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PS4-025

Translation down-regulation during transient global ischaemia in the rat brain: involvement of mRNA binding to ribosome

C Martin de la Vega[1], J Burda[2], M Nemethova[2], V Danielisova[2] and M Salinas[1]
[1]Servicio de Bioquimica-Investigación, Hospital Ramón y Cajal, Madrid, Spain; [2]Institute of Neurobiology, Slovak Academy of Sciences, Kosice, Slovak Republic

The striking correlation between neuronal vulnerability and translation down-regulation suggests that this cellular process is a critical part in the cascade of pathologenetic events leading to ischemic cell death. Translation inhibition is exerted at the initiation level and this study explore the participation of initiation factors involved in the binding of mRNA to the ribosome. Incomplete forebrain ischemia (30-min) was induced in rats by using the 4-vessels-occlusion model. Initiation factors 4E, 4G and 4E-BP1 levels and phosphorylation status, initiation factor 4F complex formation, as well as ribosomal protein S6 kinase activity, were determined in different subcellular fractions from cortex and hippocampus (CA1 and remaining subfields), at several postischemic times. eIF4E and 4E-BP1 were significantly dephosphorylated during ischemia and total eIF4E levels decreased during reperfusion both in the cortex and hippocampus, with values normalising at 6 h reperfusion only in the cortex. Conversely, S6 kinase activity that was inhibited in both regions during ischemia recovered control values before in the hippocampus than in cortex. eIF4F complex formation diminished both in cortex and hippocampus during ischemia and reperfusion and it was lower in CA1-subfield, roughly paralleling the observed decrease in eIF4E and eIF4G levels. Our findings are consistent with a potential role for eIF4E, 4E-BP1 and eIF4G in translation down-regulation during ischemia. eIF4G and S6 kinase are positively implicated in the translational inhibition induced at early reperfusion, whereas eIF4F complex formation is likely to contribute to the translation inhibition observed at longer reperfusion times.

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PS4–026

Association of the perimicrovilar membranes with the haemoglobin-derived heme in the *Rhodnius prolixus* midgut

M Dansa-Petretski[1], J R Silva[1], M F Oliveira[2], C M Braga[3] and P L Oliveira[2]
[1]Laboratorio de Quimica e Funcao de Proteinas e Peptideos, CBB, UENF, Campos dos Goytacazes, RJ; [2]Depto. de Bioquimica Medica, ICB, CCS,UFRJ, Rio de Janeiro, RJ; [3]Divisao de Quimica, CENPES, Petrobras, Cidade Universitaria, Rio de Janeiro, RJ, Brazil

Rhodnius prolixus is a hematophagous insect. During the blood digestion, high concentrations of heme (Hm) are generated, as consequence of hemoglobin degradation. In the *Rhodnius* midgut Hm is sequestred into an aggregated form, Hemozoin (Hz). Hz was identified in other Triatomines species by FTIR and Absorption Spectrophotometry. In the *Rhodnius prolixus*, perimicrovillar membranes (PMVM) are, in fact, the first structures to come into contact with hemoglobin-derived heme. When we used 3,3- DAB to detect heme on the PMVM we could observe a positive staining. The heme–PMVM association could suggest their role as a physical barrier against heme. We tested the PMVM of both *R. prolixus* and *Dysdercus peruvianus* (a phytophagous Hemiptera) in a heme aggregation assay and both successfully induced the Hz synthesis. We still tested lipid and protein moieties from *R. prolixus* PMVM and verified that both of them were able to induced heme aggregation. In the first days after feeding only 4% of heme is in the aggregated form. In the later days, up to 90% of heme is as Hemozoin. This increase in the Hz synthesis is coincident with the increase in the α-glucosidase activity, used as the parameter for the PMVM production. Our results show that PMVM are in fact responsible for the Hz synthesis in the *R. prolixus* and probably the ability to form Hz could have been present in a phytophagous Hemipteran ancestral. Supported by IFS,FENORTE,CNPq and FAPERJ.

PS4-027

Blood antioxidant parameters in subjects from Azorean populations with different sociocultural profile

M L Pavão[1], S António[1], T Figueiredo[1], M C Santos[2], J Nève[3] and A M Viegas-Crespo[2]
[1]University of Azores, Ponta Delgada, Portugal; [2]University of Lisbon, Lisbon, Portugal; 3Free University of Brussels, Brussels, Belgium

Age, sex, physiological and pathological conditions, as well as geographical location reflected in diet, social and environmental conditions and even in life habits are relevant factors in the assessment of the prooxidant/antioxidant status of individuals.

The aim of this work is to compare some antioxidant parameters, such as whole blood Se-glutathione peroxidase (GSH-Px) and erythrocyte Cu,Zn-superoxide dismutase (SOD) activities, serum selenium, copper and zinc levels in healthy subjects from three populations with different sociocultural characteristics. Volunteer men and women aged 20–60 were selected from Ponta Delgada (urban population), Ribeira Quente (fishing population) and Água Retorta (rural population) located in the island of S. Miguel (Azores' Archipelago, Portugal).

No significant differences in GSH-Px activity were found in interpopulation analysis, but the activity tended to be higher in women than in men; in turn, selenium levels, which were maximum in subjects from Ribeira Quente, were significantly higher in male than in female groups, except in the rural population where they were similar. SOD activities, as well as zinc levels were significantly higher in both men and women from the fishing population than in the others, where they did not differ. Also SOD, but not zinc or copper, was higher by 13% in women than in men from Ribeira Quente. The rural population exhibited the highest copper concentrations, being much higher in these women than in those from Ribeira Quente or Ponta Delgada.

Diet, either food or drinking water might be a major cause for the differences observed.

PS4-028

Genomic organization and promoter analysis of the human heat shock factor 2 gene

P Nykanen[1], T-P Alastalo[1], J Ahlskog[1], N Horelli-Kuitunen[2], L Pirkkala[1] and L Sistonen[3]
[1]Turku Centre for Biotechnology, University of Turku, Abo Akademi University, Turku; [2]Department of Biology, Abo Akademi University, Turku; [3]Laboratory Department of Helsinki University Hospital, Helsinki, Finland

The cellular stress response is characterized by the inducible transcription of heat shock genes. By studying the transcriptional activation of these genes, the family of heat shock factors (HSFs) was found. The HSF family consists of factors which share the property of binding to heat shock element (HSE). To date, three members of this family, HSF1, HSF2, and HSF4, have been identified in mammals. HSF2 is a nonclassical member of the heat shock transcription factor family, as activation of HSF2 has been shown during differentiation and development rather than upon cellular stress. Here we report the isolation and characterization of the human hsf2 gene and its 5′-flanking region. The transcription unit of the human hsf2 gene consists of 13 exons dispersed over 33 kbp of genomic DNA on chromosome 6. The hsf2 mRNA is transcribed from multiple sites and initiation from the major start site results in a transcript of 2.45 kb. Examination of the core promoter sequence revealed a high GC content and lack of a canonical TATA box. This feature seems to be common among various species, as comparison of the hsf2 proximal promoter sequences from human, mouse and rat revealed certain highly conserved regions. A functional promoter, as determined by the ability to direct expression of a transiently transfected luciferase reporter gene, resides in a 950-bp upstream region of the human hsf2 gene. This proximal promoter fragment appeared not to be inducible, suggesting that the hsf2 mRNA and protein levels are mainly post-transcriptionally regulated.

PS4-029

Metabolic regulation by Hsp104 protein as a protector of heat shock, oxidative stress and heavy metal stress

K Lee and J Eum
Department of Applied Chemistry, Sejong University, Seoul, South Korea

Abstract withdrawn

PS4-030

Acute stress-induced tissue injury in mice: differences between emotional and social stress

M Soley, O Sánchez, A Arnau, M Pareja and I Ramirez
Department de Bioquimica i Biologia Molecular, Facultat de Biologia, Universitat de Barcelona, Avda. Diagonal 645, 08028-Barcelona, Spain

Emotional stress affects cellular integrity in many tissues including heart. Much less is known about effects of social stress. We studied the effect of emotional (tape-immobilization or restraint, without or with cold exposure) or social (intermale confrontation) stress in mice. Tissue injury was measured by means of the release of enzyme activities to blood plasma: lactate dehydrogenase (LDH), creatine kinase (CK), aspartate transaminase (AST), and alanine transaminase (ALT). Immobilization induced heart damage as indicated the pattern of enzyme activities in plasma, and