Article: EPA-0075
Topic: S509 - Symposium: Genetic component of suicidal behavior

Genome wide association study on suicidal behavior

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Genome-wide association studies of suicidal behaviour

Family and twin studies have shown that both common genetic variants and environmental factors contribute to vulnerability to suicide behaviour. Interactions between several candidate genes and environmental factors have been reported. In order to discover new candidate gene using an agnostic method we examined the association between common genome-wide variations and lifetime suicide behaviour (suicide attempt, SA, and completion, SC) (genome-wide association study, GWAS).
In the first, discovery, analysis allele frequencies of the common non-imputed 282'738 single nucleotide polymorphisms (SNPs) were compared between 833 SA, 235 SC and 1360 controls from the French-Swiss collaboration, genotyped with the Illumina Human 660W-Quad bead chips and HumanHap300 BeadChipsSNPs platforms respective. Thirty SNPs were associated at level p<10-5 for SA and 5 for SC. Strongest evidence of association for SA was observed 150kb from PLXNA2 (rs10779481, p=4x10-8) and for SC in the DROSHA locus (rs7726209, p=9.9 x10-6). The combined sample of suicide attempters and completers, identified two SNPs (rs9038 and rs2574852) located at chromosome 17q25.3 within a gene encoding the septin 9 (*SEPT9*) that showed a trend for an association with SB (p=2.04x10-7 and 7.52x10-7).
Replication studies are now in progress by analysing existing comparable samples, a second new French-Swiss sample, and imputation. These results suggest that GWAS could identify new candidate genes involved in new candidate pathways involved in vulnerability to SA and SC.

https://doi.org/10.1016/S0924-9338(14)77572-8 Published online by Cambridge University Press