Aviles canyon

BIOMETRIC	L (mm)	L (mm)	L (mm)
Total length	199	193	170
Standard length	180	177	165
Head length	39	36	32
Snout length	9	9	7
Postorbital length	17	15	13
Eye diameter	13	12	12
Interorbital length	8	6	7
$Predorsal_1$ length	41	40	36
$Predorsal_2$ length	47	45	40
$Dorsal_1$ base length	5	4	3
$Dorsal_2$ base length	117	118	105
Maxilla length	17	17	13
Anal base length	85	89	76
Pectoral length	27	27	21
Ventral length	25	23	19
Preanal length	75	69	63
Caudal peduncle Length	6	6	4
Minimum height of caudal peduncle	3	3	2
Body depth	30	28	24
Body width	18	16	13
MERISTIC			
First dorsal rays	5	4	5
Second dorsal rays	58	57	56
Anal rays	52	50	49
Pectoral rays	23	22	23
Ventral rays	8	8	8
Branchiostegal rays	7	7	7
Gillrakers in first arch	5+15	5+14	6+14

ANEXO III-2

Bañón, R., Arronte, J.C., Isbert, W., Coscelli, G. & Sánchez, F. 2014. Melanic hyper-pigmentation in the genus *Lepidion* (Gadiformes: Moridae). Cybium, 38 (3): 231-234.

Abstract

Two cases of melanic hyper-pigmentation in *Lepidion lepidion* are reported from two localities in Spanish Atlantic waters. A bibliographic search revealed the occurrence of this chromatic anomaly in another two *Lepidion* specimens, the first of them reported in the late 19th century. Macroscopically, the colour abnormality was characterized by the presence of numerous cutaneous irregular dark patches over the head, body and fins. Microscopically, melanosis corresponds with hyperplasia of dermal melanophores. Although the cause of the hyperplasic proliferation of pigmented cells could not be determined, possible aetiologic agents were proposed. This is the first histopathological study of a melanic specimen of the genus *Lepidion*.

INTRODUCTION

Pigmentation and integumentary colours in fish are the result of a combination of coloured substances or biochromes, contained in various pigmented cells or chromatophores. There are three major chromatophore cell types: melanophores, xantophores and iridophores (Fujii, 1993). Melanophores contain melanin, which gives a brown or black colouration. In teleosts, melanophores are commonly located in the dermis of the skin, forming a pigmented layer, but they can also appear in the epidermis and hypodermis (Beeching et al., 2013). The pigmentation patterns are regulated by several intrinsic physiological conditions (Quigley and Parichy, 2002) and they are also influenced by numerous environmental stressors such as exposure to light and ultraviolet ray, temperature, osmolarity and pH of the water, mechanical pressure and nutrition (Greenwood et al., 2012).

Many fish species may develop skin pigment abnormalities both in wild or farming conditions, mainly associated to melanophore disorders. Hyper-pigmentation is one of these disorders, characterized by the occurrence of focal or generalized spots, patches or bands of dark coloration (Groff, 2001; Simon et al., 2009). It has been commonly observed associated with pathological conditions such as chronic inflammation, hyperplasic or neoplastic proliferation of melanophores (Roberts, 2012; Lévesque et al., 2013).

Skin lesions, including hyper-pigmentation, have received considerable attention in the last few years, as they represent indicators of water pollution and/or otherwise stressed aquatic environments (Vethaak and Jol, 1996). The purpose of this study is to

describe the occurrence of two specimens of *Lepidion lepidion* displaying external hyper-pigmentation. In one specimen, the hyper-pigmented skin was evaluated macroscopically and characterized by histopathological analysis.

MATERIALS AND METHODS

Two specimens of *L. lepidion* with melanistic coloration were recorded in Spanish Atlantic waters (NE Atlantic).

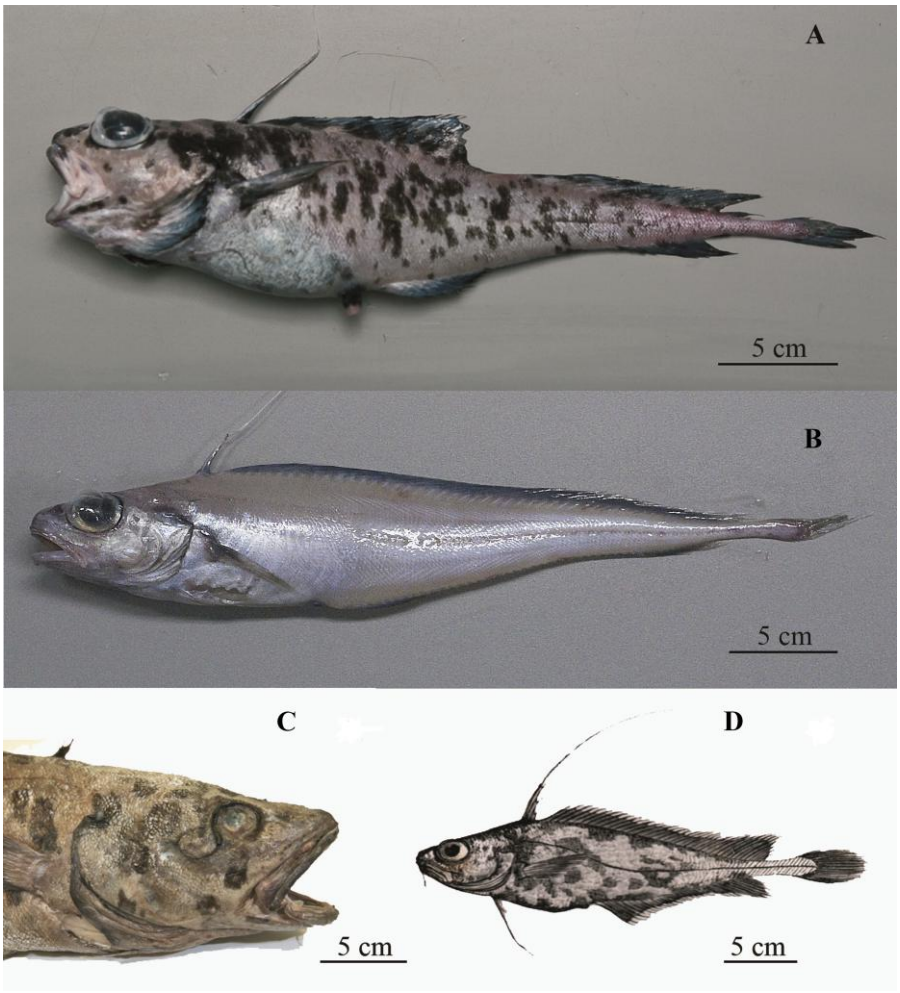

Figure. 1.- Melanic and normal pigmentation in the genus *Lepidion*: (A) Hyperpigmentation in *L. lepidion* IEOST10052, (B) Specimen of *L. lepidion* showing a normal pigmentation (C) Detail of *L. guentheri* specimen reported in Bañón et al. (2010) and (D) *L. lepidion* in Moreau (1881).

One specimen (captured specimen) measuring 345 mm total length (Fig. 1A), was caught by bottom trawl on 18 August 2010 on the Galician Bank (42º34'ºN-11º57'W) at

a depth of 1,100 m during the research survey INDEMARES-BANGAL 0810. The specimen was frozen onboard and then fixed in 10% neutral buffered formalin. It was later transferred to 70% ethanol and deposited in the fish collection of the Instituto Español de Oceanografía in Santander (IEOST10052). The second specimen of about 32 cm (video-recorded specimen) was filmed alive in its natural habitat by the remotely operated vehicle (ROV) Liropus 2000 on 4 May 2012 during a research survey (INDEMARES-AVILES 0412) in a cold-water coral reef in the La Gaviera Canyon (43º 55'N - 5º 46'W) at a depth of 792 m (Fig. 2).

Figure. 2.- One specimen of *L. lepidion* with advanced melanistic hyper-pigmentation swimming over *Madrepora aculeata* and *Cerianthus* sp. in La Gaviera Canyon (Cantabrian Sea).

Macroscopic and microscopic examination

A detailed visual examination of fins and body for external parasites, malformations, amputations and any other morphological alterations of the captured specimen was carried out. A sample of the skin and muscle (~ 2 cm2) with a distinct melanotic pigmentation was randomly selected and removed from the body to detect the presence of metazoan parasites. The muscle was separated from the skin and the tissue was sliced and squeezed between two glass plates and examined under a stereo-microscope with transmitted light. Likewise, samples of skin and underlying skeletal muscle, including hyper-pigmented and adjacent normal areas were removed for histopathological

analysis. Fixed tissues were routinely processed and paraffin-embedded. Sections of 3-4 µm thickness were cut and stained with haematoxylin and eosin (H-E), periodic acid-Schiff (PAS) and Fontana-Masson (FM) staining. Alternatively, additional sections were bleached with 3% H2O2 for 24 h (in a humid chamber at room temperature) before H-E stainings. Skin samples of three specimens displaying normal pigmentation were used as a reference for normal histological structure.

RESULTS

Normal pigmentation

The typical pigmentation of *L. lepidion* is uniformly pale, varying from light brown to grey-pink, with the fin extremities lightly pigmented (Fig. 1B).

Altered skin pigmentation

Macroscopic examination

The captured and video-recorded specimens of *L. lepidion*, both exhibited darkened skin with evident hyper-pigmented areas, including the head, operculum and body surface. In the captured specimen, lesions were characterized by generalized, multifocal dark brown and black macules and spots with a smooth surface (Fig. 1A). Lesions were variable in shape and size, varying from well-demarcated spots to irregular and diffuse patches. Transverse sections of the body showed that hyper-pigmentation was restricted to the skin and was not found deep in the musculature. In addition, the captured fish exhibited a partial amputation on its dorsal profile, specifically in the middle of its second dorsal fin. The video-recorded specimen exhibited a similar skin colour pattern, but a higher proportion of skin surface was covered by hyper-pigmentation.

Microscopic examination

The parasitological examination did not reveal any parasites either on the skin or in the muscular tissue. The histological examination of hyper-pigmented skin showed hyperplasia of dermal melanophores (Fig. 3A). Pigmented cells were largely distributed throughout the stratum laxum of the dermis, beneath the epidermis and above the scales, but not extending into the deep dermis. They formed a thick, continuous and compact pigmented row, parallel to the basement membrane (Fig. 3B). Demelanized samples showed melanophores with rounded to fusiform nuclei and indistinguishable

cytoplasmatic edges (Fig. 3C). Mitotic figures were not observed. Staining with the FM technique confirmed the presence of melanin granules in pigmented cells (Fig. 3D). There was no evidence of inflammatory or necrotic changes. No bacterial, fungal or parasites structures were observed in any of the analysed sections.

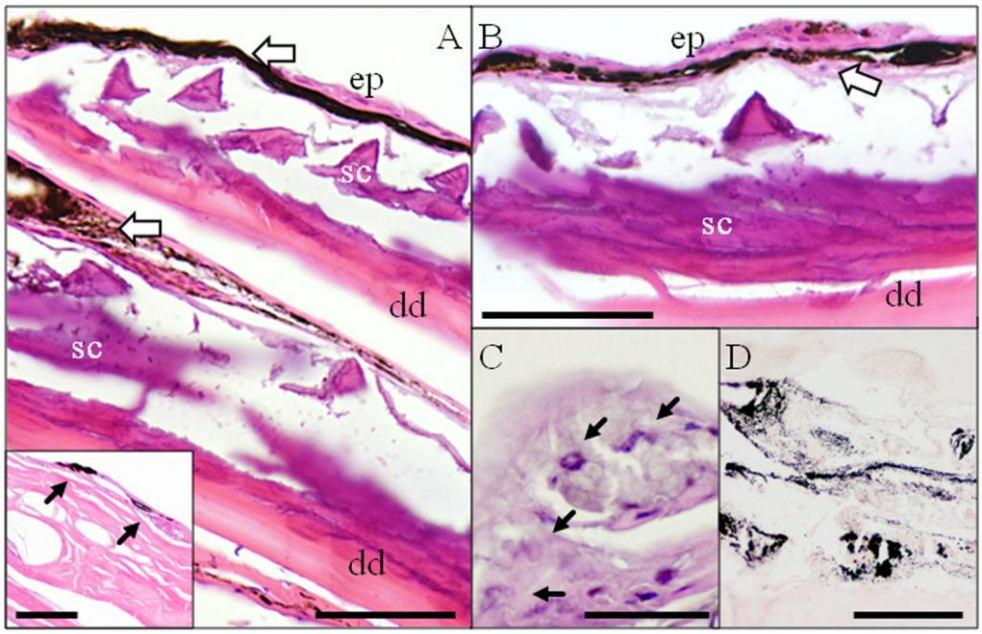

Figure. 3.- Microphotographs of hypermelanized skin sections. A, pigmented cell proliferation in the superficial dermis (stratum laxum) (arrows); epidermis (ep), scale (sc), deep dermis (dd). H-E, bar=50 µm. Insert: distribution of melanophores (arrows) in normal pigmented skin. H-E, bar=50 µm. B, hyperplasia of melanophores in superficial dermis forming a thick heavily pigmented layer beneath the epidermis (arrow); epidermis (ep), scale (sc), deep dermis (dd). H-E, bar=50 µm. C, foci of hyperplasic melanophores densely clustered. H-E, bar= 20 µm. D, Positive argentaffin reaction of melanin granules. FM staining, bar=100 µm.

DISCUSSION

Following a recent revision of the genus, the Atlantic *L. eques* has been proposed as a junior synonym of the Mediterranean *L. lepidion* (Bañón *et al.*, 2013). Therefore, *L. lepidion* is a deep-water species widely distributed in the North Atlantic Ocean and the Mediterranean Sea.

Macroscopically, the anomalous colouration pattern was quite similar in both specimens. A similar colouration pattern was previously reported in a specimen of the congeneric *L. guentheri* from the Bay of Biscay (Bañón *et al.*, 2010) (Fig. 1C) and in a specimen of *L. lepidion* from the Mediterranean Sea (Moreau, 1881; Vinciguerra, 1883) (Fig. 1D). Thus, the Moreau original drawing (1881, Vol. 3 p. 262), would appear to

represent the first documented case of melanosis in the genus *Lepidion* and one of the first, if not the first, among marine fishes.

Microscopically, the histopathological examination of tissues revealed that the skin melanosis corresponded with a severe hyperplasia of dermal melanophores, which resulted in the darkened skin. However, the aetiology of melanophore hyperplasia could not be established.

Hyperplasia is characterized by an increase in organ size or tissue involved that can be caused by an excessive and/or prolonged stimulation of hormones or growth factors on target cells, but also by inflammatory response to certain bacterial and viral infections or physical agents, such as radiation or trauma (Cockerell and Cooper, 2002; Sweet *et al*., 2012; Lévesque *et al*., 2013).

Melanophore hyperplasia seems to be a frequent cause of hyper-pigmentation in fishes and has been described previously in other fish species, such as *Sebastes sp*., *Pagellus acarne, Limanda limanda* and *Xiphophorus sp*. (Gimenez-Conti *et al*., 2001; Noguera *et al*., 2013; Ramos *et al*., 2013).

The microscopic examination showed neither dermal inflammatory changes nor histological evidence of viral, bacterial, fungal or parasite infection. However, a preceding inflammatory process cannot be ruled out because the inductor stimuli could have been activated long before the specimen was examined.

Thus, the lesion observed in the second dorsal fin of the captured fish may represent a sequel to a traumatic event, which may have been the initial stimulus that triggered the proliferation of melanophores. Although aetiology was not considered in the original publication, the specimen of *L. guentheri* with hyper-pigmentation reported by Bañón *et al*. (2010) also showed a sequel scar as a result of a traumatic injury in the suborbital area of the specimen's right eye (Fig. 1C). Unfortunately, the presence of wounds or injuries in both Moreau's drawing and the video-recorded specimen of *L. lepidion* could not be confirmed.

Chromatic alterations in fish species related to traumas, wounds and injuries have previously been reported in other fish species as *Carassius auratus* (Smith, 1931) and flatfishes (Norman, 1934; Dahlberg, 1970).

The four compiled cases confirm the presence of melanic hyper-pigmentation within the genus *Lepidion*. However, considering the relatively small number of melanic specimens found to date, the prevalence of this condition in wild populations seems to be very low. Nevertheless, specific attention to these anomalies is required in order to

achieve a more comprehensive knowledge about the occurrence of melanic hyper-pigmentation in deep-water fish species.

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ANEXO IV

Bañón, R., Arronte, J.C., Barros-García, D., Vázquez-Dorado, S. & de Carlos, A. 2013. Taxonomic study of Bathygadidae fishes (Gadiformes) from Atlantic Spanish waters combining morphological and molecular approaches. Zootaxa, 3746 (4): 552–566.

Abstract From 2009 to 2011 eleven specimens belonging to four bathygadid species of the family Bathygadidae were captured in two different locations in the northern waters of Spain. The morphometric measurements and meristic characters of these specimens are given. The specimens were identified as belonging to the genera *Gadomus* Regan, 1903, and *Bathygadus* Günther, 1878, including the following species: *Gadomus dispar* (Vaillant, 1888), *Gadomus longifilis* (Goode & Bean, 1885), *Gadomus arcuatus* (Goode & Bean, 1886) and *Bathygadus melanobranchus* Vaillant, 1888. As a result, a new northern limit of distribution of *G. arcuatus* from the northeastern Atlantic is reported. The first molecular identification and genetic interrelationships of Bathygadidae species, based on the mitochondrial COI nucleotide sequences -DNA barcodes- is reported. Sequences corresponding to specimens from the same species were identical and the overall mean genetic diversity (uncorrected p-distance) was 0.096 ± 0.008. Based on a morphological and meristic examination of the specimens, as well as on the available literature, an updated key of the members of the family Bathygadidae from the north-eastern Atlantic Ocean is provided.

Introduction

The grenadiers or rattails, traditionally included in the family Macrouridae, are now divided in three families: Bathygadidae, Macrouridae and Trachyrincidae (Howes, 1989; Roa-Varón & Ortí, 2009). The family Bathygadidae, also known as bathygadids, contains two genera, the genus *Bathygadus*, with 13 species, and the genus *Gadomus*, with about 13 species. Bathygadids show a worldwide distribution from tropical to subtropical seas, at depths of between 100 and 3,000 m. They can be found in the Atlantic Ocean, between 40ºN and 40ºS, principally along the African continental slope, in the west confined to the Gulf of Mexico and Caribbean Sea, extending east to the mid-oceanic ridge; the Indian Ocean, the Natal and Somali basins, the Arabian Sea and the Bay of Bengal; the Pacific Ocean, the Philippine Seas, the southern slope of Japan, north of New Zealand, the Hawaiian islands and from the Sala-y-Gomez Ridge (Howes, 1991; Sazonov & Iwamoto, 1992).

Bathygadids are characterized by the presence of two dorsal fins, with the second beginning immediately behind the first without a pronounced gap; first dorsal fin with two spinous rays, the first one rudimentary and the second one smooth and flexible; dorsal rays are longer than anal rays; 20 or more lathlike long outer gill rakers appear on the first arch; 7 branchiostegal rays; no membrane restricts the first gill slit; 8-10 pelvic

fin rays; the caudal fin is absent; there are no spinules on the scales; the swim bladder has two or four retia mirabilia; the mouth is large and terminal and there is no protruding snout (Marshall & Iwamoto, 1973; Iwamoto & Graham, 2001). Differences in functional morphology between bathygadids and macrourids seem to be related with their respective strategies for capturing prey. As a general rule, bathygadids, as pelagic feeders, have a wide mouth and terminal and dorsal rays longer than the anal ones whereas macrourids, as benthic to benthopelagic feeders, have subterminal or inferior mouths and longer anal rays than the dorsal ones (Marshall, 1965; McLellan, 1977).The taxonomic position of the Bathygadids is controversial, being a subject of scientific debate. Some authors assigned this group to the suborder Macrouroidei (Iwamoto, 1989) whereas others to the suborder Gadoidei (Howes, 1989; Howes & Crimmen, 1990). On the other hand, Bathygadus and Gadomus have been traditionally constituting the subfamily Bathygadinae of the family Macrouridae (Marshall & Iwamoto, 1973; Maul, 1976). However, based on morphological and molecular evidences, this group has been recognized at the family level (Howes & Crimmen, 1990; Iwamoto & Graham, 2001; Shao *et al*. 2008).

Morphologically, the bathygadids are chiefly distinguished from macrourids in having the combination of second dorsal fin better developed (higher) than the anal fin; the outer gill rakers long and slender (vs tubercular); the first gill slit no restricted by folds of skin connecting the dorsal and ventral regions of the arch with the operculum, a terminal mouth, viliform teeth, the body scales without spinules and all members have seven branchiostegal rays (Iwamoto & Anderson, 1994). Molecular data based on mitochondrial and nuclear DNA sequence analysis (average p-distance calculations) among the Gadiformes also suggest that Bathygadinae could be ranked at the family level (Roa-Varón & Ortí, 2009).

Recent morphological and genetic analyses support that bathygadids are basal to the other grenadiers (Endo, 2002; Satoh et al. 2006; Iwamoto 2008; Roa-Varón & Ortí, 2009). However, the fossil records might imply that Macrouridae (with *Nezumia lindsay*) is the oldest and probably most basal group, whereas Bathygadidae (the oldest representative is *Bathygadus novus* from the Late Eocene of Italy) might be more derived (Kriwet & Hecht 2008).

Differences among cytochrome oxidase *c* subunit I (COI) mitochondrial gene sequences from distinct species can be used as a barcode in order to facilitate identification of species, highlight cases of range expansion for known species, flag

previously overlooked species and enable identifications where traditional methods cannot be applied (Hebert *et al.* 2003). The analysis is focused on approximately 650 base pairs at the 5´end of the COI gene and the benefits in facilitating the identification of species have been extensively proved for marine fish (Ward *et al*. 2009).

DNA barcoding data from bathygadid fishes are scarce in the ichthyiological literature and only a few species have been barcoded until now. A barcode from *Bathygadus antrodes* (Jordan & Starks, 1904) was obtained during the course of the complete sequencing of a mtDNA genome in order to illustrate the phylogenetic relationships among grenadier fishes by comparing the arrangement of their mitochondrial genes (Satoh *et al*. 2006). In the largest COI database of macrourid fishes of New Zealand, composed of 27 species, a barcode from the filamentous rattail *Gadomus aoteanus* McCann & McKnight, 1980 is also mentioned (Smith *et al*. 2008).

At the moment of writing this paper, there are no published COI sequence records of *Gadomus* and only five records of *Bathygadus* can be found in the BOLD database (URL: http://v3.boldsystems.org/ accessed September 26, 2013), representing 3 species: *B. antrodes*, *B. favosus* Goode & Bean,1886 and *B. melanobranchus*.

Taxonomic revisions of bathygadids have been previously carried out (Iwamoto, 1970; Marshall & Iwamoto, 1973; Howes & Crimmen, 1990; Iwamoto & Anderson, 1994). In the eastern Atlantic Ocean, the specific composition from the western Africa waters has been recently updated, reporting seven bathygadid species, four *Gadomus*: *G. dispar*, *G. longifilis*, *G. arcuatus* and *G. capensis* (Gilchrist & von Bonde, 1924) and three *Bathygadus*: *B. melanobranchus*, *B. macrops* Goode & Bean, 1885 and *B. favosus* Goode & Bean (Sobrino *et al*. 2012); only three of them, *G. dispar*, *G. longifilis* and *B. melanobranchus* reaching the Atlantic European waters northward (Quéro *et al.* 2003). However, little is known about the distribution and abundance of these species in Atlantic European waters and our knowledge is based only on a few scattered records. The aim of the current paper is to revise the species composition of the family Bathygadidae from the Atlantic northern waters of Spain combining both the morphological analysis and the molecular DNA barcoding method.

Material and methods

Sample collection, species identification and morphological analysis

A total of eleven specimens of the family Bathygadidae were caught between 2009 and 2011 during 4 research cruises carried out in the Galicia Bank and the Avilés Canyon in north-eastern Atlantic Ocean (northern Spanish waters). All specimens were tentatively identified and subsequently frozen on board. Once in the laboratory, identification of specimens to the species level was carried out according to Marshall & Iwamoto (1973) and Howes & Crimmen (1990). Measurements to the nearest mm and meristic characters were determined mainly according to Marshall & Iwamoto (1973).

Muscle samples were removed from thawed individuals and stored in 90% ethanol. The specimens were then fixed in 10% formalin, prior to their storage in 70% ethanol. Voucher specimens were deposited in the Museo de Historia Natural da Universidade de Santiago de Compostela (MHNUSC, Santiago de Compostela, Spain). Photographs of specimens used in this study and DNA sequence data are available in the project entitled "Barcoding of the family Bathygadidae" (code BATGA) in the Barcode of Life Database (BOLD).

DNA extraction, PCR amplification and sequencing

Total DNA was purified from 25 mg of muscle tissue taken from each specimen using the spin-column protocol of the DNeasy Blood and Tissue Kit (QIAGEN). The standard 5´ barcoding region of the COI gene (ca. 650 bp) was amplified by PCR using primers LCOI1490 and HCOI2198 (Folmer *et al*. 1994). The following reaction conditions were applied: initial denaturation at 94 ºC for 3 min followed by 35 cycles of 94 ºC for 30 s, annealing at 52 ºC for 45 s and 72 ºC for 1 min, with a final extension at 72 ºC for 7 min. Polymerase chain reaction mixtures contained 1 x reaction buffer (TaKaRa), 25 pmol of each primer, 0.2 mM of each dNTP, 2 mM $MgCl_2$, 0,25 U ExTaq DNA Polymerase (TaKaRa) and 50-100 ng of template DNA. PCR reaction products were visualized on 1.2% agarose gels (Seakem LE Agarose) stained with ethidium bromide and, due to the specificity of the results, purified directly with ExoSAP-IT (USB) following the manufacturer´s instructions. DNA sequencing reactions were carried out in the direct and reverse senses using the same primers and the BigDye Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems). The resulting products were resolved on an ABI 3130 Genetic Analyser and the consensus sequences were obtained after assembling the direct and reverse traces with SeqScape v2.5.

Sequence alignment and phylogenetic analysis

Phylogenetic and molecular evolutionary analyses were conducted in MEGA version 5 (Tamura *et al*., 2011). Twelve COI partial nucleotide sequences and their deduced

amino acid alignments were built with the Alignment Explorer using the MUSCLE program (Edgar, 2004). The number of base differences per site between sequences (p-distance) served as genetic divergence estimation and was applied for the comparison of pairs of haplotypes in general and also within and between congeners. The evolutionary history among the bathygadid COI sequences was inferred by using the Maximum Likelihood (ML) method based on the Hasegawa-Kishino-Yano model (Hasegawa *et al.*, 1985). Initial tree(s) for heuristic search were obtained automatically by applying Nieghbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites (*G* parameter = 0.1660). Codon positions included were 1st+2nd+3rd+Noncoding. The species and gene sequences included in the phylogenetic analysis are listed in the Table 1. For comparisons, the data set was completed with a sample of *G. arcuatus* from the Canary Islands (28º 08,077' N, 14º 37,903' W) and barcodes of *B. antrodes* from Japan (GenBank Accession No NC008222) and *B. favosus* (BIN BOLD: AAW2815) from the North Atlantic Ocean. Sequences in BOLD of *B. melanobranchus* (MAECO390-09 and MAECO391-09) were rejected of this analyses due to high genetic divergence found, which seems indicate that they could be wrongly named. The barcode from a voucher specimen representing the Atlantic cod *Gadus morhua* Linnaeus, 1758 (GenBank Accession No EU752090) was used as outgroup in order to root the ML tree.

TABLE 1. Species used in the present study and gene sequences included in the phylogenetic analysis.

Species	Location	Sample ID	BOLD specimen no.	GenBank accession no.
Gadomus dispar	Galicia Bank	GAD001	BATGA003-13	KC959895
	Galicia Bank	GAD002	BATGA004-13	KC959900
	Galicia Bank	GAD003	BATGA005-13	KC959899
	Galicia Bank	GAD004	BATGA006-13	KC959898
	Aviles Canyon	GAD005	BATGA007-13	KC959897
	Galicia Bank	GAD006	BATGA008-13	KC959896
Gadomus longifilis	Galicia Bank	GAL001	BATGA009-13	KC959903
	Galicia Bank	GAL002	BATGA010-13	KC959901
	Galicia Bank	GAL003	BATGA011-13	KC959902
Gadomus arcuatus	Aviles Canyon	GAC001	BATGA002-13	KC959894
	Canary Islands	GAC002	BATGA012-13	KC959893
Bathygadus melanobranchus	Galicia Bank	BGN001	BATGA001-13	KC959892

Results

Genetics

Twelve COI DNA sequences were obtained from four different species of bathygadids caught in the Galicia Bank, the Avilés Canyon and the Canary Islands: *B. melanobranchus* (1 sequence), *G. arcuatus* (2 sequences), *G. dispar* (6 sequences) and *G. longifilis* (3 sequences). The alignment of 651 nucleotides revealed the presence of 542 conserved and 109 variable sites from which 76 were parsimony informative (i.e. containing at least two types of nucleotides and at least two of them occurring with a minimum frequency of two) while 33 positions corresponded to singletons. Regarding the 217 putative amino acid positions all but two were identical with the exception of V138 (codon GUU) and T152 (codon ACC) in *Bathygadus* replaced by I138 (codons AUC or AUU) and I152 (codons AUU or, AUC) in *Gadomus*.

The values of number of nucleotide differences per site (uncorrected p-distance) between haplotypes from the specimens of the family Bathygadidae are shown in Table 2.

TABLE 2. Number of nucleotide differences per site (uncorrected p-distance) from averaging over all COI haplotype pairs between bathygadids. Standard error estimates are shown above the diagonal and were obtained by a bootstrap procedure (100 replicates).

	B. antrodes	*B. favosus*	*B. melanobranchus*	*G. arcuatus*	*G. dispar*	*G. longifilis*
B. antrodes[1]		0.009	0.010	0.012	0.012	0.012
B. favosus[2]	0.051		0.009	0.013	0.013	0.012
B. melanobranchus	0.060	0.057		0.012	0.011	0.011
G. arcuatus	0.123	0.121	0.124		0.009	0.010
G. dispar	0.114	0.123	0.108	0.084		0.010
G. longifilis	0.109	0.106	0.103	0.071	0.084	

[1]GenBank Accession No. NC008222.
[2]BIN BOLD:AAW2815 (MAECO389-09)

Sequences obtained from *G. arcuatus*, *G. dispar* and *G. longifilis*, produced only one haplotype each. The mean overall distance (d ± S.E.) value among bathygadid haplotypes was 0.096 ± 0.008. The within group mean distance was 0.056 ± 0.008 for *Bathygadus* and 0.080 ± 0.009 for *Gadomus*. The group mean distance between the two genera was 0.115 ± 0.010. The highest divergence occurred between *B.*

melanobranchus and *G. arcuatus* (d = 0.124 ±0.012) while the lowest was between *B. antrodes* and *B. favosus* (0.051 ± 0.009).

ML analysis was conducted with the HKY+G model of nucleotide substitution and produced a phylogenetic tree showing that all species formed statistically well-supported and coherent clades (Fig. 1). Two separated branches representing the two genera of the family Bathygadidae can be observed. Regarding the sequences obtained in this investigation, the various *Gadomus* sequences formed one clade and the only *B. melanobranchus* sequence formed a second clade together with the congeneric ones from *B. antrodes* and *B. favosus* mined from the databases. All sequences previously assigned by taxonomy at the species level formed monophyletic clades with high bootstrap values.

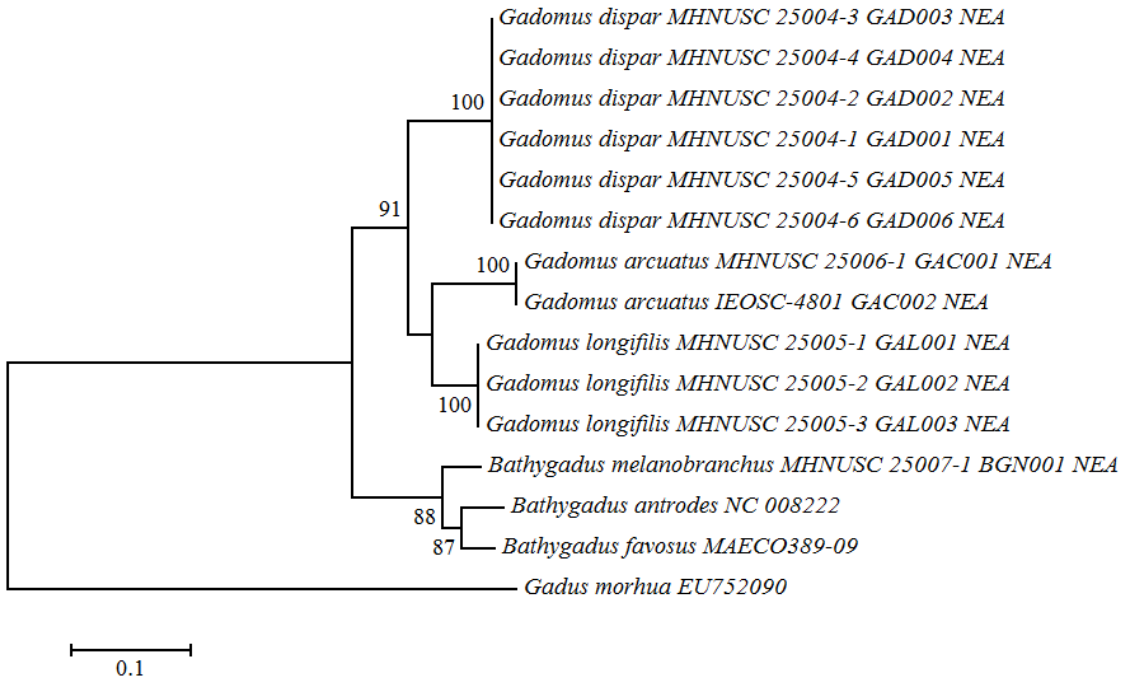

FIGURE 1. Molecular phylogenetic analysis of bathygadid COI barcoding sequences by Maximum Likelihood method. For each specimen a code followed by a location abbreviation (NEA, Northeast Atlantic) was given. Voucher specimens were deposited in the Museo de Historia Natural da Universidade de Santiago de Compostela (MHNUSC) and Instituto Español de Oceanografía de Canarias (IEOSC). A *Gadus morhua* sequence (EU752090) was employed as out-group. The percentage of trees in which the associated taxa clustered together is shown above the branches. The scale bar represents 1 fixed mutation per 10 nucleotide sequence positions.

Taxonomic descriptions

Family BATHYGADIDAE

Genus *Gadomus* Regan, 1903

***Gadomus dispar* (Vaillant, 1888)**: Fig. 2.

Hymenocephalus dispar Vaillant, 1888: 221, Pl. 24 (Fig. 1). Off Morocco, 33°43'N, 9°02'W, station 20, depth 1105 meters. Holotype (unique): MNHN 1986-0551. Marshall & Iwamoto, 1973: 518–530 (description, key); Howes & Crimmen 1990: 192–201 (description, key).

Material examined. MHNUSC 25004-1, 367 mm TL, 23th July 2009, Galicia Bank; 42º42.170 N—11º44.880' W; 765-766 m depth; MHNUSC 25004-2, 197 mm TL, 17th August 2010, Galicia Bank; 42º39.968'N—11º43.327'W; 764-766 m depth; MHNUSC 25004-3, 171 mm TL, 21th August 2010, Galicia Bank; 42º42.960'N—11º43.000'W; 775 m depth; MHNUSC 25004-4, 187 mm TL, 21th August 2010, Galicia Bank; 42º42.960'N—11º43.000'W; 775 m depth; MHNUSC 25004-5, 292 mm TL, 12th May 2011, Avilés Canyon; 43º 54.970'N—6º 15.250'W; 1051 m depth; MHNUSC 25004-6, 260 mm TL, 3th August 2011, Galicia Bank; 42º 49.180'N—11º 46.890'W; 909 m depth.

Description. Body elongated and attenuated to the caudal peduncle; head small, 5.7-6.7 times in total length; snout moderately acute, 4.3-5.8 into head; interorbital width lower than horizontal eye diameter; barbel filamentous of moderate length, about as long as the length of head, 0.8-1.2 in head length; dorsal, pectoral and ventral fins with a single elongated ray; elongated second dorsal ray 1.6-2.7, elongated second pectoral ray 1.7-2.2 and elongated first pelvic ray 0.9-2.0 in the head length. The main morphometric and meristic characteristics are presented in Table 3.

Habitat and Distribution. Benthopelagic between 548 and 1,543 m depth in tropical and subtropical North Atlantic (Marshall & Iwamoto, 1973; Sobrino *et al*. 2012). Amphi-Atlantic distribution; in western Atlantic it occurs in Norfolk Canyon, eastern Gulf of Mexico and the Caribbean Sea and in eastern Atlantic in the Cantabrian Sea, Portugal, Morocco, Mauritania and Guinea-Bissau (Middleton & Musick, 1986; Marques & Saldanha, 1998; McEachran & Fechhelm, 1998; Sánchez *et al*. 2008; Sobrino *et al*. 2012).

TABLE 3. Comparison of morphometric, meristic data and respective body proportions for specimens of *Gadomus dispar*

Gadomus dispar	MHNUSC 25004(1—6)	Marshall & Iwamoto (1973)	Howes &Crimmen (1990)
Total Length (mm)	171-367	—	—
Head length (mm)	30-61	31-56	—
As % TL			
Head length	15.0-17.5	15-20	—
As % HL			
Eye diameter	24.6-29.0	26.8-31.6	27.6-29.5
Preorbital length	17.4-23.3	22.6-27.3	—
Postorbital length	48.4-56.5	—	—
Interorbital length	16.1-20.5	15.2-17.1	18.6-19.1
Upper jaw length	48.4-56.7	51.6-56.3	—
Barbel length	83.6-119.4	83.9-103.2	75.4-90.0
1st Predorsal length	95.7-119.4	112.9-117.7	—
2nd Predorsal length	136.7-159.0	138.7-154.2	—
1st Dorsal base length	22.6-38.5	—	—
Preanal length	200-233.3	192.8-206.4	—
Length of longest ray of first dorsal	161-270	126-135	—
Pectoral length	174.2-216	164-208	—
Ventral length	93.3-108.7	96-116	—
Body depth	70.5-120	67.7-85.3	—
Meristic features			
1st Dorsal fin rays	II+9-11	12-13	II+9-11
Ventral fin rays	8	8	8
Pectoral fin rays	19-21	19-20	17-18
Gill rakers	4-5+19-21	4-5+20-21	4+20-21
Pyloric caeca	>50	—	35+

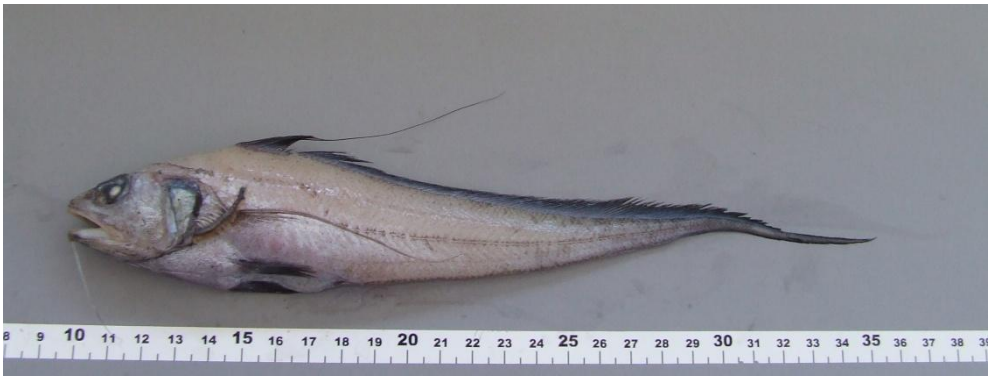

FIGURE 2. *Gadomus dispar* from the north-east Atlantic Ocean, MHNUSC 25004-6, 260 mm total length.

***Gadomus longifilis* (Goode & Bean, 1885)**: Fig. 3.

Bathygadus longifilis Goode & Bean, 1885: 599. Albatross station 2392, 28°47'30"N, 87°27'00"W, depth 724 fathoms. Syntypes: ?SU 9546 (1), USNM 37338 (2). Type catalog: Böhlke 1953:56. Parr, 1946: 8-17 (description, key); Iwamoto, 1970:

327–352 (description, key); Marshall & Iwamoto, 1973: 518–530 (description, key); Howes & Crimmen, 1990: 192–201 (description, key).

Material examined. MHNUSC 25005-1, 278 mm TL, 6th August 2011, Galicia Bank; 42º 40.390'N—11º 31.670'W; 1,450 m depth; MHNUSC 25005-2, 291 mm TL, 6th August 2011, Galicia Bank; 42º 40.390'N—11º 31.670'W; 1,450 m depth; MHNUSC 25005-3, 295 mm TL, 7th August 2011, Galicia Bank; 42º 58.51'N—11º 59.23'W; 1,683 m depth.

Description. Body elongated and attenuated to the caudal peduncle; head small, 6.7-7.7 times in total length; snout blunt, 3.7-4.4 times into head; interorbital width about equal to horizontal diameter of orbit; long chin barbel present, strongly developed and 1.9-2.4 in head length; dorsal, pectoral and ventral fins with a single elongated ray, elongated second dorsal ray 1.8-2.4, elongated second pectoral ray 2.0-2.3 and elongated first pelvic ray 2.0-2.2 in the head length. The main morphometric and meristic characteristics are presented in Table 4.

Habitat and Distribution. Benthopelagic in tropical and subtropical North Atlantic between 520 and 2,165 m depth (Geistdoerfer, 1990). Amphi-Atlantic distribution; in western Atlantic it occurs in West Greenland (a single specimen), off east coast of Florida, Straits of Florida, Gulf of Mexico and Caribbean sea and in eastern Atlantic from the northwest of Spain (Galicia), Portugal, Azores, Canary Islands, Morocco, Mauritania and Gulf of Guinea (Marshall & Iwamoto, 1973; Maul, 1976; Geistdoefer, 1990; Jørgensen, 1996; Bañón *et al*. 2010; Sobrino *et al*. 2012).

FIGURE 3. *Gadomus longifilis* from the north-east Atlantic Ocean, MHNUSC 25005-3, 295 mm total length.

TABLE 4. Comparison of morphometric, meristic data and respective body proportions for specimens of *Gadomus longifilis*.

Gadomus longifilis	MHNUSC 25005(1—3)	Parr (1946)	Iwamoto (1970)	Marshall & Iwamoto (1973)	Howes & Crimmen (1990)
Total Length (mm)	278-296	—	117-290	—	—
Head length (mm)	38-41	—	19-45	25-46	—
As % TL					
Head length	13.1-14.9	15-18	—	~15	—
As % HL					
Eye diameter	17.1-22.7	21-23	24-28	23.1-28.0	23.5-27.7
Preorbital length	22.7-26.8	28-30	26-31	26.3-28.9	—
Postorbital length	54.5-57.9	—	46-53	—	—
Interorbital length	21.1-22.7	23-25	21-28	21.1-25.0	19.7-24.8
Upper jaw length	56.1-60.5	60	57-65	52.6-60.0	—
Barbel length	40.9-51.2	40-45	13-48	31.6-40.0	40.0-50.0
1st Predorsal length	112.2-113.6	—	—	105.3-116.0	—
2nd Predorsal length	152.6-156.8	—	—	135.1-146.1	—
1st Dorsal base length	34.2-39.0	30	—	—	—
Preanal length	197.6-202.6	—	—	171.1-182.8	—
Length of longest ray of first dorsal	175.0-243.9	200	190	—	—
Pectoral length	204.5-234.1	180	200	—	—
Ventral length	204.5-217.1	160-170	250	—	—
Body depth	87.8-94.7	—	—	65.8-77.1	—
Meristic features					
1st Dorsal fin rays	II+9-10	—	II+8-10	9-11	II+9-10
Ventral fin rays	8	8	8	8	8
Pectoral fin rays	16-17	14-16	14-18	14-16	13-16
Gill rakers	7+29-31	—	7-8+26-31	5-7+1+27-29	6-8+27-29
Pyloric caeca	9-12	10-12	9-13	—	5-12

***Gadomus arcuatus* (Goode & Bean, 1886)**: Fig. 4.

Bathygadus arcuatus Goode & Bean, 1886: 158. Off Martinique Island, West Indies, Blake station 205, depth 334 fathoms. Holotype: MCZ 28007. Parr, 1946: 8-17 (description, key); Marshall & Iwamoto, 1973: 518–530 (description, key); Howes & Crimmen 1990: 192–201 (description, key).

Material examined. MHNUSC 25006-1, 566 mm TL, 13th May 2011, Avilés Canyon; 43º 57.850'N—6º 28.050'W; 1,450 m depth.

Description. Body elongated and attenuated to the caudal peduncle; upper profile to first dorsal fin strongly inclined, with a pronounced hump-backed appearance; head moderately large, 6.2 times in total length; snout 4.8 times into head; interorbital width about equal to horizontal eye diameter and 5.4 times into head length; chin barbel present and of moderate size, 0.7 in head length; mouth large and terminal jaws beyond the posterior margin of the orbit; only one pelvic ray elongated but broken is patent, all

rest of elongated rays are presumably broken, elongated first pelvic rays 1.3 and elongated first pectoral rays 1.3 in the head length. The main morphometric and meristic characteristics are presented in Table 5.

TABLE 5. Comparison of morphometric, meristic data and respective body proportions for specimens of *Gadomus arcuatus.*

Gadomus arcuatus	MHNUSC (25005-1)	Parr, 1946	Marshall & Iwamoto (1973)	Howes &Crimmen (1990)
Total Length (mm)	566	—	—	—
Head length (mm)	91	—	43-101	—
As % TL				
Head length	16.1	19-22	~20	—
As % HL				
Eye diameter	18.7	17-20	17.8-26.7	20.6-27.0
Preorbital length	20.9	25-30	28.0-30.3	—
Postorbital length	60.4	—	—	—
Interorbital length	18.7	15-16	16.7-20.0	17.0-21.8
Upper jaw length	52.7	55	52.0-57.3	—
Barbel length	72.5	60-65	65.6-87.3	67.1-94.8
1st Predorsal length	118.7	—	117.4-125.4	—
2nd Predorsal length	160.4	—	150.0-160.4	—
1st Dorsal base length	41.8	—	—	—
Preanal length	214.3	—	172.7-192.0	—
Pectoral length	128.6	80	—	—
Ventral length	128.6	125-130	—	—
Body depth	113.2	—	80-90	—
Meristic features				
1st Dorsal fin rays	II+10	12	11-13	II+10-11
Ventral fin rays	8	8	8	8
Pectoral fin rays	25	21-25	22-25	20-22
Gill rakers	5+21	+18-20	4-6+18-21	4-5+19-23
Pyloric caeca	38	30	—	25-30

Habitat and Distribution. Benthopelagic in tropical and subtropical Atlantic at depths between 610 and 1,631 m (Iwamoto, 1990; Sobrino *et al*. 2012). Amphi-Atlantic distribution; in western Atlantic from Nova Scotia (Canada), Gulf of Mexico, Caribbean, Surinam, French Guyana, north-eastern coast of South America and Brazil and in eastern Atlantic from Morocco, Azores, Canary Islands, Mauritania, Guinea-Bissau and Gabon (Marshall & Iwamoto, 1973; Iwamoto, 1990; Geistdoerfer, 1990; Howes & Crimmen, 1990; Melo & Menezes, 2002; Melo *et al*. 2010; Halliday *et al*. 2012; Sobrino *et al*. 2012).

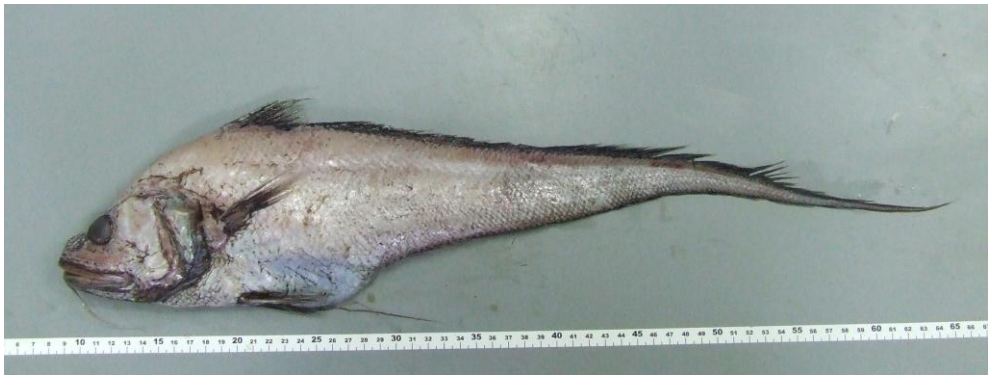

FIGURE 4. *Gadomus arcuatus* from the north-east Atlantic Ocean, MHNUSC 25006-1, 566 mm total length.

Genus *Bathygadus* Günther, 1878

***Bathygadus melanobranchus* Vaillant, 1888:** Fig. 5.

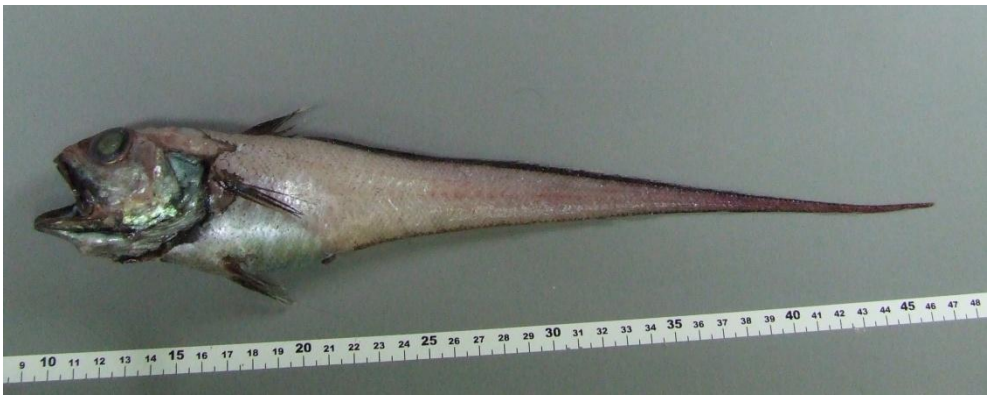

FIGURE 5. *Bathygadus melanobranchus* from the north-east Atlantic Ocean, MHNUSC 25007-1, 370 mm total length.

Description. Body elongated and attenuated to the caudal peduncle; head large, 6 times in total length; snout blunt, 4.1 times into head; mouth large and terminal, jaws do not reaching the posterior margin of the orbit; snout as long as eye diameter and 4.1 times into head length; chin barbel absent; only first ventral ray slightly produced, 0.8 in the head length. The main morphometric and meristic characteristics are presented in Table 6.

Habitat and Distribution. Benthopelagic in tropical and subtropical Atlantic at depths between 450 and 2,650 m, but generally from 700 to 1400 m (Marshall & Iwamoto, 1973). Amphi-Atlantic distribution; in western Atlantic from the Gulf of Mexico, Caribbean sea and off Suriname and in eastern Atlantic from the Irish continental slope, Azores, Madeira, Canary Islands, Morocco, Mauritania, Guinea-

Bissau, Senegal and Gabon (Farran, 1924; Marshall & Iwamoto, 1973; Sobrino *et al*. 2012). The records from South Africa were not included because they cannot be verified (Howes & Crimmen, 1990).

TABLE 6. Comparison of morphometric, meristic data and respective body proportions for specimens of *Bathygadus melanobranchus.*

Bathygadus melanobranchus	MHNUSC (25007-1)	Parr (1946)	Iwamoto (1970)	Marshall & Iwamoto (1973)
Total Length (mm)	370	—	70-400	—
Head length (mm)	62	—	—	28-89
As % TL				
Head length	16.8	—	—	15-20
As % HL				
Eye diameter	24.2	27-29	—	24.7-34.2
Preorbital length	24.2	—	25-33	24.7-29.2
Postorbital length	51.6	—	46-52	—
Interorbital length	29.0	—	25-35	24.7-33.9
Upper jaw length	54.8	54-57	51-60	46.1-56.5
1st Predorsal length	111.3	—	—	102.3-115.8
2nd Predorsal length	151.6	—	—	128.2-147.9
1st Dorsal base length	35.5	40	—	—
Preanal length	195.2	—	—	166.1-187.0
Length of longest ray of first dorsal	51.6	50-55	< 50	—
Pectoral length	66.1	55-60	—	—
Ventral length	83.9	80-85	—	—
Body depth	83.9	—	—	71.9-80.3
Meristic features				
1st Dorsal fin rays	II+10	—	II+9-11	11-13
Ventral fin rays	8	—	8	7-8
Pectoral fin rays	16	—	16-20	16-19
Gill rakers	6+24	+21	6-7+21-24	5-7+0-1+21-23
Pyloric caeca	26	28	25-40	—

Key to species of Bathygadidae from the north-eastern Atlantic Ocean waters (adapted from Iwamoto, 2003)

1a. Chin barbel very small or absent; no elongated fin rays in dorsal and pectoral fins and only slightly elongated in the ventral fin.....Genus *Bathygadus* (2)

1b. Chin barbel long, well developed; elongated fin rays in dorsal, pectoral and ventral fins.....Genus *Gadomus* (4)

2a.- Very small barbel present on chin; body integument relatively tough, not readily torn; head bones strong; gill filaments pale.....*Bathygadus macrops*

2b. No barbel on chin; body integument weak, easily torn; head bones weak, easily broken; gill filaments dusky or pale.....3

3a. Pelvic-fin rays 8; gill filaments dusky; interorbital width moderate, 4 or more times into head length.....*Bathygadus melanobranchus*

3b. Pelvic-fin rays 9; gill filaments pale; interorbital wide, 2.5-3.0 into head .....*Bathygadus favosus*

4a. Two elongated rays in pelvic fin; pectoral-fin soft rays 20 to 28....*Gadomus arcuatus*

4b. One elongated ray in pelvic fin; pectoral-fin soft rays 14 to 21.....5

5a. Gill rakers on lower limb of first arch 26 to 31; interorbital length 21-28% head length; pectoral-fin soft rays 14 to 18; orbit 17.1-28.0% head length; 9-13 pyloric caeca in adult specimens.....*Gadomus longifilis*

5b. Gill rakers on lower limb of first arch 19 to 21; interorbital length 15.2-20.5% head length; pectoral-fin soft rays 17 to 21; orbit 24.6-31.6% head length; more than 50 pyloric caeca in adult specimens.....*Gadomus dispar*

Discussion

The latitudinal and depth distributions found in this study are in the same range of previous records, with the exception of *G. arcuatus*, whose finding, in the Avilés Canyon, constitutes a new northern limit of distribution from the eastern Atlantic Ocean. The higher abundance of bathygadids in the eastern Atlantic seems to be restricted to north-western Africa, specifically in the Morocco-Western Sahara area. Merrett & Marshall (1981) found that *B. melanobranchus* is one of the most numerous species of the fishes collected in this area, occupying a depth range of 734-1,017 m. Ramos *et al*. (2006) reported *B. melanobranchus* and *G. longifilis* as two of the dominant species in the global catch of deep demersal fauna in northern Morocco between 500 and 2,000 m and Sobrino *et al*. (2012), pointed out that *B. melanobranchus* and *B. macrops* are the most abundant macrourid fishes caught in the Morocco-Saharan area.

The absence of both a long chin barbel and elongated fin rays separate the *Bathygadus* from the *Gadomus* species (Howes & Crimmen, 1990). *B. melanobranchus* can be separated from the other congeneric Atlantic species by the number of pelvic fin rays (7-8 vs 9-10 in *B. favosus*), greater number of gillrakers (5-7+21-24 vs 5-6+19-21 in *B. macrops*) and wider interorbital length (24.5-33.9 vs 19.7-25.0 %HL in *B.*

macrops) (Howes & Crimmen, 1990). The morphological measurements and counts of our specimen, are in agreement with these ranges, confirming its correct identification (Table 6).

In sampled specimens of *Gadomus*, the higher number of pectoral fins rays separate *G. arcuatus* from the other two *Gadomus* species (25 vs 16-21). *G. longifilis* can be easily differenced from *G. dispar* by the lower number of pectoral fin rays (16-17 vs 19-21), greater gill raker counts on the lower limb of the first arch (29-31 vs 19-21), wider interorbital length (21.1-22.7 vs 16.1-20.5 %HL), lower barbel length (40.9-51.2 vs 83.6-119.4 %HL) and lower number of pyloric caeca (9-12 vs more than 50). Also, *G. dispar* can be differentiated from *G. longifilis* and *G. arcuatus* in having a greater eye diameter and shorter head length (Howes & Crimmen, 1990). Our results confirm the first diagnostic but not the second. The eye diameter was 24.6-29.0 %HL in *G. dispar* compared to 17.1-22.7 in the other two congeners. However, *G. dispar* showed a greater head length (15-17.5 %TL) than in the other two congeners (13.1-16.1%TL).The morphometric and meristic data of *Gadomus* are generally in agreement, apart from minor exceptions, with previous descriptions (Tables 3–6).

The presence of attenuated anterior dorsal, pectoral and pelvic fin rays is one of the main distinctive characters in the genus *Gadomus* (Howes & Crimmen, 1990). Nevertheless, due to their fragility, it is very frequent to find these rays partially or completely broken. This fact can complicate the correct taxonomic identification and also seems to be the cause of erroneous descriptions in the literature. In the first dorsal fin of all bathygadids examined in this study, the second and flexible spinous ray was the longest. In *B. melanobranchus* it is only slightly larger than the others rays, whereas in the *Gadomus* species it is very elongated (broken in our specimen of *G. arcuatus*).

The presence of an enlarged dorsal ray in *G. arcuatus* has been described in some specimens (Koefoed, 1927; Marshall & Iwamoto, 1973) but also its absence has been observed in several individuals (Iwamoto, 1990). In *G. dispar*, the absence of an elongated ray in the first dorsal and pelvic fins has been erroneously proposed as a distinctive character (Iwamoto, 2003). The description of the holotype reported that from state of preservation, it was not possible to determine if the second dorsal fin ray was elongated or not. However, the presence of an elongated ray in pectoral and ventral fins had already been described (Vaillant, 1888). In all of our specimens, as well as in previous descriptions (Marshall & Iwamoto, 1973; Geistdoefer, 1986), the presence of an elongated ray in dorsal, pectoral and ventral fins was observed.

The second pectoral fin ray is elongated in the three *Gadomus* species (broken in our specimen of *G. arcuatus*). This is in agreement with McEachran & Fechhelm (1998), although some authors have described the first pectoral fin rays as the elongated one (Maul, 1976; Geistdoerfer, 1986). After our revision, the following radial formulae with respect to the position of the elongated fin ray is proposed: 2:2:1 for *G. dispar* and G. *longifilis* and 2:2:1-2 for *G. arcuatus*, with reference to dorsal, pectoral and ventral fins, respectively. The formula 2:2:1 could probably be applicable to the rest of the *Gadomus* species, but this should be confirmed in future studies.

The counts of pyloric caeca are in agreement with those previously reported, 5-13 for *G. longifilis* (Iwamoto, 1970; Howes & Crimmen, 1990), 25-40 for *G. arcuatus* (Cohen et al. 1990; Howes & Crimmen, 1990) and 25-40 for *B. melanobranchus* (Iwamoto, 1986). For *G. dispar*, only a count of +35 has been reported (Howes & Crimmen, 1990). Our specimens of *G. dispar* have numerous pale, long and thin pyloric caeca. Although they were very difficult to count, they exceeded 50 in each count (about 58 in a specimen of 292 mm TL). The number of pyloric caeca increases with the size (Howes & Crimmen, 1990), which could be the main origin of the intraspecific differences reported in literature.

Despite the fact that most of the specimens had been caught in different locations and/or dates, the COI sequences from the six *G. dispar*, the three *G. longifilis* and the two *G. arcuatus* are identical and represent a single barcode each. The zero value of the intra-specific divergence in the *Gadomus* species may indicate that the COI gene appears to be conserved in this genus, but this aspect should be proved in future researches.

The bootstrap values of the ML phylogenetic tree support the formed clades, validating the haplotype sequences as barcodes for the six species investigated. Following the established procedure (Ward *et al.* 2009), it is provided for the first time a barcode sequence for the species *G. dispar*, derived from six voucher specimens that yield a single haplotype. The presence of various bathygadid sequences deposited in BOLD Databases probably resembles other scientists initiatives related to the barcoding of this or a similar group of species and will be reflected in the inclusion of these sequences in future research papers. Although only 6 out of 26 (20.7 %) bathygadid species are involved, this is the first approach to the genetic interrelationships into the family Bathygadidae.

The 'Integrative taxonomy' is defined as the science that aims to delimit the units of life's diversity from multiple and complementary perspectives (Dayrat, 2005). The DNA barcoding technique has been successfully integrated with traditional morphological analysis in the systematic studies of fishes (Baldwin & Weigt, 2012; Bañón *et al*. 2013). Taxonomic studies including morphological and molecular data could help to resolve identification mistakes and incongruities between DNA and morphological results. Molecular tools have the potential to complement taxonomic investigations by helping to reveal cryptic species, the identification of immature specimens, and the clarification of problems of synonymy (Pires & Marinoni, 2010). On the other hand, morphological analyses should be necessary to prove the correct identification of all DNA barcoded species. Errors in identification are the primary source of inaccuracies in FISH-BOL barcode data (Becker *et al*. 2011). Without verified reference sequences from voucher specimens that have been authenticated by qualified taxonomists, there is no reliable library for newly generated query sequences to be compared with (Taylor & Harris, 2012).

There were no incongruities among morphological and molecular identification in this study of the family Bathygadidae. The taxonomic identification supported the genetic analysis and viceversa, which reinforces the resulting taxonomic identification.

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