

SCIENTIFIC SEMINAR



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Genetic underpinnings of reading ability and associated phenotypes

Reading and dyslexia are highly heritable, with twin studies showing heritability estimates ranging from 0.4 to 0.8, and SNP-based heritability estimates around 0.25. Despite this clear genetic influence, the field has progressed more slowly in the genomic revolution, persisting in the candidate gene era for longer than other behavioural and psychiatric traits. One contributing factor may be the phenotypic complexity of reading, which makes it challenging to assess reading-related traits in large, diverse cohorts. Recent years have marked a turning point in the field of reading genetics, with the first large-scale GWAS meta-analysis ($N \sim 35,000$) for reading quantitative measures revealing significant genetic overlaps with behavioural and brain measures (Eising et al. 2022), and the first GWAS hits being discovered for dyslexia (Doust et al. 2022). These discoveries have led to new insights into the molecular underpinnings of reading, potentially implicating specific genes involved in neurodevelopment. Moreover, they have provided datasets to assess within and cross-trait prediction using reading-related polygenic scores. In this talk, I will provide an overview of the latest advances in this field and highlight new avenues for this research by integrating it with large-scale and phenotype-rich databases. I will present our recent work on associations between reading and structural measures across the brain, at the phenotypic and genetic levels, and provide evidence of how these can be studied to further understand the relative and intertwined roles of environment and genetic factors on reading.

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