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Genome-wide association study reveals two new risk loci for bipolar disorder

Thomas W. Mühleisen, Markus Leber, Thomas G. Schulze, Jana Strohmaier, Franziska Degenhardt, Jens Treutlein, Manuel Mattheisen, Andreas J. Forstner, Johannes Schumacher, René Breuer, Sandra Meier, Stefan Herms, Per Hoffmann, André Lacour, Stephanie H. Witt, Andreas Reif, Bertram Müller-Myhsok, Susanne Lucae, Wolfgang Maier, Markus Schwarz *et al.*

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Abstract

Bipolar disorder (BD) is a common and highly heritable mental illness and genome-wide association studies (GWAS) have robustly identified the first common genetic variants involved in disease aetiology. The data also provide strong evidence for the presence of multiple additional risk loci, each contributing a relatively small effect to BD susceptibility. Large samples are necessary to detect these risk loci. Here we present results from the largest BD GWAS to date by investigating 2.3 million single-nucleotide polymorphisms (SNPs) in a sample of 24,025 patients and controls. We detect 56 genome-wide significant SNPs in five chromosomal regions including previously reported risk loci *ANK3*, *ODZ4* and *TRANK1,* as well as the risk locus *ADCY2* (5p15.31) and a region between *MIR2113* and *POU3F2* (6q16.1). *ADCY2* is a key enzyme in cAMP signalling and our finding provides new insights into the biological mechanisms involved in the development of BD.

Subject terms: Biological sciences Genetics Neuroscience

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Download references

Author information

These authors contributed equally to this work

Thomas W. Mühleisen, Markus Leber, Thomas G. Schulze, Marcella Rietschel, Markus M. Nöthen & Sven Cichon

Affiliations

Institute of Human Genetics, University of Bonn, D-53127 Bonn, Germany

Thomas W. Mühleisen, Franziska Degenhardt, Andreas J. Forstner, Johannes Schumacher, Stefan Herms, Per Hoffmann, Lutz Priebe, Peter Propping, Markus M. Nöthen & Sven Cichon

Department of Genomics, Life & Brain Center, University of Bonn, D-53127 Bonn, Germany

Thomas W. Mühleisen, Franziska Degenhardt, Andreas J. Forstner, Johannes Schumacher, Stefan Herms, Per Hoffmann, Lutz Priebe, Markus M. Nöthen & Sven Cichon

Institute of Neuroscience and Medicine (INM-1), Research Centre Jülich, D-52425 Jülich, Germany
Thomas W. Mühleisen, Per Hoffmann & Sven Cichon

Institute for Medical Biometry, Informatics, and Epidemiology, University of Bonn, D-53127 Bonn, Germany
Markus Leber & Tim Becker

German Center for Neurodegenerative Diseases (DZNE), Bonn, Germany, D-53175 Bonn, Germany
Markus Leber, André Lacour & Tim Becker

Department of Psychiatry and Psychotherapy, University of Go¨ttingen, D-37075 Göttingen, Germany
Thomas G. Schulze

Department of Genetic Epidemiology in Psychiatry, Central Institute of Mental Health, Medical Faculty Mannheim/Heidelberg University, D-68159 Mannheim, Germany
Jana Strohmaier, Jens Treutlein, René Breuer, Sandra Meier, Stephanie H. Witt & Marcella Rietschel

Department of Biomedicine, Aarhus University, DK-8000 Aarhus C, Denmark
Manuel Mattheisen

Institute for Genomic Mathematics, University of Bonn, D-53127 Bonn, Germany
Manuel Mattheisen

National Centre Register-Based Research, Aarhus University, DK-8210 Aarhus V, Denmark
Sandra Meier

Division of Medical Genetics, Department of Biomedicine, University of Basel, Basel CH-4012, Switzerland
Stefan Herms, Per Hoffmann & Sven Cichon

Department of Psychiatry, Psychosomatics and Psychotherapy, University of Würzburg, D-97070 Würzburg, Germany
Andreas Reif

Statistical Genetics, Department of Translational Psychiatry, Max Planck Institute of Psychiatry, D-80804 Munich, Germany
Bertram Müller-Myhsok & Susanne Lucae

Munich Cluster for Systems Neurology (SyNergy), D-80336 Munich, Germany
Bertram Müller-Myhsok

Institute of Translational Medicine, University of Liverpool, L69 3BX Liverpool, UK
Bertram Müller-Myhsok

Department of Psychiatry, University of Bonn, D-53127 Bonn, Germany
Wolfgang Maier

Psychiatric Center Nordbaden, D-69168 Wiesloch, Germany
Markus Schwarz, Helmut Vedder & Jutta Kammerer-Ciernioch

Department of Psychiatry and Psychotherapy, University Hospital, D-01307 Dresden, Germany
Andrea Pfennig & Michael Bauer

Department of Psychology, Clinical Psychology and Psychotherapy, Eberhard Karls University Tübingen, D-72074 Tübingen, Germany
Martin Hautzinger

Institute of Medical Informatics, Biometry, and Epidemiology, University Duisburg-Essen, D-45147 Essen, Germany
Susanne Moebus

Department of Psychiatry, Poznan University of Medical Sciences, Poznan PL-60-572, Poland
Piotr M. Czerski & Joanna Hauser

Department of Cancer Epidemiology and Prevention, Maria Sklodowska-Curie Memorial Cancer Centre and Institute of Oncology, Warsaw PL-02-781, Poland
Jolanta Lissowska

Department of Epidemiology, Nofer Institute of Occupational Medicine, Lodz PL-91-348, Poland
Neonila Szeszenia-Dabrowska

Genetic Epidemiology Group, International Agency for Research on Cancer (IARC), 69372 Lyon CEDEX 08, France
Paul Brennan

Genetic Cancer Susceptibility Group, International Agency for Research on Cancer (IARC), 69372 Lyon CEDEX 08, France
James D. McKay

School of Psychiatry, University of New South Wales, Randwick, New South Wales 2052, Australia
Adam Wright & Philip B. Mitchell

Black Dog Institute, Prince of Wales Hospital, Randwick, New South Wales 2031, Australia
Adam Wright & Philip B. Mitchell

Neuroscience Research Australia, Randwick, Sydney, New South Wales 2031, Australia
Janice M. Fullerton & Peter R. Schofield

School of Medical Sciences, Faculty of Medicine, University of New South Wales, Sydney, New South Wales 2052, Australia
Janice M. Fullerton & Peter R. Schofield

Queensland Institute of Medical Research (QIMR), Brisbane, Queensland 4006, Australia
Grant W. Montgomery, Sarah E. Medland, Scott D. Gordon & Nicholas G. Martin

Moscow Research Institute of Psychiatry, Moscow 107258, Russian Federation
Valery Krasnow

Institute of Pulmonology, Russian State Medical University, Moscow 105077, Russian Federation
Alexander Chuchalin & Gulja Babadjanova

Russian Academy of Medical Sciences, Mental Health Research Center, Moscow 115522, Russian Federation
Galina Pantelejeva, Lilia I. Abramova & Alexander S. Tiganov

Department of Biology, Medical Genetics and Ecology, Kursk State Medical University, Kursk 305041, Russian Federation
Alexey Polonikov

Institute of Biochemistry and Genetics, Ufa Scientific Center of Russian Academy of Sciences, Ufa 450054, Russian Federation
Elza Khusnutdinova

Department of Psychiatry, Dalhousie University, Halifax, Nova Scotia, Canada B3H 2E2

Martin Alda

The International Group for the Study of Lithium-Treated Patients (IGSLI), Berlin, Germany
Martin Alda & Paul Grof

Mood Disorders Center of Ottawa, Ottawa, Ontario, Canada K1G 4G3
Paul Grof

Department of Psychiatry, University of Toronto, Toronto, Ontario, Canada M5T 1R8
Paul Grof

Department of Neurology and Neurosurgery, Montreal Neurological Hospital and Institute, McGill University, Montreal, Québec, Canada H3G 1A4
Guy A. Rouleau

Department of Psychiatry, Douglas Hospital Research Institute, McGill University, Montreal, Quebec, Canada H4H 1R3
Gustavo Turecki

Département des sciences fondamentales, Université du Québec à Chicoutimi (UQAC), Saguenay, Canada G7H 2B1
Catherine Laprise

Department of Psychiatry, Hospital Regional Universitario Carlos Haya, Malaga 29009, Spain
Fabio Rivas & Fermin Mayoral

Center for Research in Environmental Epidemiology (CREAL), Barcelona 08003, Spain
Manolis Kogevinas

Biometric Psychiatric Genetics Research Unit, Alexandru Obregia Clinical Psychiatric Hospital, Bucharest RO-041914, Romania
Maria Grigoroiu-Serbanescu

Contributions

MooDS management group: M.M.N., M.R., P.P., S.C.; writing group: T.W.M, M.L., T.G.S., M.R., M.M.N. and S.C. coordinated the work and prepared the manuscript, with feedback from the other authors who approved the manuscript; statistical analysis group: M.L., M.M., A.L. and T.B.; bioinformatical analysis group: J.T., S.H. and T.W.M.; sample management, DNA extraction, genotyping, QC in Bonn and Mannheim: F.D., AJ.F., J.S., S.H., P.H., L.P., R.B., S.M. and S.H.W.; recruitment and characterization of patients and controls and generation of control data for Germany I and II: T.G.S., Ja. St., A.R., M.G.-S., W.M., M.S., H.V., J.K.-C., A.P., M.B., M.H., B.M.-M., S.L. and Su.Mo.; recruitment and characterization of patients and controls and generation of control data for Poland: P.M.C., J.H., J.L., N.S.-D., P.B. and J.D.M.; recruitment and characterization of patients and controls and generation of control data for Australia: A.W., P.B.M., J.M.F., P.R.S., G.W.M., S.E.M., S.D.G. and N.G.M.; recruitment and characterization of patients and controls and generation of control data for Russia: V.K., A.C., G.B., G.P., L.I.A., A.S.T., Al.Po., E.K.; recruitment and characterization of patients and controls and generation of control data for Canada: M.A., P.G., G.A.R., G.T. and C.L.; recruitment and characterization of patients and controls and generation of control data for Spain: F.R., F.M. and M.K.

Competing financial interests

The authors declare no competing financial interests.

Corresponding authors

Correspondence to: Marcella Rietschel or Markus M. Nöthen or Sven Cichon

Supplementary information

PDF files

1. Supplementary Figures, Tables and References (1,402 KB)
   Supplementary Figures 1-2, Supplementary Tables 1-8 and Supplementary References

Excel files

1. Supplementary Data 1 (16 KB)
   Quality control procedure for the genotype and the imputed MooDS data.

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