Analysis of genome-wide significant bipolar disorder genes in borderline personality disorder

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The objective of this study was to investigate the hypothesis that borderline personality disorder (BPD) and bipolar disorder (BD) share genetic variation through analysis of known genetic risk factors for BD in a well-characterized BPD case-control cohort. Genotyping of five genome-wide significant variants identified for BD (in CACNA1C, ANK3, and ODZ4) was performed in 673 BPD cases and 748 controls. A nominally significant association with BPD was found for rs1006737 in CACNA1C (P=0.0498). Sex-specific analysis showed that this signal was present only in women. This is the first report of an association between a BD risk gene and BPD where selection was not based on a priori hypotheses about its function, but on an unbiased hypothesis-free screening of the genome. Genome-wide association data of large samples of BPD are warranted and will eventually identify new risk genes and the overlap between BPD and BD if it exists.
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