The clinical use of determination of gene expression of RNA in non-small cell lung cancer (NSCLC)

Abstract

Introduction

Non-small cell lung cancer (NSCLC) belongs to the most frequent causes of cancer deaths worldwide. Chemotherapy (CHT) has still (except pemetrexed) administered according to stages and patients comorbidities, without the use of other predictive markers. It results into only low objective therapeutical response that differs in indivial patients without more clearly known causes.

Aims

The aim of our research was to find possible predictive markers in the form of mRNA or miRNA, which would help to reduce the effect of NSCLC / CHT for selected groups of patients.

Methods

In three groups of patients (42 patients with radically resected adenocarcinomas stage 1; 90 patients with NSCLC who have undergone surgical resection and 59 of them consequently adjuvant CHT; 81 patients palliatively treated in combination platinum derivative + paclitaxel/gemcitabine +/- sequential radiotherapy with advanced squamous NSCLC stages 3B, 4), we examined the effect of expression of mRNA and miRNA until relapse (DFI) / progression (PFS) and overall survival (OS). Expressions were determined with the real-time PCR methodology using UPL probes. Statistical analysis used cox regression model and Kaplan - Meier distribution functions.

Results

In the first group of patients we demonstrated no statistically significant relationship between expression of selected markers and DFI / OS in the whole set. Only a subset of smokers/exsmokers shown significant relationship between levels of mRNA BRCA1and OS. The second group of patients of the general population has no significant relationship to DFI and OS, these results were significant only for the selected subgroups. In the analysis of more variables we found no reinforcing/debilitating combinations of expression of given mRNA. In palliativelly treated patients we didn´t prove relationship arranged markers to PFS and in the overall group neither to OS. Statistically significant differences in the OS were obtained in certain subgroups for some miRNA (miR - 342 - 3p, miR - 34a and miR – 224). We also pointed out the complex links between these miRNAs.

Conclusion

In patients with lung adenocarcinomas stage 1 we didn´t manage to find in the selected panel the marker, which would be an appropriate predictor of administration or non-administration of adjuvant chemotherapy. Patients with non-advanced disease with a high expression of DNA repair genes have had good prognosis after surgery, our investigation hasn´t confirmed the predictive significance of predictive genes which we investigated to adjuvant CHT. In the palliatively treated patients with squamous NSCLC of stages 3B and 4 on the basis of our results the expression of certain miRNA is associated with OS and may serve as a potential prognostic markers in these groups of patiens.