This study was supported by the Research Strenghtening Grant from BIOTEC-NSTDA, Thailand.

512 Poster

Characterization of bladder tumoral lineages established in vitro

R. Marrakchi[1], S. Ouerhani[1], K. Bougatef[1], A. Darwiche[2], Y. Messai[1], N. Kourda[3], M. Chebil[2], A. Ben Ammar Elgaaied[2]
[1]Faculté des Sciences de Tunis, Biologie, Tunis, Tunisia; [2] Hospital Charlles Nicolles, Urologie, Tunis, Tunisia; [3] Hospital Charlles Nicolles, Anathomopathologie, Tunis, Tunisia

Introduction: On the basis of the epidemiological data in Tunisia, we were interested in the establishment of tumoral lineages from biopsies of bladder taken from the patients presenting a vesical tumor. Tumoral lineages in culture allow the characterization at the phenotype and functional level. Our objective is to study the cell lines from the point of view of their susceptibility to immunity effectors and to test them towards drugs used in chemotherapy with the aim of understanding the phenomena of tumoral cells escape to apoptose.

Methods: We have undertaken several approaches for the establishment of tumoral lineages which have been obtained after 12 months. The phenotypic characterization of two tumoral lineages was realized by cytometry and immunohistochemical test using monoclonal antibodies specific for cell surface markers, tumoral antigens and various receptors with domains of death.

Results:We observed a reduction of expression of CMH class molecules on the surface of the tumoral cells. This result was expected since it was already described that the transformation into maligant cells is often associated with a reduction of these CMH class, this reduction being a marker of bad forecast.On the contrary, we observed an increase of the expression of ICAM-1 adhesion molecule that is usually correlated with a fast tumoral progress, because it facilitates angiogenesis. In the second stage, we studied the susceptibility to apoptose of the two lineages, using adapted positive control lines; For that purpose, we studied the receivers with domains of death such as Fas, TRAIL and TNF. Apoptose induction in vitro was realized by using the way of the TNF, of Fas L or the TRAIL at the end to understand the tumoral resistance to lysis. At a last stage, we realized the immunohistochimical characterization of the established lineages and biopsies of cancer of patients' bladder recruited at the hospital by means of antibodies used in the immunofluorescence.

Conclusions: This comparison is interesting because it is not obvious that the phenotype of the lineage is identical to the that of the biopsy: the in vitro culture selects clones the most adapted to the culture conditions.

513 Poster

Polyamine analogue treatment of neuroblastoma

E. Söderstjerna[1], K. Hellman[1], S. Oredsson[1]
[1]Lund University, Cell and Organismbiology, Lund, Sweden

Neuroblastoma is a malignant childhood cancer of the sympathetic nervous system. It is one of the most common tumours found in childhood cancers with a mortality of 50%. Children with cancer are given the same treatment as adults – surgery, chemotherapy or radiation. This is not optimal as growing and developing children are more sensitive than adults. Our aim is to find chemotherapeutic agents that have fewer or no side effects. Such possible chemotherapeutic drugs are polyamine analogues. Polyamines are essential for all living cells and they are involved in cell proliferation, cell differentiation and apoptosis. Their levels are tightly regulated and increased polyamine levels are a hallmark of cell proliferation. Polyamine analogues reduce cellular polyamine pools without taking over the function of the natural polyamine. In several types of cancer cells decreased polyamine levels result in growth inhibition followed by apoptosis, while normal, healthy cells will survive undamaged. Some of these compounds have shown exceptional efficacy in animal tumour models. Several polyamine analogues are in clinical trails and they have shown surprisingly low toxicity in humans. There are thoughts of using them in the treatment of childhood tumours. In the present project neuroblastoma cell lines are grown as multicellular spheroids. Multicellular spheroids resemble tumour growth in vivo better than cells cultured in monolayer. Flow cytometric analysis has shown that polyamine analogue treatment results in cell death. We are studying multicellular spheroids of two neuroblastoma cell lines, SH-SY5Y and LA-N-1, composed of 10 000, 20 000, 50 000, 100 000, and 200 000 cells. Presently we are cryo sectioning spheroids that have been labelled with bromodeoxyuridine to investigate cell proliferation after treatment with polyamine analogues. The sections will also be used for investigation of the level of hypoxia with antibodies against hypoxia inducible factor 1 (HIF1).

514 Poster

Expression of S100 proteins in the progression of melanocytic lesions

C. Enerback[1], E. Shubbar[1], S. Petersson[1]
[1]Institute of Biomedicine, Department of Clinical Genetics, Gothenburg, Sweden

Background: S100 proteins are differentially expressed in tumors of epithelial origin, exemplified by a high expression of S100A7 in ductal carcinoma in situ (DCIS) correlated to poor prognosis. Less is known about their expression in melanocytes and melanocyte-derived tumors, of neuroectodermal origin.

Materials and Methods: We compared the expression of seven S100 proteins, using Western blotting, in a panel of cell lines comprising normal melanocytes, melanoma cells, normal keratinocytes and squamous carcinoma cells under different conditions of culture. We also examined the immunohistochemical expression of S100 A7, S100A9 and S100 A10 in a panel of 47 melanocyte-derived lesions comprising melanocyte nevi and melanomas.

Results: S100A1 was expressed at a low level in two studied cancer cell lines, but was absent in their normal counterparts. No differential expression was observed in S100A4, S100A7, S100A8, S100A9 and S100A11. In contrast, S100A10 was downregulated in three melanoma cell lines compared to normal melanocytes. SAGE informatics of NCI 60 microarray expression data cell lines revealed a significant correlation between the expression of S100A10 and the expression of the proliferation marker Ki67. S100A7 and S100A9 were not expressed in any of the melanocytic lesions but strongly expressed in hyperplasic epithelium covering the lesions. S100A10, on the other hand, was variably expressed in the melanocytic lesions with the highest expression in regions with a strong proliferating or differentiating capacity, especially in regions in or near the epidermis.

Conclusion: Our results suggest that S100A10 may have a role in the regulation of proliferation or maturation of melanocytes and may have a potential value as a biomarker of activity.

515 Poster

Expression profile of genes coding for DNA repair in human pancreatic cancer

D.I. Gheonea[1], A. Saftoiu[1], M. Ioana[1], T. Ciurea[1]
[1]University of Medicine and Pharmacy Craiova, Research Center in Gastroenterology and Hepatology, Craiova, Romania

BACKGROUND: Pancreatic adenocarcinoma is the fifth leading cause of cancer death and has the lowest survival rate for any solid cancer. Unfortunately, only 10–15% of patients present with small, resectable cancers. The aim of our study was to compare genes expression profiles of malignant and benign pancreatic masses samples in order to distinguish differentially expressed genes by quantitative real-time reverse transcription-polymerase chain reaction (RT-PCR) in endoscopic ultrasound guided fine needle aspiration (EUS-FNA) specimens.

PATIENTS AND METHOD: We analyzed 10 genes associated with DNA repair in 26 EUS-FNA specimens including pseudotumoral chronic pancreatitis (n=8) and pancreatic cancer patients (n=16). The final diagnosis was obtained by EUS-FNA cytology analysis, by surgical pathology or 6 months follow-up. Quantitative RT-PCR was performed to measure the expression of these 10 selected genes in EUS-FNA specimens. Our selected mismatch repair genes were: ABL1, ANKRD17, EXO1, MLH1, MLH3, MSH2, MSH3, MSH4, MSH5, MSH6. In order to asses the RNA quality we analyzed the 18S and 28S ribosomal RNA bands integrity by electrophoresis on a denaturing agarose gel. For every sample 100 ng of total RNA were available.

RESULTS: In pancreatic cancer samples we detected a significantly ($p<0.05$) reduced expression of four DNA repair genes (EXO1, MLH1, MLH3, MSH2) than in chronic pancreatitis specimens.

CONCLUSION: Expression profiling is a useful method to identify potential target genes. Molecular analysis of EUS-guided FNA samples in pancreatic cancer appears as a valuable strategy for improving our knowledge of molecular mechanism of cancer initiation and progression.

516 Poster

Clinical and pathologic characteristics of Gastrointestinal Stromal Tumors in 11 Egyptian patients/implications for surgical management at Cairo university hospitals

A. Mohsen[1], Y. El-Nahas[2]
[1]Faculty of Medicine-Cairo University, General Surgery, Cairo, Egypt; [2] National Cancer Institute [NCI]-Cairo University, Clinical Pathology, Cairo, Egypt

Background: Gastrointestinal sromal tumors (GISTs) are rare, but have clinical relevance. The majority is gastric with diverse symptoms, and there