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Título	Association of polygenic risk scores with ADHD trajectories and brain structural features
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Background: Attention-deficit/hyperactivity disorder (ADHD) is a highly heritable neuropsychiatric disorder, very common among children and adults. Although it has common genetic variants that contribute to its susceptibility, its aetiology is not entirely understood. Neuroimaging studies have shown several altered brain regions in children and adults with ADHD. The ENIGMA cross-sectional mega-analysis has confirmed these alterations and provided a model of ADHD as a disorder of maturation delay, based on more pronounced effects in childhood. Also, cohorts and longitudinal studies have demonstrated both late-onset of symptoms and age-independent remission, questioning if it is a neurodevelopmental disorder.

Objective: Our aim is to evaluate the relationship between symptoms remission and the brain alterations reported in the ENIGMA mega-analysis (accumbens, amygdala, caudate, hippocampus, putamen and intracranial volume) and how they are related with polygenic risk scores associated with ADHD in an independent sample.

Methods: This study assessed a target sample (n=227) that had been diagnosed with ADHD and later evaluated in a 7-year follow up, this third wave of evaluation includes the acquisition of magnetic resonance imaging (MRI – 3 Tesla) data and an extensive clinical-sociodemographic characterization. The images acquired were structural (T1, T2-weighted, DTI), functional resting state and spectroscopy, with a major focus in the structural data, processed with the FreeSurfer software. All samples were genotyped through Illumina PsychChip. The polygenic risk scores were performed using the PRSice software, comparing a discovery sample from PGC-ADHD 2017 (https://www.med.unc.edu/pgc/results-and-downloads) with our target sample.

Results and Conclusion: Individuals were genotyped in our sample and standard quality controls measures were performed, so related individuals were removed and genetic outliers were excluded based on principal component analysis (variants with imputation INFO score <0.8 or minor allele frequency (MAF) <0.001). Thereby 82 (mean age 46 years old) individuals were included so far in this third assessment. The imputation was performed through Ricopili pipeline. To this moment the neuroimaging results followed those previously reported in the literature. Image quality control was made with the ENIGMA protocol (http://enigma.ini.usc.edu/protocols/imaging-protocols/). Our next step will be to investigate the association within symptoms remission in the last three assessments and ADHD polygenic risk scores.