clearance is a marker of pathogenicity, diagnosis or prognosis in plasma cell dyscrasias requires further study.

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Identification of potential diagnostic markers in bronchial fluid of patients with non small cell lung cancer (NSCLC)

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Background: Lung cancer ranks among the most common and most lethal malignancies worldwide. Given the fact that survival of lung cancer patients is very poor, it is logical to speculate that early detection might result in more favourable outcomes for these individuals. New proteomic techniques can identify potential diagnostic and prognostic markers. The aim of this study was to find protein markers in bronchial fluid which could enable early diagnosis in NSCLC.
Materials and Methods: We have included 96 patients with NSCLC diagnosed using bronchoscopy (64 scamous/29 adenocarcinoma/3 others) and 49 consecutive patients with non pathological bronchoscopy. Bronchial fluid was obtained from each patient and potential protein markers were studied. Bronchial fluid was centrifuged and supernatant proteins were analysed using bidimensional electrophoresis with poliacrilamid gel stained with silver nitrate. Gel was scanned and analysed with *Progenesis* PG6220 program, which measures intensity of each spot. Resultant intensities in each group of patients (NSCLC/non pathological bronchoscopy) were compared using T-Student method. We selected as potential markers those spots with a p value of less than 0.05. We calculated "fold change" of each spot as the ratio between mean intensity in NSCLC bronchoscopies samples and non pathological bronchoscopies samples.
Results: We analysed 300 spots in each sample and we found 31 potential markers whose fold-change ranges from 1.49 to 7.41; 15 of the markers were expressed in a higher level in NSCLC samples and the other 16 were expressed in a lower level.
Conclusions: We have identified 31 differential protein markers in bronchial fluid among our patients. These results could lead in an early diagnostic test which must be validated in future studies.

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Free light chains in patients with renal impairment associated or not with hypergammaglobulinemia

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Introduction: Serum immunoglobulin-free light chain (FLC) assay is a major marker in the evaluation and management of patients with plasma cell dyscrasias. However FLC are known to be metabolized by kidneys and these patients frequently present renal insufficiency. We retrospectively assessed the effect of renal impairment on serum and urinary polyclonal FLC values in patients with or without polyclonal hypergammaglobulinemia.
Methods: K and L FLC concentrations were measured by nephelometry (Freelite ®, The binding site) in serum and 24-h urines from 80 patients [73 (22−91) years]. Patients with monoclonal protein detected by serum and/or urinary protein immunofixation electrophoresis were excluded. Three arbitrarily groups of patients with normal serum immunoglobulins concentrations and FLC K/L ratio (rFLC) were defined with respect to type of proteinuria (Hydragel Proteinuria, Sebia) and to K and L FLC renal clairance ratio (CK/CL) as physiologic (C, n = 11), predominant tubular (T, n = 27) or predominant glomerular (G, n = 31) groups. A fourth group of patients had renal impairement and polyclonal hypergammaglobulinemia (H, n = 11). Results: median (ranges); Mann-Withney test (significance: $P < 0.05$), Spearman correlations (significance: $P < 0.02$).
Results: Throughout C, T and G groups, K and L FLC serum concentrations, urinary excretions and renal clearances were significantly inversely correlated with glomerular filtration (as evaluated by 1/serum creatinine concentration), regardless of the type of proteinuria. Serum rFLC was inversely correlated while urinary rFLC and CK/CL were positively correlated with glomerular filtration. In H as compared to G group, glomerular filtration and CK, CL, CK/CL were similar suggesting similar renal impairment; however, in H as compared to G group, FLC serum concentrations of K [101 (57–344) vs 34 (20–120) mg/L, respectively] and L [60 (42–174) vs 34 (15−78) mg/L, respectively], urinary excretions of K [327 (91–1328) vs 140 (35–537) mg/24 h, respectively] and L [57 (24–371) vs 40 (10–252) respectively] and serum rFLC [1.3 (1.0−2.3) vs 1.0 (0.4−1.7) respectively] were significantly higher.
Conclusions: K and L FLC serum concentrations, urinary excretions and serum rFLC increased with progressive renal impairment, an effect that was reinforced by polyclonal hypergammaglobulinemia. Therefore, interval references for K and L values and serum and urinary rFLC probably should be related to creatinine for the evaluation and management of patients with plasma cell dyscrasias presenting renal insufficiency with or without polyclonal hypergammaglobulinemia.

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Study of EGFR mutation expression in adenocarcinoma of lung and their implication in the specific treatment – institutional experience

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Background: In the last years, the work groups that are contributing to the study of the treatment of the non-small-cell lung cancer (NSCLC), being one of the emergent lines, the epidermal growth factor receptor (EGFR). Retrospective analyses of the biopsies of patients, mutation of the tyrosine kinase domain of the EGFR confer to the patients a strong sensitivity to gefinitib.
Purpose: Examine retrospectively EGFR mutations at exones 18, 19 and 21 to evaluate the prevalence in a small series of our institution with pulmonary confirming biopsy of adenocarcinoma.
Materials and Methods: We studied 23 patients, of them 7 were females an 16 males, with median age was 58 years (32−76). The stage of patients at diagnosis, according the TNM staging system was: 9 patients (39%) were classified at stage I; 1 (4.5%) at stage II; 7 (30.5%) at stage III; and 6 (26%) at stage IV. Depending on personal background, 20 patients (87%) were smokers and the rest (13%) non-smokers. The study took place on samples peripheral blood and paraffin-embedded tissue. The analysis of gene that codifies the EGFR made by means of genomic obtaining of DNA: 1) from blood-EDTA, 2) from the rich paraffin tissue in tumour. The exones identification 18, 19, and 21 of gene EGFR was made by means of PCR. In each series two controls were used: one positive with genomic DNA of a patient control and one negative (without DNA) to detect possible contaminations. The patients previously were informed about the test that was going away to make, following the effective ethical norms in our country.
Results: Mutations were not detected DNA from peripheral blood of the 23 studied cases. Sixteen of 23 (69%) patients harbored mutations in EGFR gene. 4/23 (17%) presented prognostic therapeutic meaning mutations according to those described before, and were 3 cases of deletion LREA in exon 19 and one mutation L858 of exon 21. These 4 cases corresponded to females.
Conclusions: In our environment, the mutations frequency of EGFR gene in adenocarcinoma pulmonary with therapeutic-clinical meaning is very low and predominantly in female sex.
The systematic study of the EGFR gene mutations may allow the individualization of therapy for patiens with lung adenocarcinoma.

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Potential diagnostic markers in bronchial fluid of small cell lung cancer (SCLC)

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Background: Lung cancer is a major cause of mortality worldwide and overall survival rate has not improved significantly over the past 20 years. Although the incidence of SCLC is declining, it remains a worldwide public health problem. An early diagnosis could improve prognosis and survival among these patients. The aim of this study was to identify protein markers obtained from bronchial fluids of SCLC patients which may differ from non-pathological bronchoscopy samples.
Materials and Methods: We have included 43 patients with SCLC diagnosed using bronchoscopy and 49 consecutive patients with non pathological bronchoscopy. Bronchial fluid was obtained from each patient and potential protein markers were studied. After being centrifuged, supernatant proteins were analysed using bidimensional electrophoresis