

Novel risk genes for bipolar disorder

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Bipolar disorder (BD), characterized by mood swings between positive manic/hypomanic and negative/depressive states, is a common psychiatric disorder with a lifetime prevalence of ~1%. Although epidemiological studies indicate that genetic components contribute to BD development, several genome-wide association studies (GWASs) identified limited number of susceptibility (risk) genes for BD, most of which are yet unidentified.

Collaborative research in Japan, under the guidance of the principle investigators from Fujita Health University and RIKEN, led to the identification of a novel risk gene (FADS1 and FADS2) for [bipolar disorder](#) via GWAS performed using samples collected in Japan (2,964 cases and 61,887 comparison subjects). The function of this gene is well established: metabolism of lipids, including blood lipids (e.g., cholesterol and triglyceride) and omega3/6 polyunsaturated fatty acids (PUFA). Previous epidemiological surveys have shown that prevalence of hyperglycemia or metabolic syndrome in patients with BD was higher than that of the general population; hence, the researchers concluded that lipid abnormality may be involved in BD pathophysiology.

To maximize the sample size, the researchers then conducted a meta-analysis between their samples and results from the publicly available BD GWAS database (Psychiatric GWAS Consortium). They identified an additional novel gene for BD (NFIX) and supported three previously implicated [genes](#) (ODZ4, MAD1L1, and TRANK1).

The sample size analyzed in this study is one of the largest, especially as

samples were collected in Asian populations. However, because of the extremely small effect size of the BD risk (i.e., odds ratio ~1.2), Prof. Nakao Iwata says, "a large number of risk genes are still unidentified. Therefore further study is essential." In addition, he says, "We cannot use this information in the clinical setting yet. After elucidating a concrete association of these genes with BD, in terms of their function, new therapeutic strategies may be developed, including the development of new drugs."

More information: M Ikeda et al, A genome-wide association study identifies two novel susceptibility loci and trans population polygenicity associated with bipolar disorder, *Molecular Psychiatry* (2017). [DOI: 10.1038/MP.2016.259](https://doi.org/10.1038/MP.2016.259)

Provided by Fujita Health University

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