Identification of alternative splicing alterations in small cell lung cancer

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INTRODUCTION

Small cell lung cancer is the most aggressive type of lung cancer, showing poor survival rates. The lack of knowledge about their underlying tumorigenic mechanisms and the lack of effective treatments make the situation more dramatic.

Our main goal is to obtain a specific splicing signature for SCLC that may provide novel molecular targets for prognosis and therapy.

RESULTS

We identified 510 unique genes that show differential transcript expression in SCLC compared to other lung cancers or normal tissues. Results from different analyses were consistent and presented high score and IG values. S1 values were greater than 0.85, many of them reaching the maximum value of 1. Results from analyses comparing similar samples showed lower scores (0.3-0.6) that confirmed the reliability of the obtained values for SCLC analyses.

We also obtained a list of 49 genes for fresh tumours and 46 genes for cell lines that appeared recurrently as a result of at least 7 out of the total 8 performed analyses.

CONCLUSIONS

A set of distinct transcripts are expressed in SCLC compared to other samples.

The identified genes may have functional relevance shedding light to the study of new molecular mechanisms for SCLC.

Identification of these alterations in alternative splicing can benefit the development of prognostic and therapeutic targets of SCLC tumours.

REFERENCES