

Identifying Gene-Environment Interactions in Schizophrenia: Contemporary Challenges for Integrated, Large-scale Investigations

European Network of National Networks studying Gene-Environment Interactions in Schizophrenia (EU-GEI)*

*A full list of authors and affiliations appears in the Appendix.

Recent years have seen considerable progress in epidemiological and molecular genetic research into environmental and genetic factors in schizophrenia, but methodological uncertainties remain with regard to validating environmental exposures, and the population risk conferred by individual molecular genetic variants is small. There are now also a limited number of studies that have investigated molecular genetic candidate gene-environment interactions ($G \times E$), however, so far, thorough replication of findings is rare and $G \times E$ research still faces several conceptual and methodological challenges. In this article, we aim to review these recent developments and illustrate how integrated, large-scale investigations may overcome contemporary challenges in $G \times E$ research, drawing on the example of a large, international, multi-center study into the identification and translational application of $G \times E$ in schizophrenia. While such investigations are now well underway, new challenges emerge for $G \times E$ research from late-breaking evidence that genetic variation and environmental exposures are, to a significant degree, shared across a range of psychiatric disorders, with potential overlap in phenotype.

Key words: schizophrenia/gene-environment interaction/psychosis/epidemiology/genetics

The Environment and Schizophrenia: Evidence Beyond Reasonable Doubt?

Over the past decades, substantial and consistent evidence has accrued that implicates environmental factors in the development of schizophrenia. Numerous studies have consistently reported an increased incidence of schizophrenia in urban areas^{1–8} as well as in migrant and minority ethnic groups.^{4,7,9–12} Evidence further suggests cannabis use^{13–17} and childhood adversity^{18–20} confer substantial risk for psychotic disorder. For these environmental factors, pooled effects sizes from meta-analyses in the range of a 2- to 4-fold increase in risk,^{4,5,8–10,13–17,20} evidence of dose-response gradient,^{10,20–26} and population attributable risk fractions of 20%–35%^{20,27} have been reported. These advances notwithstanding, a

number of methodological uncertainties remain in validating environmental exposures, including risk of systematic information bias, confounding by genetic and other factors, and possible reverse causality.^{19,28–32}

Recent Gene Discoveries in Schizophrenia: (Some) More Light in the Dark

While the initial surge for the molecular genetic basis of schizophrenia was characterized by slow progress and methodological concerns,^{32,33} recent years have seen more rapid advances through large-scale collaboration in genome-wide association studies (GWAS), which have generated replicated findings on a number of common risk alleles.^{34–38} Recent advances have further produced consistent findings that rare copy number variants (CNVs) increase schizophrenia risk substantially and to a greater extent than individual common risk alleles identified by GWAS.^{39–42}

However, the common variants identified to date explain only a small proportion of the genetic risk of schizophrenia and a large number of common risk alleles (with small effects) remain to be identified.^{35,41,43} Also, heritability estimates of the overall contribution of common genetic variants based on molecular genetic data are considerably smaller (ie 23%–33%)^{38,44} than heritability estimates from twin studies (ie 81%).^{45,46} What is more, while the reported effect sizes for CNVs tend to be much larger, they are rare and therefore contribute even less to total risk.^{40–42} There are several potential explanations that may account for this pattern in molecular genetic findings, but, given the consistent evidence that environmental factors confer substantial, and much greater risk than individual common genetic risk variants, it seems reasonable that gene-environment interactions ($G \times E$) play an important role.

Gene-Environment Interactions: Contemporary Challenges

The $G \times E$ approach posits that the effect of an individual's genotype depends on environmental exposure

and, vice versa, the effect of environmental exposure on risk depends on an individual's genotype.^{32,47} Since both environmental and genetic factors have consistently been implicated in etiology, but there is considerable variation in phenotype, in so far as not all individuals exposed to environmental risk or carrying genetic risk variants go on to develop the disorder, $G \times E$ appears to be particularly relevant in schizophrenia.^{29,48} $G \times E$ would also plausibly account for the large discrepancy in heritability estimates from twin and molecular genetic studies.^{44–46} This heritability gap may come about because $G \times E$ involving shared environmental factors within families are included in heritability estimates of twin studies, but not molecular genetic studies of unrelated subjects.⁴⁶

While long ignored in molecular genetic analyses, and still an emerging field, the beginning of this century has seen a limited number of $G \times E$ studies on candidate genes in schizophrenia.^{29,49,50} These studies have tested individual, a priori selected single-nucleotide polymorphisms (SNPs), with very few attempts at replication^{49–52} and limited evidence on the potential mechanisms underlying $G \times E$ in schizophrenia.^{31,32} Indeed, there remain a number of conceptual and methodological challenges in contemporary molecular $G \times E$ research. These include (a) the validation of environmental exposures, consistently measured in sufficiently large, epidemiologically characterized samples for $G \times E$ analysis^{33,46}; (b) selecting optimal strategies for (1) the use of complex GWAS data, (2) a priori, hypothesis-based vs exploratory approaches, and (3) the type of genetic variation to be used in $G \times E$ analysis; (c) a relative paucity of validated and scalable experimental methods for investigating modifiable mechanisms underlying $G \times E$ in schizophrenia; (d) the different phenotypic levels of schizophrenia at which $G \times E$ may impact, including intermediate phenotypes, prodrome, onset, severity, and course of schizophrenia; (e) statistical modeling of the likely simultaneous presence of $G \times E$, $G \times G$ and $E \times E$ interactions; (f) ethical issues that may arise if $G \times E$ analyses produce evidence of substantial risks to be leveraged in risk assessment and early prediction; and (g) the need for translation of $G \times E$ findings to clinical practice.

It has repeatedly been noted that current challenges in molecular genetic $G \times E$ research warrant integrated, large-scale investigations that bring together international experts at the forefront of research in epidemiology, genetics, experimental psychiatry, statistics, social psychiatry, brain imaging, and clinical psychiatry.^{31–33,47,50,53} While in molecular genetic research large-scale collaborations such as the International Schizophrenia Consortium³⁵ or the Psychiatric Genomics Consortium⁵⁴ are increasingly common, there are only few examples in $G \times E$ research; one is “The European Network of National Networks studying Gene-Environment Interactions in Schizophrenia” (EU-GEI)^{32,47} (see also www.eu-gei.eu).

The European Network of National Schizophrenia Networks Studying Gene-Environment Interactions (EU-GEI)

EU-GEI is a large, international, multi-center study of $G \times E$ in schizophrenia using family-based, multidisciplinary research paradigms in more than 15 countries (the Netherlands, the UK, Germany, Turkey, Spain, France, Belgium, Greece, Austria, Switzerland, Hong Kong (China), Brazil, Australia, Ireland, Italy, and other European and non-European countries represented by EU-GEI affiliated centers) for testing a priori $G \times E$ hypotheses. The overall aim of EU-GEI is the identification and translational application of clinical, genetic, and environmental interactions in the development, severity, and course of schizophrenia in patients and their families. To this end, several work packages are currently underway that amalgamate expertise from multiple disciplines for addressing contemporary challenges in $G \times E$ research (see [figure 1](#)).

The “Functional Enviromics” work package has developed and currently applies methods for the detailed assessment of candidate, individual- and area-level environmental exposures of public health relevance (ie with the largest attributable fractions and most relevant to the EU study population).¹² The work package employs a number of strategies for validating environmental exposures by using an optimum, family-based, case-control design in a diverse range of settings across Europe, drawing on corroborative sources of information in the assessment of childhood and adult adversity to minimize recall bias, and taking account of potential confounding by direct and indirect measures of genetic risk as well as other relevant factors. In doing so, “Functional Enviromics” aims to investigate the impact of hypothesized individual- and area-level environmental exposures on risk of first episode psychosis and to identify proximal explanatory factors that account for high rates of psychotic disorder in urban areas and in migrant and ethnic minority groups. The work package further aims, together with “Discovery Genetics” and “ $G \times E$ Data & Statistics,” to examine evidence for hypothesized $G \times E$ and environment \times environment ($E \times E$) interactions.

The “Discovery Genetics” work package aims to identify novel genes and biological pathways and implement new approaches for CNVs that will allow, jointly with all other work packages, to test specific, a priori $G \times E$ hypotheses. Specifically, this work package combines available with newly generated GWAS data to identify common variants, showing robust genome-wide evidence for association, to test specific, a priori SNP-based $G \times E$ hypotheses. “Discovery Genetics” further constructs, in collaboration with “ $G \times E$ Data & Statistics,” polygenic pathway scores based on pathway-wide evidence for association of SNPs in genes that are involved in specific biological pathways underlying environmental risks.

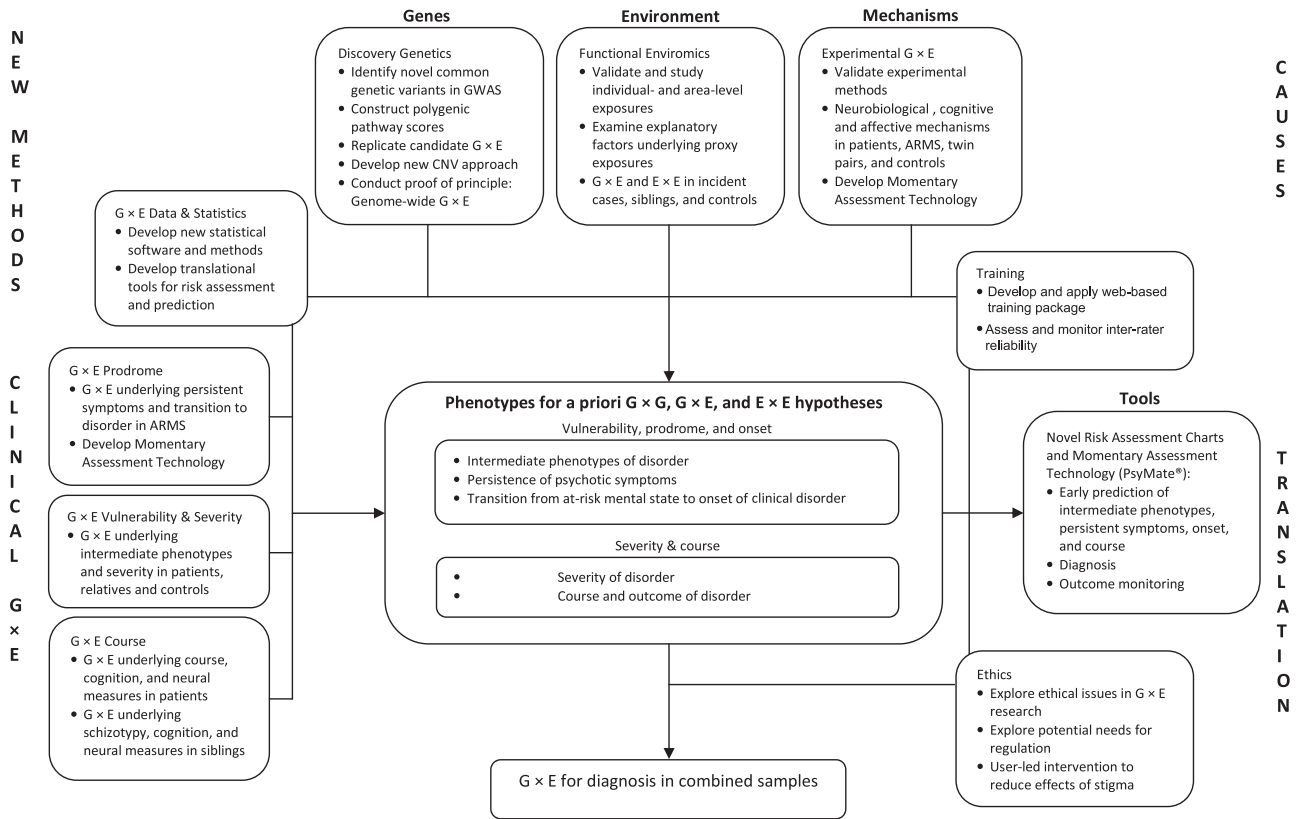


Fig. 1. General approach and overview of European Network of National Networks studying Gene-Environment Interactions in Schizophrenia.

In addition, this work package targets previously identified candidate $G \times E$ for replication, develops and implements new approaches to $G \times E$ analysis with CNVs, and conducts proof of principle for genome-wide $G \times E$ analysis, with the aim of identifying novel risk-environment interplays that are not predicated upon the existence of observed genetic main effects.

In the “Experimental $G \times E$ ” work package, validated and scalable experimental methods have been developed for investigating neural, cognitive, and affective mechanisms underlying the interplay of genetic and environmental factors under experimental conditions, controlling for measured and unmeasured confounding factors, including genetic factors (and, thereby, gene-environment correlation). Work by the experimental $G \times E$ work package also supports the view that epidemiologically validated risk factors such as migration or urban living and upbringing have a social component, as proposed by the social defeat hypothesis.⁵⁵ Specifically, findings from this work package suggest a specific impact of social stress on activation in a perigenual cingulate-amygdalar circuit in healthy populations exposed to urban living and upbringing⁵⁶ and migration.⁵⁷ This suggests that this circuit may be a core convergence region for risk of mental disorders arising through social stressors.⁵⁸ The experimental $G \times E$ approach is also of considerable potential value for generating translational knowledge. Therefore,

this work package has developed innovative Momentary Assessment Technology (ie the PsyMate) to investigate stress sensitivity in daily life as an important affective mechanism underlying environmental and genetic risk in the development of schizophrenia.⁵⁹

The “ $G \times E$ Prodrome,” “ $G \times E$ Vulnerability and Severity,” and “ $G \times E$ Course” work packages take into account the different phenotypes and clinical stages of disorder at which gene-environment interactions may impact, including intermediate phenotypes, prodrome, onset, severity, and course of schizophrenia. These work packages aim to investigate clinical, environmental, and genetic determinants as well as $G \times E$ at all these levels, with initial evidence of candidate $SNP \times$ cannabis interaction for psychosis liability.^{60,61} The “ $G \times E$ Data & Statistics” work package provides coordination and support for statistical methodology to examine, jointly with all other work packages, $G \times E$, $G \times G$, and $E \times E$ interactions underlying disease risk, course, and outcome of schizophrenia. The work package further develops novel statistical software and methodology for examining $G \times E$ interactions. In the “Training” work package, a web-based training environment has been developed for addressing a key issue in large multi-national collaborations, i.e. inter-rater reliability in the assessment of environmental exposures, diagnosis, intermediate phenotypes, prodrome, onset, severity, and course. Given the potential

ethical issues raised by $G \times E$ research in schizophrenia, the “Ethics” work package explores these, detects potential needs for regulation and, in collaboration with the “Dissemination” work package, will include ethical and legal perspectives in the dissemination activities. Lastly, the entire project is coordinated by the “Management” work package.

Evidence on $G \times G$, $G \times E$, and $E \times E$ generated by EU-GEI will aggregate in the development of risk prediction algorithms that will be implemented in innovative, translational risk assessment charts and momentary assessment technology for early prediction of intermediate phenotypes, persistent symptoms, transition to, as well as onset, severity, course, and outcome of, schizophrenia. Application of these tools will allow the targeting of prevention, treatment and resources to modifiable mechanisms as well as subgroups of individuals with the greatest vulnerability, highest risk of developing persistent symptoms and psychotic disorder and, once diagnosed, to those with greatest severity and highest risk of poor course and outcome.

Conclusion and Future Prospects

Recent years have seen significant advances in epidemiological and molecular genetic research, consistently implicating environmental and genetic factors in the etiology of schizophrenia. However, methodological uncertainties remain with regard to validating environmental exposures and the population risk conferred by the molecular genetic variants identified to date remains small. While $G \times E$ may account for the latter, so far, replication of the limited number of molecular genetic candidate $G \times E$ findings is rare. Important conceptual and methodological challenges of $G \times E$ research in schizophrenia are currently being addressed in integrated, large-scale investigations, such as EU-GEI.

While EU-GEI is now well underway, new challenges emerge at the horizon of $G \times E$ research. It now appears increasingly likely that genetic variation⁴⁴ and environmental exposures (such as childhood adversity)¹⁸ are, to a significant degree, shared across a range of psychiatric disorders, with some emerging evidence of overlap in phenotypes.⁶² Therefore, as for mono-disciplinary, epidemiological and molecular-genetic research, the study of $G \times E$ needs to be extended beyond individual disorders to investigations of all major psychiatric disorders in order to unpick the complex interplay of genes, environment, and underlying mechanisms that push some people along a pathway to psychosis, whilst others to non-psychotic or no disorder. Not only cross-discipline, but also large-scale cross-disorder investigations are now required to more fully realize the potential of $G \times E$ research in elucidating the etiology of, and, ultimately, improving prevention and treatment for, schizophrenia.

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European Network of National Networks studying Gene-Environment Interactions in Schizophrenia (EU-GEI)

Authors

Jim van Os^{1,2}, Bart P. Rutten¹, Inez Myin-Germeys¹, Philippe Delespaul^{1,3}, Wolfgang Viechtbauer¹, Catherine van Zelst¹, Richard Bruggeman^{1,4}, Ulrich Reininghaus^{1,5}, Craig Morgan⁵, Robin M. Murray², Marta Di Forti², Philip McGuire², Lucia R. Valmaggia⁶, Matthew J. Kempton², Charlotte Gayer-Anderson⁵, Kathryn Hubbard⁵, Stephanie Beards⁵, Simona A. Stilo^{2,5}, Adanna Onyejiaka⁵, Francois Bourque⁵, Gemma Modinos², Stefania Tognin², Maria Calem², Michael C. O’Donovan⁷, Michael J. Owen⁷, Peter Holmans⁷, Nigel Williams⁷, Nicholas Craddock⁷, Alexander Richards⁷, Isla Humphreys⁷, Andreas Meyer-Lindenberg⁸, F. Markus Leweke⁸, Heike Tost⁸, Ceren Akdeniz⁸, Cathrin Rohleder⁸, J. Malte Bumb⁸, Emanuel Schwarz⁸, Köksal Alptekin⁹, Alp Üçok¹⁰, Meram Can Saka^{11,12}, E. Cem Atbaşoğlu^{11,12}, Sinan Gülöksüz^{1,13}, Guvem Gumus-Akay¹², Burçin Cihan¹⁴, Hasan Karadağ¹⁵, Haldan Soygür¹⁶, Eylem Şahin Cankurtaran¹⁵, Semra Ulusoy¹⁷, Berna Akdede⁹, Tolga Binbay⁹, Ahmet Ayer¹⁸, Handan Noyan¹⁹, Gülşah Karadayı¹⁰, Elçin Akturan¹⁰, Halis Ulaş⁹, Celso Arango²⁰, Mara Parellada²⁰, Miguel Bernardo²¹, Julio Sanjuán²², Julio Bobes²³, Manuel Arrojo²⁴, Jose Luis Santos²⁵, Pedro Cuadrado²⁶, José Juan Rodríguez Solano²⁷, Angel Carracedo²⁸, Enrique García Bernardo²⁹, Laura Roldán²⁰, Gonzalo López²⁰, Bibiana Cabrera²¹, Sabrina Cruz²², Eva M^a Díaz Mesa²³, María Pouso^{24,28,30}, Estela Jiménez²⁵, Teresa Sánchez²⁰, Marta Rapado²⁰, Emiliano González²⁰, Covadonga Martínez²⁰, Emilio Sánchez²⁹, M^a Soledad Olmeda²⁹, Lieuwe de Haan³¹, Eva Velthorst³¹, Mark van der Gaag^{32,33}, Jean-Paul Seltén^{1,34}, Daniella van Dam³¹, Elsje van der Ven^{1,34}, Floor van der Meer³¹, Elles Messchaert^{31,34}, Tamar Kraan^{31,33}, Nadine Burger^{31,33}, Marion Leboyer^{35–38}, Andrei Szoke^{35–38}, Franck Schürhoff^{35–38}, Pierre-Michel Llorca^{38–40}, Stéphane Jamain^{36–38}, Andrea Tortelli^{36,41}, Flora Frijda⁴¹, Jeanne Vilain^{35–38}, Anne-Marie Galliot³⁶, Grégoire Baudin^{35,36}, Aziz Ferchiou^{35,36}, Jean-Romain Richard^{36,38}, Ewa Bulzacka³⁵, Thomas Charpeaud^{38,39,40}, Anne-Marie Tronche^{38,39,40}, Marc De Hert⁴², Ruud van Winkel^{1,42}, Jeroen Decoster⁴³, Catherine Derom^{44,45}, Evert Thiery^{45,46}, Nikos C. Stefanis⁴⁷, Gabriele Sachs⁴⁸, Harald Aschauer⁴⁸, Iris Lasser⁴⁸, Bernadette Winklbaur⁴⁸,

Monika Schlögelhofer⁴⁸, Anita Riecher-Rössler⁴⁹, Stefan Borgwardt⁵⁰, Anna Walter⁵⁰, Fabienne Harrisberger⁵⁰, Renata Smieskova⁵⁰, Charlotte Rapp⁴⁹, Sarah Ittig⁴⁹, Fabienne Soguel-dit-Piquard⁴⁹, Erich Studerus⁴⁹, Joachim Klosterkötter⁵¹, Stephan Ruhrmann⁵¹, Julia Paruch⁵¹, Dominika Julkowski⁵¹, Desiree Hilboll⁵¹, Pak C. Sham⁵², Stacey S. Cherny⁵², Eric Y. H. Chen⁵³, Desmond D. Campbell⁵², Miaoxin Li⁵², Carlos María Romeo-Casabona⁵⁴, Aitziber Emaldi Cirión⁵⁴, Asier Urruela Mora⁵⁵, Peter Jones⁵⁶, James Kirkbride^{56,57}, Mary Cannon⁵⁸, Dan Rujescu⁵⁹, Ilaria Tarricone⁶⁰, Domenico Berardi⁶⁰, Elena Bonora⁶¹, Marco Seri⁶¹, Thomas Marcacci⁶⁰, Luigi Chiri⁶⁰, Federico Chierzi⁶⁰, Viviana Storbini⁶⁰, Mauro Braca⁶⁰, Maria Gabriella Minenna⁶², Ivonne Donegani⁶², Angelo Fioritti⁶², Daniele La Barbera⁶³, Caterina Erika La Cascia⁶³, Alice Mulè⁶⁴, Lucia Sideli⁶³, Rachele Sartorio⁶³, Laura Ferraro⁶⁴, Giada Tripoli⁶³, Fabio Seminerio⁶⁴, Anna Maria Marinaro⁶⁴, Patrick McGorry⁶⁵, Barnaby Nelson⁶⁵, G. Paul Amminger⁶⁵, Christos Pantelis⁶⁶, Paulo R. Menezes^{67,68}, Cristina M. Del-Ben^{68,69}, Silvia H. Gallo Tenan^{68,69}, Rosana Shuhama^{68,69}, Mirella Ruggeri⁷⁰, Sarah Tosato⁷⁰, Antonio Lasalvia⁷⁰, Chiara Bonetto⁷⁰, Elisa Ira⁷⁰, Merete Nordentoft⁷¹, Marie-Odile Krebs⁷², Neus Barrantes-Vidal⁷³⁻⁷⁶, Paula Cristóbal⁷³, Thomas R. Kwapił⁷⁵, Elisa Brietzke⁷⁷, Rodrigo A. Bressan⁷⁷, Ary Gadelha⁷⁷, Nadja P. Maric⁷⁸, Sanja Andric⁷⁸, Marina Mihaljevic⁷⁸, and Tijana Mirjanic⁷⁸

Affiliations

¹Department of Psychiatry and Neuropsychology, School for Mental Health and Neuroscience, South Limburg Mental Health Research and Teaching Network, Maastricht University Medical Centre, Maastricht, The Netherlands; ²Department of Psychosis Studies, Institute of Psychiatry, King's College London, London, UK; ³Mondriaan Mental Health Trust, South Limburg, Maastricht/Heerlen, Heerlen, The Netherlands; ⁴University Centre of Psychiatry, Rob Giel Clinical Research, University of Groningen, University Medical Centre Groningen, Groningen, The Netherlands; ⁵Department of Health Service and Population Research, Institute of Psychiatry, King's College London, London, UK; ⁶Department of Psychology, Institute of Psychiatry, King's College London, London, UK; ⁷Medical Research Council (MRC) Centre for Neuropsychiatric Genetics and Genomics, Cardiff University Cardiff, UK; ⁸Department of Psychiatry and Psychotherapy, Central Institute of Mental Health, Mannheim, Germany; ⁹Department of Psychiatry, School of Medicine, Dokuz Eylül University, Konak, Turkey; ¹⁰Psychotic Disorders Research Unit, Department of Psychiatry, Istanbul Faculty of Medicine, Istanbul University, Istanbul, Turkey; ¹¹Department of Psychiatry, School of Medicine, Ankara University, Cebeci Hospital, Mamak cad, Ankara, Turkey; ¹²Ankara University Brain Research Center, Ankara University, Ankara, Turkey; ¹³Department

of Psychiatry, Yale University Medical School, Department of Psychiatry, New Haven, CT; ¹⁴Department of Psychology, Middle East Technical University ODTÜ Üniversiteler Mah., Ankara, Turkey; ¹⁵Dışkapı Y.B. Research and Training Hospital, İrfan Baştuğ Cad, Dışkapı, Ankara, Turkey; ¹⁶Turkish Federation of Schizophrenia Associations, Ankara, Turkey; ¹⁷Psychiatry Clinic, Atatürk Training and Research Hospital, Ankara, Turkey; ¹⁸Manisa Mental Health Hospital, Manisa, Turkey; ¹⁹Department of Advanced Neurological Sciences, Institute for Experimental Medical Research, Istanbul Faculty of Medicine, Istanbul University, Istanbul, Turkey; ²⁰Department of Child and Adolescent Psychiatry, Hospital General Universitario Gregorio Marañón, School of Medicine, Universidad Complutense, IiSGM (CIBERSAM), Madrid, Spain; ²¹Department of Psychiatry, Hospital Clinic, IDIBAPS, Centro de Investigación Biomédica en Red de Salud Mental (CIBERSAM), Universidad de Barcelona, Barcelona, Spain; ²²Department of Psychiatry, School of Medicine, Universidad de Valencia, Centro de Investigación Biomédica en Red de Salud Mental (CIBERSAM), Valencia, Spain; ²³Department of Medicine, Psychiatry Area, School of Medicine, Universidad de Oviedo, Centro de Investigación Biomédica en Red de Salud Mental (CIBERSAM), Oviedo, Spain; ²⁴Department of Mental Health and Drug-addiction assistance, Health Service of Galicia, Psychiatric Genetic Group IDIS, Hospital Clínico Universitario de Santiago de Compostela, affiliated center to Centro de Investigación Biomédica en Red de Salud Mental, (CIBERSAM), Servicio Gallego de Salud. Edificio Administrativo de San Lázaro s/n 15706 Santiago de Compostela, Spain; ²⁵Department of Psychiatry, Servicio de Psiquiatría Hospital "Virgen de la Luz," C/Hermanidad de Donantes de Sangre, Cuenca, Spain; ²⁶Villa de Vallecas Mental Health Department, Villa de Vallecas Mental Health Centre, Hospital Universitario Infanta Leonor/Hospital Virgen de la Torre, Madrid, Spain; ²⁷Puente de Vallecas Mental Health Department, Hospital Universitario Infanta Leonor/Hospital Virgen de la Torre, Centro de Salud Mental Puente de Vallecas, Madrid, Spain; ²⁸Fundación Pública Galega de Medicina Xenómica, Hospital Clínico Universitario, Santiago de Compostela, Spain; ²⁹Department of Psychiatry, Hospital General Universitario Gregorio Marañón, School of Medicine, Universidad Complutense, Madrid, Spain; ³⁰Hospital Psiquiátrico de Conxo. ext 251951, Santiago de Compostela, A Coruña, Spain; ³¹Department of Psychiatry, Early Psychosis Section, Academic Medical Centre, University of Amsterdam, Amsterdam, The Netherlands; ³²Department of Clinical Psychology, VU University and EMGO Institute of Health and Care Research, Amsterdam, The Netherlands; ³³Department of Psychosis Research, Parnassia Psychiatric Institute, The Hague, The Netherlands; ³⁴Rivierduinen Psychiatric

Institute, Leiden, The Netherlands; ³⁵AP-HP, Groupe Hospitalier “Mondor”, Pôle de Psychiatrie, Créteil, France; ³⁶INSERM, U955, Equipe 15, Créteil, France; ³⁷Faculté de Médecine, Université Paris-Est, Créteil, France; ³⁸Fondation Fondamental, Créteil, France; ³⁹CMP B CHU, BP 69, 63003 Clermont-Ferrand, Cedex 1, France; ⁴⁰Université d’Auvergne, EA 7280, Clermont-Ferrand, France; ⁴¹EPS Maison Blanche, Paris, France; ⁴²UPC KU Leuven, Campus Kortenberg, Department of Neurosciences, UPC, Kortenberg, Belgium; ⁴³Research Group Psychiatry, Department of Neurosciences, UPC, Leuven, Belgium; ⁴⁴Department of Human Genetics, University Hospital Gasthuisberg, Katholieke Universiteit Leuven, Leuven, Belgium; ⁴⁵Association for Scientific Research in Multiple Births, Ghent, Belgium; ⁴⁶Department of Neurology, Ghent University, Ghent University Hospital, Ghent, Belgium; ⁴⁷National and Kapodistrian University of Athens, Medical School Eginition Hospital, Athens, Greece; ⁴⁸Department of Psychiatry and Psychotherapy, Medical University of Vienna, Vienna, Austria; ⁴⁹Center for Gender Research and Early Detection, Psychiatric University Clinics Basel, Basel, Switzerland; ⁵⁰Diagnostic and Crisis Intervention Centre, Psychiatric University Clinics Basel, Basel, Switzerland; ⁵¹Department of Psychiatry and Psychotherapy, University of Cologne, Cologne, Germany; ⁵²Centre for Genomic Sciences, State Key Laboratory of Brain and Cognitive Sciences and Department of Psychiatry, Li Ka Shing Faculty of Medicine, The University of Hong Kong, Hong Kong SAR, PR China; ⁵³State Key Laboratory of Brain and Cognitive Sciences and Department of Psychiatry, Li Ka Shing Faculty of Medicine, The University of Hong Kong, New Clinical Building, Queen Mary Hospital, Hong Kong SAR, PR China; ⁵⁴Inter-University Chair in Law and the Human Genome (Provincial Government of Biskay) in University of Deusto, University of the Basque Country, Bilbao, Bizkaia, Spain; ⁵⁵Criminal Law, University of Zaragoza, Zaragoza, Spain; ⁵⁶Department of Psychiatry, University of Cambridge, Herchel Smith Building for Brain & Mind Sciences, Cambridge, UK; ⁵⁷Division of Psychiatry, University College, Charles Bell House, London, UK; ⁵⁸Department of Psychiatry, Royal College of Surgeons in Ireland, Education and Research Centre, Beaumont Hospital, Dublin 9, Ireland; ⁵⁹Division of Molecular and Clinical Neurobiology, Department of Psychiatry, Ludwig-Maximilians University, Munich, Germany; ⁶⁰Department of Medical and Surgical Science, Psychiatry Unit, Alma Mater Studiorum Università di Bologna, Bologna, Italy; ⁶¹Department of Medical and Surgical Science, Genetic Unit, Alma Mater Studiorum Università di Bologna, Bologna, Italy; ⁶²Department of Mental Health and Pathological Addictions, Local Health Trust, Bologna, Italy; ⁶³Department of Experimental Biomedicine and Clinical Neuroscience, Section of Psychiatry, University of Palermo, Palermo,

Italy; ⁶⁴Unit of Psychiatry, “P. Giaccone” General Hospital, Palermo, Italy; ⁶⁵Centre for Youth Mental Health, University of Melbourne Parkville, Victoria, Australia; ⁶⁶Melbourne Neuropsychiatry Centre, University of Melbourne, Carlton South, Victoria, Australia; ⁶⁷Departamento de Medicina Preventiva, Faculdade de Medicina, Universidade de São Paulo, Avenida Doutor Arnaldo 455, CEP 01246-903, São Paulo, Brazil; ⁶⁸Núcleo de Pesquisa em Saúde Mental Populacional, Universidade de São Paulo, São Paulo, Brazil; ⁶⁹Departamento de Neurociências e Ciências do Comportamento, Faculdade de Medicina de Ribeirão Preto, Universidade de São Paulo, Ribeirão Preto, Brazil; ⁷⁰Section of Psychiatry, Department of Public Health and Community Medicine, University of Verona, Verona, Italy; ⁷¹Copenhagen University Hospital, Research Unit, Mental Health Centre Copenhagen, Copenhagen, Denmark; ⁷²Hôpital Sainte-Anne, Service Hospitalo-Universitaire, Faculté de Médecine Paris Descartes, University Paris Descartes, Paris, France; ⁷³Departament de Psicologia Clínica i de la Salut, Universitat Autònoma de Barcelona, Barcelona, Spain; ⁷⁴Departament de Salut Mental, Sant Pere Claver-Fundació Sanitària, Barcelona, Spain; ⁷⁵Department of Psychology, University of North Carolina at Greensboro, Greensboro, NC; ⁷⁶Spanish Mental Health Research Network, CIBERSAM, Spain; ⁷⁷PRISMA Early Intervention Program, Department of Psychiatry, Federal University of São Paulo, São Paulo, Brazil; ⁷⁸School of Medicine, University of Belgrade, Beograd, Serbia

Correspondence

Bart P. Rutten, Department of Psychiatry and Neuropsychology, School for Mental Health and Neuroscience, South Limburg Mental Health Research and Teaching Network, Maastricht University Medical Centre, PO Box 616, 6200 MD Maastricht, The Netherlands; tel: 31-43-388-1263, fax: 31-43-388-4086, e-mail: b.rutten@maastrichtuniversity.nl

Ulrich Reininghaus, Department of Psychiatry and Neuropsychology, School for Mental Health and Neuroscience, South Limburg Mental Health Research and Teaching Network, Maastricht University Medical Centre, PO Box 616, 6200 MD Maastricht, The Netherlands; tel: 31-43-388-3896, fax: 31-43-388-4122, e-mail: u.reininghaus@maastrichtuniversity.nl

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