

Supervisor statement – Nikolas Tolar

In our laboratory, we study mole-rats as a model of longevity, long female fertility and the effect of ovulations on oocyte quality. The most famous mole-rat is undoubtedly naked mole-rat with publicly available genome. However, as a comparison with this species, and also due to the best availability of aged females, we also study Mechow's mole-rat. This species shares characteristics with naked mole-rat, but did not have available genome sequence to map our sequencing data to. Therefore, the aim of Nik's thesis was to assemble and annotate its genome using our Nanopore and Illumina sequencing data, annotate its transposable elements and compare their expression in the oocytes to the expression in other mammalian species with available oocyte RNA-seq datasets. It was a purely bioinformatics project, using sequencing data generated in our laboratory. For genome assembly and gene annotation, Nik was advised by our collaborator, Anna Voleníková from Petr Nguyen's laboratory.

During work on his project, Nik gained skills in using programs for hybrid genome assembly with long Nanopore reads corrected by short Illumina reads, genome annotation through transcriptome assembly our our and published RNA-seq datasets, as well as in silico predictions, transposon annotation using RepeatModeler and RepeatMasker, RNA-seq data processing and mapping, work with sequencing data visualisation and analysis tool Seqmonk, and developed own Python scripts to further analyse transposon expression. His results will contribute to two publications and the genome assembly will be used as a reference for our future research and research of our collaborators, who already showed interest in this assembly. In addition to work on his Master's project, Nik significantly contributed to a collaborative project with the group of Hana Cahova from Institute of Organic Chemistry and Biochemistry in Prague, helped with other projects in our laboratory whenever some programming of sophisticated use of existing programs was needed, and he also worked on other projects at the Informatic Department of our faculty. Considering all Nik's contributions to our research from the start of his Bachelor's studies, I think that without him, our research would not be where it is now – he can do things that other people in the team, including me, cannot do (and I would probably never be able to or have time to do myself).

Nik is exceptionally talented, hardworking, self-motivated, and has a very nice and easy-going personality, making our interactions and collaboration pleasant and smooth. Thanks to his programming skills, the ability to self-study to extend his knowledge and skills and the ability to critically evaluate the results, he could easily be a Ph.D. student already. I think it is fair to say his programming abilities are more advanced than biological knowledge, but this was considerably improved during the course of his studies, especially from the point of view of the application of programming to solve biological problems.

Nik produced a high quality first draft of methods, results and discussion sections of his thesis which required almost zero changes and comments from my side. In contrast, the first draft of biological part of theoretical background (about mole-rat biology, genomes and transposons) resembled rather a popular science magazine, not a scientific text. I appreciate that Nik then put considerable effort in improving the language and adding more factual information, during the limited time before the deadline (limited time was my fault, as GAČR deadlines and Easter holidays clashed with thesis submission deadlines) – although it could be improved further, in my opinion.

I can conclude that I was more than happy with Nik's work and I am also very happy that he resisted offers of Petr Nguyen and others and decided to stay in our team for his Ph.D. studies.

In České Budějovice on 15/5/2023

Mgr. Lenka Gahurová, Ph.D.