Novogene's Single-Cell Sequencing Services Facilitate Mammalian Stem Cell Regeneration Research

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Introduction

Scientists have long sought answers to the regenerative capabilities of mammals, often focusing on highly regenerative lower vertebrates such as zebrafish and salamanders. However, a comprehensive understanding of mammalian regenerative mechanisms remains elusive. In February 2023, a groundbreaking study titled "A population of stem cells with strong regenerative potential discovered in deer antlers" was published in the prestigious journal, *Science*. We are honored to have Prof. Qiang Qiu, One of the corresponding author of this study from School of Ecology and Environment of Northwestern Polytechnical University and an expert in the field of evolutionary genomics and evolutionary medicine, presented a novel understanding of mammalian regenerative abilities. Notably, Novogene contributed to this project by providing sample preparation and single-cell sequencing services.

Utilizing cutting-edge techniques, 10X Genomics single-cell gene expression, the researchers established a spatial and temporal cellular atlas of deer antler regeneration. They systematically characterized the cellular and molecular mechanisms underlying the rapid growth and regeneration of deer antlers. The study demonstrated that the regenerative process in deer antlers aligns with stem cell-based mammalian regeneration. Furthermore, the researchers identified a population of regenerative progenitor cells known as Antlerogenic Bone and Cartilage Progenitor Cells (ABPCs) that possess self-renewal, bone-to-cartilage differentiation, and bone tissue repair capabilities. This cellular foundation provides valuable insights into deer antler regeneration and offers novel perspectives on mammalian regenerative biology, thereby paving the way for future advancements in regenerative medicine.

Q: Can you introduce the key areas of your research group's current research? Why you chose to focus on the organ tissue of deer antlers?

A: We are engaged in evolutionary genomics research, using ruminants as models, applying multi-level omics data to elucidate the genetic basis of complex animal traits across species at a large scale, especially traits with major evolutionary significance. Ultimately, we validate our omics analysis results through functional experiments, recreating phenotypes in experimental systems and regulating complex animal traits.

Deer antler is the only accessory organ in mammals that can regenerate and is a valuable model for studying mammalian regeneration. In our 2019 Science article, we analyzed the mechanism of antler regeneration from a genetic perspective, and in our 2023 Science article, we further elucidated the cellular and molecular mechanisms of antler regeneration and development.

Q: What do you think is the value of choosing deer antler tissue as a research tool for mammalian organ regeneration and stem cell development and differentiation?

A: Mammals have very limited regenerative ability, for example, it is difficult for humans to recover from fractures, and heal wounds after skin injuries, both of which are manifestations of weak regenerative ability. Velvet antler is the only organ that can fully regenerate in mammals. This process includes complete regeneration of bone, skin, nerve, blood vessels and other tissues. A thorough analysis of its regeneration mechanism is of great significance for understanding the basis for the lack of mammalian regeneration capability and advancing human regenerative medicine. Our recent Science paper advanced our understanding of a population of antler stem cells responsible for velvet antler regeneration. These stem cells show a robust ability to affect osteogenesis, chondrogenesis and bone repair. Currently, we are also actively exploring the application of this group of stem cells to human regenerative medicine.

Q: What biological problems or technical challenges need to be addressed during the research process?

A: We strive to overcome the challenge of identifying progenitor cells, elucidating their cellular composition, and determining the process of cellular transformation during antler regeneration. From an evolutionary perspective, we would like to know if the regeneration process of deer antlers is similar to that of salamanders and zebrafish.

Q: Why choose single cell technology to study this topic? Can we solve the research difficulties? What are the advantages?

A: Single cell transcriptome technology can be used to draw a spatiotemporal cellular atlas of velvet antler regeneration, simulate cellular development in the process of regeneration, extend previous research from the molecular level to the cellular level, and can effectively reveal the transformation of specific cell types in the process of development and regeneration. Velvet antler regeneration is based on the activity of stem cells. Single cell transcriptome technology has facilitated the successful identification of a population of core velvet antler stem cells responsible for this process.

Q: What are the results of your single-cell transcriptome sequencing research? What methods have been adopted to verify this result?

A: In this study, we isolated 74730 cells, which were divided into 8 cell classes, including mesenchymal cells, chondroblasts, chondrocytes, osteoblasts, fibroblasts, endothelial cells, pericytes, and immune cells. We further divided these cell types into 20 cell subpopulations. Using temporal analysis of scRNA-seq data, we identified the key stem cells responsible for deer antler regeneration and localized this cell population using tissue immunofluorescence staining. Next, we separated the stem cell population from deer antler tissue using flow cytometry and demonstrated its strong regenerative potential through a series of in vivo and in vitro experiments.

Q: Compared with other similar studies, what are the innovations of your research results obtained through single cell transcriptome sequencing?

A: We constructed a complete regeneration map of deer antler for the first time, depicting the sequence of cellular events in deer antler regeneration.

We also conducted cross species comparative analysis of single cell profiles and found that deer antler stem cells play an important role in mammalian regeneration. Importantly, we successfully identified and isolated the key stem cells of velvet antler with the help of single cell transcriptome technology.

Q: Have you considered using other sequencing techniques to further deepen your research? What are the plans?

A: We plan to use spatial transcriptome technology to further refine the spatial map of velvet antler regeneration, and explore the location and distribution of cell populations and the interaction of cell populations during regeneration.

Q: What technical challenges did you encounter while conducting this study? Has our sequencing technology helped you solve these challenges? Will you continue to choose Novogene's sequencing service in future research, and why?

A: Deer antler regeneration tissue belongs to a special type of tissue, and tissue processing and the preparation of cell suspensions present unique challenges. We would like to express our gratitude to the sample preparation specialists at Novogene for their dedication to optimizing the experimental conditions and successfully completing the preparation of our deer antler samples. We would also like to express our appreciation to the sales staff of Novogene for their excellent communication and assistance in facilitating the successful sequencing our deer antler samples during the epidemic. In the future, we will continue to collaborate extensively with Novogene to explore the field of deer antler research.

Read the original article about Mammalian regenerative mechanisms here: **A population of stem cells with strong regenerative potential discovered in deer antlers | Science**

Learn more about Novogene single-cell sequencing services here: **Single Cell Sequencing - Novogene**

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