Linkage and association of novel DRD2 variants to the comorbidity of type 2 diabetes and depression

M. AMIN1,2, R. WU3,4, T.T. POSTOLACHE5,6,7, C. GRAGNOLI3,8,9

1INSERM, US14-Orphanet, Paris, France
2Department of Biochemistry and Molecular Biology, Faculty of Medicine, Al-Neelain University, Khartoum, Sudan
3Department of Public Health Sciences, Penn State College of Medicine, Hershey, PA, USA
4Department of Statistics, Penn State College of Medicine, Hershey, PA, USA
5Department of Psychiatry, Mood and Anxiety Program, University of Maryland School of Medicine, Baltimore, MD, USA
6Rocky Mountain Mental Illness Research Education and Clinical Center (MIRECC), Veterans Integrated Service Network (VISN) 19, Military and Veteran Microbiome: Consortium for Research and Education (MVM-CoRE), Denver, CO, USA
7Mental Illness Research Education and Clinical Center (MIRECC), Veterans Integrated Service Network (VISN) 5, VA Capitol Health Care Network, Baltimore, MD, USA
8Department of Medicine, Division of Endocrinology, Creighton University School of Medicine, Omaha, NE, USA
9Molecular Biology Laboratory, Bios Biotech Multi-Diagnostic Health Center, Rome, Italy

Abstract. – OBJECTIVE: The dopamine receptor 2 (DRD2) binds dopamine in both central tissues (e.g., basal ganglia, pituitary gland) and peripheral tissues (e.g., adrenal gland, kidneys, intestine) and mediates dopamine actions in cognition, emotional processing, and prolactin-secretion inhibition and stimulation, and in DRD2–/– knockout mice insulin secretion is impaired. Variants in or around the DRD2 gene have been implicated in major depressive disorder (MDD), schizophrenia, obesity, and type 2 diabetes (T2D) but not in comorbid MDD-T2D patients; DRD2 agonists (e.g., bromocriptine) are approved treatments in T2D. This study aimed to detect whether the DRD2 gene plays a role in T2D, MDD, and T2D-MDD comorbidity in Italian families.

SUBJECTS AND METHODS: In 212 Italian families with T2D and MDD, we investigated the presence of linkage and linkage disequilibrium of variants in the DRD2 gene with T2D and/or MDD. A test was considered statistically significant if \( p \) was <0.05.

RESULTS: We found 3 novel variants (rs6276, rs35608204, and rs1800499) significantly linked to and/or associated with the risk of T2D and 1 novel variant (rs112646785) significantly linked and associated to the comorbidity of T2D and MDD.

CONCLUSIONS: This is the first study to link and associate DRD2 variants with the comorbidity of T2D and MDD.

Key Words: Dopamine receptor 2, DRD2 gene, Dopamine, Prolactin, PRL, Major depressive disorder, Depression, MDD, Psychiatric disorder, Type 2 diabetes, T2D, Metabolic, Comorbidity, Mental-metabolic, Linkage disequilibrium, LD block, Single nucleotide polymorphism, SNP, Schizophrenia, SCZ, Insulin secretion, Glucose intolerance, Obesity, Cognition, Emotional processing, DRD2–/–, Knockout mice, Basal ganglia, Pituitary gland, Peripheral tissues, Adrenal gland, Kidneys, Intestine, Locomotion, Energy homeostasis, Antipsychotic medications, \( \beta \)-cells, Agonists, History, Diagnostic criteria, DSM-IV, Mendelian error, PLINK, Pseudomarker, Parametric, Dominant, Recessive, Complete penetrance, Incomplete penetrance, Inheritance model, Statistically significant, Risk allele, RegulomeDB, rs6276, rs35608204, rs1800499, rs112646785, Chromatin state, Endocrine pancreas, Hyperglycemia, Anxiety, Migraine.
Introduction

Dopamine is an important neurotransmitter that exerts a multitude of physiologic functions, including emotional processing, locomotion, cognition, and behavior and energy homeostasis. The dopamine system has long been studied in relation to susceptibility and treatment of psychiatric disorders [e.g., schizophrenia (SCZ), depression], and it has also been studied in relation to metabolic disorders [e.g., obesity, type 2 diabetes (T2D)]. The roles of dopamine are mediated by five dopamine receptors (DRD1-DRD5). The dopamine receptor 2 (DRD2) is the main target for antipsychotic medications. DRD2 binds dopamine in both central tissues (e.g., basal ganglia, pituitary gland) and peripheral tissues (e.g., adrenal gland, kidneys, intestine), mediates its actions in cognition, emotional processing, and prolactin-secretion inhibition and stimulation, and impairs insulin secretion in DRD2-/- knockout mice. Recent evidence shows that modulating the activity of DRD2 affects pancreatic insulin production in mice and cultured β-cells. DRD2 agonists (e.g., bromocriptine) are approved treatments in T2D. Variants in or around the DRD2 gene which encodes DRD2 have been implicated in major depressive disorder (MDD), SCZ, obesity, and T2D but not in comorbid MDD-T2D patients. In this study, we aimed at investigating the role of DRD2 variants in the susceptibility to familial T2D and MDD comorbidity.

Subjects and Methods

We accessed the deidentified data of 212 Italian families with T2D, rich T2D familial history, phenotyped for the presence or absence of MDD (diagnostic criteria of DSM-IV). Participants were recruited from central Italy following the Helsinki Declaration guidelines and provided written informed consent. The study was institutionally approved by the Bios Ethical Committee.

Statistical Analysis

We amplified 21 microarray-based single nucleotide polymorphisms (SNPs) in the DRD2 gene and excluded genotyping and Mendelian error via PLINK. Using Pseudomarker, we analyzed the 21 SNPs for 2-point parametric-linkage to and linkage-disequilibrium (LD) with T2D with the recessive complete penetrance (R1) model. Subsequently, we tested the variants for the dominant complete penetrance (D1), dominant incomplete penetrance (D2), and recessive incomplete penetrance (R2) models. The T2D-risk variants were tested for linkage to and LD with MDD under the same models. Only tests with p < 0.05 were considered statistically significant. The risk SNPs were labelled “independent” if they were not found in a specific LD block in the Tuscany Italian population (https://www.internationalgenome.org/data-portal/population/TSI).

Results

We found a total of 3 variants (rs6276, rs35608204, and rs1800499) significantly linked to and/or associated with T2D and 1 variant (rs112646785) significantly linked and associated to the comorbidity of T2D and MDD (Table I). Linkage and LD (i.e., linkage and association) were statistically significant across different inheritance models (Figure 1).

Discussion

The 3 T2D-risk variants and the MDD-risk variant identified in the present study are novel and have not been previously reported with T2D, MDD, or T2D-MDD comorbidity. The two T2D-risk variants (rs6276 and rs1800499) were studied with SCZ and the non-risk allele C of rs6276 (but not rs1800499) was significantly associated with SCZ-risk. Regulatory predictions for the SNPs in our study using RegulomeDB revealed that all T2D and MDD risk variants detected in our study intersect with repressed chromatin state in the endocrine pancreas, which is consistent with impaired insulin secretion and glucose intolerance reported in DRD2-/- knockout mice.

Interestingly, variants in the DRD2 gene were previously associated with the comorbidity of hyperglycemia and SCZ, and the comorbidity of MDD and anxiety and migraine.
Table I. Risk Single Nucleotide Polymorphisms (SNPs) in the *DRD2* Gene Linked to and/or in Linkage Disequilibrium (LD) with Major Depressive Disorder (MDD) and/or Type 2 Diabetes (T2D).

<table>
<thead>
<tr>
<th>Disease</th>
<th>Model</th>
<th>SNP</th>
<th>Position</th>
<th>Ref</th>
<th>Alt</th>
<th>Risk Allele</th>
<th>Consequence</th>
<th>LD Block</th>
<th>Reported in MDD or T2D?</th>
</tr>
</thead>
<tbody>
<tr>
<td>MDD</td>
<td>D2, R1, R2</td>
<td>rs112646785</td>
<td>113444554</td>
<td>T</td>
<td>C</td>
<td>T</td>
<td>Intronic</td>
<td>Independent</td>
<td>Novel</td>
</tr>
<tr>
<td>T2D</td>
<td>D2</td>
<td>rs6276</td>
<td>113410675</td>
<td>C</td>
<td>T</td>
<td>T</td>
<td>3'UTR</td>
<td>NA</td>
<td>Novel</td>
</tr>
<tr>
<td></td>
<td>D1, D2</td>
<td>rs35608204</td>
<td>113415071</td>
<td>A</td>
<td>G</td>
<td>G</td>
<td>Intronic</td>
<td>Independent</td>
<td>Novel</td>
</tr>
<tr>
<td></td>
<td>D1, D2, R1, R2</td>
<td>rs1800499</td>
<td>113416972</td>
<td>C</td>
<td>T</td>
<td>T</td>
<td>Synonymous</td>
<td>Independent</td>
<td>Novel</td>
</tr>
<tr>
<td></td>
<td>D1, R1, R2</td>
<td>rs112646785</td>
<td>113444554</td>
<td>T</td>
<td>C</td>
<td>T</td>
<td>Intronic</td>
<td>Independent</td>
<td>Novel</td>
</tr>
</tbody>
</table>

1Models: D1: dominant, complete penetrance, D2: dominant, incomplete penetrance, R1: recessive, complete penetrance, R2: recessive, incomplete penetrance. The MDD-T2D comorbid risk variant is bolded.
Conclusions

Our study is the first linking and associating DRD2 variants with the comorbidity of T2D and MDD. Peninsular families are powerful and genetically informative as they allow the reveal of gene variants contributing to complex disorders, such as T2D and MDD as well as to their comorbidity.

Conflict of Interest

The Authors declare that they have no conflict of interests.

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Ethics Approval

Subjects provided written informed consent and were recruited following the Helsinki declaration guidelines. Bios Ethical Committee approved the study.

Informed Consent

Written informed consent was obtained by participants before the study.

Authors’ Contribution

Claudia Gragnoli conceived and supervised the project, including statistical analysis and manuscript drafting. M.
Amin helped with the bioinformatic analysis, literature search, and manuscript drafting. R.-L. Wu and T.T. Postolache critically helped in data interpretation and critical revision of the manuscript. All authors have approved the final manuscript.

Data Availability
The study data are available on reasonable request, and due to lacking specific patients’ consent and privacy restrictions, they are not publicly available.

Authors’ Information
C. Gragnoli is Professor of Medicine and Chief of Endocrinology, Creighton University School of Medicine, Omaha, NE, and Adjunct Professor of Public Health Sciences, Penn State University College of Medicine, Hershey, PA; M. Amin has an MD and a Ph.D in Genetics (University of Paris) and is a geneticist at Orphanet | INSERM-US14, Paris, France, and member of the executive committee, European Reference Network for the Intellectual Disabilities (ERN-ITHACA) and the International Consortium of Gene Curation Coalition (GenCC); R.-L. Wu is Professor of Statistics and Public Health Sciences and Director of the Center for Statistical Genetics at Penn State University College of Medicine, Hershey, PA; T.T. Postolache is Professor of Psychiatry and Director of the Mood and Anxiety Program, Department of Psychiatry, University of Maryland School of Medicine, Baltimore, MD.

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