P-704 - COPY NUMBER VARIANTS (CNV) AND IMPULSIVE-DISINHIBITED TRAIT

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Introduction: Impulsivity/disinhibition trait has been defined as the predisposition to respond to internal or external stimuli without regard to the potentially negative consequences. The genetic of personality traits has been evaluated in relation to microsatellites and SNPs, however, the contribution of copy number variation (CNV) is poorly known. We hypothesize that CNV may be part of the genetic component of the impulsivity/disinhibition trait.
Objectives: To evaluate the distribution of CNV in a cohort of impulsive/disinhibited subjects.
Aims: To detect CNV, CNV regions (CNVR) and candidate genes involved in impulsive-disinhibited trait.
Methods: Comparative genome hybridization (CGH) analysis in a group of subjects that scores the highest values in impulsivity/disinhibition questionnaires. DNA from each high scoring subject was compared with a pool of DNA obtained from low scoring controls. Data was analysed by Agilent Genomic Workbench using ADAM2 algorithm to identify CNVs and CNVR with statistical threshold of 7.5 and a minimum of 4 probes.
Results: A list of 68 genes, from the 38 selected CNVRs, was obtained from Human Genome build 37 (h19). Enrichment of genes for biological attributes and disease association were captured from *Phenotype-Genotype Integrator* and *GeneDecsk* web resources. Experimental validation of enriched genes, by Taqman copy number assays and MLPA, are in progress.
Conclusions: As an exploratory strategy we will be able to capture genes differentially represented in subjects analyzed, that could be experimentally validated in the entire cohort.

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