EUROPEAN RESPIRATORY SOCIETY
INTERNATIONAL CONGRESS 2023
MILAN Italy, 9-13 September

Identification of potential biomarkers for diagnosis of lung adenocarcinoma

I. Tegami (Barretos, Brazil), G. Maria Stanfoca Casagrande (Barretos, Brazil), L. Sussuchi Da Silva (São Paulo, Brazil), R. Oliveira Cavagna (Barretos, Brazil), M. Gonçalves (Barretos, Brazil), F. Ferreira Da Silva (Barretos, Brazil), E. Caetano Albino Da Silva (Barretos, Brazil), V. Duval Da Silva (Botucatu, Brazil), P. De Marchi (Rio de Janeiro, Brazil), R. Manuel Reis (Barretos (Brazil); Braga/Guimarães, Portugal), L. Ferro Leal (Barretos, Brazil)

Background: Lung cancer is the deadliest cancer worldwide. Therapeutic options for lung adenocarcinoma(LUAD) have dramatically increased, but late diagnosis remains a challenge. Differentially expressed genes(DEG) may be employed as biomarkers for LUAD detection. Aim: To identify potential biomarkers for diagnosis of LUAD. Materials and Methods: We evaluated fresh-frozen tumoral tissues from patients with LUAD(n=53). Gene expression analysis was performed using the nCounter® PanCancer Pathways panel(NanoString® Technologies). Upregulated and downregulated genes were selected according to fold-change(FC≥|2|) and p-value(p≤0.01) using the ROSALIND® software. DEG were in silico validated using The Cancer Genome Atlas Lung Adenocarcinoma dataset. Enrichment analysis was performed using STRING database. Median normalized counts were used as cut-offs for stratification of genes for survival analysis. Results: We identified a 78-gene signature comparing LUAD tissue and non-tumoral lung tissue. Seventy-seven out of the 78-gene signature were validated($p<0.05$), being considered biologically connected(PPI p-value=1.0e-16). Patients were stratified into groups based on gene expression levels into higher, intermediate and lower groups. An association with survival was noted($p=0.001$), whereas the intermediate group had a hazard ratio(HR) of 1.58(95%CI:0.4-5.9;$p=0.48$) and the lower group had a HR of 4.29(95%CI:1.1-16.5;$p=0.034$). Notably, the downregulation of CD19, IL1R2, and TLR4 showed HRs of 2.75(95%CI:1.27-5.91;$p=0.10$), 2.34(95%CI:1.09-5.04;$p=0.29$), and 2.15(95%CI:1.02-4.55;$p=0.043$), respectively. Conclusion: We identified a 78-gene signature that might help define a more accurate diagnosis for lung adenocarcinoma.