PO-485 LOW ABUNDANCE CIRCULATING PROTEINS IN GIANT CELL TUMOURS OF BONE

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Introduction Circulating low-abundance proteins/fragments generating from tumour cells and tissues, represent the most important source of cancer biomarkers useful for early diagnosis and prognosis. Giant cell tumour of bone (GCT) is a benign neoplasm occurring in the long bone and in the axial skeleton of young adults. Approximately 5% of GCT develop pulmonary metastases. Although many biomarkers have been proposed, identification of circulating low abundance molecules may be useful to predict metastasis with a non invasive method.
Material and methods The hydrogel nanoparticles technique followed by mass spectrometry was used to detect low molecular weight serum proteins or protein fragments in serum of 20 GCT patients with different clinical course and in 10 healthy sera used as control. The most representative low-abundant *de novo* or differentially abundant proteins were submitted to String database in order to define protein-protein interaction network. Cluster analysis was performed to identify prognostic groups of patients with similar abundance of proteins that significantly discriminate between the groups.
Results and discussions For the 25 low-abundant *de novo* or differentially abundant proteins identified, we recognised that the top interconnected pathways included protein activation cascade, wound healing, blood coagulation, cell-substrate adhesion. Proteoma cluster analysis separated metastasis-free from metastatic GCT patients in two well-defined groups where serum levels of signalling transduction mediators and regulators of kinase activity presented a high discriminatory power. Increased expression of proteins STAT5B, GRB2 and OXSR1 was related to a higher probability of metastasis.
Conclusion In conclusion, using a no invasive technique, we identified differentially abundant serum biomarkers, also providing prognostic information in patients with GCT of bone. Future studies are ongoing to establish the interplay between these biomarkers in order to fully understand the mechanism involved in tumour development and to focus on the planning of tailored therapies that should be more effective and less toxic.

PO-486 SURROGATE BIOMARKERS OF CLINICAL EFFICACY IN STAGE IIIB/IV NON-SMALL-CELL LUNG CANCER PATIENTS TREATED WITH AN OPTIMISED EGF-BASED VACCINATION SCHEDULE

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Introduction In previous clinical trials were reported that an EGF-based vaccine administration was immunogenic in advanced non-small cell lung cancer (NSCLC) patients and the elicited immune response was associated with patient´s survival. However, the description of additional key features associated with a 'protective' humoral response, using an optimised immunisation schedule, remained unknown.
Material and methods A phase III trial was designed using an optimised immunisation schedule. It included higher antigen dose and injections at multiple vaccination sites. Immune response and circulating biomarkers were studied in a subset of patients. EGF-specific antibody titers, IgG subclasses and peptide immunodominance was assessed by ELISA. *In vitro* EGF-neutralisation capacity of immune sera was evaluated by Western Blot and EGF-IgG binding kinetics by surface plasmon resonance (SPR) technology. Additionally, circulating levels of EGFR ligands (EGF, TGFα, AR) and others NSCLC-associated circulating factors were measured.
Results and discussions EGF vaccine administration elicited antibody titers higher than 1:4000 in 80% of vaccinated patients after 3 months of treatment. The EGF-specific humoral response was directed against the central region of the EGF molecule and was mainly composed by IgG3/IgG4 antibody subclasses. The capacity of post-immune sera to inhibit EGFR phosphorylation increased during the course of the immunisation scheme and was associated with EGF-specific antibody affinity maturation. Basal concentrations of EGF and TGFα in the serum were affected by EGF- based immunisation. The avidity and the EGFR phosphorylation inhibition capacity of elicited polyclonal antibodies was associated with the clinical benefit of treated patients.
Conclusion Optimising the vaccination schedule allowed to induce the development of a protective humoral response in a high percent of NSCLC vaccinated patients. Quality of induced anti-EGF polyclonal antibodies was associated with clinical benefit (clinical trial registration number: RPCEC00000161).

PO-487 PROGNOSIS OF TRIPLE NEGATIVE BREAST CANCER IS ASSOCIATED WITH MHC II GENES

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Introduction Triple negative breast cancer (TNBC) is clinically to denote women with invasive breast cancer whose tumours lack expression of oestrogen receptor (ER-), progesterone receptor (PR-), or overexpression of HER2/Neu. TNB tumours behave aggressively and are not candidates for ER or HER2/Neu targeted therapy. In previous published study of 47 TNBC patients with RNA-seq data, we discovered that twenty-four genes related MCH pathway exhibited significantly higher expression in tumour tissue from patients who did not relapse, including eleven genes representation of the MHC II pathway. In this study, we further investigated 24 genes in MCH pathway in prognosis of TNBC. This work will lead in future guidance in treatment of TNB based on patient's' gene profile and also provides means to assess prognosis in TNBC.
Material and methods Forty-seven snap frozen primary TNBC tumour specimens were analysed using RNA-seq. Descriptive analysis and logistic regression model were used to identify