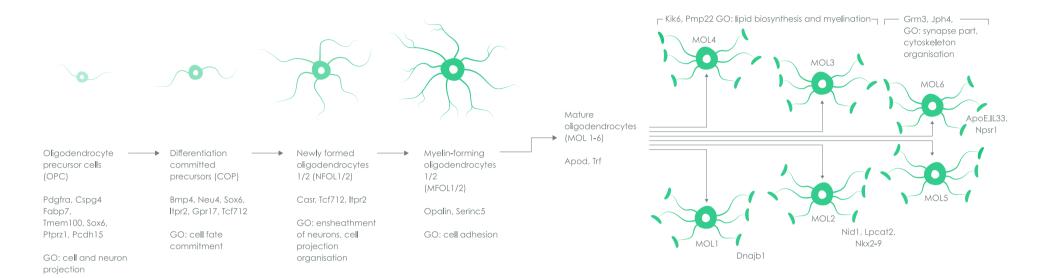
Oligodendrocyte lineage in the mouse CNS

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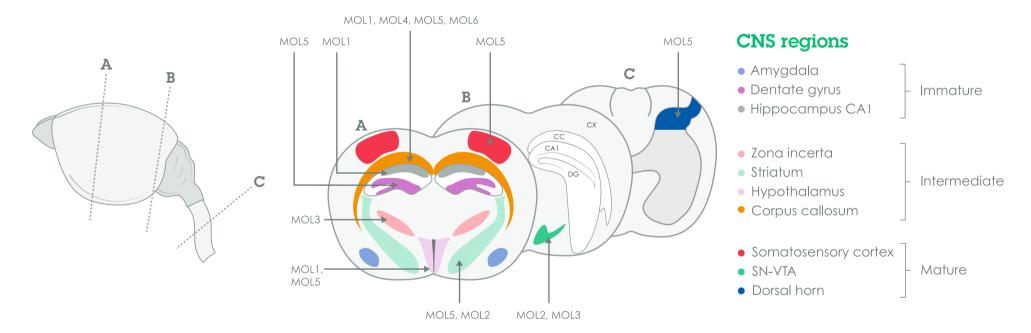
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Oligodendrocytes (OLs) play a number of essential roles in the central nervous system (CNS) including providing metabolic support for neurons and myelination of axons, which allows rapid action potential conduction. Although they have previously been considered a homogenous cell population, single-cell RNA-sequencing has unveiled their transcriptional heterogeneity, revealing twelve distinct oligodendrocyte subpopulations/cell states during mouse CNS development and adulthood^{1,2}.



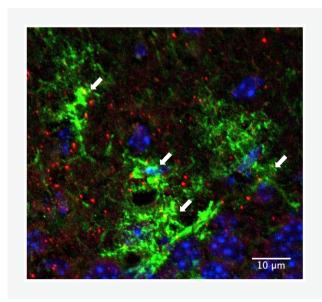
Transcriptional heterogeneity of oligodendrocyte populations in the CNS

OL subpopulations exhibit specific gene expression throughout the maturation process. Pan OL markers SOX10, Olig2, Olig1, MBP, and CNP are not shown, but are present from the COP stage onwards, whilst MOG is present from the MFOL stage onwards. All OL populations/cell states can be found in the juvenile CNS. In the adult corpus callosum and cortex, OPCs, MOL5 and MOL6 predominate. Of note, MOL6 expresses genes involved in synaptic function. GO: gene ontology.



Distribution of mature oligodendrocytes in the juvenile CNS

Mature oligodendrocyte populations are enriched in different regions of the juvenile mouse CNS (P21-P30). These regions have been classified as immature, intermediate and mature regions.



Hippocampus of juvenile mouse (P20) stained with anti-Grm3 (ab140741, red) and DAPI. Green is from the PdgfraCre-GFP reporter line (3). White arrows highlight the oligodendrocytes that are double positive for GFP and Grm3.

References

- 1. Zeisel, A. et al. Cell types in the mouse cortex and hippocampus revealed by single-cell RNA-seq. Science (80-.). 347, 1138–42 (2015).
- 2. Marques, S. et al. Oligodendrocyte heterogeneity in the mouse juvenile and adult central nervous system. Science 352, 1326–9 (2016).
- 3. Roesch, K. et al. The transcriptome of retinal Müller glial cells. J. Comp. Neurol. 509, 225-238 (2008).

Disclaimer: The markers presented in this poster have been revealed by RNA sequencing and were not tested by immunohistochemistry. Due to the similiar transcription profile of MOLs, a combination of markers would be recommended for identifying specific cell states/populations.

