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ORIGINAL ARTICLE

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Shared genetic risk between eating disorder- and substance-use-related phenotypes: Evidence from genome-wide association studies

Melissa A. Munn-Chernoff[1] | Emma C. Johnson[2] | Yi-Ling Chou[2] | Jonathan R.I. Coleman[3,4] | Laura M. Thornton[1] | Raymond K. Walters[5,6] | Zeynep Yilmaz[1,7] | Jessica H. Baker[1] | Christopher Hübel[3,4,8] | Scott Gordon[9] | Sarah E. Medland[9] | Hunna J. Watson[1,10,11] | Héléna A. Gaspar[3,4] | Julien Bryois[8] | Anke Hinney[12] | Virpi M. Leppä[8] | Manuel Mattheisen[13,14,15,16] | Stephan Ripke[5,6,17] | Shuyang Yao[8] | Paola Giusti-Rodríguez[7] | Ken B. Hanscombe[18] | Roger A.H. Adan[19,20,21] | Lars Alfredsson[22] | Tetsuya Ando[23] | Ole A. Andreassen[24] | Wade H. Berrettini[25] | Ilka Boehm[26] | Claudette Boni[27] | Vesna Boraska Perica[28,29] | Katharina Buehren[30] | Roland Burghardt[31] | Matteo Cassina[32] | Sven Cichon[33,34,35] | Maurizio Clementi[32] | Roger D. Cone[36] | Philippe Courtet[37] | Scott Crow[38] | James J. Crowley[7,14] | Unna N. Danner[39] | Oliver S.P. Davis[40,41] | Martina de Zwaan[42] | George Dedoussis[43] | Daniela Degortes[44] | Janiece E. DeSocio[45] | Danielle M. Dick[46,47,48] | Dimitris Dikeos[49] | Christian Dina[50] | Monika Dmitrzak-Weglarz[51] | Elisa Docampo[52,53,54] | Laramie E. Duncan[55] | Karin Egberts[56] | Stefan Ehrlich[26] | Geòrgia Escaramís[52,53,54] | Tõnu Esko[57,58] | Xavier Estivill[52,53,54,59] | Anne Farmer[3] | Angela Favaro[44] | Fernando Fernández-Aranda[60,61] | Manfred M. Fichter[62,63] | Krista Fischer[57] | Manuel Föcker[64] | Lenka Foretova[65] | Andreas J. Forstner[34,66,67,68] | Monica Forzan[32] | Christopher S. Franklin[28] | Steven Gallinger[69] | Ina Giegling[70] | Johanna Giuranna[12] | Fragiskos Gonidakis[71] | Philip Gorwood[72,73] | Monica Gratacos Mayora[52,53,54] | Sébastien Guillaume[37] | Yiran Guo[74] | Hakon Hakonarson[74,75] | Konstantinos Hatzikotoulas[28,76] | Joanna Hauser[77] | Johannes Hebebrand[12] | Sietske G. Helder[3,78] | Stefan Herms[33,34] | Beate Herpertz-Dahlmann[30] | Wolfgang Herzog[79] | Laura M. Huckins[28,80] | James I. Hudson[81] | Hartmut Imgart[82] | Hidetoshi Inoko[83] | Vladimir Janout[84] | Susana Jiménez-Murcia[60,61] | Antonio Julià[85] | Gursharan Kalsi[3] | Deborah Kaminská[86] | Leila Karhunen[87] |

Cynthia M. Bulik and Arpana Agrawal joint last authors

Andreas Karwautz[88] | Martien J.H. Kas[19,89] | James L. Kennedy[90,91,92] | Anna Keski-Rahkonen[93] | Kirsty Kiezebrink[94] | Youl-Ri Kim[95] | Kelly L. Klump[96] | Gun Peggy S. Knudsen[97] | Maria C. La Via[1] | Stephanie Le Hellard[98,99,100] | Robert D. Levitan[90,91,92] | Dong Li[74] | Lisa Lilenfeld[101] | Bochao Danae Lin[19] | Jolanta Lissowska[102] | Jurjen Luykx[19] | Pierre J. Magistretti[103,104] | Mario Maj[105] | Katrin Mannik[57,106] | Sara Marsal[85] | Christian R. Marshall[107] | Morten Mattingsdal[108] | Sara McDevitt[109,110] | Peter McGuffin[3] | Andres Metspalu[57,111] | Ingrid Meulenbelt[112] | Nadia Micali[113,114] | Karen Mitchell[115,116] | Alessio Maria Monteleone[105] | Palmiero Monteleone[117] | Benedetta Nacmias[118] | Marie Navratilova[65] | Ioanna Ntalla[43] | Julie K. O'Toole[119] | Roel A. Ophoff[120,121] | Leonid Padyukov[122] | Aarno Palotie[58,123,124] | Jacques Pantel[27] | Hana Papezova[86] | Dalila Pinto[80] | Raquel Rabionet[125,126,127] | Anu Raevuori[93] | Nicolas Ramoz[72] | Ted Reichborn-Kjennerud[97,128] | Valdo Ricca[129] | Samuli Ripatti[130] | Franziska Ritschel[26,131] | Marion Roberts[3] | Alessandro Rotondo[132] | Dan Rujescu[70] | Filip Rybakowski[133] | Paolo Santonastaso[134] | André Scherag[135] | Stephen W. Scherer[136,137] | Ulrike Schmidt[138] | Nicholas J. Schork[139] | Alexandra Schosser[140] | Jochen Seitz[30] | Lenka Slachtova[141] | P. Eline Slagboom[142] | Margarita C.T. Slof-Op't Landt[143,144] | Agnieszka Slopien[145] | Sandro Sorbi[118,146] | Beata Świątkowska[147] | Jin P. Szatkiewicz[7] | Ioanna Tachmazidou[28] | Elena Tenconi[44] | Alfonso Tortorella[148,149] | Federica Tozzi[150] | Janet Treasure[138] | Artemis Tsitsika[151] | Marta Tyszkiewicz-Nwafor[145] | Konstantinos Tziouvas[152] | Annemarie A. van Elburg[20,153] | Eric F. van Furth[143,144] | Gudrun Wagner[88] | Esther Walton[26] | Elisabeth Widen[123] | Eleftheria Zeggini[28,76] | Stephanie Zerwas[1] | Stephan Zipfel[154] | Andrew W. Bergen[155,156] | Joseph M. Boden[157] | Harry Brandt[158] | Steven Crawford[158] | Katherine A. Halmi[159] | L. John Horwood[157] | Craig Johnson[160] | Allan S. Kaplan[90,91,92] | Walter H. Kaye[161] | James Mitchell[162] | Catherine M. Olsen[163] | John F. Pearson[164] | Nancy L. Pedersen[8] | Michael Strober[165,166] | Thomas Werge[167] | David C. Whiteman[163] | D. Blake Woodside[91,92,168,169] | Jakob Grove[13,170,171,172] | Anjali K. Henders[173] | Janne T. Larsen[170,174,175] | Richard Parker[9] | Liselotte V. Petersen[170,174,175] | Jennifer Jordan[176,177] | Martin A. Kennedy[178] | Andreas Birgegård[8,14,15] | Paul Lichtenstein[8] | Claes Norring[14,15] | Mikael Landén[8,179] | Preben Bo Mortensen[170,174,175] | Renato Polimanti[180,181] | Jeanette N. McClintick[182] | Amy E. Adkins[46,47] | Fazil Aliev[46,183] |

Silviu-Alin Bacanu[184,185,186] | Anthony Batzler[187] | Sarah Bertelsen[188] | Joanna M. Biernacka[189,190] | Tim B. Bigdeli[191] | Li-Shiun Chen[2] | Toni-Kim Clarke[192] | Franziska Degenhardt[193] | Anna R. Docherty[194] | Alexis C. Edwards[185,186] | Jerome C. Foo[195] | Louis Fox[2] | Josef Frank[195] | Laura M. Hack[55] | Annette M. Hartmann[70] | Sarah M. Hartz[2] | Stefanie Heilmann-Heimbach[193] | Colin Hodgkinson[196] | Per Hoffmann[33,67,197] | Jouke-Jan Hottenga[198] | Bettina Konte[70] | Jari Lahti[199] | Marius Lahti-Pulkkinen[200] | Dongbing Lai[201] | Lannie Ligthart[198] | Anu Loukola[123] | Brion S. Maher[202] | Hamdi Mbarek[198] | Andrew M. McIntosh[203] | Matthew B. McQueen[204] | Jacquelyn L. Meyers[205] | Yuri Milaneschi[206] | Teemu Palviainen[123] | Roseann E. Peterson[185,186] | Euijung Ryu[189] | Nancy L. Saccone[207] | Jessica E. Salvatore[46,185,186] | Sandra Sanchez-Roige[161] | Melanie Schwandt[208] | Richard Sherva[209] | Fabian Streit[195] | Jana Strohmaier[195] | Nathaniel Thomas[46,47] | Jen-Chyong Wang[188] | Bradley T. Webb[184,185,186] | Robbee Wedow[5,6,210,211] | Leah Wetherill[201] | Amanda G. Wills[212] | Hang Zhou[180,181] | Jason D. Boardman[213,214] | Danfeng Chen[6] | Doo-Sup Choi[215] | William E. Copeland[216] | Robert C. Culverhouse[217] | Norbert Dahmen[218] | Louisa Degenhardt[219] | Benjamin W. Domingue[220] | Mark A. Frye[190] | Wolfgang Gäebel[221] | Caroline Hayward[222] | Marcus Ising[223] | Margaret Keyes[224] | Falk Kiefer[225] | Gabriele Koller[226] | John Kramer[227] | Samuel Kuperman[227] | Susanne Lucae[223] | Michael T. Lynskey[228] | Wolfgang Maier[229] | Karl Mann[225] | Satu Männistö[230] | Bertram Müller-Myhsok[231] | Alison D. Murray[232] | John I. Nurnberger[201,233] | Ulrich Preuss[234,235] | Katri Räikkönen[200] | Maureen D. Reynolds[236] | Monika Ridinger[237] | Norbert Scherbaum[238] | Marc A. Schuckit[161] | Michael Soyka[239,240] | Jens Treutlein[195] | Stephanie H. Witt[195] | Norbert Wodarz[241] | Peter Zill[242] | Daniel E. Adkins[194,243] | Dorret I. Boomsma[198] | Laura J. Bierut[2] | Sandra A. Brown[161,244] | Kathleen K. Bucholz[2] | E. Jane Costello[245] | Harriet de Wit[246] | Nancy Diazgranados[247] | Johan G. Eriksson[248,249] | Lindsay A. Farrer[209,250,251,252,253] | Tatiana M. Foroud[201] | Nathan A. Gillespie[185] | Alison M. Goate[188] | David Goldman[196,254] | Richard A. Grucza[2] | Dana B. Hancock[255] | Kathleen Mullan Harris[256,257] | Victor Hesselbrock[258] | John K. Hewitt[259] | Christian J. Hopfer[260] | William G. Iacono[224] | Eric O. Johnson[255,261] | Victor M. Karpyak[190] | Kenneth S. Kendler[185,186] | Henry R. Kranzler[262,263] | Kenneth Krauter[264] | Penelope A. Lind[9] |

Matt McGue[224] | James MacKillop[265,266] | Pamela A.F. Madden[2] | Hermine H. Maes[185] | Patrik K.E. Magnusson[8] | Elliot C. Nelson[2] | Markus M. Nöthen[193] | Abraham A. Palmer[161,267] | Brenda W.J.H. Penninx[268] | Bernice Porjesz[205] | John P. Rice[2] | Marcella Rietschel[195] | Brien P. Riley[184,185,186] | Richard J. Rose[269] | Pei-Hong Shen[196] | Judy Silberg[185,186] | Michael C. Stallings[259] | Ralph E. Tarter[236] | Michael M. Vanyukov[236] | Scott Vrieze[224] | Tamara L. Wall[161] | John B. Whitfield[9] | Hongyu Zhao[270] | Benjamin M. Neale[5,6] | Tracey D. Wade[271] | Andrew C. Heath[2] | Grant W. Montgomery[9,173,272] | Nicholas G. Martin[9] | Patrick F. Sullivan[1,7,8] | Jaakko Kaprio[93,123] | Gerome Breen[3,4] | Joel Gelernter[180,181,273,274] | Howard J. Edenberg[182,201] | Cynthia M. Bulik[1,8,275] | Arpana Agrawal[2]

[1]Department of Psychiatry, University of North Carolina at Chapel Hill, Chapel Hill, North Carolina, USA

[2]Department of Psychiatry, Washington University School of Medicine, Saint Louis, Missouri, USA

[3]Social, Genetic and Developmental Psychiatry (SGDP) Centre, Institute of Psychiatry, Psychology and Neuroscience, King's College London, London, UK

[4]National Institute for Health Research Biomedical Research Centre, King's College London and South London and Maudsley National Health Service Trust, London, UK

[5]Analytic and Translational Genetics Unit, Department of Medicine, Massachusetts General Hospital and Harvard Medical School, Boston, Massachusetts, USA

[6]Stanley Center for Psychiatric Research, Broad Institute of MIT and Harvard, Cambridge, Massachusetts, USA

[7]Department of Genetics, University of North Carolina at Chapel Hill, Chapel Hill, North Carolina, USA

[8]Department of Medical Epidemiology and Biostatistics, Karolinska Institutet, Stockholm, Sweden

[9]QIMR Berghofer Medical Research Institute, Brisbane, Queensland, Australia

[10]School of Psychology, Curtin University, Perth, Western Australia, Australia

[11]School of Paediatrics and Child Health, University of Western Australia, Perth, Western Australia, Australia

[12]Department of Child and Adolescent Psychiatry, University Hospital Essen, University of Duisburg-Essen, Essen, Germany

[13]Department of Biomedicine, Aarhus University, Aarhus, Denmark

[14]Department of Clinical Neuroscience, Karolinska Institutet, Stockholm, Sweden

[15]Center for Psychiatry Research, Stockholm Health Care Services, Stockholm County Council, Stockholm, Sweden

[16]Department of Psychiatry, Psychosomatics and Psychotherapy, University of Würzburg, Germany

[17]Department of Psychiatry and Psychotherapy, Charité - Universitätsmedizin, Berlin, Germany

[18]Department of Medical and Molecular Genetics, King's College London, Guy's Hospital, London, UK

[19]Department of Translational Neuroscience, Brain Center Rudolf Magnus, University Medical Center Utrecht, Utrecht, The Netherlands

[20]Center for Eating Disorders Rintveld, Altrecht Mental Health Institute, Zeist, The Netherlands

[21]Sahlgrenska Academy, University of Gothenburg, Gothenburg, Sweden

[22]Institute of Environmental Medicine, Karolinska Institutet, Stockholm, Sweden

[23]Department of Behavioral Medicine, National Institute of Mental Health, National Center of Neurology and Psychiatry, Kodaira, Tokyo, Japan

[24]NORMENT Centre, Division of Mental Health and Addiction, NORMENT Centre, University of Oslo, Oslo University Hospital, Oslo, Norway

[25]Department of Psychiatry, Center for Neurobiology and Behavior, University of Pennsylvania Perelman School of Medicine, Philadelphia, Pennsylvania, USA

[26]Division of Psychological and Social Medicine and Developmental Neurosciences, Faculty of Medicine, Technische Universität Dresden, Dresden, Germany

[27]Centre of Psychiatry and Neuroscience, INSERM U894, Paris, France

[28]Wellcome Sanger Institute, Wellcome Genome Campus, Hinxton, Cambridge, UK

[29]Department of Medical Biology, School of Medicine, University of Split, Split, Croatia

[30]Department of Child and Adolescent Psychiatry, Psychosomatics and Psychotherapy, RWTH Aachen University, Aachen, Germany

[31]Klinikum Frankfurt/Oder, Frankfurt, Germany

[32]Clinical Genetics Unit, Department of Woman and Child Health, University of Padova, Italy

[33]Institute of Medical Genetics and Pathology, University Hospital Basel, Basel, Switzerland

[34]Department of Biomedicine, University of Basel, Basel, Switzerland

[35]Institute of Neuroscience and Medicine (INM-1), Research Center Juelich, Germany

[36]Department of Molecular and Integrative Physiology, Life Sciences Institute, University of Michigan, Ann Arbor, Michigan, USA

[37]Department of Emergency Psychiatry and Post-Acute Care, CHRU Montpellier, University of Montpellier, Montpellier, France

[38]Department of Psychiatry, University of Minnesota, Minneapolis, Minnesota, USA

[39]Altrecht Eating Disorders Rintveld, Altrecht Mental Health Institute, Zeist, The Netherlands

[40]MRC Integrative Epidemiology Unit, University of Bristol, Bristol, UK

[41]School of Social and Community Medicine, University of Bristol, Bristol, UK

[42]Department of Psychosomatic Medicine and Psychotherapy, Hannover Medical School, Hannover, Germany

[43]Department of Nutrition and Dietetics, Harokopio University, Athens, Greece

[44]Department of Neurosciences, University of Padova, Padova, Italy

[45]College of Nursing, Seattle University, Seattle, Washington, USA

[46]Department of Psychology, Virginia Commonwealth University, Richmond, Virginia, USA

[47]College Behavioral and Emotional Health Institute, Virginia Commonwealth University, Richmond, Virginia, USA

[48]Department of Human & Molecular Genetics, Virginia Commonwealth University, Richmond, Virginia, USA

[49]Department of Psychiatry, Athens University Medical School, Athens University, Athens, Greece

[50]l'institut du thorax, INSERM, CNRS, Univ Nantes, Nantes, France

[51]Department of Psychiatric Genetics, Poznan University of Medical Sciences, Poznan, Poland

[52]Barcelona Institute of Science and Technology, Barcelona, Spain

[53]Universitat Pompeu Fabra, Barcelona, Spain

[54]Centro de Investigación Biomédica en Red en Epidemiología y Salud Pública (CIBERESP), Barcelona, Spain

[55]Department of Psychiatry and Behavioral Sciences, Stanford University, Stanford, California, USA

[56]Department of Child and Adolescent Psychiatry, Psychosomatics and Psychotherapy, Centre for Mental Health, University Hospital of Würzburg, Würzburg, Germany

[57]Estonian Genome Center, University of Tartu, Tartu, Estonia

[58]Program in Medical and Population Genetics, Broad Institute of MIT and Harvard, Cambridge, Massachusetts, USA

[59]Genomics and Disease, Bioinformatics and Genomics Programme, Centre for Genomic Regulation, Barcelona, Spain

[60]Department of Psychiatry, University Hospital of Bellvitge –IDIBELL and CIBERobn, Barcelona, Spain

[61]Department of Clinical Sciences, School of Medicine, University of Barcelona, Barcelona, Spain

[62]Department of Psychiatry and Psychotherapy, Ludwig-Maximilians-University, Munich, Germany

[63]Schön Klinik Roseneck affiliated with the Medical Faculty of the University of Munich, Munich, Germany

[64]Department of Child and Adolescent Psychiatry, University of Münster, Münster, Germany

[65]Department of Cancer, Epidemiology and Genetics, Masaryk Memorial Cancer Institute, Brno, Czech Republic

[66]Centre for Human Genetics, University of Marburg, Marburg, Germany

[67]Institute of Human Genetics, School of Medicine & University Hospital Bonn, University of Bonn, Bonn, Germany

[68]Department of Psychiatry (UPK), University of Basel, Basel, Switzerland

[69]Department of Surgery, Faculty of Medicine, University of Toronto, Toronto, Ontario, Canada

[70]Department of Psychiatry, Psychotherapy and Psychosomatics, Martin-Luther-University Halle-Wittenberg, Halle (Saale), Germany

[71]1st Psychiatric Department, National and Kapodistrian University of Athens, Medical School, Eginition Hospital, Athens, Greece

[72]Institute of Psychiatry and Neuroscience of Paris, INSERM U1266, Paris, France

[73]CMME (GHU Paris Psychiatrie et Neurosciences), Paris Descartes University, Paris, France

[74]Center for Applied Genomics, Children's Hospital of Philadelphia, Philadelphia, Pennsylvania, USA

[75]Department of Pediatrics, University of Pennsylvania Perelman School of Medicine, Philadelphia, Pennsylvania, USA

[76]Institute of Translational Genomics, Helmholtz Zentrum München - German Research Centre for Environmental Health, Neuherberg, Germany

[77]Department of Adult Psychiatry, Poznan University of Medical Sciences, Poznan, Poland

[78]Zorg op Orde, Delft, The Netherlands

[79]Department of General Internal Medicine and Psychosomatics, Heidelberg University Hospital, Heidelberg University, Heidelberg, Germany

[80]Department of Psychiatry, and Genetics and Genomics Sciences, Division of Psychiatric Genomics, Icahn School of Medicine at Mount Sinai, New York, New York, USA

[81]Biological Psychiatry Laboratory, McLean Hospital/Harvard Medical School, Boston, Massachusetts, USA

[82]Eating Disorders Unit, Parklandklinik, Bad Wildungen, Germany

[83]Department of Molecular Life Science, Division of Basic Medical Science and Molecular Medicine, School of Medicine, Tokai University, Isehara, Japan

[84]Faculty of Health Sciences, Palacky University, Olomouc, Czech Republic

[85]Rheumatology Research Group, Vall d'Hebron Research Institute, Barcelona, Spain

[86]Department of Psychiatry, First Faculty of Medicine, Charles University, Prague, Czech Republic

[87]Department of Clinical Nutrition, Institute of Public Health and Clinical Nutrition, University of Eastern Finland, Kuopio, Finland

[88]Eating Disorders Unit, Department of Child and Adolescent Psychiatry, Medical University of Vienna, Vienna, Austria

[89]Groningen Institute for Evolutionary Life Sciences, University of Groningen, Groningen, The Netherlands

[90]Centre for Addiction and Mental Health, Toronto, Ontario, Canada

[91]Institute of Medical Science, University of Toronto, Toronto, Ontario, Canada

[92]Department of Psychiatry, University of Toronto, Toronto, Ontario, Canada

[93]Department of Public Health, University of Helsinki, Helsinki, Finland

[94]Institute of Applied Health Sciences, School of Medicine, Medical Sciences and Nutrition, University of Aberdeen, Aberdeen, UK

[95]Department of Psychiatry, Seoul Paik Hospital, Inje University, Seoul, Korea

[96]Department of Psychology, Michigan State University, East Lansing, Michigan, USA

[97]Department of Mental Disorders, Norwegian Institute of Public Health, Oslo, Norway

[98]Department of Clinical Science, Norwegian Centre for Mental Disorders Research (NORMENT), University of Bergen, Bergen, Norway

[99]Dr. Einar Martens Research Group for Biological Psychiatry, Center for Medical Genetics and Molecular Medicine, Haukeland University Hospital, Bergen, Norway

[100]Department of Clinical Medicine, Laboratory Building, Haukeland University Hospital, Bergen, Norway

[101]The Chicago School of Professional Psychology, Washington DC Campus, Washington, District of Columbia, USA

[102]Department of Cancer Epidemiology and Prevention, M Skłodowska-Curie Cancer Center - Oncology Center, Warsaw, Poland

[103]BESE Division, King Abdullah University of Science and Technology, Thuwal, Saudi Arabia

[104]Department of Psychiatry, University of Lausanne-University Hospital of Lausanne (UNIL-CHUV), Lausanne, Switzerland

[105]Department of Psychiatry, University of Campania "Luigi Vanvitelli", Naples, Italy

[106]Center for Integrative Genomics, University of Lausanne, Lausanne, Switzerland

[107]Department of Paediatric Laboratory Medicine, Division of Genome Diagnostics, The Hospital for Sick Children, Toronto, Ontario, Canada

[108]NORMENT KG Jebsen Centre, Division of Mental Health and Addiction, University of Oslo, Oslo University Hospital, Oslo, Norway

[109]Department of Psychiatry, University College Cork, Cork, Ireland

[110]Eist Linn Adolescent Unit, Bessborough, Health Service Executive South, Cork, Ireland

[111]Institute of Molecular and Cell Biology, University of Tartu, Tartu, Estonia

[112]Molecular Epidemiology Section (Department of Biomedical Datasciences), Leiden University Medical Centre, Leiden, The Netherlands

[113]Department of Psychiatry, Faculty of Medicine, University of Geneva, Geneva, Switzerland

[114]Division of Child and Adolescent Psychiatry, Geneva University Hospital, Geneva, Switzerland

[115]National Center for PTSD, VA Boston Healthcare System, Boston, Massachusetts, USA

[116]Department of Psychiatry, Boston University School of Medicine, Boston, Massachusetts, USA

[117]Department of Medicine, Surgery and Dentistry "Scuola Medica Salernitana", University of Salerno, Salerno, Italy

[118]Department of Neuroscience, Psychology, Drug Research and Child Health (NEUROFARBA), University of Florence, Florence, Italy

[119]Kartini Clinic, Portland, Oregon, USA

[120]Center for Neurobehavioral Genetics, Semel Institute for Neuroscience and Human Behavior, University of California Los Angeles, Los Angeles, California, USA

[121]Department of Psychiatry, Erasmus MC, University Medical Center Rotterdam, Rotterdam, The Netherlands

[122]Department of Medicine, Center for Molecular Medicine, Division of Rheumatology, Karolinska Institutet and Karolinska University Hospital, Stockholm, Sweden

[123]Institute for Molecular Medicine FIMM, HiLIFE, University of Helsinki, Helsinki, Finland

[124]Center for Human Genome Research, Massachusetts General Hospital, Boston, Massachusetts, USA

[125]Saint Joan de Déu Research Institute, Saint Joan de Déu Barcelona Children's Hospital, Barcelona, Spain

[126]Institute of Biomedicine (IBUB), University of Barcelona, Barcelona, Spain

[127]Department of Genetics, Microbiology and Statistics, University of Barcelona, Barcelona, Spain

[128]Institute of Clinical Medicine, University of Oslo, Oslo, Norway

[129]Department of Health Science, University of Florence, Florence, Italy

[130]Department of Biometry, University of Helsinki, Helsinki, Finland

[131]Department of Child and Adolescent Psychiatry, Faculty of Medicine, Eating Disorders Research and Treatment Center, Technische Universität Dresden, Dresden, Germany

[132]Department of Psychiatry, Neurobiology, Pharmacology, and Biotechnologies, University of Pisa, Pisa, Italy

[133]Department of Psychiatry, Poznan University of Medical Sciences, Poznan, Poland

[134]Department of Neurosciences, Padua Neuroscience Center, University of Padova, Padova, Italy

[135]Institute of Medical Statistics, Computer and Data Sciences, Jena University Hospital, Jena, Germany

[136]Department of Genetics and Genomic Biology, The Hospital for Sick Children, Toronto, Ontario, Canada

[137]McLaughlin Centre, University of Toronto, Toronto, Ontario, Canada

[138]Department of Psychological Medicine, Institute of Psychiatry, Psychology and Neuroscience, King's College London, London, UK

[139]J. Craig Venter Institute (JCVI), La Jolla, California, USA

[140]Department of Psychiatry and Psychotherapy, Medical University of Vienna, Vienna, Austria

[141]Department of Pediatrics and Center of Applied Genomics, First Faculty of Medicine, Charles University, Prague, Czech Republic

[142]Molecular Epidemiology Section (Department of Medical Statistics), Leiden University Medical Centre, Leiden, The Netherlands

[143]Center for Eating Disorders Ursula, Rivierduinen, Leiden, The Netherlands

[144]Department of Psychiatry, Leiden University Medical Centre, Leiden, The Netherlands

[145]Department of Child and Adolescent Psychiatry, Poznan University of Medical Sciences, Poznan, Poland

[146]IRCCS Fondazione Don Carlo Gnocchi, Florence, Italy

[147]Department of Environmental Epidemiology, Nofer Institute of Occupational Medicine, Lodz, Poland

[148]Department of Psychiatry, University of Naples SUN, Naples, Italy

[149]Department of Psychiatry, University of Perugia, Perugia, Italy

[150]Brain Sciences Department, Stremble Ventures, Limassol, Cyprus

[151]Adolescent Health Unit, Second Department of Pediatrics, "P. & A. Kyriakou" Children's Hospital, University of Athens, Athens, Greece

[152]Pediatric Intensive Care Unit, "P. & A. Kyriakou" Children's Hospital, University of Athens, Athens, Greece

[153]Faculty of Social and Behavioral Sciences, Utrecht University, Utrecht, The Netherlands

[154]Department of Internal Medicine VI, Psychosomatic Medicine and Psychotherapy, University Medical Hospital Tuebingen, Tuebingen, Germany

[155]BioRealm, LLC, Walnut, California, USA

[156]Oregon Research Institute, Eugene, Oregon, USA

[157]Christchurch Health and Development Study, University of Otago, Christchurch, New Zealand

[158]The Center for Eating Disorders at Sheppard Pratt, Baltimore, Maryland, USA

[159]Department of Psychiatry, Weill Cornell Medical College, New York, New York, USA

[160]Eating Recovery Center, Denver, Colorado, USA

[161]Department of Psychiatry, University of California San Diego, La Jolla, California, USA

[162]Department of Psychiatry and Behavioral Science, University of North Dakota School of Medicine and Health Sciences, Fargo, North Dakota, USA

[163]Population Health Department, QIMR Berghofer Medical Research Institute, Brisbane, Queensland, Australia

[164]Biostatistics and Computational Biology Unit, University of Otago, Christchurch, New Zealand

[165]Department of Psychiatry and Biobehavioral Science, Semel Institute for Neuroscience and Human Behavior, University of California Los Angeles, Los Angeles, California, USA

[166]David Geffen School of Medicine, University of California Los Angeles, Los Angeles, California, USA

[167]Department of Clinical Medicine, University of Copenhagen, Copenhagen, Denmark

[168]Centre for Mental Health, University Health Network, Toronto, Ontario, Canada

[169]Program for Eating Disorders, University Health Network, Toronto, Ontario, Canada

[170]The Lundbeck Foundation Initiative for Integrative Psychiatric Research (iPSYCH), Aarhus, Denmark

[171]Centre for Integrative Sequencing, iSEQ, Aarhus University, Aarhus, Denmark

[172]Bioinformatics Research Centre, Aarhus University, Aarhus, Denmark

[173]Institute for Molecular Bioscience, University of Queensland, Brisbane, Queensland, Australia

[174]National Centre for Register-Based Research, Aarhus BSS, Aarhus University, Aarhus, Denmark

[175]Centre for Integrated Register-based Research (CIRRAU), Aarhus University, Aarhus, Denmark

[176]Department of Psychological Medicine, University of Otago, Christchurch, New Zealand

[177]Canterbury District Health Board, Christchurch, New Zealand

[178]Department of Pathology and Biomedical Science, University of Otago, Christchurch, New Zealand

[179]Department of Psychiatry and Neurochemistry, Institute of Neuroscience and Physiology, The Sahlgrenska Academy at the University of Gothenburg, Gothenburg, Sweden

[180]Department of Psychiatry, Division of Human Genetics, Yale School of Medicine, New Haven, Connecticut, USA

[181]Veterans Affairs Connecticut Healthcare System, West Haven, Connecticut, USA

[182]Department of Biochemistry and Molecular Biology, Indiana University School of Medicine, Indianapolis, Indiana, USA

[183]Faculty of Business, Karabuk University, Karabuk, Turkey

[184]Virginia Commonwealth University Alcohol Research Center, Virginia Commonwealth University, Richmond, Virginia, USA

[185]Virginia Institute for Psychiatric and Behavioral Genetics, Virginia Commonwealth University, Richmond, Virginia, USA

[186]Department of Psychiatry, Virginia Commonwealth University, Richmond, Virginia, USA

[187]Psychiatric Genomics and Pharmacogenomics Program, Mayo Clinic, Rochester, Minnesota, USA

[188]Department of Neuroscience, Icahn School of Medicine at Mount Sinai, New York, New York, USA

[189]Department of Health Sciences Research, Mayo Clinic, Rochester, Minnesota, USA

[190]Department of Psychiatry and Psychology, Mayo Clinic, Rochester, Minnesota, USA

[191]Department of Psychiatry and Behavioral Sciences, State University of New York Downstate Medical Center, Brooklyn, New York, USA

[192]Division of Psychiatry, University of Edinburgh, Edinburgh, UK

[193]Institute of Human Genetics, University of Bonn School of Medicine & University Hospital Bonn, Bonn, Germany

[194]Department of Psychiatry, University of Utah, Salt Lake City, Utah, USA

[195]Department of Genetic Epidemiology in Psychiatry, Central Institute of Mental Health, Medical Faculty Mannheim, Heidelberg University, Mannheim, Germany

[196]Laboratory of Neurogenetics, NIH/NIAAA, Bethesda, Maryland, USA

[197]Human Genomics Research Group, Department of Biomedicine, University of Basel, Basel, Switzerland

[198]Department of Biological Psychology, Amsterdam Public Health Research Institute, Vrije Universiteit Amsterdam, Amsterdam, The Netherlands

[199]Turku Institute for Advanced Studies, University of Turku, Turku, Finland

[200]Department of Psychology and Logopedics, University of Helsinki, Helsinki, Finland

[201]Department of Medical and Molecular Genetics, Indiana University School of Medicine, Indianapolis, Indiana, USA

[202]Johns Hopkins Bloomberg School of Public Health, Baltimore, Maryland, USA

[203]Division of Psychiatry, Centre for Cognitive Ageing and Cognitive Epidemiology, University of Edinburgh, Edinburgh, UK

[204]Department of Integrative Physiology, University of Colorado Boulder, Boulder, Colorado, USA

[205]Department of Psychiatry and Behavioral Sciences, Henri Begleiter Neurodynamics Laboratory, SUNY Downstate Medical Center, Brooklyn, New York, USA

[206]Department of Psychiatry, Amsterdam Public Health Research Institute, VU University Medical Center/GGz inGeest, Amsterdam, The Netherlands

[207]Department of Genetics, Washington University School of Medicine, Saint Louis, Missouri, USA

[208]Office of the Clinical Director, NIH/NIAAA, Bethesda, Maryland, USA

[209]Department of Medicine (Biomedical Genetics), Boston University School of Medicine, Boston, Massachusetts, USA

[210]Department of Epidemiology, Harvard T.H. Chan School of Public Health, Harvard University, Cambridge, Massachusetts, USA

[211]Department of Sociology, Harvard University, Cambridge, Massachusetts, USA

[212]Department of Pharmacology, University of Colorado School of Medicine, Aurora, Colorado, USA

[213]Institute of Behavioral Science, University of Colorado, Boulder, Colorado, USA

[214]Department of Sociology, University of Colorado, Boulder, Colorado, USA

[215]Department of Molecular Pharmacology and Experimental Therapeutics, Mayo Clinic, Rochester, Minnesota, USA

[216]Department of Psychiatry, University of Vermont Medical Center, Burlington, Vermont, USA

[217]Department of Medicine, Division of Biostatistics, Washington University School of Medicine, Saint Louis, Missouri, USA

[218]Department of Psychiatry, University of Mainz, Mainz, Germany

[219]National Drug and Alcohol Research Centre, University of New South Wales, Sydney, New South Wales, Australia

[220]Stanford University Graduate School of Education, Stanford University, Stanford, California, USA

[221]Department of Psychiatry and Psychotherapy, University of Düsseldorf, Duesseldorf, Germany

[222]MRC Human Genetics Unit, Institute of Genetics and Molecular Medicine, University of Edinburgh, Edinburgh, UK

[223]Max-Planck-Institute of Psychiatry, Munich, Germany

[224]Department of Psychology, University of Minnesota, Minneapolis, Minnesota, USA

[225]Department of Addictive Behavior and Addiction Medicine, Central Institute of Mental Health, Medical Faculty Mannheim, Heidelberg University, Mannheim, Germany

[226]Department of Psychiatry and Psychotherapy, University Hospital, LMU Munich, Munich, Germany

[227]Department of Psychiatry, University of Iowa Roy J and Lucille A Carver College of Medicine, Iowa City, Iowa, USA

[228]Addictions Department, Institute of Psychiatry, Psychology & Neuroscience, King's College London, London, UK

[229]Department of Psychiatry, University of Bonn, Bonn, Germany

[230]Department of Public Health Solutions, National Institute for Health and Welfare, Helsinki, Finland

[231]Department of Statistical Genetics, Max-Planck-Institute of Psychiatry, München, Germany

[232]Aberdeen Biomedical Imaging Centre, School of Medicine, Medical Sciences & Nutrition, University of Aberdeen, Foresterhill, Aberdeen, UK

[233]Department of Psychiatry, Indiana University School of Medicine, Indianapolis, Indiana, USA

[234]Department of Psychiatry, Psychotherapy and Psychosomatics, Martin-Luther-University Halle-Wittenberg, Herborn, Germany

[235]Department of Psychiatry and Psychotherapy, Vitos Hospital Herborn, Herborn, Germany

[236]School of Pharmacy, University of Pittsburgh, Pittsburgh, Pennsylvania, USA

[237]Department of Psychiatry and Psychotherapy, University of Regensburg Psychiatric Health Care Aargau, Regensburg, Germany

[238]Department of Psychiatry and Psychotherapy and Department of Addictive Behaviour and Addiction Medicine, Medical Faculty, LVR-Hospital Essen, University of Duisburg-Essen, Essen, Germany

[239]Medical Park Chiemseeblick in Bernau-Felden, Ludwig-Maximilians-University, Bernau am Chiemsee, Germany

[240]Psychiatric Hospital, Ludwig-Maximilians-University, Bernau am Chiemsee, Germany

[241]Department of Psychiatry and Psychotherapy, University of Regensburg, Regensburg, Germany

[242]Department of Psychiatry, Psychiatric Hospital, Ludwig-Maximilians-University, Munich, Germany

[243]Department of Sociology, University of Utah, Salt Lake City, Utah, USA

[244]Department of Psychology, University of California San Diego, La Jolla, California, USA

[245]Department of Psychiatry and Behavioral Sciences, Duke University Medical Center, Durham, North Carolina, USA

[246]Department of Psychiatry and Behavioral Neuroscience, University of Chicago, Chicago, Illinois, USA

[247]NIAAA Intramural Research Program, Bethesda, Maryland, USA

[248]Department of General Practice and Primary Health Care, University of Helsinki, Helsinki, Finland

[249]National Institute for Health and Welfare, Helsinki, Finland

[250]Department of Neurology, Boston University School of Medicine, Boston, Massachusetts, USA

[251]Department of Ophthalmology, Boston University School of Medicine, Boston, Massachusetts, USA

[252]Department of Epidemiology, School of Public Health, Boston University, Boston, Massachusetts, USA

[253]Department of Biostatistics, School of Public Health, Boston University, Boston, Massachusetts, USA

[254]Office of the Clinical Director, NIH/NIAAA, Besthesda, Maryland, USA

[255]Center for Omics Discovery and Epidemiology, Behavioral Health Research Division, RTI International, Research Triangle Park, North Carolina, USA

[256]Department of Sociology, University of North Carolina at Chapel Hill, Chapel Hill, North Carolina, USA

[257]Carolina Population Center, University of North Carolina at Chapel Hill, Chapel Hill, North Carolina, USA

[258]Department of Psychiatry, University of Connecticut School of Medicine, Farmington, Connecticut, USA

[259]Institute for Behavioral Genetics, University of Colorado Boulder, Boulder, Colorado, USA

[260]Department of Psychiatry, University of Colorado Denver, Aurora, Colorado, USA

[261]Fellow Program, RTI International, Research Triangle Park, North Carolina, USA

[262]Center for Studies of Addiction, University of Pennsylvania Perelman School of Medicine, Philadelphia, Pennsylvania, USA

[263]VISN 4 MIRECC, Crescenz VAMC, Philadelphia, Pennsylvania, USA

[264]Department of Molecular, Cellular, and Developmental Biology, University of Colorado Boulder, Boulder, Colorado, USA

[265]Peter Boris Centre for Addictions Research, McMaster University/St. Joseph's Healthcare Hamilton, Hamilton, Ontario, Canada

[266]Michael G. DeGroote Centre for Medicinal Cannabis Research, McMaster University/St. Joseph's Healthcare Hamilton, Hamilton, Ontario, Canada

[267]Institute for Genomic Medicine, University of California San Diego, La Jolla, California, USA

[268]Department of Psychiatry, Amsterdam UMC, VU University and GGZinGeest, Amsterdam, The Netherlands

[269]Department of Psychological & Brain Sciences, Indiana University Bloomington, Bloomington, Indiana, USA

[270]Department of Biostatistics, Yale School of Public Health, Yale University, New Haven, Connecticut, USA

[271]School of Psychology, Flinders University, Adelaide, South Australia, Australia

[272]Queensland Brain Institute, University of Queensland, Brisbane, Queensland, Australia

[273]Department of Genetics, Yale School of Medicine, New Haven, Connecticut, USA

[274]Department of Neuroscience, Yale School of Medicine, New Haven, Connecticut, USA

[275]Department of Nutrition, University of North Carolina at Chapel Hill, Chapel Hill, North Carolina, USA

Correspondence
Melissa A. Munn-Chernoff, Department of Psychiatry, University of North Carolina at Chapel Hill, 101 Manning Drive, Campus Box 7160, Chapel Hill, NC 27599.
Email: melissa_chernoff@med.unc.edu

Abstract

Eating disorders and substance use disorders frequently co-occur. Twin studies reveal shared genetic variance between liabilities to eating disorders and substance use, with the strongest associations between symptoms of bulimia nervosa and problem alcohol use (genetic correlation [r_g], twin-based = 0.23-0.53). We estimated the genetic correlation between eating disorder and substance use and disorder phenotypes using data from genome-wide association studies (GWAS). Four eating disorder phenotypes (anorexia nervosa [AN], AN *with* binge eating, AN *without* binge eating, and a bulimia nervosa factor score), and eight substance-use-related phenotypes (drinks per week, alcohol use disorder [AUD], smoking initiation, current smoking, cigarettes per day, nicotine dependence, cannabis initiation, and cannabis use disorder) from eight studies were included. Significant genetic correlations were adjusted for variants associated with major depressive disorder and schizophrenia. Total study sample sizes per phenotype ranged from ~2400 to ~537 000 individuals. We used linkage disequilibrium score regression to calculate single nucleotide polymorphism-based genetic correlations between eating disorder- and substance-use-related phenotypes. Significant positive genetic associations emerged between AUD and AN (r_g = 0.18; false discovery rate q = 0.0006), cannabis initiation and AN (r_g = 0.23; q < 0.0001), and cannabis initiation and AN *with* binge eating (r_g = 0.27; q = 0.0016). Conversely, significant negative genetic correlations were observed between three non-diagnostic smoking phenotypes (smoking initiation, current smoking, and cigarettes per day) and AN *without* binge eating (r_{gs} = −0.19 to −0.23; qs < 0.04). The genetic correlation between AUD and AN was no longer significant after co-varying for major depressive disorder loci. The patterns of association between eating disorder- and substance-use-related phenotypes highlights the potentially complex and substance-specific relationships among these behaviors.

KEYWORDS
eating disorders, genetic correlation, substance use

1 | INTRODUCTION

Well-established phenotypic associations exist between eating disorder and substance use phenotypes, with evidence for specific relations between particular types of eating disorders and substance use disorders. The prevalence of an alcohol use disorder (AUD) is greater among individuals with bulimia nervosa and binge-eating disorder than individuals with anorexia nervosa (AN) or healthy controls.[1,2] Similarly, individuals with bulimia nervosa or binge-eating disorder are at increased risk for smoking, nicotine dependence,[3,4] and cannabis use,[4,5] compared with individuals with AN or healthy controls, though these results are not consistent.[1] Importantly, women with the binge-eating/purging subtype of AN report a higher prevalence of AUD, smoking, nicotine dependence, and cannabis use than women with the restricting subtype of AN.[1,5,6] Thus, binge eating—a trans-diagnostic symptom defined as eating a large amount of food in a

short period of time while experiencing loss of control—may be a key component of the observed association.

However, prior research has only partially addressed whether binge eating is the critical eating disorder symptom in the comorbidity, especially across different milestones of substance use (ie, initiation through substance use disorder) and across a variety of substances (ie, alcohol, nicotine, and cannabis). Elucidating shared sources for these associations is crucial because of the increased morbidity and mortality associated with comorbid presentations[7,8] and because improvements in one disorder may exacerbate (or weaken) symptoms of the other disorder.[9] Refining our understanding of these associations could improve prevention and treatment approaches for these debilitating disorders, their comorbidity, and their sequelae.

Accumulating findings from twin studies implicate shared genetic factors between eating disorder- and substance-use-related phenotypes. The strongest reported association is between bulimia nervosa symptoms (including binge eating) and problem alcohol use, with a genetic correlation (r_g) ranging from 0.23 to 0.53.[10] Although there has been less focus on genetic associations between bulimia nervosa symptoms and regular smoking and bulimia nervosa symptoms and illicit drug use disorder, twin-based r_gs of 0.35 and approximately 0.38, respectively, have been reported.[11,12] Limited information exists regarding whether less problematic aspects of substance use exhibit a significant r_g with eating disorder phenotypes. The impact of genetic factors influencing this comorbidity may significantly increase once an individual has progressed to problematic alcohol use, as genetic effects are more prominent in problem substance use, such as abuse and dependence, than with the initiation and general use of substances.[13-16] No study has comprehensively examined a range of eating disorder- and substance-use-related phenotypes to determine whether the r_g varies with different aspects of substance use and whether the r_g varies depending on the eating disorder and substance examined.

Recent advances in genomic methods allow for an assessment of r_g using existing genome-wide association study (GWAS) summary statistics. Unlike twin studies, these genome-wide methods allow for use of unrelated cases and controls, typically yielding sample sizes in the tens to hundreds of thousands. One such method, linkage disequilibrium score regression (LDSC),[17,18] estimates single nucleotide polymorphism (SNP)-based heritability and r_g between phenotypes. Of particular relevance to low prevalence phenotypes, such as AN, estimation of SNP-based r_g does not require both phenotypes to be measured in the same individual; thus, independent studies assessing only one phenotype can be jointly examined.

The current study estimated SNP-based genetic correlations (r_gs) between eating disorder- and substance-use-related phenotypes based upon summary statistics from the largest published eating disorder GWAS and existing GWAS encompassing a range of substance-use-related phenotypes (ie, alcohol, nicotine, and cannabis), using robust data from twin studies to shape our three hypotheses. First, we hypothesized that the strongest SNP-based r_g would be between eating disorder phenotypes that have binge eating as a core symptom and alcohol use phenotypes, rather than between eating disorder phenotypes and nicotine and cannabis use-related phenotypes.[10] Second, we hypothesized that for binge eating-related phenotypes, the SNP-based r_g would be higher when assessing AUD than typical alcohol consumption,[10] because we expected that two problem behaviors are more likely to share genetic risk than a problem behavior (eg, binge eating) and a normative pattern (eg, alcohol consumption). Because we have less information from twin studies about genetic associations between liabilities to eating disorders and tobacco (nicotine) and cannabis use-related phenotypes, we do not forward specific hypotheses for these substances. Finally, prior studies document robust genetic associations for major depressive disorder and schizophrenia with both eating disorders and substance-use-related phenotypes.[19-21] We hypothesized that r_gs between eating disorders and substance use and disorder would be attenuated when accounting for variants associated with major depressive disorder and schizophrenia. Findings from this study will yield important information about the role of genetics in this clinically challenging pattern of comorbidity.[22]

2 | METHOD

2.1 | Participants

We included summary statistics from two existing GWAS of eating disorder phenotypes where participants were primarily of European ancestry[21,23] and data from individuals of European ancestry from six existing GWAS of substance-use-related phenotypes.[19,20,24-27] The eating disorder phenotypes (Table 1) included a diagnosis of AN (which was further parsed into AN *with* binge eating or AN *without* binge eating) and a bulimia nervosa factor score derived from the Eating Disorder Examination,[28] a well-established structured clinical interview for eating disorders. We did not examine bulimia nervosa or binge-eating disorder because there are currently no published GWAS for either disorder; thus, the bulimia nervosa factor score represents the closest to a GWAS of bulimia nervosa available. Substance-use-related phenotypes ranged from typical use (eg, drinks per week, smoking initiation, and cannabis initiation) to substance use disorder (ie, AUD, nicotine dependence, and cannabis use disorder). Sample sizes for the phenotypes ranged from 2442 (bulimia nervosa factor score) to 537 349 (drinks per week) individuals. Table 2 provides individual study details.

2.2 | Statistical analysis

We used LDSC[17,18] to evaluate SNP-based genetic correlations (r_g) between samples. This method uses the linkage disequilibrium (LD) structure of the genome to estimate the distribution of effect sizes for individual SNPs as a function of their LD score. Under a polygenic model, causal SNPs are likely to be overrepresented in higher LD score bins (ie, including additional SNPs in high LD), such that associations with SNPs in these LD bins will make stronger

contributions to the phenotypic variation under study. This polygenic distribution of effect sizes across LD score bins provides an estimate of SNP-based heritability, that is, the proportion of phenotypic variance that is attributable to the aggregate effects of genome-wide SNPs. The correlation of effect sizes across LD bins between two phenotypes then provides an estimate of SNP-based r_g.

Genetic correlations range from −1 to +1, where the sign indicates that the same genetic factors are contributing to variation in the target traits in *opposite* or *same* directions, respectively. The LDSC intercept for the genetic covariance provides evidence about sample overlap across two traits. SNPs (MAF > 0.01) found in the HapMap3 EUR population were used to calculate LD scores. We used the false discovery rate[29] to correct for multiple testing (n = 66 tests; q < 0.05). Finally, post hoc analyses examined whether significant differences between two r_gs existed, using the jackknife procedure implemented through LDSC.[17]

We used GNOVA[30] to stratify significant r_gs between the eating disorder- and substance-use-related phenotypes into both tissue-specific (for seven broadly defined tissue classes: brain, cardiovascular, epithelial, gastrointestinal, immune-related, muscular, and "other") and nontissue-specific functional regions of the genome. GenoCanyon[31] and GenoSkyline[32,33] annotation methods, which integrate transcriptomic and epigenomic data from ENCODE[34] and the Roadmap Epigenomics Project,[35] were used to define functional regions of the genome.

Finally, for significant r_gs detected in LDSC, multitrait-based conditional and joint analysis using GWAS summary data (mtCOJO)[36] was used to condition both input GWAS (eg, AN and AUD) for variants associated with major depressive disorder[37] at $P < 5 \times 10^{-7}$ and schizophrenia[38] at $P < 5 \times 10^{-8}$. Because fewer genome-wide significant SNPs were identified for major depressive disorder than schizophrenia, we chose a more lenient P value threshold for major depressive disorder to capture a comparable number of SNPs. LDSC was used to compute r_gs using the resulting genome-wide summary statistics for each trait after separately adjusting for major depressive disorder or schizophrenia variants to examine whether conditioning on either disorder would affect the observed genetic relationships.

TABLE 1 Eating disorder-related phenotype descriptions

Phenotype	Definitions
Anorexia nervosa (AN)[a]	Diagnostic criteria included the following: 1. Body mass index less than minimally expected 2. Intense fear of gaining weight 3. Weight or shape disturbance, undue influence of weight or shape, or denial of the seriousness of the disorder
AN *with* binge eating[b]	Individuals with AN who also engaged in binge-eating episodes, defined as eating a large amount of food in a short period of time while having a sense of loss of control over the eating episode.
AN *without* binge eating[b]	Individuals with AN who did not engage in binge-eating episodes.
Bulimia nervosa (BN)[c] factor	Derived from a factor analysis that included the following items: 1. Reporting self-induced vomiting to control body weight 2. Reporting suffering from or being treated for binge eating 3. Reporting suffering from or being treated for bulimia

[a]A fourth diagnostic criterion for AN includes amenorrhea. However, amenorrhea was excluded as a required criterion for cases in the Psychiatric Genomics Consortium datasets because it is no longer a diagnostic criterion in the DSM-5.
[b]The DSM and ICD include two subtypes of anorexia nervosa (AN)—a binge-eating/purging subtype and a restricting subtype. Although it would have been ideal to examine differences between the AN binge-eating/purging subtype and AN restricting subtype, this was not possible with current Psychiatric Genomics Consortium data. However, there was sufficient information about presence or absence of binge eating, which resulted in creating the AN *with* binge-eating and AN *without* binge-eating subtypes.
[c]Bulimia nervosa is defined as (a) recurrent episodes of binge eating, (b) recurrent inappropriate compensatory behaviors (eg, self-induced vomiting or laxative use) to prevent weight gain, (c) the binge eating and inappropriate compensatory behaviors occurring an average of twice a week for 3 mo, (d) having undue influence of body weight and shape, and (e) disturbance not occurring during AN.

3 | RESULTS

The overall SNP-based heritability for the eating disorder phenotypes ranged from 0.20 to 0.39, whereas the corresponding heritabilities for the substance-use-related phenotypes ranged from 0.03 to 0.35 (Table S1). Figure 1 and Table S1 show the genetic correlations (r_gs) between all four eating disorder phenotypes and eight substance-use-related phenotypes. Broadly speaking, there were significant r_gs across substance-use-related phenotypes, ranging from 0.21 (AUD and cigarettes per day) to 0.70 (drinks per week and AUD). Cannabis initiation risk was not significantly genetically correlated with cigarettes per day or nicotine dependence. For the remaining results, we focus on previously unexplored associations of interest in this study—correlations between eating disorder- and substance-use-related phenotypes. For these associations, the genetic covariance intercepts ranged from −0.03 (standard error [SE] = 0.01; AN and cannabis initiation) to 0.01 (SE = 0.01; AN and cannabis use disorder), indicating some sample overlap (or low-level confounding) existed,[39] although the LDSC approach parses this overlap from the r_g estimation.

Significant positive r_gs were observed for alcohol- and cannabis use-related phenotypes. First, the r_g was significant between AN and AUD (r_g = 0.18; SE = 0.05; q = 0.0006) but not between AN and drinks per week (r_g = 0.01; SE = 0.03; q = 0.91), suggesting that genetic factors that increase risk for AN also increase risk for AUD, but little evidence exists for shared genetic risk between AN and typical alcohol consumption. These two correlations significantly differed from each other (z-score = 3.51, P = 0.0005). Intriguingly, there was a significant difference in r_gs for AN and AUD versus AN *without* binge eating and AUD (z-score = 2.28, P = 0.02) but not for AN and AUD versus AN *with* binge eating and AUD (z-score = 0.23, P = 0.82). The genetic

covariance estimates between AN and AUD were significant in both functional (corrected ρ_g = 0.01; corrected r = 0.23; corrected q = 0.007) and nonfunctional categories (corrected ρ_g = 0.01; corrected r = 0.19; corrected q = 0.002; Table S2) but not in any specific tissue type. No significant association between the bulimia nervosa factor score, which included items pertaining to both binge eating and compensatory behaviors, and either alcohol-use-related phenotype was observed.

Second, the significant r_g between AN and cannabis initiation was 0.23 (SE = 0.04, q < 0.0001) and the significant r_g between AN *with* binge eating and cannabis initiation was 0.27 (SE = 0.08, q = 0.0017), indicating that genetic factors that increase the risk for AN may also increase risk for cannabis initiation. However, cannabis initiation was not significantly correlated with the bulimia nervosa factor score (r_g = 0.15, SE = 0.18, q = 0.57) or with AN *without* binge eating (r_g = 0.10, SE = 0.08, q = 0.31). No significant associations were observed between any eating disorder phenotype and cannabis use disorder (r_gs = −0.08-0.23; SEs = 0.01; qs ≤ 0.57). Post hoc analyses revealed significant differences in the r_gs for AN and cannabis initiation versus AN and cannabis use disorder (z-score = 2.70, P = 0.01). However, the r_g between AN *with* binge eating and cannabis initiation, while significant, was statistically different from the r_g between AN *with* binge eating and cannabis use disorder. The genetic covariance estimate between AN *with* binge eating and cannabis initiation was significant in both functional (corrected ρ_g = 0.01; corrected r = 0.60; corrected q < 0.0001) and nonfunctional categories (corrected ρ_g = 0.01; corrected r = 0.30; corrected q = 0.004; Table S3) but not in any specific tissue type. The genetic covariance estimate between AN *without* binge eating and cannabis initiation was only significant in nonfunctional categories (corrected ρ_g = 0.01; corrected r = 0.27; corrected q = 0.004; Table S4).

TABLE 2 Details of samples included in analyses

Study	Sample/Consortium	Phenotype(s)	Definition	Sample Size (cases/controls if binary)	Number of SNPs in Summary Statistics File
Eating disorder phenotype					
Watson et al (2019)	PGC-ED	1. Anorexia nervosa	DSM-III-R, DSM-IV, ICD-8, ICD-9, ICD-10, or self-reported anorexia nervosa	16 992/55 525	8 219 102
		2. Anorexia nervosa *with* binge eating		2381/10 249	8 982 440
		3. Anorexia nervosa *without* binge eating		2262/10 254	8 671 192
Wade et al (2013)	Australian Twin Registry	Bulimia nervosa factor	Eating Disorder Examination	151/2291	6 150 213
Substance use-related phenotype					
Kranzler et al (2019)	MVP	Alcohol use disorder	ICD-9 or ICD-10	34 658/167 346	6 895 251
Walters et al (2018)	PGC-SUD	Alcohol dependence	DSM-IV	8485/20 272	9 271 145
Liu et al (2019)	GSCAN	1. Drinks per week[a]	Average number of drinks each week	537 349	11 916 707
		2. Smoking initiation	Ever vs never regular smoker	311 629/321 173	11 733 344
		3. Current smoking[c]	Current vs former smokers	92 573/220 248	12 197 133
		4. Cigarettes per day[a]	Average number of cigarettes smoked per day	263 954	12 003 613
Hancock et al (2017)	14 samples	Nicotine dependence[b]	Mild (FTND score 0-3)Moderate (FTND score 4-6)Sever (FTND score 7-10)	14 184 (Mild) 9206 (Moderate) 5287 (Severe)	10 622 668
Pasman et al (2018)	ICC UK Biobank	Cannabis initiation	Lifetime cannabis use	43 380/118 702	11 733 371
Demontis et al (2019)	iPSYCH	Cannabis use disorder	ICD-10	2387/48 985	8 969 939

Abbreviations: DSM, Diagnostic and Statistical Manual; FTND, Fagerström Test of Nicotine Dependence; GSCAN, GWAS & Sequencing Consortium of Alcohol and Nicotine use; ICC, International Cannabis Consortium; ICD, International Classification of Diseases; iPSYCH, Lundbeck Foundation Initiative for Integrative Psychiatric Research; MVP, Million Veteran Program; PGC-ED, Eating Disorders Working Group of the Psychiatric Genomics Consortium; PGC-SUD, Substance Use Disorders Working Group of the Psychiatric Genomics Consortium; SNPs, single nucleotide polymorphisms.

[a]Treated as a continuous phenotype.

[b]Treated as an ordinal phenotype.

[c]In Lui et al (2019), the phenotype is labeled as "smoking cessation." It was renamed as "current smoking" to reflect the coding scheme and for ease in comparing across all smoking phenotypes.

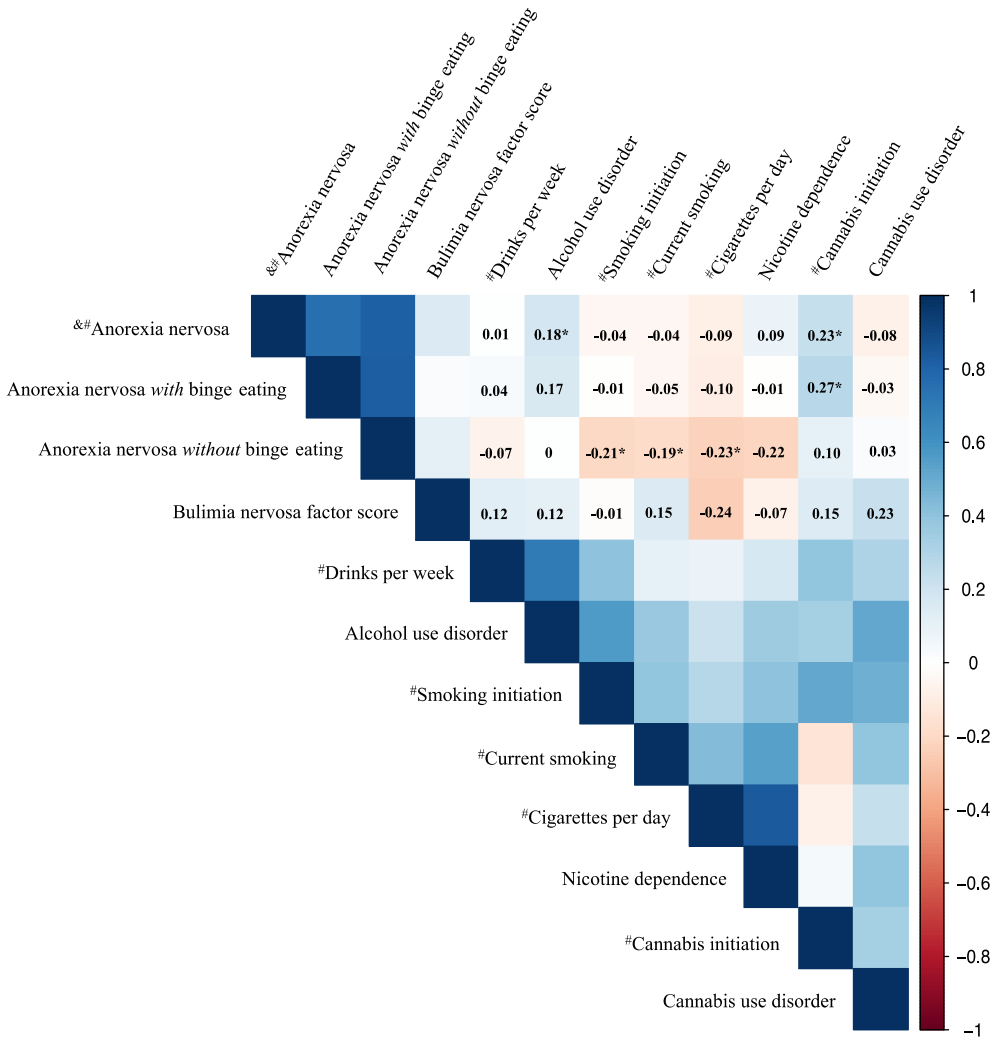

FIGURE 1 Genetic correlations between eating disorder subtypes and substance-use-related phenotypes. *Note*. # indicates known or potential sample overlap with UK Biobank, and & indicates known sample overlap with iPSYCH. Starred values denote significant genetic correlations after correcting for multiple comparisons using False Discovery Rate (n tests = 66; q < 0.05) [Colour figure can be viewed at wileyonlinelibrary.com]

Conversely, for smoking phenotypes, significant correlations were only observed for the AN *without* binge eating subtype. Smoking initiation (r_g = −0.21, SE = 0.06, q = 0.0006), current smoking (referred to as smoking cessation in Liu et al[20])* (r_g = −0.19, SE = 0.08, q = 0.03), and cigarettes per day (r_g = −0.23, SE = 0.07, q = 0.003) were significantly and negatively associated with AN *without* binge eating. Although the correlation between nicotine dependence and AN *without* binge eating was in the same direction as the other smoking phenotypes, it was not significant (r_g = −0.22, SE = 0.12, q = 0.14). The r_gs for AN diagnosis and each of the three nondiagnostic smoking traits versus AN *without* binge eating and these same smoking traits all differed significantly from each other (z-scores ranged from −3.22 to −2.11; P values ≤ 0.04). The genetic covariance estimate between AN *without* binge eating and smoking initiation was only significant in the nonfunctional category (corrected ρ_g = −0.01; corrected r = −0.17; corrected q = 0.007; Table S5). For AN *without* binge eating and current smoking, the genetic covariance estimate was significant in both functional (corrected ρ_g = −0.01; corrected r = −0.32; corrected q = 0.01) and nonfunctional categories (corrected ρ_g = −0.01; corrected r = −0.21; corrected q = 0.03; Table S6). Finally, the genetic covariance estimate between AN *without* binge eating and cigarettes per day was only significant in the nonfunctional category (corrected ρ_g = −0.02; corrected r = −0.35; corrected q = 0.003; Table S7).

After conditioning the AN and AUD GWAS summary statistics for loci associated with major depressive disorder, the positive r_g between AN and AUD was attenuated (r_g = 0.07; SE = 0.05, q = 0.125; Table S8) and significantly lower than the unadjusted r_g (z-score = 2.48, P = 0.01). In contrast, after conditioning the AN *with* binge eating and cannabis initiation GWAS for major depressive disorder, the resulting r_g was marginally smaller but remained significant after correction for multiple tests (r_g = 0.21, SE = 0.08, q = 0.016). After conditioning for the major depressive disorder GWAS, r_gs between AN *without* binge eating and smoking initiation, current smoking, and cigarettes per day remained significant and modestly increased in magnitude (r_gs = −0.27 to −0.31; SEs = 0.05 to 0.09; qs < 0.0009). All r_gs

*In Liu et al (2019), the phenotype is noted as "smoking cessation," where current smokers were coded as 2 and former smokers were coded as 1. Because the comparison group is "current smokers," we have renamed this phenotype as "current smoking" for clarification and ease of interpretation across all smoking phenotypes.

remained significant after conditioning the AN and substance-use-related phenotypes for schizophrenia (r_gs = −0.20 to 0.27; SEs = 0.04 to 0.08; qs < 0.03; Table S9).

4 | DISCUSSION

Using existing GWAS data, we investigated genetic associations between liabilities to four eating disorder- and eight substance-use-related phenotypes spanning initiation and typical use to substance use disorder. We found differential patterns of association between AN *with* and *without* binge eating and substance-use-related traits, which may point toward substance-specific genetic relationships. Additionally, there may be some degree of symptom overlap contributing to these associations.

Three main patterns emerged. First, in line with prior twin studies, we observed a positive genetic correlation (r_g) between problem alcohol use (ie, AUD) and AN diagnosis. Second, we observed positive, significant r_gs between cannabis initiation and AN diagnosis, as well as cannabis initiation and the AN *with* binge eating subtype. This is a novel finding not previously examined in twin research. The positive genetic associations suggest that some genetic loci may be influencing these traits in the same direction. Finally, negative r_gs emerged between the three nondiagnostic smoking phenotypes and AN *without* binge eating but not with the other three eating disorder phenotypes. These negative r_gs indicate that some of the loci influencing liability to these eating disorder and smoking phenotypes might be shared but are affecting the liability to these traits in opposite directions. Indeed, r_gs cannot identify specific loci or underlying mechanisms that contribute to the shared risk. Nevertheless, the results provide initial evidence for differential genetic associations between the liability to varying eating disorder- and substance-use-related phenotypes.

Based on findings from twin studies, we hypothesized that (a) the strongest SNP-based r_g would be between eating disorder phenotypes that have binge eating as a core symptom and alcohol use phenotypes and (b) a significant positive r_g between eating disorder phenotypes with binge eating as a key symptom and AUD would emerge. In line with these hypotheses, we found a significant genetic association between AUD and AN diagnosis but not between typical alcohol consumption (ie, drinks per week) and AN. No twin study has examined genetic associations between AN and alcohol-use-related phenotypes, and previous studies[21,26] using LDSC have not reported significant r_gs between these traits. That we found a significant association most likely reflects the larger AN sample size in our study (from 3495 cases and 10 982 controls to 16 992 cases and 55 525 controls), as well as combining two large existing GWAS of AUD, emphasizing the importance of increasing sample sizes for GWAS.

Importantly, the r_gs between the eating disorder- and substance-use-related phenotypes were robust to conditioning on schizophrenia loci. However, the r_g between AN and AUD was not robust to the adjustment for major depressive disorder-associated variants. Major depressive disorder is among the most prominent comorbidities in individuals with AN and AUD,[40] and GWAS for both traits document strong r_gs between major depressive disorder and these disorders.[19,21,26] Our results indicate that the three disorders share genetic underpinnings. We cannot discount the possibility of a genetic relationship between AN and AUD that is distinct from major depressive disorder; however, much larger sample sizes may be required to detect such an association.

Intriguingly, although we did not detect a significant r_g for AN *with* binge eating with AUD, the point estimate for the r_g between AUD and AN *with* binge eating was similar to that for AUD and AN diagnosis (0.17 vs 0.18, respectively) and higher than that for AUD and AN *without* binge eating (0.01). Sample sizes for these AN subtypes were smaller than for AN diagnosis; however, the two subtypes included approximately equal numbers of cases and controls. Indeed, binge eating was assessed in such a way that we were unable to tease apart purging behaviors, and AN diagnosis is heterogenous even within subtypes. Therefore, binge eating may be one plausible key component of the observed genetic association. For example, binge eating has been shown to activate brain reward circuitry in a similar manner to substances,[41,42] and administration of naltrexone, an opioid antagonist approved by the US Food and Drug Administration for the treatment of AUD,[43] has been shown to reduce the frequency of binge eating episodes among individuals with an eating disorder.[44,45] We did not detect a significant r_g with the bulimia nervosa factor score, although that GWAS was relatively underpowered. Thus, our findings highlight the importance of expanding GWAS to include bulimia nervosa and binge-eating disorder, where a core symptom of both disorders is binge eating, to elucidate whether binge eating is a critical eating disorder symptom in the comorbidity with AUD and to home in on relevant shared mechanisms.

The significant genetic associations between cannabis initiation and AN are novel, yet consistent with the negative genetic association between cannabis use and body mass index, and with observational[25] and experimental[46,47] studies regarding the role of endocannabinoids in appetite regulation, energy expenditure, stress, and reward. One of the principal psychoactive agents of cannabis, delta-9-tetrahydrocannabinol (THC), a partial agonist of the endogenous cannabinoid 1 (CB1) receptor, is presumed to be orexigenic and may acutely increase appetite and food intake, contributing to its potential role as an appetite stimulant in patients with an anorexia or cachexia syndrome[48] due to a disease (eg, HIV or AIDS) or in response to treatment (eg, chemotherapy). An antagonist of the CB1 receptor was previously tested as a highly promising anti-obesity medication (Rimonabant, SR141716), which is particularly relevant because some genes may influence AN and obesity in opposite directions.[21] Further, the endocannabinoid anandamide has been shown to be elevated in individuals with acute AN,[49] indicating disruption in food-related reward and eating behavior regulation. Animal and human studies have also provided initial evidence for the therapeutic effectiveness of cannabinoid agonists in treating eating disorders.[50,51] It is also likely that individuals with high genetic liability to AN are less likely to experiment with a substance that has a documented hyperphagia component. Thus, there is evidence of a complex

biological relationship between cannabis use and eating disorders, as well as body mass index.

Finally, the significant negative r_gs between three tobacco-smoking phenotypes—smoking initiation, current smoking, and cigarettes per day—and AN *without* binge eating are intriguing, suggesting that AN *without* binge eating and tobacco-smoking behaviors are alternate expressions of shared mechanisms. Phenotypic studies are inconsistent about the association between the restricting subtype of AN and smoking. Some studies suggest that individuals with restricting AN have a higher prevalence of various smoking phenotypes than controls,[5] whereas other studies indicate no significant difference between the two groups.[6] A recent meta-analysis did not find differences in the odds of lifetime smoking between individuals with AN and healthy controls,[3] yet the authors did not assess differences by AN subtype. Individuals with AN may smoke as a way to control or lose weight,[52] and temporary weight gain does occur with smoking cessation.[53] However, a positive phenotypic correlation need not be accompanied by a r_g in the same direction (or genetic contributors to the phenotypic association at all). Still, there is plausible support for the negative r_g. Although not significant, a negative r_g between smoking and AN has been reported.[18,21] Notably, our study includes individuals from these earlier reports and extends findings by including larger sample sizes for both AN and smoking phenotypes. Unfortunately, there are no twin studies of AN or AN-like traits and smoking with which to compare findings.

One explanation for the negative genetic association is that it is due to a third, underlying variable influencing both AN *without* binge eating and smoking. We tested for the potential role of variants associated with major depressive disorder and schizophrenia and found the r_gs to be robust to those adjustments. In the largest GWAS of smoking phenotypes, positive r_gs were also observed between smoking initiation and cigarettes per day with multiple cardiometabolic traits, including type 2 diabetes and fasting glucose.[20] These same metabolic traits were negatively genetically correlated with AN.[21,54] Thus, the patterns of r_gs might point to metabolic, rather than psychiatric, factors in influencing the apparent genetic association between smoking phenotypes and AN. However, the associations could also reflect adoption of unhealthy lifestyles that promote obesity and are correlated with smoking. In addition, the r_gs between smoking and body mass index, as well as AN and body mass index, may reflect underlying disinhibitory pathways, as variants associated with body mass index show enrichment in the central nervous system.[55] The current approach is not designed to disentangle these putative etiological mechanisms, but our findings do encourage careful study of the specific relationships between eating and substance use disorders.

Substance use and substance use disorders are partially distinct, and although excessive substance use is a necessary component of substance use disorders, the latter is associated with psychological and physiological impairment related to excess use and aspects of loss of control over the behavior. Consistent with our findings for alcohol, accumulating evidence suggests that genetic liability to other psychiatric traits (eg, schizophrenia) is strongly correlated with liability to substance use disorders (eg, AUD) but not substance use (eg, alcohol consumption).[19-21] Genetic liability to alcohol use has also been correlated with liabilities to psychiatric disorders (eg, major depressive disorder) in opposite directions depending on level of involvement.[19] However, we did not find similar elevations in r_gs when contrasting ever smoking and nicotine dependence nor comparing cannabis initiation to cannabis use disorder. It is possible that the lack of genetic overlap between AN and nicotine dependence, as well as AN and cannabis use disorder, is related to the relatively modest sample size of those discovery GWAS. A similar non-significant r_g was noted for AUD when the Walters et al[26] alcohol dependence GWAS was used as the sole source of summary statistics for problem drinking in the current study. Several other explanations for this divergence in findings exist. For instance, for tobacco, the highly addictive nature of nicotine may result in convergence in genomic effects on earlier and later stages of smoking (ie, a much larger proportion of those who ever smoke become dependent compared with the proportion of those who drink alcohol and develop AUD). For cannabis, given its lower addictive potential, we might have expected stronger associations with cannabis use disorder than with cannabis initiation. In addition to the considerably smaller sample size of the cannabis use disorder GWAS, the association with cannabis initiation could also be attributed to the small number of cohorts in that discovery GWAS that included individuals with a high likelihood of cannabis use disorder. It is also possible that the relationship between AN and cannabis use is distinct and that earlier but not later stages of cannabis use are genetically related to liability to AN. Future studies should consider the multistage nature of substance use and misuse when examining cross-trait correlations.

This is the largest and most comprehensive assessment of shared genetic risk between eating disorder- and substance-use-related phenotypes, using existing GWAS data from large cohorts (up to ~537 000 individuals per phenotype). We were able to separately assess approximate AN subtypes (ie, *with* binge eating vs *without* binge eating) to evaluate the extent to which binge eating, in the context of AN, may share genetic risk with substance-use-related phenotypes. Using these large datasets—many of which are publicly available—allows for the rapid development of scientific knowledge regarding the underlying etiology of psychiatric disorder and substance use comorbidity. Nevertheless, some limitations exist. First, sample sizes for the bulimia nervosa factor score and cannabis use disorder GWAS were relatively small compared with the other GWAS, resulting in large standard errors and low power. Second, we were unable to uniformly examine sex differences in these r_gs. Because the prevalence of eating disorders is higher in women than men and the prevalence of substance use disorders is higher in men than women,[40] it will be important to explore possible sex differences in genetic associations as the GWAS data become available. Notably, we previously did not find evidence for sex differences in the r_g between binge eating and problem alcohol use.[56] Third, even though we did not detect significant r_gs for all pairs of traits, it is possible that local genetic associations exist for some of these trait

pairs. Such local correlations, for instance, in certain chromosomal regions but not others, particularly when in opposing directions (eg, a positive local correlation at one chromosomal location and a negative local correlation at another) might dilute the overall r_g estimate. Although such a systematic evaluation of each pair of traits is beyond the scope of this report, we did note some support for enrichment of the aggregated genetic covariance in both functional and nonfunctional genomic regions for several of the significant r_gs. Finally, SNP coverage was limited in the earlier GWAS of the bulimia nervosa factor score because that study used older genotyping platforms and imputation panels that included fewer SNPs than current imputation panels. The Eating Disorders and Substance Use Disorders Working Groups of the Psychiatric Genomics Consortium are continuously adding samples and releasing data freezes with incrementally larger sample sizes, while collecting information on multiple substances (eg, opioids). In coming years, the statistical power is expected to increase for AN (including the *with* and *without* binge eating subtypes), bulimia nervosa, and binge-eating disorder, as well as AUD, nicotine dependence, and cannabis use disorder, from within and outside the Psychiatric Genomics Consortium. This will allow for a more refined assessment of specific eating disorder symptoms, including binge eating, in relation to substance-use-related phenotypes.

In conclusion, findings from this study suggest that the shared sources of variation in liabilities to eating disorder- and substance-use-related phenotypes are not consistent across traits or levels of substance involvement, extending results from twin studies to a genome-wide SNP approach. Despite the typically high co-occurrence of alcohol, tobacco, and cannabis use and their genetic overlap,[25] the differential patterns seen between the eating disorder- and substance-use-related phenotypes highlight the uniqueness and complexity of their shared etiology. Potential clinical implications include watching for the emergence of symptoms of one disorder (eg, AN) while being treated for the other behavior (eg, AUD) and understanding that, for example, women with AN who use nicotine may not be able to quit successfully both because they are afraid of gaining weight and they have high genetic susceptibility for smoking via the shared genetic risk between AN and smoking-related traits. Additional research using contemporary genomic methods, such as cross-disorder association studies, could identify the specific loci contributing to this comorbidity. Future research that combines genome-wide data with measured environmental constructs, such as trauma,[9] that may increase risk for this comorbidity could enhance the prediction, prevention, and treatment of co-occurring eating disorder- and substance-use-related traits.

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Eating Disorders Working Group of the Psychiatric Genomics Consortium (PGC-ED)

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DATA ACCESS

This manuscript was a joint collaboration between the Eating Disorders and Substance Use Disorders Working Groups of the Psychiatric Genomics Consortium. These data can be found at https://www.med.unc.edu/pgc/data-index/. Additional datasets included in this study were obtained multiple ways. We recieved summary statistics directly from the first author of the primary GWAS manuscript for the bulimia nervosa factor score (Australian Twin Registry), alcohol use disorder (Million Veteran Program), nicotine dependence (multiple samples), and cannabis initiation (International Cannabis Consortium and UK Biobank). Summary statistics for drinks per week, smoking initiation, smoking cessation, and cigarettes per day (GSCAN) were downloaded from https://conservancy.umn.edu/handle/11299/201564 on 7 March 2019. Summary statistics for cannabis use disorder (iPSYCH) were downloaded from https://ipsych.dk/forskning/downloads/ on 27 June 2019.

CONFLICT OF INTERESTS

The authors report the following potential competing interests. O. Andreassen received a speaker's honorarium from Lundbeck. G. Breen received grant funding and consultancy fees in preclinical genetics from Eli Lilly, consultancy fees from Otsuka, and has received honoraria from Illumina. C. Bulik served on Shire Scientific Advisory Boards, is a consultant for Idorsia, and receives author royalties from Pearson. D. Degortes served as a speaker and on advisory boards and has received consultancy fees for participation in research from various pharmaceutical industry companies including AstraZeneca, Boehringer, Bristol Myers Squibb, Eli Lilly, Genesis Pharma, GlaxoSmithKline, Janssen, Lundbeck, Organon, Sanofi, UniPharma, and Wyeth; he has received unrestricted grants from Lilly and AstraZeneca as director of the Sleep Research Unit of Eginition Hospital (National and Kapodistrian University of Athens, Greece). J. 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unrelated research. All other authors have no conflicts of interest, relevant to the contents of this paper, to disclose.

AUTHORS CONTRIBUTION

MM-C, CB, and AA were responsible for the study concept and design. MM-C, ECJ, and Y-LD performed the statistical analyses, and JC, RW, and ZY assisted with the data analysis. MM-C, ECJ, Y-LD, JC, LT, RW, ZY, JB, CH, JK, HE, CB, and AA assisted with interpretation of findings. TDW facilitated access to and interpretation of the summary statistics for the bulimia nervosa factor score. HK, JG, and HZ facilitated access to and interpretation of the Million Veteran Program summary statistics for AUD. DH facilitated access to and interpretation of the summary statistics for nicotine dependence. MM-C, ECJ, LT, CB, and AA drafted the manuscript. All remaining authors provided data for this study and consulted on the analytic plan. All authors critically reviewed the content and approved the final version for publication.

ORCID

Melissa A. Munn-Chernoff https://orcid.org/0000-0001-9368-9457

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SUPPORTING INFORMATION

Additional supporting information may be found online in the Supporting Information section at the end of this article.

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