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BIOMARKERS BASED ON GENE EXPRESSION IN LUNG CANCER

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Introduction

Lung cancer is the most common neoplasm and also has the highest mortality, so early histological diagnosis is essential. The real-time PCR technique is a reliable and widely used method for the identification of possible biomarkers. The main objective of this work is to corroborate in a larger population cohort the possible utility of gene expression changes identified by our research group in previous works as lung cancer biomarkers. (1)

Materials and methods

A population sample of 23 patients, with lung adenocarcinoma (n=13) or squamous cell carcinoma (n=10) in its early stages, were recruited. From previous work, where massive sequencing was used, we have identified changes in the expression of ten genes as potential cancer biomarkers (1). We applied the qPCR technique in tumour and healthy lung tissue for each of these possible biomarkers.

Results

Of the ten possible genes as expression biomarkers, we have been able to corroborate the validity of four of them in lung adenocarcinoma, being CA5BPB, IYD, SLC44A4 and TMC5. While in the case of patients with squamous cell carcinoma it was not possible to corroborate the usefulness of any of them.

Conclusions

We have been able to validate that the expression changes of the CA5BPB, IYD, SLC44A4 and TMC5 genes could be used as specific biomarkers. On the other hand, we remark that the alteration of the expression profiles in adenocarcinoma is more marked, which would make it subsidiary to a search for biomarkers due to its high genetic load.
