P35

Identification of epigenetic biomarkers in COPD and lung cancer using minimally invasive samples

Teresa Morales-Ruiz[1,2,3]*, Adriana Patricia Rojas Moreno[4], Litzy Gisella Bermúdez Liscano[4], Camila Bernal Forigua[4], David Segorbe[1,2,3], María Isabel Martínez -Macías[1,2,3], Dolores Córdoba-Cañero[1,2,3], Bernabé Jurado Gámez[1,3], Laura Caballero Ballesteros[1,3], María del Sol Arenas de Larriva[1,3], Rafael R. Ariza[1,2,3], Teresa Roldán-Arjona[1,2,3]

[1]Maimonides Biomedical Research Institute of Cordoba (IMIBIC), Córdoba, Spain.
[2]Department of Genetics. University of Cordoba, Córdoba, Spain.
[3]Reina Sofia University Hospital, Córdoba, Spain.
[4]Institute of Human Genetics, School of Medicine,
Pontificia Universidad Javeriana, Bogotá, Colombia.
** e-mail: b52morum@uco.es*

Lung cancer (LuCa) is the leading cause of cancer deaths worldwide, partially because is an asymptomatic disease in early stages. It also shares many symptoms with chronic obstructive pulmonary disease (COPD), which is considered a risk factor for development of lung cancer, as is tobacco use. In addition, lung cancer and COPD are difficult to diagnose due to sampling complexity and the absence of biomarkers.

5-methylcytosine (5-meC) is an epigenetic mark that causes gene silencing. Altered DNA methylation patterns are common in a growing number of human diseases, such as cancer. Tumour cells display local hypermethylation of tumour-suppressor gene promoters and global hypomethylation of gene-poor regions and repetitive sequences.

In this work, we aimed to develop a highly sensitive methodology for detection of epigenetic biomarkers for early diagnosis of lung cancer and COPD using minimally invasive samples (exhaled breath condensate and blood plasma)

.For this purpose, samples were classified into four groups: 1) control group without risk factor (healthy); 2) smokers risk factor group (Smokers); 3) chronic obstructive pulmonary disease risk factor group (COPD) and 4) lung cancer group (LuCa). DNA was extracted, bisulfite-modified, and quantitative methylation specific PCR (qMSP) perfomed to determine methylation status for a group of genes selected previously associated with COPD or LuCa (p16, Rassf1, Shox2, pTGER4 and Line1).

To date, blood plasma samples have been analysed and preliminary data show Rassf1 methylation in 38% LuCa, 10% COPD, 12.5% Smokers and 12.5% healthy subjects. Furthermore in Shox2, methylation was observed in 22% of patients in LuCa group and no methylation was observed in the rest of selected genes in any patient. These preliminary data suggest that methylation of Rassf1 and Shox2 could be useful epigenetic biomarkers for diagnosis of lung cancer using minimal invasive samples.

Keywords:
Lung cancer, COPD, epigenetics, DNA methylation, early diagnosis, minimally invasive samples.