**Project Title:** From normative to poor readers: looking for genetic associations underlying reading abilities in adults.

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**Webpage:** The CBMR group (http://cbmr.ualg.pt/; http://gnc.cbmr.ualg.pt/); The CCMAR group (BioSkel, bioskel.ccmar.ualg.pt/).

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**Location of research lab/research center:** The research centers involved (CBMR and CCMAR) are highly suitable for the implementation of this project.

**Summary: (1000 characters)**

Dyslexia is a neurologically-based developmental learning specific deficit affecting word recognition, reading and writing, with a prevalence around 5-10% in school-aged children across different populations. An individual diagnosed with dyslexia in childhood typically remains diagnosed as dyslexic throughout life. Problems in learning to read and write constitute a major constraint for educational and vocational training in modern knowledge-based societies and are associated with academic underachievement, incomplete high school/college studies, and underemployment as well as all consequent psychological-behavioral problems. According to Pennington (2006), a substantial amount of the variance in reading ability is explained by inherited factors: genetic variance explains about 20-80% of the total variance in reading skills. Although many studies associate certain genes variants with reading and their disorders, so far this association remains inconclusive because many results have not been consistently replicated. The lack of consistency could be partially explained by the age and educational stage at which the diagnosis of dyslexia affection status and the quantitative trait measurement took place (Carrion-Castillo et al., 2017).

One way of overcoming these age-varying effects is to genotype a sample of adults with dyslexia and normative readers. A critical open question is how some adults, called compensated dyslexics, attain age-appropriate reading skills and succeed in their academic career despite a history of reading difficulties (compensated) while others do not (non-compensated dyslexics). Therefore, genetic analysis is an open window to understand the both the heterogeneity of reading difficulties and the fact that some of dyslexics compensate and succeed.

We plan to (1) identify the correlation between the observed reading phenotypes in adult readers (assessed with an extensive cognitive battery) and their genotype and (2) to understand the role of the identified genetic variations in compensated vs. non-compensated dyslexics. An add value of this proposal is to develop a close collaboration between research in human genetics and cognitive neurosciences by identifying human gene mutations affecting cognitive profile responsible for reading disorders in adults. This will serve as an important stepping stone in the pursuit of a deeper causal understanding of developmental reading difficulties, including dyslexia and other impaired attainments of reading expertise.

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