

Applying advanced statistical modeling to genetic predictors of personality dimensions associated with addiction

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Family adversity, impulsivity, and internalizing and externalizing problems have known associations with addiction, but the underlying genetic etiology of these phenotypes is unclear. This presentation describes two analytic frameworks for examining the influence of target SNPs on personality and negative outcomes: multi-group structural equation modelling and latent class analysis. Chinese college students (N = 200, 38% male) completed a psychometric battery of family adversity measures, personality dimensions, and psychiatric outcomes. Saliva samples were used to sequence 16 target SNPs, including genes within dopaminergic (DRD2, COMT), serotonergic (HTR1A, HTR2A, HTR2B), HPA-axis (CRHR1, FKBP5), neurotrophic (BDNF), GABA (GABRA2), and oxytocin (OXTR) pathways. Latent class analysis on these 16 SNPs produced two genetic variables of clustered SNPs, one of which contained more high-risk alleles for impulsivity and negative behavioral outcomes. We then examined the moderating effects of each latent genetic cluster on the associations between early family adversity, personality, and outcome dimensions. The higher-risk latent genetic variable predicted stronger correlations between family adversity and impulsivity, internet addiction, and other health-risk phenotypes. Thus, family adversity's impact on personality and behavioral issues in adulthood may be influenced by genetic risk. Separately, multi-group structural equation modelling examined the moderating effects of GABRA2 and OXTR on associations between clustered genes from dopaminergic, serotonergic, and HPA-axis systems and impulsivity. Genotype combinations of alleles associated with oxytocin inducement and GABA inhibition appeared to moderate the association between each neurotransmitter system and impulsivity. To our knowledge, this work represents the first examination of polygenic influences and moderating effects on family adversity and personality traits associated with addiction. Although these analyses include only 16 SNPs and our sample is small, we hope that our statistical methods offer heuristic value for larger-scale genetic risk modelling (e.g. polygenic and polypathway risk scores) of the personality and behavioral dimensions associated with addiction.