# Somatic Mutation Profiling in Head and Neck Squamous Cell Carcinoma: Early Insights from an Ongoing Cohort Study

Melichar Vojtěch 1,2, Galiyeva Liliya 1,4, Netušil Jiří 1,3, Kolář Michal 1,2, Vomastek Tomáš 5, Plzák Jan 4, Šáchová Jana 1

1 Laboratory of Genomics and Bioinformatics, Institute of Molecular Genetics of the Czech Academy of Sciences

2 Department of Informatics and Chemistry, University of Chemical Technology Prague

*3 Faculty of Science, Charles University, Prague*

*4 Department of Otorhinolaryngology and Head and Neck Surgery, First Faculty of Medicine, Charles
 University Prague, Faculty Motol Hospital*

*5 Laboratory of Cell Signalling, Institute of Microbiology of the Czech Academy of Sciences*

Head and neck squamous cell carcinoma (HNSCC) is a genetically heterogeneous disease with a complex mutational landscape. In this study, we aim to identify recurrent somatic mutations in a cohort of 70 HNSCC patients using high-throughput sequencing. Currently, variant calling has been performed on an initial subset of 18 matched tumour-normal samples. Surprisingly, the number of high-confidence somatic variants passing standard filters according to GATK’s Best Practices is relatively low. The most frequent causes of variant exclusion include normal artifact, strand bias and low base quality. The basis for this phenomenon is unclear. Preliminary analysis indicates that TP53, KMT2D and FAT1 are the most commonly mutated genes in the cohort so far, which is consistent with previous studies. As additional samples are processed, we aim to refine the mutational landscape of HNSCC and explore correlations with clinical and pathological features. Transcriptomic data from the same patients are generated and analysed in parallel. This work highlights the technical challenges of somatic variant calling in HNSCC and the importance of rigorous filtering to ensure high-quality and validity of called genomic variants.