

中国科学家首次解析人脑“中央处理器”，领先美国脑计划

A single-cell RNA-seq survey of the developmental landscape of the human prefrontal cortex

【Nature 系列】人脑前额叶皮层是人类大脑高级功能的关键组成部分，堪称人脑的“中央处理器”。人类的前额叶皮层占到了大脑皮层总面积的三分之一，主要负责人脑的高级智力活动，是人类思想的重要物质基础。主要参与记忆形成、短期储存以及调取功能、语言功能、认知能力、行为决策、情绪的调节等功能。

该团队经研究确认了六大主要类型共计 35 个亚型的细胞，并追踪这些细胞的发育轨迹。同时，通过对神经元单细胞转录组数据的系统分析和深度挖掘，还首次揭示了在人类大脑前额叶皮层发育过程中兴奋性神经元生成、迁移和成熟的三个关键阶段。作者王晓群认为，随着其研究团队此番成果的发表，中国在这方面的研究“应该比美国脑计划快了一步”。

A single-cell RNA-seq survey of the developmental landscape of the human prefrontal cortex 啉
关于人前额皮层发育状况的单细胞 RNA 测序研究

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The mammalian prefrontal cortex comprises a set of highly specialized brain areas containing billions of cells and serves as the centre of the highest-order cognitive functions, such as memory, cognitive ability, decision-making and social behaviour^{1,2}. Although neural circuits are formed in the late stages of human embryonic development and even after birth, diverse classes of functional cells are generated and migrate to the appropriate locations earlier in development. Dysfunction of the prefrontal cortex contributes to cognitive deficits and the majority of neurodevelopmental disorders; there is therefore a need for detailed knowledge of the development of the prefrontal cortex. However, it is still difficult to identify cell types in the developing human prefrontal cortex and to distinguish their developmental features. Here we analyse more than 2,300 single cells in the developing human prefrontal cortex from gestational weeks 8 to 26 using RNA sequencing. We identify 35 subtypes of cells in six main classes and trace the developmental trajectories of these cells. Detailed analysis of neural progenitor cells highlights new marker genes and unique developmental features of intermediate progenitor cells. We also map the timeline of neurogenesis of excitatory neurons in the prefrontal cortex and detect the presence of interneuron progenitors in early developing prefrontal cortex. Moreover, we reveal the intrinsic development-dependent signals that regulate neuron generation and circuit formation using single-cell transcriptomic data analysis. Our screening and characterization approach provides a

blueprint for understanding the development of the human prefrontal cortex in the early and mid-gestational stages in order to systematically dissect the cellular basis and molecular regulation of prefrontal cortex function in humans.