CHARACTERISATION OF FGFR1-4 AND MET EXPRESSION STATUS IN SQUAMOUS NON-SMALL LUNG TUMORS AND ADJACENT NORMAL LUNG TISSUE

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Background: FGFRs inhibitors are investigated as a potential treatment option for patients with squamous non-small cell lung cancer. While FGFR1-4 are part of multiple biological pathways, their expression in Sq-NSCLC has not been well characterized. Furthermore, MET activation is one of the suggested mechanisms of the resistance towards FGFR inhibitors.

Study Aims: The **aim of the study was to evaluate and compare the *FGFR1-4* and *MET* mRNA expression in** Sq-NSCLC **tumors vs** corresponding lung tissue using **the** optimal set of reference genes

Materials and Methods: **The *FGFR1, FGFR2, FGFR3, FGFR4* and *MET* expression** was determined in 32 primary lung carcinomas (stage IA3 – IIIA) and in 15 corresponding adjacent normal lung tissue samples, by the Real-time PCR **with the use of *P****OLR2* and *ACTB* as reference genes.

Results: The median *FGFR1* and *FGFR4* gene expression on mRNA level was significantly decreased in tumors as compared to control lung samples: *FGFR1* (0.04 vs 0.12, p=0.0005); *FGFR4* (0.01 vs 0.21, p=0.00001). Additionally, the overexpression of *FGFR1-3* and *MET* genes *(FC>2)* was observed in individual samples.

Conclusions: Our preliminary data show that *FGFR1* and *FGFR4* expression is significantly decreased in most of the Sq-NSCLC vs corresponding adjacent normal lung tissue. Yet, the limited size of the study group, necessitates further research to confirm our observations in larger series. Additionally, we recommend the *POLR2A* and *ACTB* as the optimal set for gene expression normalization in the Sq-NSCL carcinomas.

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