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Cell Type Diversity During Sea Urchin Development: A Single Cell Approach to Reveal Different Neuronal Types and Their Evolution

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Abstract

An essential step towards understanding the biology and development of an organism is identifying the molecular fingerprint of its cell types, while to understand its evolution, cell type inventories must be obtained and compared across taxa. This thesis aims to provide a thorough characterization of the genetic program employed in the cell types of a non-chordate deuterostome, the sea urchin. To this end, single cell RNA sequencing (scRNA-seq) was used as a tool to recognize the major cell types in place during the late embryonic and early larval development of the sea urchin Strongylocentrotus purpuratus. The outcome of this thesis was the generation of scRNA-seq cell type atlases for the late gastrula and two early pluteus larval stages, depicting their specific molecular signatures. Extensive analysis of the scRNA-seq data revealed complex regulatory states and novel gene markers. Moreover, the scRNA-seq analysis showed that known gene interactions could be traced back at a single-cell level and that novel functional domains of known gene regulatory modules can be described. In addition, a thorough analysis of the nervous system showed signs of increased neuronal complexity and diversity and identified pre-neuronal cell types employing a similar genetic program to the one utilized by the vertebrate cells that will give rise to the forebrain region. Furthermore, a detailed analysis of the early larva cell types led to identifying specific gastrointestinal and neuronal larval populations with a pancreatic-like genetic program. Lastly, the data presented in this thesis demonstrate that the sea urchin homolog of the master regulator Pdx1, which in vertebrates controls endocrine pancreas differentiation, has an evolutionary conserved role in promoting secretory fate by regulating the differentiation of a specific neuronal type with a strong pancreatic-like molecular signature.