DOI 10.18699/SBB-2022-016

First insight into regeneration potential of the ears of *Acomys cahirinus* in the single-cell resolution

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Key words: regeneration, single-cell RNA sequencing

Motivation and Aim: It is well-known that spiny mouse, *Acomys*, shows exceptional regenerative ability after damaging its internal organs, full-thickness excision of dorsal skin and biopsy punch of ears. However, investigating such outstanding model of regeneration using modern molecular and bioinformatics methods is limited not only due to challenges associated with breeding and colony maintenance, but also due to inaccessibility of high quality *Acomys* genome information. This research presents the first attempt of looking into regeneration process of the *A. cahirinus* ear by RNA sequencing of individual cells.

Methods and Algorithms: We utilized 10X Genomics Single Cell 5' R2-only protocol for RNA-sequencing of the control (right after punch biopsy) and regenerating external ear cells (2 days of regeneration after operation). Due to inaccessibility of high quality genome assembly and annotation for *A. cahirinus*, we chose mouse genome for mapping with cellranger count, using some relaxed settings for STAR (that gave us approximately 97 % mapping rate and 71 % of reads uniquely mapped). Further processing was carried out with Seurat and Conos R packages.

Results: Approximately 4600 and 6800 cells (control and regenerating dataset respectively) were recovered during reads processing and quality control. Using certain gene markers for mouse cell types, we were able to identify all major types of external ear cells, including endothelial cells, cartilage, keratinocytes, smooth muscle cells, fat cells and dermis, glia, neurons and immune cells. Integration of two datasets showed us some differences in clusters structure, and the most remarkable notion was formation of specific cartilage subcluster in the regenerating dataset.

Conclusion: The first results obtained in the given research suggest that, even if the genome assembly for the non-model organism is currently unavailable, usage of closely-related genome may be a good alternative. This is especially applicable to single-cell studies, where good annotation is crucial for successive analysis – for example, for mitochondrial contamination deletion and finding cell-cycle dependent variation.

Acknowledgements: The study is supported by Ministry of Science and Higher Education of the Russian Federation grant 075-15-2021-1344.