PW01-233 - **SEARCHING FOR ALCOHOLISM VULNERABILITY GENES: UK-COGA PROVISIONAL CLINICAL FINDINGS**

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**Background:** Alcoholism has a high prevalence and impacts on morbidity, mortality, life quality, and the economy. Heritability estimates of alcohol dependence are 50-61%. Putative psychological, cultural, and genetic susceptibilities to alcoholism have been identified but understanding of the genetic components is still underdeveloped.

**Aim:** Identify genetic vulnerabilities predisposing individuals to alcoholism and co-morbid psychiatric disorders in the largest study of its kind.

**Method:** 12 centres including 10 trainees are currently collecting blood and clinical samples. Nearly 1700 of 2000 cases of ICD-10/DSM-IV alcohol dependence have been collected; 500 with standardized assessments of alcohol use and comorbdity; and 2000 ancestrally-matched supernormal controls from UCL/collaborators. Genomic DNA will be isolated following standard procedures. Genotyping will be performed using the Affymetrix Gene Chip Human Mapping 1M Array to type up to 1 million single nucleotide polymorphism (SNP) and copy number variant (CNV) markers. Chi-square analysis of allelic association for the alcoholic sample versus controls will occur.

**Results:** n=65; 57% male; mean age 45years; mean age onset harmful alcohol use 19years; mean age onset withdrawals 32y; mean alcohol intake 21 units; primary depression 27%; secondary depression 49%; antisocial personality disorder 14%. The candidate gene approach in this sample has shown that the GABA receptor B1 (GABRB1) and the tachykinin receptor 1 (TACR1) are involved in genetic susceptibility to alcoholism. The D2 dopamine receptor is next.

**Conclusion:** Preliminary data suggests high psychiatric comorbidity in a clinical alcohol dependence sample and implicated candidate genes. Next is genomewide analysis of markers, sequencing and biological pathway/systems alterations.

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