WILEY-BLACKWELL

the FEBS Journal

Volume 277 Supplement 1 June 2010

www.febsjournal.org

35TH FEBS CONGRESS
MOLECULES OF LIFE

June 26–July 1, 2010 • Gothenburg, Sweden

Welcome to FEBS 2010, jointly organised by the Swedish Society for Biochemistry and Molecular Biology and the Norwegian Biochemical Society

Abstracts
35th FEBS Congress

Gothenburg, Sweden
26 June – 1 July 2010

SFBM The Swedish Society for Biochemistry and Molecular Biology

N:B:S Norwegian Biochemical Society

explored the gene expression profiles of HIF-1α and BNP-45 as master regulatory gene of oxygen homeostasis and biomarker of HF, respectively. Rats, male, were randomized into seven groups (n = 4 per group), control normoxia exposed to room air, hypoxia group were housed in hypoxic chamber (028%) for 1, 3, 7, 14, 21 and 28 days respectively.

Result: Histopathologic examination shows: Massive hypertrophy of cardiomyocytes accompanied by alterations of intercalated disk, necrosis, fibrosis and apoptosis as a hallmark ventricular remodeling. A drastic increase in plasma BNP-45 levels at 21-day exposure. The BNP-45 mRNA and HIF-1α mRNA expression increased and the activities of HIF-1α were significantly increased compared with control group.

Conclusions: Chronic hypoxia causes: Ventricular hypertrophy accompanied by myocardial structural damage and then progress to heart failure. There were changes in the gene expression either in transcription and post-transcription level.

B4.44
An early zygotic genome activator in tissue patterning formation, a multipotent Drosophila nuclear protein

P. Giannios[1], C. Delidakis[2] and **S. Tsitilou**[1]
[1]University of Athens, Biochemistry and Molecular Biology, Athens, Greece, [2]Foundation for Research and Technology, Institute of Molecular Biology and Biotechnology, Heraklion, Greece

The zinc finger protein Zelda, a key activator of the early zygotic genome in Drosophila, is shown to be necessary for patterning the wing structure during late developmental stages of the fly. This protein has been shown to play crucial roles during embryogenesis. Our data suggest that Zelda affects major components of signalling pathways such as Hedgehog and Notch. Spatiotemporal overexpression and knockout of zelda's gene product in the larval stages of the fly, impair wing development resulting in abnormal adult tissue formation. In these experiments several changes in the production patterns of proteins such as Patched and Wingless are observed, indicating a direct involvement of Zelda in the signalling cascade involving these proteins. A prominent role of Zelda in cell cycle progression has been suggested by previous experiments. However, cell cycle promotion could be linked to or divorced from patterning decisions. Zelda is known to be involved in both processes and it remains to be elucidated the exact mechanism of this involvement.

B4.45
Nuclear myc promoter-binding protein-1 (MBP-1) expression is a prognostic factor in invasive ductal breast carcinoma

C. Mazzarella[1], A. Ferro[2], M. Lo Presti[2], F. Contino[2], S. Sbacchi[2], E. Roz[3], C. Lupo[3], G. Perconti[4], A. Giallongo[4], A. Marrazzo[1] and S. Feo[2]
[1]University of Palermo, Dipartimento di Oncologia Sperimentale e Applicazioni Cliniche, Palermo, Italy, [2]University of Palermo, Department of Experimental Oncology and Clinical Applications, Palermo, Italy, [3]La Maddalena Hospital, Anatomical Pathology Department, Palermo, Italy, [4]CNR, Institute of Biomedicine and Molecular Immunology, Palermo, Italy

Myc Promoter-Binding Protein-1 (MBP-1) is a transcriptional repressor, generated by alternative translation of the α-enolase mRNA, that negatively regulates c-Myc gene expression (1) and plays a suppressive role on tumorogenesis (2, 3). We analyzed α-enolase and MBP-1 expression and localization in normal breast epithelium and primary infiltrating ductal breast carcinoma (IDC) from 177 patients by Western blotting and immunohistochemical analyses, using specific anti-α-enolase mAbs. A significantly increase in α-enolase expression was observed in 98% of the analysed tumors, compared to normal tissues. Nuclear MBP-1 has been found in almost all normal tissues while its expression is retained in only 35% of the matched tumours. Statistically significant inverse correlation was observed between expression and nuclear localization of MBP-1 and ErbB2 and Ki-67 expression, node positivity and tumor grade. Furthermore, nuclear MBP-1 is associated with good disease-free survival of patients with primary IDC. Transfection experiments in human breast SKBr3 cells (ErbB2+) demonstrated that MBP-1 ectopic expression results in down regulation of ErbB2 expression, and led us to identify the ErbB2 promoter region involved in the binding, indicating that, like c-Myc gene, ErbB2 is a direct target of MBP-1 transcriptional repression fuctions in breast cancer. Owing to the prognostic influence of nuclear-MBP-1 expression in a subgroup of small tumors and among patients with node-negative and ErbB2- cancers, where the need for prognostication is the greatest, MBP-1 nuclear expression may prove to be a clinically valuable prognostic variable for breast cancer patients.

B4.46
GAPDH regulation in human tumor cells under hypoxic oxygenation conditions from different origin and their suitability as experimental housekeeping genes

H. M. Said[1], B. Polat[1], C. Hagemann[2], B. Schoemig[2], A. Staab[3], M. Flentje[1] and D. Vordermark[4]
[1]University of Würzburg, Medical Faculty, Radiation Oncology, Wuerzburg, Germany, [2]Department of Neurosurgery, University of Würzburg, Medical Faculty, Tumor Research Laboratory, Wuerzburg, Germany, [3]Paul Scherer Institute, Proton Research, Villigen, Switzerland, [4]Martin-Luther-University-Halle-Wittenberg,, Radiation Oncology, Halle, Germany

Gene expression studies related to cancer diagnosis and treatment are important. In order to conduct such experiment accurately, absolutely reliable housekeeping genes are essential to normalize cancer related gene expression. However, no single gene of this group of genes manifests always stable expression levels under all experimental conditions. Incorrect choice of housekeeping genes leads to interpretation errors of experimental results including evaluation and quantification of pathological gene expression. Here, we examined (a) the degree of GAPDH expression regulation in Hep-1-6 mouse hepatoma and Hep-3-B and HepG2 human hepatocellular carcinoma cell lines as well as in human lung adenocarcinoma epithelial cell line (A-549) in addition to both HT-29, and HCT-116 colon cancer cell lines, and 4 glioblastoma cell lines under hypoxic conditions *in vitro* in comparison to other housekeeping genes like β-actin, serving as experimental loading controls.

Results: No hypoxia-induced regulatory effect on GAPDH expression was observed in cell lines studied *in vitro* that were; Hep-1-6 mouse hepatoma and Hep-3-B and HepG2 human hepatocellular carcinoma cell lines, Human lung adenocarcinoma epithelial cell line (A-549), both colon cancer cell lines HT-29, and HCT-116, glioblastoma U373, U251,U87-MG and GaMG.

Conclusions: As it is the case for human hepatocellular carcinoma, mouse hepatoma, human colon cancer, and human lung adenocarcinoma, brain cancer GAPDH represents an optimal choice of a housekeeping gene and / (or) loading control to determine the expression of hypoxia induced genes in tumors of different origin.