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Tese de Doutorado

Aspectos Genéticos no Transtorno do Pânico

Carolina Blaya

Orientadora: Prof. Dra. Gisele Gus Manfro

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Carolina Blaya

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3. Lista de abreviaturas

5-HTT – Gene transportador da serotonina ou *Serotonergic transporter gene*

5-HTTLPR – Polimorfismo na região promotora do gene transportador da serotonina ou *Serotonin Transporter Promoter Polymorphism*

AMPc – Adenosina monofosfato cíclico

BDNF – Fator neurotrófico neuronal

CBT – *Cognitive Behavioral Therapy*

CI – Comportamento inibido

CI95% – *Confident Interval of 95%*

CIDI – *Composite International Diagnostic Interview*

COMT – Gene *Catechol O-Methyltransferase*

CREB – *AMPc responsive-element binding protein*

CREB1 – *AMPc responsive-element binding protein gene*

CRH – Hormônio liberador de Corticotrofina

CRHR1 – Receptor 1 do Hormônio liberador de Corticotrofina

DL – Desequilíbrio de ligação

DNA – Ácido desoxirribonucléico

DSM – Manual diagnóstico e estatístico de transtorno mental ou *Diagnostic and Statistical Manual*

EFHC2 – *EF-hand domain containing 2*

GWA – *Genome-wide association*

GxA – Interação Gene-Ambiente

HCPA – Hospital de Clínicas de Porto Alegre

HPA – Eixo Hipotálamo-hipófise-adrenal

HTR1A – Receptor de serotonina 1A

HTR1B – Receptor de serotonina 1B

HTR2A – Receptor de serotonina 2A

HTR2C – Receptor de serotonina 2C

HTR3A – Receptor de serotonina 3A

HWE – Equilíbrio de Hardy-Weinberg ou *Hardy-Weinberg Equilibrium*

ICD – *International Classification of Diseases*

ISRS – Inibidores seletivos de recaptação da serotonina

L – *long*

MAOA – Monoamino oxidase A

Met – Metionina

MGH – *Massachusetts General Hospital*

MINI – *MINI International Neuropsychiatric Interview*

MOOSE – *Meta-analysis of Observational Studies in Epidemiology*

OR – *Odds ratio*

PD – *Panic Disorder*

RFLP – *Restriction fragment length polymorphism*

RGS2 – *Regulator of G-protein signaling 2*

S – *short*

SLC6A4 – Solute Carrier Family 6 (Neurotransmitter transporter serotonin), member 4

SNC – Sistema Nervoso Central

SNP – *Single nucleotide polymorphism*

SNPs – *Single nucleotide polymorphisms*

SSRIs – *Serotonin Selective Reuptake Inhibitors*

TCLE – Termo de Consentimento livre e esclarecido

TP – Transtorno do Pânico

TPH – Triptofano hidroxilase

UFRGS – Universidade Federal do Rio Grande do Sul

Val – Valina

VNTR – Número variável de repetições em *tandem*

4. Apresentação Parcial dos Resultados

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- Blaya C, Heldt E, Moorjani P, Salum Júnior G, Leistner-Segal S, Smoller J, Manfro GG. Marcadores genéticos como preditores à Terapia Cognitiva Comportamental para Transtorno do Pânico. XXV Congresso Brasileiro de Psiquiatria, Porto Alegre, 2007.
- Blaya C, Moorjani P, Heldt E, Salum Júnior G, Leistner-Segal S, Perlis R, Smoller J, Manfro GG. Genetic markers as a predictor to Cognitive Behavioral Therapy (CBT) for Panic Disorder (PD). XVth World Congress in Psychiatric Genetics, Nova Iorque, 2007.
- Salum Júnior G, Blaya C, Moorjani P, Seganfredo AC, Heldt E, Kipper L, Smoller J, Manfro GG. Interação Gene-Ambiente (GxA): Moderação de um

polimorfismo no receptor da serotonina 1A (5-HTR1A) na relação com Transtorno do Pânico e estressores precoces de vida. XIX Salão de Iniciação Científica da UFRGS, Porto Alegre, 2007. Prêmio destaque.

- Acosta JR, Blaya C, Salum Júnior G, Manfro GG. Polimorfismo Val66Met do Fator Neurotrófico Derivado do Cérebro (BDNF) e Transtorno do Pânico: estudo de caso-controle. XIX Salão de Iniciação Científica da UFRGS, Porto Alegre, 2007.

5. Resumo

A herdabilidade estimada do Transtorno do Pânico (TP) é de 28 a 43%, embora ainda permaneça como questão de pesquisa quais os genes envolvidos na sua etiologia. A busca dos genes candidatos para os estudos de associação geralmente é baseada em moléculas envolvidas no tratamento farmacológico, nos agentes que induzem ataques de pânico ou nos estudos de neuroimagem. Genes relacionados ao sistema serotoninérgico, noradrenérgico, eixo hipotálamo-hipófise-adrenal, entre outros, já foram investigados no TP. Os resultados são ainda pouco conclusivos. Para ampliar o conhecimento nessa área, foram realizados quatro estudos nessa tese.

O polimorfismo no promotor do gene transportador da serotonina (*5-HTTLPR*) foi estudado por alguns autores no TP. Realizamos então o estudo 1, que é composto pela revisão sistemática e meta-análise dos estudos de caso-controle que avaliaram esse gene no TP. Foram revisados artigos publicados entre janeiro de 1996 e abril de 2007 nas bases PubMed, PsychInfo, Lilacs e ISI. Identificou-se 19 artigos potenciais, e foram incluídos na análise 10 estudos. Não houve associação do gene *5-HTTLPR* e o TP (OR=0,91, CI95% 0,80 to 1,03, p=0,14). Três subanálises divididas de acordo com a etnia, qualidade do grupo controle e comorbidade com Agorafobia também não encontraram qualquer associação. Entretanto essa análise não possui poder para identificar associações de menor magnitude, e mais estudos são necessários.

O estudo 2 foi realizado para avaliar a associação entre polimorfismos nos genes *5-HTTLPR* e receptores da serotonina 1A (*HTR1A*) e 2A (*HTR2A*) e o TP, bem como a interação com dois fatores ambientais previamente associados ao transtorno: trauma e parentagem na infância. Foram incluídos 107 pacientes e 125 controles. O gene *HTR1A* foi associado ao TP na análise de grupo corrigido para o experimento ($p_2=0,027$). Três SNPs desse gene foram associados ao TP. Na análise de haplótipo pode-se identificar um haplótipo associado ao TP ($p=0,008$), e outro protetor para o TP ($p=0,004$). Na análise de interação, identificou-se que polimorfismos no gene *HTR2A* (rs6311 e rs6313), influenciado por ótima parentagem paterna, conferia proteção ao TP. Essa interação permaneceu significativa após a correção de Bonferroni. Não houve associação do TP com o *5-HTTLPR* mesmo considerando a interação com trauma na infância. Esse estudo replica achados prévios de associação do TP com o *HTR1A* e também reforça a evidência de interação gene-ambiente do *HTR2A* com parentagem, que possivelmente influencia a capacidade dos sujeitos de usarem as experiências familiares como suporte.

O estudo 3 avaliou o TP com o *EF-hand domain containing 2 (EFHC2)*, um gene previamente associado à percepção do medo. Nesse estudo foram incluídos 127 pacientes e 132 controles. Um dos 8 marcadores do *EFHC2* (rs1562875) foi associado ao TP, e também a dois outros fenótipos intermediários associados à ansiedade: comportamento inibido e temperamento evitação de dano. Se for

replicado, esse achado pode colaborar para a elucidação do mecanismo neurobiológico do medo.

O estudo 4 avaliou polimorfismos em 7 genes previamente envolvidos na ansiedade (*BDNF*, *CREB1*, *RGS2*, *CRHR1*, *5-HTTLPR*, *HTR2A*, *HTR1A*) com a resposta à terapia cognitivo-comportamental (TCC) no TP. Foram incluídos 74 pacientes com TP resistentes a quatro meses de tratamento prévio com antidepressivos que fizeram TCC em grupo. Na análise de grupo, houve associação do *CREB1* com melhora em 1 ano de seguimento ($p= 0,016$). Dois dos 5 marcadores do *CREB1* estiveram associados a esse desfecho (rs7594560, $p=0,003$ e rs2253206, $p=0,021$), mas não permaneceram associados após a correção por permutação. Na análise de haplótipos, um dos dez haplótipos esteve associado à melhor resposta nesse mesmo período. Apesar do limitado tamanho amostral esse estudo promoveu evidências preliminares da associação do *CREB1* na resposta à TCC.

Por fim, essa tese versa sobre alguns aspectos relacionados ao TP, abrangendo revisão sistemática da literatura, estudos de associação, de interação gene-ambiente e de resposta à TCC. Esses artigos estão de acordo com propostas atuais de estudos em genética, incluindo a pesquisa de vários genes e a análise de múltiplos marcadores que buscam aumentar o conhecimento dos fatores genéticos associados ao TP.

6. Summary

The estimated heritability of PD is between 28 to 43%, however which genes are involved in PD etiology still remains to be answered.. The search for candidate genes are usually based on molecules associated to pharmacological treatment, panic-inducing substance or neuroimage studies. Genes related to serotonergic, noradrenergic, hypothalamic-pituitary-adrenal axis and others have been previously studied with inconclusive results. In order to improve this knowledge, four studies were performed in this thesis.

The polymorphism in the promoter of serotonin transporter gene (*5-HTTLPR*) has been studied in PD. The study 1 was designed in order to perform a systematic review and meta-analysis of case-controls studies. Papers published between January 1996 and April 2007 were eligible for this study. The electronic databases searched included PubMed, PsychInfo, Lilacs and ISI. Nineteen potential articles were identified, and 10 studies were included in this meta-analysis. No statistically significant association between *5-HTTLPR* and PD was found, OR=0.91 (CI95% 0.80 to 1.03, p=0.14). Three sub-analyses divided according to ethnicity, control group and comorbidity with agoraphobia also did not find any association. However, more studies are needed in order to evaluate a possible minor effect.

The study 2 was designed to evaluate the association between *HTR1A*, *HTR2A* and *5-HTTLPR* in PD patients and controls. Besides this, we ought to evaluate the interaction between these genes and two environmental factors previously associated with PD: childhood trauma and parental bonding. In this case-control candidate gene study, 107 PD patients and 125 controls were included. *HTR1A* was experiment-wide associated with PD in set-based test ($p_2=0.027$). Three SNPs of this gene were nominally significantly associated with PD. Additionally, one haplotype was significantly associated with PD ($p=0.008$), and one haplotype was significantly protective for PD ($p=0.004$). In the interaction analysis with optimal father parenting, both interaction terms of SNPs of *HTR2A* (rs6311 and rs6313) were nominally associated with PD and remained significant after Bonferroni's correction. No association was found with *5-HTTLPR* even considering interaction with childhood trauma. This study replicates previous findings regarding the association between PD and *HTR1A*. We also reinforce evidence of gene-environment interaction in *HTR2A* gene with parenting, maybe influencing the capacity of subjects to use familiar experiences as environmental support.

In the study 3 we evaluated the association between PD and EF-hand domain containing 2 (*EFHC2*), a gene previously related to fear recognition. In this study we included 127 patients and 132 controls. One of 8 *EFHC2* markers (rs1562875) was associated with PD and also with two intermediate phenotypes related to anxiety: behavioral inhibition and harm avoidance. If replicated, this finding may contribute to elucidate the neurobiological path of fear.

In the study 4 we evaluated 7 genes previously related to anxiety (*BDNF*, *CREB1*, *RGS2*, *CRHR1*, *5-HTTLPR*, *HTR2A*, *HTR1A*) with cognitive-behavioral therapy (CBT) response. We included 74 patients resistant to 4 months of antidepressant treatment that received add-on treatment with group CBT. In the set-based test, *CREB1* achieved gene-wide significant association with improvement at 1-year follow-up (empirical p-value = 0.016). Out of the 5 *CREB1* single markers SNPs, two showed nominally significant associations (rs7594560, p-value 0.003 and rs2253206, p-value 0.021), that did not remain significant after 10,000 permutations. In the haplotype analysis, we identified one haplotype significantly associated with 1-year response (p=0.0002). Although limited by small sample size, these results provide preliminary evidence that variations in *CREB1* may be related to long-term CBT response among pharmacological-resistant patients with PD.

Finally, this thesis shows some aspects related to genetics in PD, including a systematic search, association, gene-environment and CBT response studies. Papers included are in accordance with what has been proposed for new studies in genetic, including the analysis of different genes and markers in order to contribute to the knowledge of genetic factors of PD.

7. Introdução

Transtorno do Pânico

O Transtorno do Pânico (TP) é caracterizado pela presença de ataques súbitos de ansiedade, acompanhado de ansiedade antecipatória e evitação de locais ou situações nas quais já ocorreu um ataque de pânico (1). O TP freqüentemente é complicado pela presença de Agorafobia, que é a evitação fóbica de locais nos quais é difícil de sair ou obter ajuda. Estudos recentes estimam que o TP com ou sem Agorafobia afeta em torno de 4,8% da população geral (2-4). O TP é duas ou três vezes mais comum em mulheres e geralmente inicia no final da adolescência ou início da vida adulta (5).

O TP, em geral, tem um curso crônico. Alguns estudos evidenciaram que cerca de 20 a 30% dos pacientes apresentavam sintomatologia igual ou pior após vários anos de tratamento (1, 6). Outros estudos de seguimento mostraram que o TP pode apresentar um curso crônico em até 88% dos pacientes (1, 7). Andersch *et al.* (2003) seguiram pacientes com TP ao longo de 15 anos e evidenciaram que mais de 20% da amostra seguia sintomática (8).

O diagnóstico do TP, como uma entidade nosológica individual, surgiu em 1980 a partir do DSM III (Manual Diagnóstico e Estatístico de Transtorno Mental). No DSM IV (1), o TP caracteriza-se pela presença de ataques espontâneos e recorrentes que atingem o pico máximo em até 10 minutos e são acompanhados por uma sensação de medo iminente ou urgência para escapar. Após um dos

ataques, deve haver preocupação persistente com a possibilidade de ocorrer um novo episódio, com suas implicações e consequências ou uma alteração significativa no comportamento em função dos ataques por um período de pelo menos um mês. No TP, os ataques de pânico não ocorrem como uma consequência de efeitos fisiológicos diretos de alguma substância ou condição médica, assim como não são sintomas de outro transtorno mental (1). O paciente deve ter vivenciado ataques espontâneos ao menos uma vez, embora os ataques possam passar a ser situacionais com o desenvolvimento da doença.

Etiologia

Diversos fatores vêm sendo atribuídos à gênese do Transtorno do Pânico, e tanto fatores genéticos quanto psicológicos e ambientais parecem contribuir para esse transtorno (9).

Fatores genéticos

Os Transtornos de Ansiedade geralmente se agregam em famílias (10). Estudos de famílias com TP demonstraram um padrão familiar, no qual o risco de TP em parentes de primeiro grau dos pacientes com esse transtorno é maior que no grupo controle (11). Estudos com gêmeos também corroboram esses achados, mostrando maior concordância do TP em gêmeos monozigóticos em comparação aos dizigóticos (12).

Estudos realizados em gêmeos sugerem que fatores de risco genéticos comuns provavelmente colaboram para as altas taxas de comorbidade presente nos Transtornos de Ansiedade. Togerson (13) encontrou uma concordância de 2:1 em gêmeos monozigóticos:dizigóticos quando considerou todos os Transtornos de Ansiedade, mas não encontrou essa relação quando considerou um mesmo Transtorno de Ansiedade. Estudos mais recentes em uma ampla amostra de gêmeos descreveram que tanto fatores genéticos quanto ambientais colaboram para o desenvolvimento de Fobias, Depressão Maior, Transtorno de Ansiedade Generalizada e Transtorno do Pânico (14-17).

Fatores Psicológicos

Vários estudos psicológicos sobre o TP seguem a teoria cognitivo-comportamental. Segundo Clark (18), os ataques de pânico derivam de interpretações catastróficas disfuncionais de certas manifestações corporais. A suposição é centralizada no processamento inadequado de informações vindas de um estímulo externo (ruído, luminosidade) ou interno (sensação de taquicardia, sudorese, vertigem). A interpretação é de perigo iminente que dispara ou intensifica as sensações corporais confirmando o “perigo”, gerando então mais interpretações catastróficas e ansiedade em uma espiral crescente e rápida. O modelo de Barlow (19) amplia este conceito, no qual o ataque de pânico inicial é um “alarme falso” quando ocorre um aumento momentâneo de estresse da vida em indivíduos com vulnerabilidades biológicas e/ou psicológicas. Após o primeiro ataque, a pessoa torna-se apreensiva em relação a ataques futuros. Para Barlow

(19), o medo primário no TP é o medo das sensações físicas, particularmente as associadas à ativação autonômica. Esta teoria também salienta a influência dos fatores sócio-culturais para o surgimento da Agorafobia, onde o medo estaria associado aos estímulos ambientais.

Alguns autores dedicaram-se ao estudo dos fatores psicodinâmicos associados ao início do TP ou a uma maior vulnerabilidade psicológica ao transtorno (20). Pacientes com TP freqüentemente se descrevem como crianças medrosas, nervosas e tímidas, e também referem desconforto com os sentimentos agressivos, sentimentos crônicos de baixa auto-estima, frustração e ressentimento que precediam o início do TP.

A qualidade da relação parental é um fator de risco para o TP (21). Por exemplo, os pacientes com TP freqüentemente descrevem seus pais como pessoas brabas, críticas, amedrontadoras e controladoras (22). O estudo da relação parental na psicopatologia evoluiu muito com o surgimento de instrumentos que avaliam esse constructo de forma estruturada, como o *Parental Bonding Inventory* (PBI) (23). O PBI é um instrumento auto-aplicável de 25 questões que avalia separadamente os cuidados do pai e da mãe durante os primeiros 16 anos de vida em duas dimensões: a superproteção e o afeto. Uma análise fatorial recentemente sugeriu uma estrutura de três fatores para o PBI, com a dimensão adicional do fator de autoritarismo (24-26). Alguns estudos demonstraram uma boa correlação entre os cuidados reais e a medida parental avaliada pelo instrumento (27-30). Além disso, uma coorte de 20 anos demonstrou uma boa estabilidade do instrumento em longo prazo (31). O PBI está disponível

na versão traduzida e adaptada para o português brasileiro (32). Estudos que avaliaram pacientes com TP quanto ao vínculo parental com o PBI demonstraram uma associação desse transtorno com pais com altos níveis de superproteção e baixos níveis de afeto (21, 33-36).

Fatores ambientais

Estudos prévios têm associado experiências traumáticas na infância (37-39) ao desenvolvimento do TP na idade adulta. Eventos estressantes na vida adulta também estão relacionados ao desenvolvimento de Transtornos de Ansiedade (14) e ao TP (40). Scocco *et al.* (41) descreveram que cerca de 90% dos pacientes com TP experienciaram transição de papéis e 40% tiveram perdas no ano que antecedeu o início do TP.

No entanto a aferição do trauma, principalmente do trauma infantil, é algumas vezes pouco confiável, possivelmente devido ao medo, culpa e vergonha relacionado ao evento. Alguns autores sugerem que a medida de trauma torna-se mais confiável quando realizada através de uma medida contínua (42) e auto-aplicável (43). Um instrumento usado para avaliar trauma na infância é o *Childhood Trauma Questionnaire* (CTQ), que foi traduzido e adaptado para a versão brasileira (42). O CTQ é um instrumento auto-aplicável composto por 28 questões tipo Likert que avalia cinco subescalas: abuso emocional, físico e sexual, e negligência física e emocional. Os itens são pontuados de 1 a 5, e o resultado de cada subescala varia de 5 a 25. O CTQ fornece também um escore total de maus-tratos obtido através da soma de todas as subescalas, variando de 25 a 125

pontos, sendo que os escores maiores indicam maiores maus-tratos. Estudos prévios indicam boa estabilidade do CTQ avaliado em crianças vítimas de trauma após 6 meses de tratamento. As subescalas do CTQ apresentam boa consistência interna e validade convergente com avaliação clínica (44, 45).

Delineamentos de estudos em Genética Psiquiátrica

Durante muitos anos, os estudos em genética se restringiam aos estudos de famílias (46) através de análise de ligação de marcadores moleculares utilizando um grande número de indivíduos afetados e não afetados dentro de uma mesma família. No entanto, essa abordagem não contribuiu muito para identificar genes de doenças complexas, como a doença coronariana, asma, diabetes e doenças psiquiátricas (46). Os estudos mudaram então o foco do mapeamento genético para estudos de associação.

Os estudos de associação buscam identificar se um padrão de polimorfismos varia sistematicamente em um determinado fenótipo (47). Existem dois desenhos fundamentais nos estudos de associação: os realizados em famílias (trios) e os realizados em indivíduos não-relacionados (caso-controle). Em termos de poder estatístico, os estudos de trios e caso-controle pouco se diferem (46). Já em termos de coleta de dados, os estudos de trios geralmente exigem mais esforços em comparação aos de caso-controle, exceto em crianças, pois o acesso aos pais é mais fácil (46). Por outro lado, o delineamento de trios é mais robusto que o de caso-controle na medida que permite determinar se o alelo de

risco é de origem materna ou paterna (48); além disso, o estudo de trios possibilita a construção de um modelo e teste de múltiplas hipóteses (46) e reduz as chances de associação por estratificação étnica (48, 49).

Os estudos de trios baseiam-se no teste de desequilíbrio de transmissão, que compara o número de alelos transmitidos para os sujeitos afetados com o que seria esperado pela transmissão Mendeliana. Um excesso de determinado alelo na prole afetada indica que aquele fenótipo está em desequilíbrio de ligação com o marcador (46). Já os estudos de caso-controle comparam se um determinado polimorfismo é mais freqüente em um determinado grupo (47).

Classificação dos estudos de associação

Existem mais de 30.000 genes no genoma humano, e a probabilidade *a priori* de que algum gene selecionado ao acaso possa influenciar um determinado fenótipo é muito baixa (50). Dessa forma, ou a seleção de SNPs (*Single Nucleotides Polimorphisms*) deve englobar um número muito grande de marcadores, ou os SNPs devem ser selecionados baseado em algum referencial teórico. Os estudos de associação são então classificados de acordo com método de busca dos SNPs estudados da seguinte forma:

a) Gene candidato, no qual cerca de 5-50 polimorfismos, ao redor de um determinado gene, são avaliados. O gene pode ser determinado pela sua posição, por ter estudos de ligação prévios, ou mesmo por ser um candidato funcional, ou seja, ter a sua função já demonstrada em outras espécies;

b) Mapa fino, que são estudos conduzidos numa região candidata de cerca de 1-10Mb e pode envolver centenas de genes;

c) *Genome-wide Association* (GWA), que busca identificar variações ao longo do genoma, com cerca de 300.000 SNPs.

As vantagens dos estudos de gene candidato é que o custo é infinitamente menor; no entanto, a escolha do gene deve ser feita de forma bastante criteriosa. Já os estudos que envolvem múltiplos SNPs, como o GWA, apresentam um risco elevado de encontrar associações espúrias devido às múltiplas associações, portanto o valor p deve ser adequadamente corrigido (47).

Seleção de SNPs

Nos estudos de gene candidato, o processo de seleção dos SNPs no gene deve ser feito de forma que os SNPs que retém maior variação genética sejam escolhidos, e a esse processo se denomina *Single Nucleotide Polymorphism (SNP) Tagging*. Dessa forma, dentre dois SNPs disponíveis que estão em forte desequilíbrio de ligação (DL), será escolhido apenas um, preferencialmente aquele com maior frequência alélica (47, 51). Existem programas que desempenham essa função, como por exemplo, o *Tagger program* (51) (<http://www.broad.mit.edu/mpg/tagger/>).

Peculiaridades da análise estatística

Um dos problemas da análise estatística de estudos na área da genética é que o grande número de polimorfismos possibilita encontrar associações

estatisticamente significativas ao acaso. Para evitar isso, algumas abordagens são feitas no tratamento estatístico.

A primeira etapa é avaliar a qualidade do material genotipado. Indivíduos que não foram genotipados na maioria dos polimorfismos devem-se, provavelmente, ao comprometimento da qualidade do ácido desoxirribonucléico (DNA), devendo então ser excluídos. Da mesma forma, SNPs que não forem genotipados na maioria dos indivíduos provavelmente também não são de boa qualidade (50). Testar para o equilíbrio de Hardy-Weinberg (HWE) também pode ser útil, uma vez que desvio de HWE freqüentemente se deve a consangüinidade, estratificação populacional, seleção (47) ou erro no experimento (52). Portanto, alguns autores preconizam que HWE deva também ser usado como controle de qualidade, e descartar aqueles SNPs que desviarem em controles, por exemplo, com um nível de significância alfa de 10^{-3} ou 10^{-4} .

O objetivo final dos estudos de associação é encontrar associação de determinado gene com o fenótipo avaliado. No entanto, analisar os SNPs individualmente pode negligenciar a informação conjunta (47). Uma das formas de abordar a associação conjunta do gene é analisar através do teste baseado no grupo (*set-based test*). Dessa forma, além do teste de associação individual de cada SNP com o fenótipo, obtém-se também um teste de associação para o efeito aditivo dos SNPs. Outra estratégia para avaliar um conjunto de SNPs é a análise de haplótipos, que busca a correlação de SNPs em regiões de pouca recombinação (47). Os achados da análise de haplótipo são mais consistentes quando são incluídos SNPs com forte DL entre eles. No entanto essa abordagem

oferece pouca ou nenhuma vantagem sobre a análise de grupo, particularmente quando se utiliza a estratégia de busca de SNPs através do método *Tagging*, pois esse método não inclui SNPs que estão em forte DL (47).

Esses recursos não evitam, todavia, o grande problema dos estudos genéticos: múltiplos testes. O genoma é muito grande, então qualquer SNP (ou grupo de SNP) tem uma baixa probabilidade de estar realmente associado ao fenótipo estudado. Uma estratégia para evitar falso-positivos é adotar a correção de Bonferroni, mas para SNPs com forte DL essa correção é bastante conservadora. Outra estratégia é adotar o procedimento de permutação. Dessa forma os dados do genótipo são mantidos preservando a estrutura de DL, mas os fenótipos são randomizados n vezes entre os indivíduos para gerar dados que satisfaçam a hipótese nula de ausência de associação com o fenótipo (47). Nenhuma associação biológica deve ser encontrada nos dados permutados, pois o fenótipo foi modificado. Compara-se então o melhor resultado permutado, que representa um achado ao acaso, aos dados reais obtidos (48). Como a permutação preserva o esquema de correlação entre os SNPs, torna-se um método de correção menos restrito que a correção de Bonferroni, que assume que todos os testes são independentes (53).

Meta-análise

Existem três problemas freqüentes no delineamento de estudos com grande poder em genética. O primeiro deles é a freqüência do fenótipo estudado, que torna compreensível a razão pela qual existem estudos de maior poder na

Depressão Maior que no Transtorno do Pânico. A segunda grande limitação é a frequência do polimorfismo estudado. Por exemplo, para identificar uma associação com uma razão de chances (RC) de 1,2 de um SNP cuja frequência nos controles é de 5%, seriam necessários mais de 12 mil sujeitos (50). E a terceira limitação são os custos da genotipagem de genes em tantos indivíduos (48). Dessa forma, os estudos são geralmente pequenos, incluindo de 100 a 300 sujeitos (54, 55). Os estudos pequenos possuem um papel fundamental ao gerar hipóteses, mas devem ser replicados em uma segunda amostra, preferencialmente maior (50).

De acordo com Hirschhorn *et al.* (56), de um total de 166 estudos de associação de variações genéticas com doenças, apenas 6 replicaram achados prévios. Sabe-se que a RC de associação de um polimorfismo com uma doença é geralmente baixa. Dentre os transtornos psiquiátricos, apenas a Doença de Alzheimer foi associada a um gene com RC maior que 2 (50), enquanto que as demais associações geralmente se situam numa RC entre 1,1 à 1,5 (57). Assim, a estratégia estatística final é compilar os resultados de vários pequenos estudos para averiguar o real impacto de determinada variação genética em um fenótipo, através do recurso da meta-análise.

Estratificação Étnica

Outro problema freqüente nos estudos de associação de caso-controle são os potenciais confundidores, como por exemplo, estratificação étnica. Como a frequência de muitos SNPs difere de acordo com a origem étnica, é possível que

uma determinada associação se deva a uma diferença de representação étnica dos grupos. Uma estratégia pode ser restringir as análises a um determinado grupo étnico, tornando a população mais homogênea possível (58). A desvantagem desse método é que ele pode ser influenciado pela a definição cultural de uma determinada ancestralidade (59). Por exemplo, no Brasil a ancestralidade africana é freqüentemente omitida e alguns autores preconizam que a descrição fenotípica não prediz a ancestralidade do brasileiro (60). No entanto, no Rio Grande do Sul o percentual de mistura africana em indivíduos classificados fenotipicamente como caucasianos é de cerca de 6% (61), sugerindo que a avaliação fenotípica é um bom parâmetro de ancestralidade para essa região.

Outro recurso é utilizar alguns marcadores para avaliar o impacto da ancestralidade da população na amostra. Uma forma descrita para controlar essa variável é o controle genômico (62), no qual se utiliza de variação de marcadores genéticos da amostra para inferir a subestrutura da população e corrigir a amostra para a estratificação. Também pode ser usado o método de associação estruturada, que parte do princípio de que uma população heterogênea é composta por subpopulações homogêneas, então se utiliza de múltiplos loci para inferir a estrutura da população de forma detalhada (63). Os testes de associação levam então em conta a estrutura inferida da população (59)

A busca de genes candidatos

O TP é considerado um transtorno psiquiátrico de herança complexa, pois não foi identificado nenhum padrão de herança Mendeliana (64). Provavelmente vários genes contribuam com um pequeno efeito para a suscetibilidade ao TP. Desta forma, a busca de genes candidatos tem sido feita baseada no conhecimento de moléculas envolvidas no tratamento farmacológico, nos agentes que induzem ataques de pânico (65) ou nos estudos de neuroimagens. Por exemplo, a resposta clínica que os pacientes com TP apresentam quando tratados com Inibidores Seletivos de Recaptação da Serotonina (ISRS) e a piora quando usam agentes serotoninérgicos colabora para a hipótese de disfunção serotoninérgica no TP (12, 66). Outros autores buscam genes candidatos baseado em modelos animais e alterações neuroendócrinas encontradas nesses pacientes.

Sistema serotoninérgico

A disfunção do sistema serotoninérgico tem sido implicada em diversas condições, como nos Transtornos de Ansiedade, enxaqueca, epilepsia e Transtornos de Humor (12). No TP, tem sido descrito que tanto o excesso, quanto a falta desse neurotransmissor em algumas regiões cerebrais estão envolvidos na sua etiopatogenia (66). Existem duas hipóteses opostas que tentam explicar a disfunção serotoninérgica no TP: excesso ou superatividade de serotonina (67, 68), e déficit ou subatividade da serotonina (69), e ambas as interpretações encontram respaldo ao serem confrontadas com a resposta farmacológica. A

teoria do excesso de serotonina sugere que os pacientes com TP apresentam liberação exagerada de serotonina na fenda sináptica ou hipersensibilidade dos receptores pós-sinápticos. A piora clínica que os pacientes com TP apresentam quando iniciam tratamento com ISRS corrobora a teoria de excesso, indicando que a hipersensibilidade dos receptores pós-sinápticos piora as crises. Por outro lado, a teoria do déficit propõe que em determinadas regiões cerebrais, como na substância cinzenta periarquedutal, a serotonina previne o pânico, e o déficit desse neurotransmissor propicia o ataque de pânico. A administração do precursor da serotonina (5-hidroxi-triptofano) (70) diminui os ataques de pânico e após um tempo os ISRS são efetivos em diminuir as crises de ansiedade. Não se espera que toda a complexidade do TP seja explicada de forma simplista por uma disfunção em um sistema monoaminérgico. Entretanto, os modelos biológicos de interpretação partem de bases simples com o intuito de explicar uma parte do transtorno que pode estar relacionada à neurotransmissão específica de uma determinada monoamina.

Existem vários genes envolvidos no sistema serotoninérgico, e um candidato freqüentemente estudados nos transtornos ansiosos e de humor (71) é o gene transportador da serotonina (*5-HTT*). O *5-HTT* está localizado no cromossomo 17q11.1-q12 (72) e codifica uma proteína de membrana integral que tem um papel na recaptção deste neurotransmissor na fenda sináptica. Existem dois polimorfismos neste gene que têm sido pesquisados: um VNTR que corresponde a um número variável de repetições em *tandem* no intron 2 (72) e o polimorfismo de tamanho de repetição (RFLP – *restriction fragment length polymorphism*) que

corresponde a uma inserção/ deleção de 44 pares de bases na região promotora deste gene (5 - *HTTLPR*), que origina 2 alelos (l- *long* e s-*short*). O alelo l, constituído de 528 pares de base, vem sendo relacionado a uma transcrição do gene transportador da serotonina duas a três vezes mais eficiente quando comparado ao alelo s de 484 pares de base (73, 74). Isso significa que o alelo s seria menos ativo, resultando numa captação em níveis menores da serotonina na fenda sináptica.

Lesch *et al.* (73) relataram que o polimorfismo 5-*HTTLPR* é responsável por 3-4% da variabilidade de neuroticismo. Indivíduos com genótipos s/s ou s/l teriam mais características associadas ao neuroticismo do que pessoas com o genótipo l/l. Osher *et al.* (75) conseguiram reproduzir os achados de Lesch *et al.*, encontrando relação entre o alelo curto do 5-*HTTLPR* e medidas de personalidade relacionadas à ansiedade. Entretanto, estudos subsequentes não replicaram esses achados (76). A associação do 5-*HTTLPR* com neuroticismo torna esse gene um bom candidato a ser avaliado no TP. No entanto, alguns estudos não encontraram qualquer relação entre esse gene e o TP (77, 78), enquanto outro grupo encontrou associação com o alelo l (79). Já os demais polimorfismos existentes nesse gene não foram associados ao TP (tabela 1).

Alguns estudos pré-clínicos e clínicos apontam para a participação do receptor de serotonina 1A (*HTR1A*) como envolvido no TP. Ratos modificados para esse gene apresentam diversos comportamentos relacionados à ansiedade em testes de conflito (80). O receptor *HTR1A* é expresso em duas populações de neurônios: como auto-receptor pré-sináptico nos núcleos da Rafe e como

heteroreceptor pós-sináptico no córtex frontal, predominantemente no hipocampo, septum e córtex (81). A ativação do receptor pré-sináptico do receptor *HTR1A* por um agonista seletivo resulta numa supressão da síntese, *turn-over* e liberação de serotonina nas áreas projetivas (82), resultando num efeito ansiolítico. Por outro lado, a ativação dos receptores pós-sinápticos resulta num efeito ansiogênico (83). Nos pacientes com TP existe uma redução da responsividade do receptor *HTR1A* (84), sugerindo que uma variação alélica no gene desse receptor possa predispor o desenvolvimento desse transtorno (9). Recentemente foi descrito que um polimorfismo (C1019G) no promotor do *HTR1A* possa contribuir para a patogênese de Agorafobia no TP (9). O alelo G libera a repressão da expressão dos auto-receptores *HTR1A* ao alterar o sítio de ligação de um fator inibitório da transcrição, resultando então na redução da neurotransmissão serotoninérgica (85). Um estudo de neuroimagem (86) descreveu uma associação entre o alelo G e a diminuição da ativação do córtex cerebral quando expostos a estímulo ansiogênico em pacientes com TP. O alelo G também foi associado à ansiedade e temperamento de evitação de dano em voluntários saudáveis (87) e ao TP com Agorafobia (88). No entanto esse achado não foi replicado num estudo de duas amostras independentes que avaliou o neuroticismo, um fenótipo intermediário da ansiedade (89).

Drogas com ação no receptor de serotonina 2A (*HTR2A*) apresentam ação ansiolítica (90). O gene do *HTR2A* consiste de dois introns e três éxons e está localizado no cromossomo 13q14-q21. Alguns polimorfismos foram descritos nesse gene (91), sendo que o polimorfismo T102C tem sido bastante estudado. O

alelo C expressa uma proteína do HTR2A menos ativo que alelo T, indicando um papel funcional para esse polimorfismo (92). Alguns estudos demonstraram associação entre variações no gene do *HTR2A* com comportamento suicida no transtorno depressivo (93, 94). No TP foi descrita associação de um polimorfismo (T102C) em duas amostras independentes (12, 95). No entanto esse achado não foi replicado em duas outras amostras (88, 96). Unschuld *et al.* (97) recentemente descreveram associação do *HTR2A* com temperamento dependente de gratificação em pacientes com TP.

A serotonina é metabolizada pela enzima monoamino oxidase A (MAOA), que é codificada pelo gene localizado no cromossomo X (Xp11.23-11.4) (98). Foi descrito um polimorfismo na região promotora do gene que influencia a atividade da enzima: os alelos longos possuem maior atividade enzimática em comparação com os alelos curtos (65). Três estudos (65, 79, 99) encontraram associação do alelo longo com TP em mulheres, enquanto que um estudo não replicou esse achado (100).

A triptofano hidroxilase 1 (*TPH1*) é uma enzima que modula a síntese de serotonina. Três polimorfismos não funcionais foram avaliados no TP, mas nenhum dos quatro estudos (96, 101-104) encontrou associação com o TP. Recentemente descobriu-se que a isoforma triptofano hidroxilase 2 (*TPH2*) é preferencialmente expressa no tecido neuronal e é então responsável pela modulação da síntese da serotonina no cérebro. Dois estudos avaliaram o *TPH2* no TP e não encontraram qualquer associação (105, 106).

Os polimorfismos estudados nos demais receptores da serotonina não mostraram resultados consistentes e replicáveis. A tabela 1 descreve os principais achados encontrados nos genes da serotonina e o TP.

Tabela 1. Estudos que avaliaram genes da serotonina no Transtorno do Pânico

Gene Candidato	Polimorfismo	Referência	Amostra	Resultado principal
5-HTT	5-HTTLPR	Hamilton <i>et al.</i> 1999(107)	45 famílias, 74 trios	Sem associação
		Deckert <i>et al.</i> 1997 (77)	158 pacientes 169 controles	Sem associação
		Ishiguro <i>et al.</i> 1997 (78)	66 pacientes 150 controles	Sem associação
		Maron <i>et al.</i> 2005 (79)	158 pacientes 215 controles	Associação com alelo l
		Matsushita <i>et al.</i> 1997 (108)	86 pacientes 213 controles	Sem associação
		Kim <i>et al.</i> (104)	244 pacientes 227 controles	Sem associação
	VNTR	Maron <i>et al.</i> 2004 (102)	158 pacientes 215 controles	Sem associação
	18784A-C 10647G-A 167G-C	Maron <i>et al.</i> 2004b (103)	127 pacientes 146 controles	Sem associação
MAO-A	VNTR	Deckert <i>et al.</i> 1999 (65)	209 pacientes 190 controles	Associação com o alelo longo em mulheres com TP
		Hamilton <i>et al.</i> 2000 (100)	70 famílias, 81 trios	Sem associação
		Maron <i>et al.</i> 2005 (79)	158 pacientes 215 controles	Associação alelo longo em mulheres com TP e Ago
		Samochowiec <i>et al.</i> 2004 (99)	101 pacientes 202 controles	Associação alelo longo em mulheres com Ago
	Fnu4HI	Tadic <i>et al.</i> 2003(109)	38 pacientes 276 controles	Sem associação
TPH 1	1095T-C	Han <i>et al.</i> 1999(101)	45 pacientes 142 controles	Sem associação

	218A-C	Fehr <i>et al.</i> 2001(96)	35 pacientes 87 controles	Sem associação
		Maron <i>et al.</i> 2004 (102)	158 pacientes 215 controles	Sem associação
		Kim <i>et al.</i> 2006 (104)	244 pacientes 227 controles	Sem associação
	779A-C	Maron <i>et al.</i> 2004b(103)	127 pacientes 146 controles	Sem associação
TPH2	19776C-T 79727C-T	Maron <i>et al.</i> (2007)(105)	213 pacientes 303 controles	Sem associação
	844G-T 4002C-T	Mössner <i>et at.</i> (2006)(106)	134 pacientes 134 controles	Sem associação
HTR1A	-1019C-G	Rothe <i>et al.</i> 2004a (88)	133 pacientes 134 controles	Associação do genótipo GG e alelo G em mulheres com Ago
		Maron <i>et al.</i> 2004b (103)	127 pacientes 146 controles	Associação do alelo C em TP com TH
		Huang <i>et al.</i> 2004(110)	87 pacientes 107 controles	Associação do genótipo GG e alelo G no ataque de pânico
	294G-A	Inada <i>et al.</i> 2003(12)	63 pacientes 100 controles	Sem associação
	-480A-del	Maron <i>et al.</i> 2004b(103)	127 pacientes 146 controles	Sem associação
HTR1B	861G-C	Fehr <i>et al.</i> 2000a (111)	32 pacientes 74 controles	Sem associação
		Maron <i>et al.</i> 2004(102)	158 pacientes 215 controles	Sem associação
	-1089T-C, -700C-A, -511G-T, -161A-T, 129C-T, 276G-A, 371T-G, 705C-T, 1180G-A	Maron <i>et al.</i> 2004b(103)	127 pacientes 146 controles	Sem associação
HTR2A	102T-C	Fehr <i>et al.</i> 2001(96)	35 pacientes 87 controles	Sem associação
		Inada <i>et al.</i> 2003 (12)	63 pacientes 100 controles	Associação do alelo C no TP com Ago

		Rothe <i>et al.</i> 2004b (9)	94/86 pacientes 94/86 controles	Sem associação
		Maron <i>et al.</i> 2004b(103)	127 pacientes 146 controles	Associação do alelo C no TP puro
		-143A-G, 73C-A, 1354 C-T Maron <i>et al.</i> 2004b (103)	127 pacientes 146 controles	Sem associação
HTR2C	Cys23Ser	Fehr <i>et al.</i> 2000b(112)	35 pacientes 89 controles	Sem associação
		Inada <i>et al.</i> 2003 (12)	63 pacientes 100 controles	Sem associação
		Maron <i>et al.</i> 2004b(103)	127 pacientes 146 controles	Associação com TP com ou sem comorbidades
	(12-18)G-T (4-5)T-G	Deckert <i>et al.</i> 2000 (113)	87/124 pacientes 131/95 controles	Sem associação
	2831T-G	Maron <i>et al.</i> 2004b(103)	127 pacientes 146 controles	Sem associação
HTR3A	1302T-C 1596G-A	Maron <i>et al.</i> 2004b(103)	127 pacientes 146 controles	Sem associação

Abreviações. TP, Transtorno do Pânico; Ago, Agorafobia; TH, Transtorno de Humor. *5-HTT*, gene transportador da serotonina. *5-HTTLPR*, polimorfismo no promotor do gene transportador da serotonina; *MAO-A*, enzima monoamino-oxidase A; *TPH 1*, triptofano hidroxilase 1; *HTR1A*, receptor da serotonina 1A; *HTR1B*, receptor da serotonina 1B; *HTR2A*, receptor da serotonina 2A; *HTR2C*, receptor da serotonina 2C; *HTR3A*, receptor da serotonina 3A; *VNTR*, número variável de repetições em tandem. Nota. Adaptado e atualizado de Maron et al. (114).

Sistema Noradrenérgico

Algumas evidências apontam para o papel da norepinefrina na patogênese do TP: elevação do seu principal metabólito em urina de pacientes (115), uso de agentes com ação noradrenérgica no tratamento farmacológico desse transtorno (66, 116, 117), e indução de ataques de pânico com o aumento da liberação da noradrenalina (118). Além disso, o *locus coeruleus*, que contém a maior

concentração de células noradrenérgicas no cérebro, é conhecido por estar envolvido no medo e na ansiedade (119, 120).

Alguns autores mostraram dados consistentes relacionando o polimorfismo Val158Met do gene *Catechol O-Methyltransferase (COMT)* com o TP (95, 121, 122). *COMT* é uma enzima que inativa as catecolaminas, incluindo a noradrenalina, adrenalina e dopamina. O gene que codifica a *COMT* está localizado no cromossomo 22q11.2. Uma substituição de um único nucleotídeo (guanina por adenosina), na primeira posição do códon 158 desse gene leva a uma mudança funcional do aminoácido valina por metionina (rs4680). Essa transição de valina por metionina está associada a um aumento de três a quatro vezes na termolabilidade. O alelo com valina (Val) apresenta uma maior atividade da enzima *COMT* que o alelo com metionina (Met) (121). O alelo Met foi associado ao Transtorno Obsessivo-Compulsivo (123), apesar de não ter sido replicado em outro estudo (124).

Alguns estudos demonstram uma relação entre o alelo de alta atividade (Val) com o TP em caucasianos (121, 122, 125), no entanto em coreanos essa relação foi inversa (126). Recentemente uma meta-análise avaliou seis estudos de associação e não encontrou qualquer associação entre o polimorfismo Val158Met com o TP (127). No entanto, foi identificada uma grande heterogeneidade nos estudos incluídos na meta-análise. Nas análises estratificadas, identificou-se uma associação do alelo valina em amostras caucasianas, enquanto que foi descrita uma associação com o alelo metionina nas amostras asiáticas.

Hormônio liberador de Corticotrofina (CRH)

O CRH é um peptídeo que regula a função da hipófise e adrenal no eixo hipotálamo-hipófise-adrenal (HPA) e é também um hormônio extra-hipotalâmico relacionado a vários comportamentos, incluindo expressões de medo (128). Os corpos celulares dos neurônios que contém CRH são largamente distribuídos no cérebro e, além dos neurônios encontrados no núcleo para-ventricular do hipotálamo, encontram-se no núcleo da estria terminal e núcleo central da amígdala. Com base em uma série de dados proveniente de estudos com animais, sabe-se que a administração central de CRH produz uma série de condutas análogas às vistas em Transtornos de Ansiedade e transtornos afetivos, incluindo: anorexia, insônia, diminuição da libido, aumento da atividade locomotora, aumento da frequência cardíaca e pressão arterial, distúrbios gastrointestinais, aumento da conduta de autolimpeza, redução da atividade exploratória e aumento da resposta de sobressalto (129). Camundongos transgênicos com alterações no gene do CRH mostraram excesso de produção do hormônio de liberação da corticotrofina. Esses camundongos exibiam também anormalidades endócrinas, incluindo elevação do hormônio adrenocorticotrófico e corticosterona, reforço da responsividade ao novo e uma resposta semelhante à que é vista no labirinto em cruz elevado. Essas manipulações genéticas reforçam a hipótese de que o CRH desempenha um importante papel nas respostas comportamentais a estressores e na psicopatologia humana (128). Há evidências de que o sistema de CRH do Sistema Nervoso Central (SNC) comumente medeia

a associação entre estresse precoce na vida e o desenvolvimento de Transtornos de Humor e Ansiedade na vida adulta (130). Um estudo recente (131) demonstrou que variações no gene do CRH estão associadas ao comportamento inibido em crianças, um temperamento que está relacionado ao desenvolvimento de Transtorno de Ansiedade na vida adulta.

O receptor 1 do CRH (*CRHR1*) está envolvido na ação ansiogênica do CRH (132, 133). Modelos animais mostraram que ratos deficientes de *CRHR1* apresentam menos comportamento ansioso em comparação com ratos selvagens (134). Alguns estudos demonstraram que antidepressivos de diferentes classes suprimem a expressão do gene CRH em roedores (135), e que a atividade do eixo HPA está deprimida em humanos saudáveis (136, 137). Além disso, foi descrito que os ISRS exercem parte do seu efeito através da redução da atividade dos neurônios do CRH (138). Liu *et al.* (139) recentemente encontraram um efeito moderado de polimorfismos do *CRHR1* e resposta em curto prazo à fluoxetina para Depressão Maior.

Neurotrofinas e mensageiros intermediários

O Fator neurotrófico neuronal (*BDNF*) é a mais abundante neurotrofina cerebral (140) e é uma molécula candidata a estar envolvida na fisiopatologia dos Transtornos de Humor (141). O *BDNF* participa da plasticidade cerebral envolvendo mecanismos como aprendizado e memória (142). O nível sérico do *BDNF* foi relacionado à resposta à Terapia Cognitiva Comportamental de pacientes com TP (143).

Um polimorfismo funcional Val66Met do gene *BDNF* foi relacionada à atividade da secreção dessa neurotrofina (144). O modelo animal recentemente mostrou que ratos Met/Met apresentam mais comportamento de ansiedade, acompanhado de uma redução de secreção de *BDNF* atividade-dependente, mas não no nível total (145). O comportamento ansioso dos ratos não foi modificado pelo uso da fluoxetina, sugerindo a importância dessa neurotrofina como mediador do efeito ansiolítico dos antidepressivos. Considerando o papel do *BDNF* na sobrevivência, diferenciação e plasticidade neuronal, o polimorfismo Val66Met passou a ser um grande candidato a ser avaliado nos transtornos psiquiátricos (142). Entretanto a associação desse polimorfismo com ansiedade é bastante errática. Por um lado, Lang *et al.* (146) encontraram associação entre o genótipo Val/Val e traços de ansiedade, enquanto o alelo Met estava associado a níveis mais elevados de temperamento ansioso em outro estudo (147). No TP esse polimorfismo somente foi avaliado em amostras orientais, e não houve associação entre esse SNP e TP em japoneses (148) e chineses (149).

Modelos animais demonstraram que a ansiedade está relacionada ao *AMPC responsive-element binding protein (CREB)* (150). O *CREB* é expresso em todas as células cerebrais e é uma proteína que age como fator de transcrição (151). Wallace *et al.* (152) demonstraram em um modelo animal que a expressão do *CREB* na amígdala basolateral influencia os comportamentos de depressão, medo e ansiedade. O aumento da expressão de *CREB* na amígdala de ratos tem um efeito semelhante ao que é visto no treinamento massivo em campo aberto no desenvolvimento do medo condicionado (153). Em humanos, o *CREB* está

associado ao Transtorno de Humor (154), suicídio (155, 156), agressividade (157) e resposta ao antidepressivo (158). O *CREB* também está envolvido no circuito de recompensa e regula então a sensibilidade individual ao estímulo emocional, contribuindo então para neuroadaptação ao estímulo (151). Alguns estudos associaram também o *CREB* à memória em diversos organismos (159). O propranolol, que é um tratamento experimental para o Transtorno do Estresse Pós-Traumático, modifica a consolidação da memória ao atuar como antagonista beta-adrenérgico, que inibe a fosforilação do AMPc (160). O TP está intimamente ligado à interpretação catastrófica dos sintomas corporais e à memória dos ataques de pânico, sendo essa a base da terapia cognitivo-comportamental (161).

O *RGS2* (*regulator of G-protein signaling 2*) é uma proteína que reduz a atividade da proteína G (162, 163). Os neurotransmissores envolvidos na biologia da ansiedade, como a serotonina e a noradrenalina, agem através da proteína G acoplada ao receptor de sinalina (164). Ratos *RGS2 knockout* mostraram-se mais ansiosos que os ratos selvagens (165), e um estudo recente (166) mostrou associação entre 4 SNPs do *RGS2* com TP.

Fenótipos intermediários

Os estudos de genética em Transtornos de Ansiedade são bastante erráticos (167), provavelmente devido à grande dificuldade em definir qual a real parte que é herdável desse fenótipo. Alguns autores descreveram que o aspecto genético dos Transtornos de Ansiedade se torna mais aparente quando a definição do

estado “afetado” é expandido, e inclui variações sub-sindrômicas (13, 168). Sabe-se que os Transtornos de Ansiedade são influenciados por fatores genéticos quando considerados como um conjunto; no entanto, os estudos de gêmeos demonstraram pouca concordância para um mesmo Transtorno de Ansiedade (13). Além disso, existe uma grande sobreposição de Ansiedade e Depressão. Estudos em família demonstraram uma maior suscetibilidade para o desenvolvimento de Depressão em familiares de pacientes com TP (169). Parece que a nosologia genética não segue os parâmetros diagnósticos propostos pelo DSM-IV (1).

Dentro desse contexto surge o conceito de fenótipos intermediários. Propõem-se então que os fatores genéticos, modulados por experiências ambientais, influenciam a expressão de “fenótipos mínimos” e o agrupamento desses determina os “fenótipos intermediários”, como o comportamento inibido, um temperamento que pode estar associado aos Transtornos de Ansiedade ou Depressivos. Os fenótipos intermediários, por sua vez, caracterizam as síndromes clínicas, como por exemplo, a síndrome ansiosa ou a síndrome depressiva, configurando o temperamento ou o funcionamento pré-mórbido. As síndromes passam então a ser consideradas transtornos quando levam a um prejuízo funcional do indivíduo. O prejuízo funcional pode ocorrer devido ao tempo de sofrimento, à desadaptação funcional, ao prejuízo na qualidade de vida ou mesmo ao aumento dos custos sociais ou da morbi-mortalidade (Figura 1). Dentro desse paradigma é possível compreender a grande sobreposição da comorbidade

Ansiedade e Depressão, uma vez que essas compartilham de endofenótipos comuns.

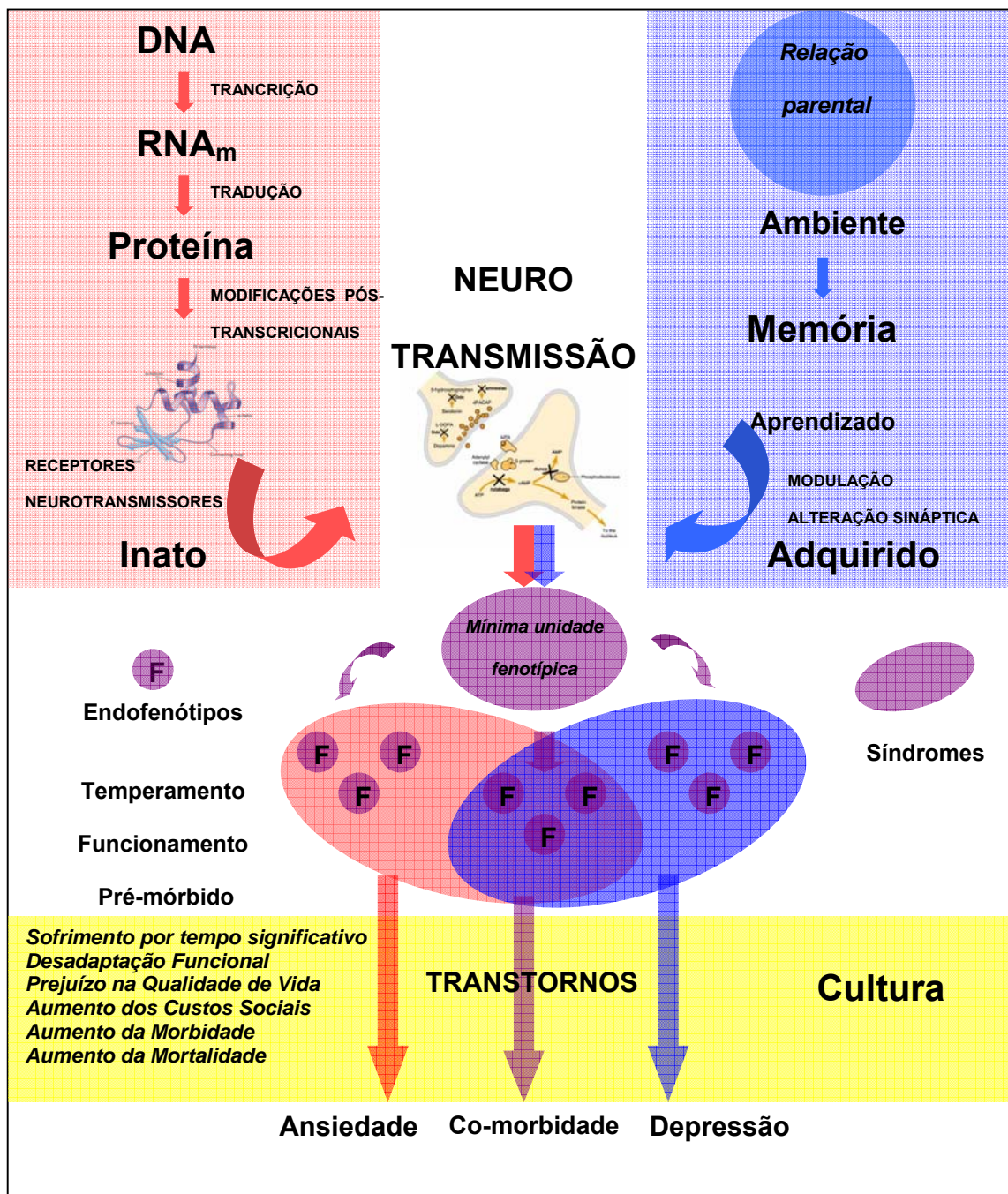


Figura 1. Modelo dimensional da nosologia genética. Autor Salum Ga, 2008.

Alguns autores sugerem que existe um pequeno número de dimensões nas quais os indivíduos diferem, e a psicopatologia representa então extremos de dimensões que compõe a personalidade normal (167). Muitas dessas dimensões ou temperamentos que contribuem para diferenças individuais na personalidade estão diretamente relacionadas com a ansiedade (167).

O temperamento dos indivíduos é um fenótipo intermediário bastante relacionado a variações herdáveis. Cloninger (170) definiu três traços de personalidade que ocorrem em resposta a estímulos específicos: os “procuradores por novidade”, que é um padrão de atividade exploratória freqüente de intensa excitação frente um novo estímulo; os “evitadores de dano”, que é uma tendência herdada a responder de forma extremamente intensa a um estímulo aversivo, aprendendo a evitar novidades; e os “dependentes de gratificação” que é uma tendência a responder de forma intensa a reforços positivos. A integração dessas dimensões neurobiológicas forma padrões de respostas diferentes a punição, recompensa e novidades, e favorece a capacidade discriminatória de situações seguras e perigosas. Existem evidências que a variação em cada dimensão está fortemente associada com alterações específicas nas vias monoaminérgicas; por exemplo, os “evitadores de dano” estão relacionados com alta atividade serotoninérgica. Nos indivíduos com alta evitação de dano, a ansiedade crônica caracteriza-se por preocupações antecipatórias freqüentes (170), um padrão clinicamente semelhante ao encontrado em pacientes com Transtorno do Pânico. Os pacientes com TP são descritos como possuírem predominantemente um temperamento de evitadores de dano (171, 172).

O comportamento inibido (CI) também é um fenótipo intermediário de ansiedade que vem sendo estudado em estudos genéticos (131). CI na infância é caracterizado pela presença de irritabilidade em bebês, timidez e medos excessivos na criança pré-escolar e, na criança em idade escolar, introversão, dificuldade e constrangimento ao enfrentar novas situações (173). O comportamento inibido apresenta tanto componentes comportamentais, tais como o retraimento social e timidez, quanto componentes fisiológicos, como aumento dos níveis de cortisol salivar, dos níveis de catecolaminas urinárias, da frequência cardíaca e dilatação pupilar (173). Comportamento inibido é mais freqüente em crianças cujos pais têm Agorafobia e Transtorno do Pânico (174), e Transtornos de Ansiedade são mais freqüentes nas famílias de crianças com comportamento inibido (175). Crianças identificadas como tendo comportamento inibido têm taxas mais altas de Transtornos de Ansiedade na infância (176).

A percepção das emoções é outro fenótipo avaliado no TP em estudos de neuroimagem (86). Kessler *et al.* (177) descreveram que o reconhecimento das emoções tende a ser pior nos pacientes com TP, que interpretam outras emoções como raiva. Esse estudo levanta a hipótese de que os pacientes com TP tendem a interpretar os estímulos sociais como sendo perigosos. A percepção do medo tem sido estudada em diferentes transtornos (178), no qual a amígdala parece desempenhar um papel crucial (179). Weiss *et al.* (180) realizaram um mapeamento do reconhecimento do medo em duas amostras independentes de pacientes com Síndrome de Turner e encontraram associação com o *EF-hand domain containing 2 (EFHC2)*, um gene localizado no cromossomo X.

Interação gene-ambiente

As associações entre marcadores genéticos com transtornos psiquiátricos vêm sendo um tanto erráticas (71), provavelmente devido à desconsideração dos fatores ambientais que interagem com fatores genéticos. Os transtornos psiquiátricos, de uma forma geral, desenvolvem-se devido à interação entre uma predisposição familiar e estressores biopsicossociais. Esse modelo é contemplado pela teoria de diátese-estresse que prediz o desenvolvimento de Depressão (71), no qual a sensibilidade a um evento estressor depende da sua genética. Mann *et al.* (181) sugerem a construção de um modelo que pode ser visto como um modelo gatilho-limiar para explicar essa suscetibilidade e compreender esse fenômeno. A diátese (vulnerabilidade) determina como um indivíduo reage a um evento estressor e depende de fatores que moldam a sua personalidade como os fatores genéticos e ambientais, experiências infantis entre outros. Baseado neste modelo, os fatores de risco podem ser categorizados como pertencentes a um desses dois domínios (gatilho ou limiar pessoal).

Essa tem sido a base dos estudos de interação gene-ambiente. Caspi *et al.* (71) ao seguir uma amostra por mais de duas décadas encontraram que a presença do alelo curto no *5-HTTLPR* influenciava a probabilidade de desenvolver um quadro Depressivo Maior frente a uma situação estressora (71). A associação gene-ambiente do *5-HTTLPR* para Depressão foi demonstrada em muitos estudos (71, 182-189), mas não em todos (190, 191). Surtees *et al.* (191), no maior estudo

disponível de interação gene-ambiente para Depressão, não encontrou relação entre o genótipo e experiências na infância ou na vida adulta com o risco de Depressão maior. Por outro lado, foi identificada uma interação somente com os homens, mas na direção oposta àquela descrita por Caspi *et al.* (71).

A interação gene-ambiente do *5-HTTLPR* com maus tratos na infância não foi estudada exclusivamente na Depressão Maior. Kaufman *et al.* (192) descreveram em um estudo de seguimento de crianças vítimas de maus-tratos e controles uma interação gene-ambiente também com o alelo *s* e uso precoce de álcool.

Nenhum estudo testou a interação gene-ambiente no TP, apenas com fenótipos intermediários da ansiedade. Stein *et al.* (193) avaliaram a interação do *5-HTTLPR* com trauma na infância e encontraram que os sujeitos com o alelo *s* estavam associados à maior sensibilidade à ansiedade quando expostos a maior abuso emocional, o que não ocorreu com os sujeitos *ll*. No entanto, não houve interação gene-ambiente com o fenótipo neuroticismo pelo inventário de personalidade NEO.

Outro gene candidato para interação gene-ambiente é o *HTR1A*. Ratos com deleção de *HTR1A*, particularmente no córtex pré-frontal, apresentam um fenótipo de ansiedade somente quando essa inativação ocorre no período pós-natal, uma vez que a inativação do *HTR1A* na vida adulta não afeta a ansiedade (194). Recentemente foi demonstrado que a expressão do *HTR1A* é menor em animais sensíveis ao estresse (195). No entanto, Mandelli *et al.* (182) não

encontrou qualquer associação entre o *HTR1A* e eventos estressantes no início da Depressão Maior.

Os estudos de interação não se restringem ao efeito deletério do ambiente, mas também avaliam o efeito protetor. Jokela *et al.* (196) avaliaram um coorte prospectiva de 21 anos e encontraram que os sujeitos portadores do alelo T do polimorfismo T102C do *HTR2A* eram mais responsivos ao aspecto protetor do cuidado materno para o desenvolvimento de depressão. Esse estudo mostra que variações genéticas podem influenciar na forma como o indivíduo utiliza os suportes ambientais.

Os estudos de interação devem ser vistos com cuidado, pois freqüentemente os achados se restringem a subanálises, o que resulta de um maior número de testes estatísticos e então uma maior probabilidade de recair no erro tipo I (197). Por exemplo, Grabe (184) e Eley (183) encontraram associação gene-ambiente com o *5-HTTLPR* apenas nas mulheres, enquanto que Surtees *et al.* (191) encontraram uma relação em homens com direção inversa (198). Já Stein *et al.* (193) descreveu uma interação do gene transportador da serotonina com uma escala de trauma na infância e sensibilidade à ansiedade, enquanto que não há referência às demais escalas, que refletem fatores de risco mais bem estabelecidos para ansiedade como o abuso sexual. Sjoberg *et al.* (199) descreveram interação entre *5-HTTLPR* e adversidades com Depressão, mas a interação foi observada em direções opostas em homens e mulheres.

Outra limitação desses estudos é que a baixa freqüência de eventos no grupo de comparação diminui o poder do estudo que provavelmente detectará

somente interações de grande efeito. Os estudos de interação geralmente apresentam um poder pequeno, e os achados iniciais freqüentemente estão superestimados, necessitando ser replicado em amostras maiores. Curiosamente, os estudos de tamanho amostral pequeno geralmente descrevem uma associação positiva, enquanto que apenas estudos grandes (190, 191) mostram resultados negativos. Possivelmente, existe um viés de publicação e a interpretação do resultado passa a ser ainda mais problemática (198). Ainda, a presença de interação estatística encontrada nos estudos não significa necessariamente uma interação biológica plausível (198).

Moffitt et al. (200) propuseram sete etapas para conduzir um bom estudo de interação, sendo que primeiramente deve-se buscar os modelos quantitativos de genética comportamental. Os coeficientes de herdabilidade não indicam apenas a contribuição de genes, mas também o efeito desses na interação com o ambiente. No caso do TP, a herdabilidade é estimada em 28%, sendo que os fatores ambientais contribuem em 70% (14). A segunda etapa é identificar o evento ambiental candidato, e ter sua medida otimizada. Posteriormente, devem-se identificar os genes candidatos, e então testar a interação. No passo seguinte, deve-se testar se a interação permanece ao substituir um gene por outro ou mesmo um evento ambiental por outro, para avaliar a especificidade da interação. Porém essa relação somente é firmada quando o achado é replicado e concluído por meta-análise (200).

Interação gene-gene

Diante do possível papel de múltiplos genes no desenvolvimento de patologias psiquiátricas, alguns autores passaram a investigar a interação gene-gene. O sucesso dessas interações depende muito de um tamanho amostral adequado (201).

Freitag *et al.* (202) avaliaram diversas interações possíveis para o desenvolvimento do TP e encontraram uma interação entre o *HTR1A* (-1019C/G) e o *COMT* (Val/Met). Os autores propõem que o alelo G do *HTR1A* levaria a um aumento da expressão dos auto-receptores no núcleo da rafe, levando então a uma diminuição da transmissão serotoninérgica. Nas células pós-sinápticas, por outro lado, o alelo G levaria à diminuição da expressão dos receptores *HTR1A* pós-sinápticos. Essa proposta está de acordo com estudos de neuroimagem nos quais se identificou diminuição de ligação nos receptores no giro do cíngulo e nos núcleos da rafe (203). A liberação de norepinefrina no *locus coeruleus* é modulada em ratos pela ação inibitória do *HTR1A* nos neurônios glutamatérgicos (204), sugerindo-se, então, que a redução da transmissão serotoninérgica causada pelo alelo G conseqüentemente levaria a um aumento da liberação de norepinefrina. Já o alelo G do *COMT* leva a uma inativação monoaminérgica mais rápida, e a redução local de norepinefrina nos hetero-receptores alfa 1 nos neurônios serotoninérgicos da rafe leva à diminuição da liberação de serotonina (205). Dessa forma, a redução da neurotransmissão serotoninérgica poderia ocorrer pela elevação da atividade da *COMT* ou pelo aumento dos auto-receptores ou

diminuição dos hetero-receptores *HTR1A*, ou mesmo pela interação desses fatores. No entanto, os autores encontraram uma razão de chances (RC) para esse achado de 1,08 em uma amostra de 230 sujeitos. Gauderman (201) sugere que quando a RC esperada em um estudo de interação for de 1,5, necessitar-se-iam mais de 2000 sujeitos, ou seja, resultados vindos de amostras pequenas podem estar recaindo no erro tipo I.

Farmacogenética

A resposta a psicofármacos também parece ser influenciada por variações genéticas. Ela é resultado da interação de múltiplas variações genômicas com influências ambientais e depende da estrutura ou expressão funcional de produtos gênicos (receptores, transportadores, enzimas), os quais são alvos diretos das drogas ou modificam indiretamente o desenvolvimento e a plasticidade de conexões neurais envolvidas em efeitos farmacológicos. Como o mecanismo de ação detalhado dos antidepressivos continua sendo enigmático, os estudos recentes modificaram o foco que vinha sendo depositado nos neurotransmissores, ou seja, sua liberação, recaptura e metabolismo para modulação da expressão gênica, plasticidade sináptica e neurogênese (206, 207).

Os estudos de farmacogenética envolvendo antidepressivos geralmente se concentram em pacientes com Depressão Maior. Serretti *et al.* (208) trataram pacientes com depressão unipolar e bipolar com fluvoxamina e encontraram uma pior resposta ao fármaco para os pacientes bipolares com a variação G do

polimorfismo (-109C/G) no *HTR1A*. Lemonde *et al.* (209) descreveram a resposta à fluoxetina, à nefazodona e ao agonista do *HTR1A* fibanserina e também encontraram uma pior resposta nos pacientes com o alelo G. Evidências indicam uma associação entre o tempo de resposta e a resposta global dos ISRS e o 5-*HTTLPR* em pacientes com Depressão (210, 211).

Apenas um estudo examinou a influência de marcadores genéticos no TP. Perna *et al.* testaram a hipótese de que a variação alélica do 5-*HTTLPR* poderia estar relacionada com a eficácia da paroxetina no tratamento do TP. A presença do alelo I em homozigose ou heterozigose foi associada com melhor resposta aos ataques de pânico em mulheres (212).

Apesar dos avanços nas pesquisas de farmacogenética, nenhum estudo avaliou a influência dos marcadores genéticos com a psicoterapia em nenhum transtorno psiquiátrico.

8. Justificativa do Estudo

Estudos de caso e controle não têm encontrado qualquer associação entre o polimorfismo do gene transportador da serotonina (*5-HTTLPR*) com o Transtorno do Pânico (TP). No entanto, os estudos geralmente são realizados com amostras que variam de 100 a 300 indivíduos, justificando o uso da meta-análise para aumentar o poder do estudo.

Além disso, nenhum estudo avaliou o *5-HTTLPR* na sua forma trialélica (213), e os resultados de associação dos genes dos receptores de serotonina *HTR1A* e *HTR2A* com o TP são bastante controversos. Não existe nenhum estudo publicado em amostras brasileiras que avalie essas variações gênicas no TP. Nenhum estudo avaliou também a interação dessas variações gênicas com estressores associados ao TP.

O gene *EFHC2* (*EF-hand domain containing 2*) esteve recentemente relacionado à percepção do medo (180) e ainda não foi avaliado no TP nem nos fenótipos intermediários da ansiedade. Como medo é um sintoma central do TP, o *EFHC2* pode ser um gene candidato para o TP.

Por fim, apesar de alguns avanços na farmacogenética, nenhum estudo avaliou a influência de marcadores gênicos à terapia cognitivo-comportamental. Esses estudos possivelmente poderiam contribuir para elucidar o mecanismo biológico envolvido no processo psicoterápico.

9. Hipóteses

Considerando que os estudos dos aspectos genéticos no TP ainda apresentam resultados controversos, as hipóteses desse estudo são:

1. Uma vez que os estudos de associação com o *5-HTTLPR* e o TP são relativamente pequenos, nossa primeira hipótese é de que com o recurso da meta-análise poderíamos encontrar uma associação. Devido à associação do alelo *s* com traços de ansiedade em sujeitos saudáveis (214), a hipótese é de que o alelo *s* também estaria associado ao TP.
2. Como estudos prévios associaram o TP com variações nos genes *HTR1A* e *HTR2A* (12, 88), nossa hipótese é de que replicaríamos esse achado na amostra brasileira. Em relação aos estudos de interação gene-ambiente, nossa hipótese é de que encontraríamos uma interação do *5-HTTLPR* com trauma na infância, e do *HTR2A* com vínculo parental no TP.
3. Como o medo é um sintoma central do TP, nossa hipótese é de que o gene *EFHC2* estaria relacionado ao TP e aos seus 2 fenótipos intermediários (comportamento inibido e temperamento de evitação de danos).
4. Alguns estudos sugerem mecanismos semelhantes para a ação da psicoterapia e de psicofármacos (215-217). Nossa hipótese é de que

algum gene previamente relacionado à ansiedade (*BDNF*, *CREB*, *CRHR1*, *RGS2*, *HTR1A*, *HTR2A*) esteja associado à resposta à Terapia Cognitivo-Comportamental.

10. Objetivos

Gerais:

- O objetivo desse estudo é pesquisar a influência do polimorfismo nos genes dos receptores de serotonina *HTR1A* e *HTR2A*, *5-HTTLPR*, *CRHR1*, *RGS2*, *BDNF*, *CREB* e *EFHC2* no TP. Como esse estudo envolve vários genes, aumentando conseqüentemente a chance de erro tipo I, os genes estudados com cada fenótipo foram estabelecidos *a priori*, resultando em quatro objetivos específicos.

Específicos:

1. Revisão sistemática da literatura em busca da associação entre Transtorno do Pânico e o gene transportador da serotonina.
2. Evidenciar associação entre o gene transportador da serotonina e os receptores *HTR1A* e *HTR2A* com o diagnóstico de TP na população brasileira e a interação entre gene-ambiente com estressores e vínculo parental na infância.
3. Evidenciar associação entre marcadores do *EFHC2* com o TP e fenótipos intermediários.
4. Evidenciar a influência dos marcadores gênicos do *BDNF*, *CREB1*, *CRHR1*, *RGS2*, *HTR1A*, *HTR2A* e transportador da serotonina na resposta à Terapia Cognitivo-Comportamental.

11. Considerações Éticas

Os sujeitos incluídos nos estudos assinaram o Termo de Consentimento livre e esclarecido (TCLE) que está em anexo e um adendo explicando a parceria internacional. O projeto está de acordo com a resolução CNS 347/05 e foi avaliado pelo Comitê de Ética e Pesquisa da HCPA (04-272 e 05-056) e do *Massachusetts General Hospital* (MGH 2007-P-000119). Os TCLE utilizados nos estudos estão no anexo A.

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13. Artigos

Artigo 1 - *Lack of association between the Serotonin Transporter Promoter Polymorphism (5-HTTLPR) and Panic Disorder: a systematic review and meta-analysis*

Artigo 2 - *Panic disorder and serotonergic genes (5-HTTLPR, HTR1A and HTR2A): association and interaction with childhood trauma and parental bonding*

Artigo 3 - *Association between EFHC2 with Panic Disorder, Harm Avoidance and Behavioral Inhibition*

Artigo 4 - *CREB1 as a predictor of long term response to cognitive-behavior therapy for pharmacotherapy-resistant panic disorder patients*

Artigo 1 – *Lack of association between the Serotonin Transporter Promoter Polymorphism (5-HTTLPR) and Panic Disorder: a systematic review and meta-analysis*

Carolina Blaya¹, Giovanni A. Salum¹, Maurício S. Lima², Sandra Leistner-Segal¹,
Gisele G. Manfro^{1*}

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Research

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Lack of association between the Serotonin Transporter Promoter Polymorphism (5-HTTLPR) and Panic Disorder: a systematic review and meta-analysis

Carolina Blaya¹, Giovanni A Salum¹, Maurício S Lima², Sandra Leistner-Segal¹ and Gisele G Manfro^{*1}

Address: ¹Post-Graduate Program in Medical Sciences, Psychiatry, Universidade Federal do Rio Grande do Sul and Anxiety Disorders Program, Hospital de Clínicas de Porto Alegre, Porto Alegre, Brazil and ²Associate Professor of Psychiatry, Universidade Católica de Pelotas & Medical Director, Eli Lilly do, Brazil

Email: Carolina Blaya - cblaya@terra.com.br; Giovanni A Salum - gsalumjr@gmail.com; Maurício S Lima - LBAA_MAUICIO_SILVA_DE@LILLY.COM; Sandra Leistner-Segal - ssegal@hcpa.ufrgs.br; Gisele G Manfro* - gmanfro@portoweb.com.br

* Corresponding author

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Abstract

Background: The aim of this study is to assess the association between the Serotonin Transporter Promoter Polymorphism (5-HTTLPR) and Panic Disorder (PD).

Methods: This is a systematic review and meta-analysis of case-control studies with unrelated individuals of any ethnic origin examining the role of the 5-HTTLPR in PD according to standard diagnostic criteria (DSM or ICD). Articles published in any language between January 1996 and April 2007 were eligible. The electronic databases searched included PubMed, PsycInfo, Lilacs and ISI. Two separate analyses were performed: an analysis by alleles and a stratified analysis separating studies by the quality of control groups. Asymptotic DerSimonian and Laird's Q test were used to assess heterogeneity. Results of individual studies were combined using the fixed effect model with respective 95% confidence intervals.

Results: Nineteen potential articles were identified, and 10 studies were included in this meta-analysis. No statistically significant association between 5-HTTLPR and PD was found, OR = 0.91 (CI95% 0.80 to 1.03, p = 0.14). Three sub-analyses divided by ethnicity, control group quality and Agoraphobia comorbidity also failed to find any significant association. No evidence of heterogeneity was found between studies in the analyses.

Conclusion: Results from this systematic review do not provide evidence to support an association between 5-HTTLPR and PD. However, more studies are needed in different ethnic populations in order to evaluate a possible minor effect.

Background

Studies in families have shown that Panic Disorder (PD) has a familial pattern: its prevalence is higher in first

degree family members than in control groups [1]. Studies involving siblings show that PD concordance is higher in monozygotic than dizygotic twins [2]. These findings pro-

pose that genetic factors contribute to the pathogenesis of PD with an estimated heritability of 30–40% [3], whereas a recent meta-analysis suggests a higher heritability of 48% [4].

Studies on candidate genes for association have been selected on the basis of the molecular therapeutic drugs and panic-provoking agents [5]. For instance, the response shown by panic patients when treated with Serotonin Selective Reuptake Inhibitors (SSRIs) and the worsening when using a serotonergic agonist suggest a possible serotonergic dysfunction in this disorder [2,6].

The serotonergic transporter gene (5-HTT) is located in chromosome 17q11.1-q12 [7] and it codes for a membrane protein that reuptakes serotonin from the synaptic cleft. A size repetition polymorphism has been related to functionality of the serotonergic transporter protein. The polymorphism is a 44 bp insertion or deletion on the promoter gene region (5-HTTLPR) resulting in two alleles (*l-long* and *s-short*). The *l* allele transcription is two or three times more efficient than the *s* allele [8,9]. The *s* allele is less active, therefore, resulting in lower serotonin reuptake and, consequently, in increased serotonin in the synaptic cleft [10].

Previous studies found a significant association between *s* allele and anxiety traits in healthy volunteers [11]. Regarding PD, studies have systematically failed to find any association between this disorder and 5-HTTLPR. This lack of association could be related to the small sample size of studies. However, a recent study has raised the possibility that the *l* allele could be involved in panic disorder [12].

Although the controversies between 5-HTTLPR in PD may be related to methodological differences between studies, such as ethnicity, another limitation is lack of statistical power [13]. According to Hirschhorn et al. [14], out of 166 studies on gene-disease associations, only six replicated previous findings. Possible causes for this inconsistency include studies with small sample sizes [15,16], as the most realistic genetic association between a polymorphic locus and a disease has been claimed to yield an odds ratio between 1.1 and 1.5 [17]. Thus at least 1000 subjects should be required to detect this association, depending on the prevalence of polymorphism. However, studies typically report sample sizes from 100 to 300 and rarely above 1000 subjects [16,18], justifying the use of meta-analysis to increase power.

The aim of this study is to attempt to answer whether there is an association between the 5-HTTLPR and PD. As the *s* allele of 5-HTTLPR is significantly involved in anxiety traits, the assumption is that this polymorphism should be involved in PD.

Methods

The search

- Electronic databases: studies were identified through PubMed (which encompasses Medline, Premedline, and HealthSTAR), PsychINFO, Lilacs and ISI. The PubMed search was run using the Mesh terms: ("Serotonin Plasma Membrane Transport Proteins" [MeSH] OR "5-HTTLPR" OR "5-HTT" OR "SLC6A4") AND "Panic Disorder" [MeSH]. In PsychINFO, Lilacs and ISI the following words were used: "Panic" AND ("serotonin transporter" OR "serotonergic transporter" OR "5-HTT" OR "5-HTTLPR" OR "SLC6A4"). This search strategy was run in June and rerun in April 2007, and included only human studies, with no language restrictions, and a time scope from January 1996 to April 2007, i.e. since the 5-HTTLPR was described by Heils [9] in 1996.

- Reference cross-checking: the list of references of included studies was searched looking for additional studies.

Contact with authors: efforts were made to contact all research groups of studies included in the analysis to identify unpublished data. Three authors replied and no additional study was identified.

Inclusion/Exclusion criteria

Studies reporting the 5-HTTLPR in PD patients of any ethnic origin were evaluated by the authors. The inclusion criteria for this systematic review were: (1) type of studies: case-control and family-based studies; (2) type of participants: diagnoses of PD according to standard diagnostic criteria (DSM or ICD); (3) Hardy-Weinberg Equilibrium (HWE). Testing for HWE is commonly used for quality control of large-scale genotyping and is one of the few ways to identify systematic genotyping errors in unrelated individuals [19], and its assumption is required for the allele analysis [20].

Exclusion criteria included (1) studies in which the main disorders were other than PD; (2) replicated data (a part of sample used for more than one publication); (3) insufficient data to perform statistical analysis (unable even after contacting authors). Regarding replicated data, the included study was selected based on the sample size and the availability of information studied in this meta-analysis. Family studies were not included in the analyses because there is only one study published [21], so no analysis could be performed.

This meta-analysis methodology was performed according to MOOSE (*Meta-analysis of Observational Studies in Epidemiology*) group guidelines [22] and stages of this methodology are presented in a flowchart here in (Figure 1).

Stage I	<p>Planning the Review</p> <p>Research question Identification of the need for a review</p>	<p>Blaya C, Salum GA, Lima M3, Segal SL and Manfro GG</p> <p>Is there an association between the 5-HTTLPR and panic disorder? Several studies with incongruent results and lack of power to detect small effects of this polymorphism determine the need for a supportive theoretical construct.</p>																								
Stage II	<p>Conducting a Review</p> <p>Identification of research</p> <p>Study quality assessments and study inclusion / exclusion criteria</p> <p>Selection of studies</p>	<p>Studies were identified through PubMed, PsychInfo, Litacs and ISI. The PubMed search was run using the Mesh terms: ("Serotonin Plasma Membrane Transport Proteins"[MeSH] OR "5-HTTLPR" OR "5-HTT" OR "SLC6A4") AND "Panic Disorder"[MeSH]. In PsychINFO, Litacs and ISI the following words were used: "panic" AND "serotonin transporter" OR "serotonergic transporter" OR "5-HTT" OR "5-HTTLPR" OR "SLC6A4". Check reference section of publications found through our search was used to identify additional studies that may have been missed. Contact was tried with all authors in order to identify unpublished data.</p> <p>Quality assessment criteria</p> <ul style="list-style-type: none"> • Panic Disorder diagnosis (DSM or ICD); • Case-control or family-based studies; • Hardy-Weinberg Equilibrium (HWE). <p>Exclusion criteria</p> <ul style="list-style-type: none"> • All patients with major psychiatric disorders other than PD; • Replicated data; • Insufficient data to perform statistical analysis. <p>Studies were selected by two authors (CB and GAB) independently. Discrepancies were resolved by mutual consent and a third opinion (GGM). Exclusion reasons can be seen below the flowchart.</p> <table border="1"> <thead> <tr> <th>Included Studies</th> <th>Excluded Studies</th> </tr> </thead> <tbody> <tr> <td>Deckert et al. (German) [34]; Deckert et al. (Italian) [34]; Ishiguro et al. [35]; Maron et al. [12]; Martinez-Barondo et al. [40]; Matsushita et al. [36]; Onara et al. [37]; Olesen et al. [39]; Samochowicz et al. [38]; Hamilton et al. [21]; Kim et al. [41].</td> <td>Hajduk [31][†]; Maron et al. [28][†]; Maron et al. [29][†]; Perez et al. [32][†]; Pena et al. [26][†]; Rotondo et al. [25][†]; Rotondo et al. [33][†]; Sand et al. [30][†].</td> </tr> </tbody> </table>	Included Studies	Excluded Studies	Deckert et al. (German) [34]; Deckert et al. (Italian) [34]; Ishiguro et al. [35]; Maron et al. [12]; Martinez-Barondo et al. [40]; Matsushita et al. [36]; Onara et al. [37]; Olesen et al. [39]; Samochowicz et al. [38]; Hamilton et al. [21]; Kim et al. [41].	Hajduk [31] [†] ; Maron et al. [28] [†] ; Maron et al. [29] [†] ; Perez et al. [32] [†] ; Pena et al. [26] [†] ; Rotondo et al. [25] [†] ; Rotondo et al. [33] [†] ; Sand et al. [30] [†] .																				
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Stage III	<p>Reporting and Dissemination</p> <p>The report</p> <p>Analysis</p> <p>Allele analysis (s vs. l)</p> <p>Stratified analysis (s vs. l)</p> <p>High Quality</p> <p>Caucasian</p> <p>Agoraphobia comorbidity</p> <p>Recommendations for further investigation</p> <p>Getting evidence into practice</p>	<table border="1"> <thead> <tr> <th></th> <th>OR (CI95%)</th> <th>p-value (z)</th> <th>Heterogeneity Q test (p-value; I²)</th> </tr> </thead> <tbody> <tr> <td>Allele analysis (s vs. l)</td> <td>0.51 (0.20-1.03)</td> <td>0.14 (1.47)</td> <td>X²_(df=1)=5.75 (0.37; 7.7%)</td> </tr> <tr> <td>Stratified analysis (s vs. l)</td> <td></td> <td></td> <td></td> </tr> <tr> <td>High Quality</td> <td>0.88 (0.75 to 1.04)</td> <td>0.13 (1.52)</td> <td>X²_(df=1)=5.51 (0.16; 38.6%)</td> </tr> <tr> <td>Caucasian</td> <td>0.86 (0.74 to 1.01)</td> <td>0.06 (1.88)</td> <td>X²_(df=1)=4.72 (0.45; 0%)</td> </tr> <tr> <td>Agoraphobia comorbidity</td> <td>0.94 (0.77 to 1.15)</td> <td>0.57 (0.57)</td> <td>X²_(df=1)=5.21 (0.16; 42.1%)</td> </tr> </tbody> </table> <p>1. Adopt a lifelong perspective of PD; 2. Appropriate analysis of HWE; 3. Larger samples to detect the expected small effect of this polymorphism; 4. An adequate control group with: (a) standardized psychiatric diagnoses (DSM or ICD), for example: assessing the lifelong absence of psychiatric disorders, (b) controls should be old enough in order to reduce the possibility for the late onset of the disorder; 5. An exploratory analysis of the clinical manifestation, considering the nuances of Panic Disorder (i.e., agoraphobia, phobic avoidance, panic attacks, etc.) and other ways to investigate the heritable portion of PD; 6. Special attention to comorbidities, considering the significant influence of this polymorphism in other psychiatric conditions; 7. The role evaluation of this polymorphism in other situations such as therapeutic responses; 8. Genotypes must be determined blinding to case-control status in order to minimize the risk of a result influenced by an investigator's preconceptions [13]; 9. Corrections for multiple comparisons (e.g., Bonferroni correction), in case of multiple diagnostic schemes, models of inheritance or multiple genes tests; 10. Caution on interpretation of results, considering the non-causal pathways, the alpha error and the prior probabilities.</p> <p>The role of 5-HTTLPR in PD still needs more adequate investigation.</p>		OR (CI95%)	p-value (z)	Heterogeneity Q test (p-value; I ²)	Allele analysis (s vs. l)	0.51 (0.20-1.03)	0.14 (1.47)	X ² _(df=1) =5.75 (0.37; 7.7%)	Stratified analysis (s vs. l)				High Quality	0.88 (0.75 to 1.04)	0.13 (1.52)	X ² _(df=1) =5.51 (0.16; 38.6%)	Caucasian	0.86 (0.74 to 1.01)	0.06 (1.88)	X ² _(df=1) =4.72 (0.45; 0%)	Agoraphobia comorbidity	0.94 (0.77 to 1.15)	0.57 (0.57)	X ² _(df=1) =5.21 (0.16; 42.1%)
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Based on CDR Report, NHS Centre for Reviews and Dissemination, University of York and Cochrane Handbook
Exclusion reasons: [†]Without control group; [‡]Replicated data; [§]All patients with major Psychiatric comorbidity other than PD; [¶]Hardy-Weinberg departure; ^{||}Insufficient data.

Figure 1
Flowchart – Stages of Systematic Review with Meta-analysis.

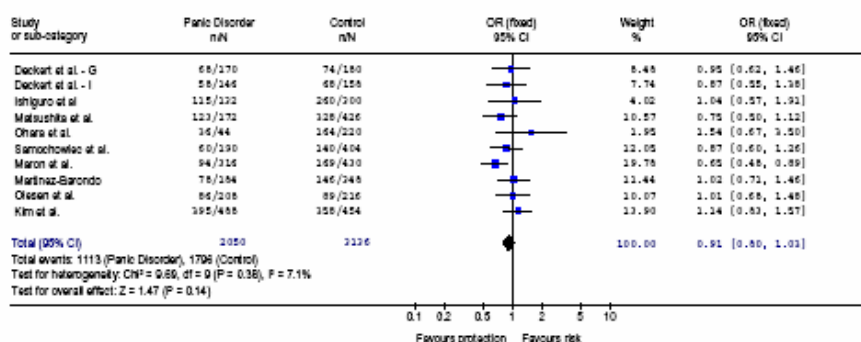


Figure 2
Forest plot with odds ratio of each study and pooled odds ratio for the association between the s allele and risk of Panic Disorder.

Data extraction

Data was independently extracted by two investigators (CB and GAS) using a standardized data extraction form. Discrepancies were resolved by discussion and if consensus was not achieved the decision was made by another reviewer (GGM). Data extracted included number of PD patients and controls for each of the three genotype groups (ll, ls, ss) in each eligible study. Only data regarding 5-HTTLPR and panic disorder were extracted regardless of other polymorphisms, disorders or outcomes reported in the studies. The male/female ratio, mean age, predominant ethnicity of the sample and psychiatric comorbidity were also extracted. Genotype frequencies were used to calculate whether they deviate significantly from HWE. In cases where data was not available in the published reports, authors were contacted directly. The information was classified as not reported when authors did not return to at least three contact trials or did not have this data available.

Statistical analysis

First, an analysis by alleles was performed because this analysis increases the power to detect differences and is the most used analysis in the current literature. Secondly, we analyze the most used model of inheritance (s dominant) to express directly the ll genotype risk [16]. In order to investigate interaction or confusion between studies, a stratified analysis was run after separating studies by ethnicity, quality of control groups and comorbidity with Agoraphobia, as recommended by Munafò and Flint [15].

It was considered as high quality control groups those with appropriate assessment diagnoses. As we performed fourteen different analyses sets of the same genetic data we also present correct p-values according to Finner's modification of the Bonferroni's procedure for multiple comparisons. Despite being an important analysis, we could not perform a stratified analysis for comorbidity with mood disorders and another anxiety disorders because this data was poorly described in studies included in this meta-analysis. We choose to perform an exploratory analysis because the heritable portion of PD that could be related to this polymorphism is not yet defined.

Asymptotic DerSimonian and Laird's Q test was used to assess heterogeneity. Because tests of heterogeneity may be underpowered to detect heterogeneity between studies when the number of studies is small [23], we also explore heterogeneity quantitatively using the I² statistic [24].

The results of individual studies, as well as the pooled odds ratio (OR), were synthesized by the fixed effect model with 95% confidence intervals. The significance of the pooled OR was determined by the z test. Publication bias was assessed with a funnel plot (allele analyses). The analyses were done with Review Manager 4.2.8, software developed by the Cochrane Collaboration. The Power Calculator for Genetic Studies software was used in order to estimate the minimum OR that could be detected in this meta-analysis.

Results

In total, 19 potential publications were identified, and 10 studies were included in this meta-analysis. No analysis was performed with family-based studies because only one was found in our search [21]. One study was excluded because all patients had Bipolar Disorder [25], three studies were excluded because there were no control groups [26-28], three studies were excluded because data were replicated [29-31], one study was excluded due to significant deviation of Hardy-Weinberg equilibrium [32] and one study [33] was excluded due to insufficient data. As one study [34] had two different sub samples clinically assessed with different methodologies, it was considered as two separate studies (Deckert German and Deckert Italian), resulting in ten studies included in our analysis (figure 1). The funnel plot suggests a couple of missing studies with OR higher than 1, but the small number of included trials does not allow drawing conclusions about publication bias.

Across all 10 case-control studies investigating 5-HTTLPR and panic disorder [12,34-41], a total of 1,025 patients and 1,568 controls were included, totaling 2,050 alleles among patients and 3,136 alleles between controls. Table 1 depicts data extracted from the included studies. Regarding the allele and stratified analyses, no evidence of heterogeneity was found. The statistics of heterogeneity Q test and I² are shown in the figure 2. We found very similar results between the OR calculated by the random-effects model and Peto OR.

In the first analysis, including 5,186 alleles, we compared the 5-HTTLPR allelic distribution between patients with PD and controls of all ten studies included. The pooled OR = 0.91 was not significant (CI95% 0.80 to 1.03; z = 1.47; p = 0.14). The results of this analysis are shown in the forest plot (figure 2). Regarding family studies, we only identified one in this search [21]. The study had evaluated 340 individuals in 45 families with at least three affected people. No linkage between the 5-HTTLPR and PD was observed (p = 0.40).

As the included studies have subjects with different ethnicity and control groups with different quality, we performed stratified analyses. Only five studies - Maron et al. [12], Deckert Italian [34], Samochowiec et al. [38], Olesen et al. [39] and Kim et al. [41] - were classified as having high quality controls. Results showed no significant association between the s allele and PD in both analyses (high and low quality). Regarding the ethnic stratified analysis, no significant association was found in Caucasian or Asian separated analyses. Some studies evaluated the comorbidity with Agoraphobia in their exploratory analysis [12,35,38,41] and no significant association was found

in this stratified analysis. Table 2 depicts all these stratified analyses for the allelic analysis and genotype analysis.

We estimated the minimum OR that could be detected in this meta-analysis by allelic analysis. Considering a power of 90%, a PD prevalence of 1.8% in Caucasoid [42], a mean frequency of s allele of 0.45 in a joint analysis with the Power Calculator for genetic studies, the minimum OR that we are capable to found is 1.14.

Discussion

This is the first systematic review between the 5-HTTLPR and PD and no statistically significant association was found. In the overall analysis, there was no evidence for heterogeneity among the studies. This indicates no greater variation among the studies than could be expected by chance and provides the validity to the meta-analysis by suggesting that studies included in this analysis are comparable. However, no association was found between this polymorphism and PD even in all stratified analyses.

The main problem in genetic studies and psychiatric disorders is probably the lack of a phenotype definition. Clinical diagnoses according to DSM-IV may be heterogeneous constructs that combine elements with distinct genetic influences [43]. Additionally, psychiatric disorders usually overlap, and comorbidity might be a bias that impairs some associations. Therefore, some authors are interested in defining 'intermediate' phenotypes that might have more direct expression of genes influencing a complex disorder and may have a simpler genetic architecture [43].

Also, a recently detected genetic variation (16A allele) [44] in the long allele of 5-HTTLPR has been linked to a lower expression of the serotonin transporter [45,46]. No study has evaluated this polymorphism neither in panic disorder nor in anxiety traits. Hence, studies should combine the evaluation of different polymorphisms that influence the protein expression.

Limitations of this study

The publication bias could not be adequately assessed in our meta-analysis by the funnel plot due to the small number of studies available. However, we believe that our search strategy was comprehensive enough. Moreover, additional sources of trials like contacting authors of included trials yield no additional study.

The sample size found in our meta-analysis is below that which is required to identify associations with minor effects [17]. In the sub-group analysis the sample size became even smaller. Thus, further investigation using larger sample sizes, in which the control group is properly diagnosed and ethnicity is evaluated, is needed. Such

Table 1: Included Case-control Studies of 5-HTTLPR and Panic Disorder

Studies	Groups (n)	Male (%)	Diagnosis	Comorbidity	Mean Age	Origin	Genotype Frequency/ Total (%)			Allele frequency/ Total (%)		HWE reported (df = 1)		
							ss	sl	ll	s	l	X ²	p	
Ishiguro et al. [35]	Panic (66)	30 (45.5)	DSM-IV	NR	40	Japanese	51/66 (77.3)	13/66 (19.7)	2/66 (3)	115/132 (87.1)	17/132 (12.9)	YES	0.986	0.321
	Control (150)	70 (46.7)	Not reported		41		114/150 (76)	32/150 (21.3)	4/150 (2.7)	260/300 (86.7)	40/300 (13.3)	YES	0.887	0.346
Matsuhita et al. [36]	Panic (86)	54 (62.7)	DSM-III-R	NR	37.0	Japanese	44/86 (51.2)	35/86 (40.7)	7/86 (8.1)	123/172 (71.5)	49/172 (28.5)	YES	<0.001	0.992
	Control (213)	96 (45.1)	Not reported		37.7		125/213 (58.7)	78/213 (36.6)	10/213 (4.7)	328/426 (77)	98/426 (23)	YES	0.242	0.623
Dedert et al. German [34]	Panic (85)	NR	DSM-III-R and CIDI	Yes (Mood); Anorexia; NR	NR	German	12/66 (14.1)	44/66 (51.8)	29/66 (34.1)	68/170 (40)	102/170 (60)	NO	0.523	0.470
	Control (90)	NR	None		NR		16/90 (17.8)	42/90 (46.7)	32/90 (35.6)	74/180 (41.1)	106/180 (58.9)	YES	0.118	0.731
Dedert et al. Italian [34]	Panic (73)	NR	DSM-III-R and SADS-LA	Mood absent; Anorexia; NR	NR	Italian	13/73 (17.8)	32/73 (43.8)	28/73 (38.4)	58/146 (39.7)	88/146 (60.3)	NO	0.523	0.470
	Control (79)	NR	DSM-III-R and DIS†		NR		12/79 (15.2)	44/79 (55.7)	23/79 (29.1)	68/158 (43)	90/158 (57)	YES	1.460	0.227
Ohara et al. [37]	Panic (22)	11 (50)	DSM-IV	Yes (Anorexia)	35.1	Japanese	14/22 (63.6)	8/22 (36.4)	0/22 (0)	36/44 (81.8)	8/44 (18.2)	NO	1.086	0.769
	Control (110)	NR	Not reported		NR		62/110 (56.4)	40/110 (36.4)	8/110 (7.3)	164/220 (74.5)	56/220 (25.5)	NO	0.192	0.661
Samochowicz et al. [38]	Panic (95)	24 (23.8)	CIDI	Yes (Anorexia)	38.7	Polonaise	10/95 (10.5)	40/95 (42.1)	45/95 (47.4)	60/190 (31.6)	130/190 (68.4)	NO	0.062	0.803
	Control (202)	54 (26.7)	KD-10		35.9		22/202 (10.9)	96/202 (47.5)	84/202 (41.6)	140/404 (34.7)	264/404 (65.3)	NO	0.492	0.483
Maron et al. [12]	Panic (158)	32 (20.2)	DSM-IV MINI	Yes (Anorexia and Mood)	38.0	Estonian	11/158 (7)	72/158 (45.6)	75/158 (47.5)	94/316 (29.7)	222/316 (70.3)	YES	1.288	0.256
	Control (215)	56 (26)	MINI†		39.8		34/215 (15.8)	101/215 (47)	80/215 (37.2)	169/430 (39.3)	261/430 (60.7)	YES	0.051	0.822
Olesen et al. [39]	Panic (104)	28 (26.9)	DSM-IV	Yes (Anorexia)	NR	Danish	15/104 (14.4)	56/104 (53.8)	33/104 (31.7)	86/208 (41.3)	122/208 (58.7)	NO	1.263	0.261
	Control (108)	30 (27.7)	Clinical interview		NR		18/108 (16.7)	53/108 (49.1)	37/108 (34.3)	89/216 (41.2)	127/216 (58.8)	NO	0.018	0.894

Table 1: Included Case-control Studies of 5-HTTLPR and Panic Disorder (Continued)

Martín e- Barond o et al. [40]	Panic (92)	28 (30.4)	DSM- IV	NR	35.8	Spanish	18/92 (19.6)	42/92 (45.7)	32/92 (34.8)	78/184 (42.4)	106/ 184 (57.6)	NO	0.392	0.531
	Control (174)	67 (38.5)	Not report ed		38.4		36/174 (20.7)	74/174 (42.5)	64/174 (36.8)	146/ 348 (42)	202/ 348 (58)	NO	2.798	0.094
Kim et al. [41]	Panic (244)	143 (58.6)	DSM- IV	Yes (Mood)	36.1	Korean	15/ 244 (6.2)	77/244 (31.6)	8/244 (3.3)	395/ 488 (80.9)	93/488 (19.1)	YES	0.1278	0.721
	Control (227)	102 (44.9)	Clinical Intervi ew		33.1		14/ 227 (6.2)	76/227 (33.5)	10/227 (4.4)	358/ 454 (78.9)	96/454 (21.1)	YES	0.0035	0.953

Note: NR, Not reported; HWE, Hardy Weinberg Equilibrium; DSM-IV, Diagnostic and Statistical Manual of Mental Disorders IV; ICD-10, International Classification of Diseases; CIDI, Composite International Diagnostic Interview; MINI, MINI International Neuropsychiatric Interview. 1 Controls with first degree relatives without psychiatric disorders.

studies should focus on exploratory analyses in order to identify the heritable features that might be related to this polymorphism. Additionally, we could not perform a subgroup analysis divided by gender, because only one study reported this data. Neither did we find any stratified analyses regarding co-morbidity (with alcohol, mood and anxiety disorders), even though associations between the 5-HTTLPR and these psychiatric disorders have been reported [30,47,48].

This meta-analysis was carried out with case-control studies. However, some authors [13] suggest that the results from this design finding a positive association between the genome and a disorder could be false. Additionally, a positive result from a case-control study might be due to population stratification rather than linkage disequilibrium [49] affected by the different disease prevalence and different marker frequencies in the subpopulation thereby producing spurious associations [50,51]. The use of Genomic Control, although with limitations [52], may be an alternative in analyzing data of case-control studies. Unfortunately, we could not perform an additional analysis with family studies because we identified only one study with this design. Family-based studies have a unique design in which population stratification is controlled.

Conclusion

In summary, results from this systematic review do not support the hypothesis of a significant association between 5-HTTLPR and PD. All the sub-analyses performed failed to find an association between PD and this polymorphism. However, more studies are needed in different ethnic populations in order to evaluate a possible minor effect. Finally, the 5-HTTLPR does not seem to play a major role in the genetics of panic disorder and, therefore, other polymorphisms should be investigated.

Abbreviations

PD, Panic Disorder

SSRIs, Serotonin Selective Reuptake Inhibitors

5-HTTLPR, Serotonin Transporter Promoter Polymorphism

DSM, Diagnostic and Statistical Manual

ICD, International Classification of Diseases

CIDI, Composite International Diagnostic Interview

MINI, MINI International Neuropsychiatric Interview.

5-HTT, Serotonergic transporter gene

SLC6A4, Solute Carrier Family 6 (Neurotransmitter transporter serotonin), member 4

HWE, Hardy-Weinberg Equilibrium

MOOSE, Meta-analysis of Observational Studies in Epidemiology

OR, Odds ratio

CI95%, Confident Interval of 95%

Competing interests

Maurício S. Lima is medical director of Eli Lilly do Brazil.

Carolina Blaya and Gisele G. Manfro are speakers of Eli Lilly Brazil.

Giovanni A. Salum and Sandra Leistner-Segal have no competing interests.

Table 2: Results of the overall studies and sub-group studies stratified by ethnicity, quality of control group and comorbidity with Agoraphobia

	n ^a	OR (95% CI)	Significance		Heterogeneity			
			Z	p-value	Finner's p	χ^2 ^c	p-value	I ²
Allelic analyses (s/ l)^b	10	0.91 (0.80–1.03)	1.47	0.14	0.58	9.75	0.37	7.7%
Ethnicity								
Caucasians	6	0.86 (0.74–1.01)	1.88	0.06	0.58	4.72	0.45	0%
Asians	4	1.02 (0.81–1.27)	0.14	0.89	0.92	3.67	0.30	18.3%
Quality of Control Group								
High quality control group	5	0.88 (0.75–1.04)	1.52	0.13	0.58	6.51	0.16	38.6%
Low quality control group	5	0.96 (0.78–1.17)	0.43	0.67	0.76	2.87	0.58	0%
Agoraphobia comorbidity								
With Agoraphobia	4	0.94 (0.77–1.15)	0.57	0.57	0.69	5.21	0.16	42.4%
Without Agoraphobia	3	0.80 (0.60–1.08)	1.48	0.14	0.58	2.30	0.32	12.9%
Genotype (s+s) vs. ll	10	0.87 (0.71–1.06)	1.39	0.17	0.58	7	0.64	0%
Ethnicity								
Caucasians	6	0.85 (0.68–1.05)	1.48	0.14	0.58	4.36	0.50	0%
Asians	4	1.01 (0.55–1.86)	0.03	0.98	0.98	2.56	0.46	0%
Quality of Control Group								
High quality control group	5	0.80 (0.63–1.03)	1.76	0.08	0.58	3.72	0.45	0%
Low quality control group	5	1.02 (0.71–1.46)	0.11	0.91	0.93	2.30	0.68	0%
Agoraphobia comorbidity								
With Agoraphobia	4	0.80 (0.57–1.11)	1.32	0.19	0.58	2.90	0.41	0%
Without Agoraphobia	3	0.85 (0.51–1.40)	0.65	0.51	0.67	1.18	0.55	0%

Abbreviations: OR, odds ratio (fixed effect); Q, Cochran's χ^2 -based Q statistic test used to assess the heterogeneity; z test used to determine the significance of the overall OR; I², inconsistency; Finner's p-value, adjusted p-value for multiple comparison

^aThe number of studies included are indicated

^bThe first allele is the risk allele

^cDegrees of freedom = number of studies - 1.

Authors' contributions

CB conceived of the study, extracted the data, participated in the design and drafted the manuscript. GAS extracted the data, participated in the design, drafted the manuscript and performed the statistical analysis. MSL helped in the statistical analysis and helped to draft the manuscript. SLS helped to draft the manuscript. GGM, participated in its design, coordination and drafted the manuscript. All authors read and approved the final manuscript.

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Artigo 2 – *Panic disorder and serotonergic genes (5-HTTLPR, HTR1A and HTR2A): association and interaction with childhood trauma and parental bonding*

Carolina Blaya¹, Giovanni Abrahão Salum¹, Priya Moorjan², Ana Carolina Seganfredo¹, Elizeth Heldt¹, Sandra Leistner-Segal¹, Jordan Smoller², Gisele Gus Manfro^{1}*

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Abstract

Background – Panic disorder (PD) has been related to both genetic and environmental risk factors. However, no study has evaluated a gene-environment interaction for this disorder. The aim of this study is to evaluate the association between *HTR1A*, *HTR2A* and 5-HTTLPR in PD patients and controls. We also evaluated the interaction between these genes and two environmental factors previously associated with PD: childhood trauma and parental bonding.

Methods - This is a case-control candidate gene study (107 PD patients and 125 controls). Diagnoses were confirmed by M.I.N.I and clinical interview. Childhood trauma was evaluated by the Childhood Trauma Questionnaire (CTQ) and Parental Bonding Instrument (PBI) was used to evaluate parenting. Genes were screened using a set-based test in PLINK followed by single marker association tests and haplotype test for genes that reached experiment-wide significance. Logistic regression was used to model the relationships between genotype in the dominant model and trauma, optimal father parenting and optimal mother parenting, independently in order to evaluate gene-environment interaction. We addressed multiple comparisons at two levels of significance correction: gene-wide (p_1) and experiment-wide (p_2).

Results – Only *HTR1A* was experiment-wide associated with PD in set-based test ($p_2=0.027$). Three SNPs of this gene were nominally significantly associated with PD, but only one (rs6449693) remained significant after correction for multiple testing. Additionally, one *HTR1A* haplotype was associated with PD ($p=0.008$), and another haplotype was protective ($p=0.004$). In the interaction analysis with optimal

father parenting, both interaction terms of SNPs of HTR2A (rs6311 and rs6313) were nominally associated with PD and rs6311 remained significant after Bonferroni correction. Among subjects with TT/TC genotype in rs6311 the protection effect of fathers with high care and low overprotection was higher than the protection effect among subjects with CC genotype ($\beta=0.134$, $t=-2.678$, $p=0.007$).

Conclusion – PD was associated with HTR1A, but not with 5-HTTLPR even considering interaction with childhood trauma. We also reinforce evidence of gene-environment interaction in HTR2A gene with parenting, maybe influencing the capacity of subjects to use familiar experiences as environmental support.

Introduction

Twin studies have established that genes contribute to panic disorder (PD), (1), but efforts to identify the specific genes involved have had mixed results (2, 3). Among the most widely studied candidate genes have been those involved in serotonergic neurotransmission (4), reflecting evidence of serotonergic dysfunction in PD and the fact that medications modulating the serotonin system are first-line treatments (5). The serotonin transporter (*5-HTTLPR*), serotonin receptor 1A (*HTR1A*) and serotonin receptor 2A (*HTR2A*) polymorphisms have been associated with PD in some studies (4, 6-8) but not in others (6, 9, 10). In addition, previous studies of the *5-HTTLPR* polymorphism have not examined a recently described functional SNP within the insertion/deletion polymorphism (11).

On the other hand, environmental risk factors such as childhood experiences have been systematically associated with psychopathology (1, 12-14). For instance, childhood sexual abuse elevates the risk for adult generalized anxiety disorder and panic disorder, as well as other psychiatric and substance use disorders (12, 13). Some authors also suggest that relationship with the primary caregiver is related to psychopathology (15-17). Studies have reported that PD is associated with parental lower care and higher overprotection scores than healthy control (17-21).

Although childhood experiences seem to be strongly associated with PD, not all people who had childhood trauma develop PD in adulthood. Diathesis-stress theories of depression and anxiety suggest that individuals' sensitivity to stressful events depends on their genetic makeup (22-26). Besides this, heritability

estimated for anxiety symptoms were larger among individuals who had reported stressor life events as compared to those without stressors, suggesting environmental moderation of genetic effects (27). Association studies attempt to identify both environmental and genetic risk factors as well as their interaction to test if a specific genotype moderates the exposure to an environmental factor (28). Serotonergic genes have been implicated in a gene-environment interaction for depression (22, 29) and for anxiety (30). However no study have accounted for gene-environment interactions in PD.

The aim of this study is to evaluate the association between *HTR1A*, *HTR2A* and *5-HTTLPR* in PD patients and controls. In addition, we evaluated the interaction between these genes and two environmental factors previously associated with PD: childhood trauma and parental bonding.

Methods

This is a case-control candidate-gene study where PD patients were recruited from the Anxiety Disorder Outpatient Clinic at the Hospital de Clínicas de Porto Alegre. Controls were employees from HCPA that were recruited between June 2006 and April 2007. The inclusion criteria were as follows: (1) PD with or without agoraphobia for patients and absence of psychiatric disorder for controls; (2) at least eighteen years old; (3) European-Brazilian ethnicity. Patients with comorbidities common to PD were included in the study provided that the symptoms were not clinically more relevant than the PD symptoms. Blood was collected from participants for DNA extraction after written informed consent.

Institutional review board approval was obtained from the ethics committee of the Hospital de Clínicas de Porto Alegre (Number 04-272).

Psychometric testing

Subjects were evaluated by a clinical interview and the Mini International Neuropsychiatry Interview (MINI) - Brazilian version (31). A semi-structured interview was used to assess sociodemographic data and clinical history.

Childhood trauma was evaluated by the Childhood Trauma Questionnaire (CTQ) – Brazilian version (32), which evaluates five subscales: childhood emotional, physical and sexual abuse and childhood physical and emotional neglect. CTQ is a self-report questionnaire with 28 items with Likert-type questions (one to five points). Each subscale score ranges from 5 to 25, with higher scores indicative of greater maltreatment. A total score (ranging from 25 to 125) was calculated by summing the values obtained on the five subscales. Previous studies indicates that CTQ remained stable after 6-months of therapy for child abuse or neglect, and subscales demonstrated good internal consistency and convergent validity with trauma-specific measures of distress and therapist rating of abuse (33, 34). Dill et al (35) showed that self-report instruments to evaluate childhood trauma are more likely to elicit truthful responses than clinical interviews. Since all subscales were associated with PD (Mann-Whitney U, $p < 0.01$) and were intercorrelated ($r > 0.4$), CTQ was only assessed as the global index to avoid multiple comparison (36).

Parenting was assessed by the Parental Bonding Inventory (PBI) – Brazilian Version (37). The original PBI (38) was intended to measure the perceived parental

rearing styles of overprotection and warmth as remembered by the respondents during their first 16 years of life. It consists of 25 items to be assessed separately for mother and father. In a number of studies the PBI proved to be a reliable and valid measure of actual and not merely perceived parenting (39-42). The long-term stability of the PBI has been demonstrated by Wilhelm et al. (43) in a 20-year cohort study. Recently some studies have used confirmatory factor analyses to show the pre-eminence of three-factor models of the PBI with the additional dimension of authoritarianism (44-46). In a previous study we were able to confirm the three factor structure in the Brazilian sample (unpublished data). Both low warmth and high overprotection were associated with PD (Mann-Whitney U, $p < 0.01$), but no association was found with authoritarianism in neither father nor mother scales. In order to avoid multiple comparisons, we generated a combined variable for father and mother scales, respectively, creating an ideally parenting subtype named “optimal father” and “optimal mother” characterized by high warmth and low overprotection scores.

Genotyping

A total amount of 1µg of genomic DNA (diluted in 1X TE buffer at 50ng/µl) from studied subjects was equally interleaved on 96-well master plates to ensure technical uniformity during the laboratory process. DNA quality control metrics were assessed prior to genotyping. Quantity of stranded DNA was assessed using PicoGreen® (Molecular Probes, Oregon, USA).

Genotyping of HTR1A and HTR2A was performed with the methods previously described with a few modifications (47). Primers were designed with SpectroDESIGNER software (Sequenom, San Diego, California). Polymerase chain reaction (PCR) was performed, followed by single base extension (SBE) reaction. Samples were analyzed in automated mode by a MassARRAY RT mass spectrometer (Sequenom) (48). The resulting spectra were analyzed by SPECTROTYPED software (Sequenom) after baseline correction and peak identification.

Genotyping was performed for HapMap single nucleotide polymorphisms (SNPs) selected within each gene and 10kb flanking region. For *5-HTTLPR* we examined functional polymorphism including the embedded SNP (rs25531). The Tagger program (49) (<http://www.broad.mit.edu/mpg/tagger/>) was used to identify tag SNPs with a minor allele frequency of greater than 5% and minimum r^2 of 0.8. A total of 9 markers were thus selected for genotyping using mass spectrometry as previously described (50).

Genotyping of the *5-HTTLPR* was performed with the following protocol - Genomic DNA (1.4 ng) was amplified in a 7 μ l reaction using KlenTaq DNA Polymerase (0.2 U), the proprietary KlenTaq Buffer (1X), dNTPs (200 μ M each), 5% glycerol, Betaine (1 M) and the marker specific primers (0.2 μ M). Amplification was performed with thirteen cycles of denaturation for 30 seconds at 93°C, annealing for 30 seconds beginning at 61.5°C and dropped 0.5° C every cycle and primer extension at 72°C for 30 second, followed by 37 cycles of denaturation for 30 seconds at 93°C, annealing for 30 seconds at 55° C and primer extension at

72°C for 30; 72°C for 1 hour. The amplified product (1µl) was combined with size standard (LIZ-250) before being analyzed on an ABI-3730. The long allele appears as a product of about 412 while the short allele shows a band at about 370. The genotype of the SNP embedded in the 5-HTTLPR (51) (rs25531) was assayed by digesting the PCR product with the restriction enzyme, *MspI* (11). This 10 µl reaction contains 2 µl of the PCR product, 1 µl of 10X restriction buffer (New England Biolabs), 1 µl of *MspI* enzyme and 6 µl of water. The reaction was incubated at 37°C for 1 hour. The digested product (1µl) was then combined with size standard (LIZ-250) before being analyzed on an ABI-3730. Post-digestion, the long allele with the A SNP allele appears as a product of about 320, the G SNP allele is indicated by the presence of a band at 148, while the short allele shows a band at about 277. The final genotype was determined from the information from the analysis of both the digested and undigested PCR product.

Markers were retained only if they met the following quality control criteria: (1) >90% genotype call rate; (2) minor allele frequency (MAF) >5%; (3) Hardy Weinberg equilibrium $P > 0.001$. Three duplicates were assessed in the experiment with 100% concordance. After applying these quality control filters, 8 markers were retained for the association analysis. Four individuals with genotyping call rates less than 90% were excluded resulting in 232 subjects included in the analysis.

Statistical Analysis

PBI and CTQ Scales

Normal distribution and sphericity were assessed previously to any statistical analysis with Kolmogorov-Smirnov test and Levene's test. Since the majority of CTQ and PBI scales are not normally distributed, the CTQ and PBI scores were dichotomized using ROC curves to maximize the accuracy of the cut-off to predict presence of PD in adulthood for risk factors, or predict absence of PD in adulthood for protection factors. The Youden's index J was used to define the optimal cut-point for the continuous variables and Area Under the Curve (AUC) was used to test significance. The best cut-points for CTQ Global Score was ≥ 41 (AUC=0.695; $p < 0.001$). The best cut-points for PBI scales were: ≥ 6 for mother overprotection (AUC=0.621; $p = 0.002$) and ≥ 4 for father overprotection (AUC=0.631; $p = 0.001$) - defined in risk factors direction; and ≥ 16 for mother warmth (AUC=0.615; $p = 0.003$) and ≥ 13 for father warmth (AUC=0.600; $p = 0.001$) - defined in protection direction.

Genetic analysis plan

A. Association

For an initial analysis, we screened each gene using the set-based test in PLINK (52) (<http://pngu.mgh.harvard.edu/purcell/plink/>) followed by single marker association for genes that reached experiment-wide significance. The set-based test is based on calculating the average test statistic for the best three SNPs per gene region, and evaluating the significance of these set-statistics by permutation (10,000). Haplotype analysis was performed for genes that reached the experiment-wide significance. The initial haplotype test is an omnibus test for any joint effect of all haplotypes observed (minor allele frequencies [MAF] $< .01$).

Where the omnibus test was significant, we performed haplotype-specific tests of each haplotype versus all others.

B. Interaction

Logistic regression techniques in Plink were used to model the relationships between genotype in the dominant model and trauma, optimal father parenting and optimal mother parenting, independently. Each model included: the SNP, one of the three environmental factors and their interaction term (SNP*environment).

C. Level of significance and corrections for multiple testing

The overall level of significance adopted was $\alpha=0.05$. Nominal p-values (uncorrected) were named p_0 . We addressed multiple comparisons at two levels of significance correction: gene-wide and experiment-wide. Gene-wide significant accounts for the SNPs within the gene, (named p_1) whereas experiment-wide (named p_2), the more restrict one, accounts for all the SNPs evaluated. For single marker association, permutation was used to correct for multiple testing yielding both gene-wise (p_1) and experiment-wise (p_2) p values. Haplotype analysis was corrected for multiple testing using a Bonferroni correction for the number of haplotypes. The interaction analysis was corrected with Bonferroni's correction accounting for the three environment covariates evaluated. Only the dominant model was evaluated for the interaction analysis. All tests were two-tailed.

Results

The sample comprised 107 patients (76.6% woman, mean age 39.94, SD 10.17 years) and 125 controls (70.4% woman, mean age 36.93, SD 9.78 years).

The mean age of PD onset was 32 (SD=10.38) years, and mean of PD duration of 7.94 year (SD=8.45). PD comorbidities included agoraphobia (89.7%), major depression (29%), generalized anxiety disorder (37.4%), social anxiety disorder (17.8%), and dysthymia (15.9%).

Table 1 depicts the set-based test for PD and shows that only *HTR1A* achieved experiment-wise significant association with PD. Table 2 shows single-marker association and haplotype association with PD. Three SNPs included in the analysis were nominally associated with PD, however only rs6449693 remained significant at experiment-wide threshold. In the haplotype analysis, Hap2 was significantly associated with PD (asymptotic p-value=0.008), whereas Hap4 was significantly protective for PD (asymptotic p-value=0.004) and remained significant after Bonferroni correction.

We could not find any significant interaction between all SNPs evaluated, optimal mother parenting or trauma in childhood and PD in adulthood (data not shown). However, optimal father parenting and rs6313 interaction term ($\beta=0.176$, $t= -2.403$, $p=0.016$) and rs6311 ($\beta=0.134$, $t=-2.678$, $p=0.007$) was nominally associated with PD, and both association remained significant after Bonferroni correction. The genotypes in rs6311 and rs6313 moderate the effect of optimal father parenting in childhood and PD in adulthood. Figure 1 illustrates this association. Among subjects with TT/TC genotype in rs6311 the protection effect of fathers with high warmth and low overprotection was higher than the protection effect among subjects with CC genotype.

Discussion

As reported in previous studies (6, 53), we observed significant association between *HTR1A* and PD. Moreover we described specific haplotypes in *HTR1A* related to this disorder. We also provide new data about gene-environment interaction between childhood experiences, PD and *HTR2A*, a gene previously associated with maternal nurturance and symptoms of major depression (29).

Preclinical (54) and clinical studies have implicated *HTR1A* in the pathogenesis of PD (55, 56). Studies in *HTR1A* knockout mice demonstrated an increased anxiety-like behavior in several tests (54, 57, 58). Besides this, PD has been associated with a reduction on both pre-synaptic and post-synaptic *HTR1A* receptors as assessed by positron emission tomography (59). However, association studies evaluating rs6295 and PD have found controversial results. Rothe et al (6) found an association with the G allele for PD with agoraphobia and Huang et al (53) found an association with panic attack, while Maron et al. (7) found an association between PD and the C allele. In our study, rs6295, rs4521432 and rs6449693 were associated with PD, but only the last SNP remained significant at experiment-wide levels. Additionally we could detect one protective haplotype and another risk haplotype significantly associated with PD even after correction.

Two independent studies have found association with *HTR2A* and PD (7, 8); however this finding was not replicated in two additional studies (6, 9). In our study, no association was found between PD and *HTR2A*, but we found a gene-environmental interaction with *HTR2A* and optimal father parenting in childhood

and PD in adulthood. This gene-environment interaction was also found with both rs6311 and rs6313. Since rs6311 and rs6313 were in high linkage disequilibrium in our sample, these two SNPs can bring redundant information to this interaction. A recent study found that individuals carrying the TT/TC genotype of rs6313 *HTR2A* were responsive to the protective aspects of nurturing mothering, so that in the presence of high maternal nurturance they expressed low levels of depressive symptoms (29). The authors hypothesize a path via the prefrontal cortex, since *HTR2A* are involved in the functioning of the prefrontal cortex involved in cognitive control and regulation of negative emotions (29). Anxiety and depression are frequently comorbidities, and studies in families have shown a high susceptibility for depression in families with PD (60), suggesting a common risk factors to these disorders (61). In our study we were not able to find a significant association with optimal mother parenting, although there was a trend in the interaction term in rs6311 (p -nominal=0.081). Lack of statistical power could explain this result. In spite of this, in the presence of father with high warmth and low overprotection, individuals carrying the TT/TC genotype of rs6313 and rs6311 were more responsive to optimal father parenting protection against PD.

The association between parenting and psychopathology seems to be influenced by cultural aspects. For instance, a study that evaluated parental bonding in six European countries found a different role to father/mother warmth and protection. In France no aspects of parental bonding were associated with PD, while in Belgium only father warmth and in Germany only mother overprotection

seems to be associated to PD (18). Maybe the *HTR2A* influences the ability of individuals to use environmental support according to cultural aspects and could be not linked to one parental figure itself.

Although *5-HTTLPR* has been associated with anxiety traits in healthy volunteers (62), no association was found with this polymorphism with PD in a recent meta-analysis (3) and our study corroborates this previous finding. This is the first study that evaluated the triallelic form (11) of *5-HTTLPR* and PD and found no association with this phenotype. Gene-environment interaction with *5-HTTLPR* for depression has been shown in many studies (22, 63-70), but not in all of them (71, 72). Besides, some studies have contradictory results (64, 65, 73). In anxiety, Stein et al (74) found an interaction between emotional abuse and the short allele with anxiety sensitivity, but not with neuroticism. In our study, we evaluate a combined trauma index instead of the subscales to avoid multiple comparisons, and no gene-environmental interaction was found with none of the SNPs evaluated in PD.

Our results should be interpreted in light of some limitations. Most importantly, the small sample size means that our analyses may be subject to Type II error. The possible confounding due to population stratification in Brazil was addressed by restricting our analyses to Caucasian subjects (75), therefore these findings are restricted to this population. The assessment of maltreatment childhood and parental bonding was retrospective and at the same time as the phenotypic evaluation. Although PBI has a long-term stability (43), biased recall could not be ruled out (28). Genes selection was performed in a no-systematic

search, and some serotonergic genes previously associated with PD were not evaluated (4, 7, 76). The interaction with optimal father parenting should be interpreted carefully since we corrected for multiple testing only considering the three phenotypes and not all SNPs included. However as this finding is similar to what has been described for depression and mother nurturance (29), the chance of spurious association by multiple testing is reduced.

In sum, we were able to demonstrate an association between *HTR1A* and PD, and a lack of association between *5-HTTLPR* and PD even considering childhood trauma or parental bonding. Besides, this study is the first analysis of gene-environment interaction in PD. We observed that fathers with high warmth and low overprotection interact with variants in *HTR2A* protecting for PD in adulthood. Clearly, additional larger studies are needed to further define this interaction effect.

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Table 1 Set-based test for the association between Polymorphisms (PMs) and Panic Disorder (PD n=107, Controls n=125)

Set	PMs in the Set	PMs	T-value	Empirical p-value 0	Empirical p-value 1	Empirical p-value 2
HTR1A	P1	rs6449693	7.495	0.0159	0.0203	0.0555
	P2	rs4521432	7.226	0.0103	0.0137	0.0383
	P3	rs6295	7.059	0.0089	0.0111	0.0303
HTR2A	P1	rs6311	0.335	0.6337	0.6493	0.9673
	P2	rs6313	0.238	0.6415	0.6493	0.9677
5-HTTLPR	P1	Biallelic	0.318	0.5975	0.5975	0.9597
SLC6A4	P1	Triallelic	0.225	0.6469	0.6469	0.9717

A multi-marker set-based test implemented in PLINK was used for the analysis of all genes. Sets that have an experiment-wide association p-value ($p < 0.05$) are shown in bold. In each set, P1 is the best PMs associated with the outcome; P2 is the second one and P3 is the third one. Maximum computed permutations were 10000.

Empirical p-value p 0: p-value for average chi-square without correction;

Empirical p-value p 1: p-value corrected for all tests within this set/ gene

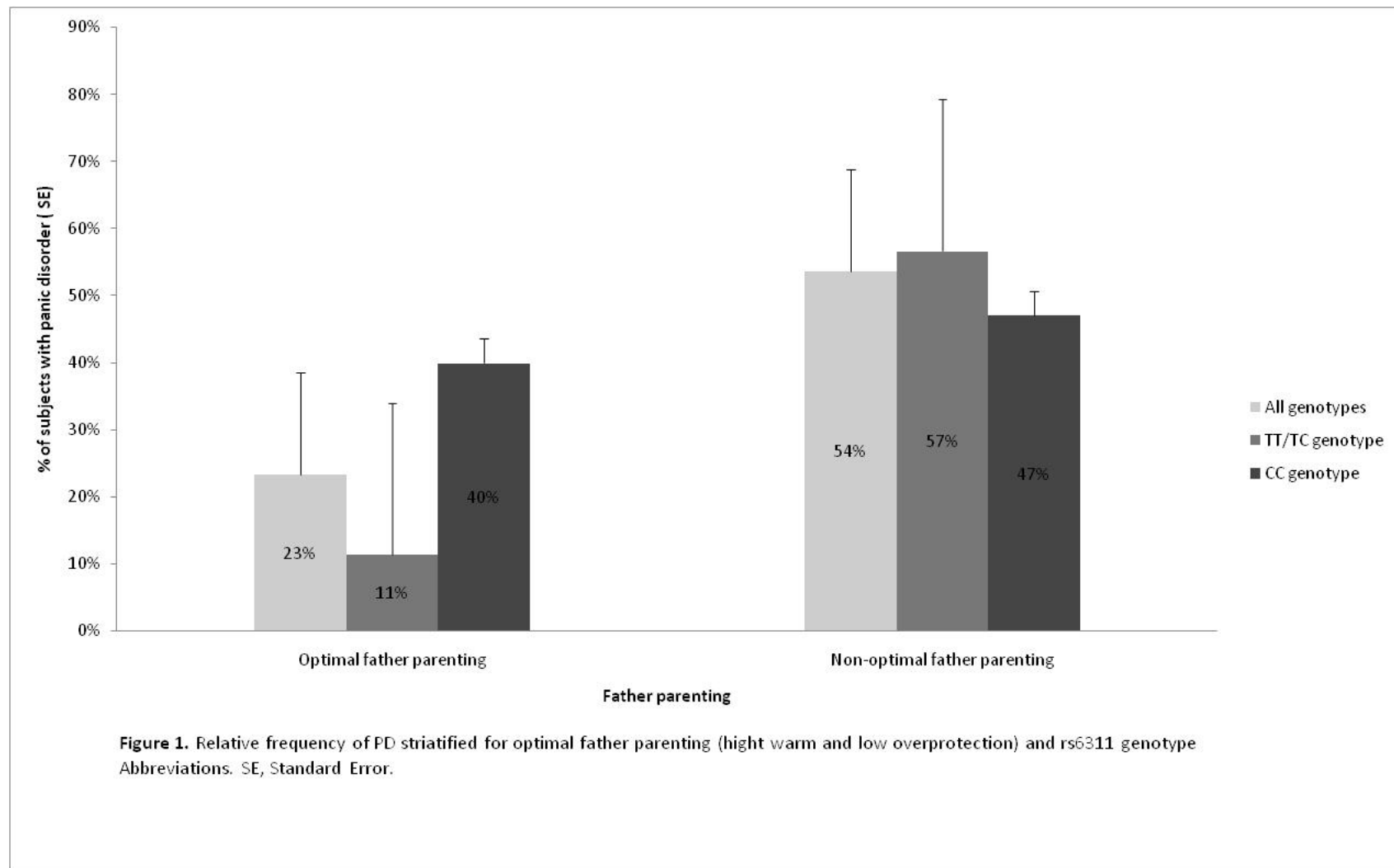
Empirical p-value p 2: p-value corrected for all tests in all sets

Abbreviations: PMs, Polymorphisms; CGI, Clinical Global Impression; HTR2A, Serotonin receptor 2A; HTR1A, Serotonin receptor 1A; 5-HTTLPR, Serotonin transporter gene.

Table 2 HTR1A single-marker association and haplotype association with Panic Disorder (107 cases and 125 controls)

	rs4521432	rs6449693	rs6295	rs13361335	Frequency in PD	Frequency in Controls	χ^2 (df=1)	Asymptotic p-value	Corrected p-value
Hap1	C	A	C	G	0.12	0.11	0.11	0.736	>0.999
Hap2	T	G	G	T	0.55	0.42	6.97	0.008	0.032
Hap3	C	A	G	T	0.01	0.02	0.03	0.871	>0.99
Hap4	C	A	C	T	0.32	0.45	8.29	0.004	0.016
					Ominbus .032				
Role	Downstream	Downstream	Promoter	Promoter					
HWE	0.695	0.794	0.794	>0.999					
Allele change	C/T	A/G	C/G	G/T					
Minor allele	T	G	G	G					
Frequency in PD	0.55	0.55	0.56	0.12					
Frequency in Controls	0.42	0.42	0.44	0.11					
χ^2 (df=1)	6.96	7.49	6.72	0.09					
Asymptotic p-value	0.008	0.006	0.009	0.764					
Empirical p-value 1	0.024	0.015	0.026	0.969					
Empirical p-value 2	0.053	0.041	0.066	0.999					
OR	1.64	1.67	1.62	1.09					

Abbreviations: PD, Panic Disorder; HTR1A, Serotonin Receptor 1A; SNP, Single Nucleotide Polymorphism; HWE, Hardy Weinberg Equilibrium p value; OR, Odds Ratio; χ^2 chi-square; df, degrees of freedom. **Bold** means $p < 0.05$.
 Asymptotic p-value: p-value for chi-square without correction;
 Empirical p-value P 1: p-value corrected for all tests within this set/ gene
 Empirical p-value P 2: p-value corrected for all tests in all sets



Artigo 3 – Association between EFHC2 with Panic Disorder,

Harm Avoidance and Behavioral Inhibition

Carolina Blaya¹, Priya Moorjani², Giovanni Abrahão Salum¹, Leonardo
Gonçalves¹, Lauren A. Weiss², Sandra Leistner-Segal¹, Gisele Gus Manfro^{1*},
Jordan Smoller²

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Anxiety-proneness is known to be influenced by genes (Munafo et al., 2004). Recent evidence suggests that anxiety traits and anxiety disorders are associated with altered limbic reactivity to fearful stimuli (Pezawas et al., 2005; Pillay et al., 2007). Previous studies have related the X-linked genes to fear recognition in which amygdale, a key structure of the limbic system, plays a critical role (Good et al., 2003). Weiss et al (Weiss et al., 2007) performed a regression-based association mapping in women with Turner syndrome and found an association between fear recognition and EF-hand domain containing 2 (*EFHC2*). This finding makes this a candidate gene for involvement in anxiety-proneness and perhaps disorder.

With this study we aim to examined whether *EFHC2* also affects non-syndromic anxiety-related traits that have been shown to reflect altered fear recognition, e.g. harm avoidance (HA) (Pezawas et al., 2005) and behavioral inhibition (BI) (Schwartz et al., 2003). We also aim to find if *EFHC2* is related to panic disorder (PD), a disorder in which reactivity to fearful stimuli has also been implicated (Pillay et al., 2007). Since the power of this study is likely to be greater for the quantitative intermediate phenotypes, we run HA and BI as a primary analyses and PD as a secondary analysis.

This is a case-control study where 127 Caucasian PD patients (75.5% females, mean age 39.05 ± 10.12 years) were recruited from the Outpatient Clinic and 132 Caucasian employees from HCPA (73.5% females mean age 36.93 ± 9.75 years) were recruited as controls. Blood was collected from

participants for DNA extraction after informed consent was signed. Institutional review board approval was obtained from the ethics committee (Number 04-272).

The Mini International Neuropsychiatry Interview - Brazilian version was used to confirm the psychiatric diagnoses. HA was assessed with the Cloninger's Temperament and Character Inventory (Cloninger, 1986). HA is described as a heritable tendency to inhibit or stop behaviors in response to signals of aversive stimuli in order to avoid punishment. The Self-Report Scale of Behavioral Inhibition - Retrospective Version (Reznick et al., 1992) was used to assess childhood BI. BI is a strong predictor of anxiety disorder and has an estimated heritability exceeding that of the anxiety disorders themselves.

Single nucleotide polymorphisms (SNPs) were selected within the *EFHC2* gene and 10KB flanking region. Genotyping of SNPs was performed according to Weiss et al. (Weiss et al., 2007) with minor modifications. Markers were retained only if they met the following quality control criteria: >90% genotype call rate, minor allele frequency (MAF) >5%, Hardy-Weinberg Equilibrium (HWE) $p > 0.001$. One SNP was excluded due to departure from HWE.

We used PLINK software (Purcell et al., 2007) to perform the basic single SNP association test for alleles. For each SNP, we calculated empirical significant value based on a Wald test and empirical significant value based on 10,000 permutations. SNPs that achieve significance in permuted analysis are safer regarding false findings due to multiple testing. Genotypic tests were

performed when allelic tests show significant in the permuted analysis. We considered an $\alpha=0.05$ as significance level.

Single marker tests of 8 *EFHC2* SNPs and HA showed one nominally significant association at rs1562875 and remained significant in the permuted analysis ($p=0.031$). In the genotype analysis, rs1562875 was also nominally associated with HA (Mean \pm SD: AA 23.6 \pm 5.8, AT 21.7 \pm 5.9 and TT 15.6 \pm 6.5, nominal p -value=0.004; permuted p -value=0.033). In the BI analysis, rs1562875 and rs17146914 were associated with this phenotype, but did not remain significant in the permuted analysis ($p=0.137$ and $p=0.184$, respectively) (table 1). In the PD analysis, the same SNP (rs1562875) was associated with this disorder (10.7% cases vs. 4.3% controls; OR 2.64, CI95% 1.23-5.66, $p=0.009$). However this association did not remain significant in the permuted analysis ($p=0.059$). Multiple logistic regression could not be performed because of high collinearity between the three phenotypes evaluated (tolerance values $< 1 - r^2$).

This is the first study that evaluates *EFHC2* and anxiety traits, a gene previously associated with fear recognition (Weiss et al., 2007). In our study, we found that rs1562875 minor allele is nominally associated with higher scores in HA and BI and is more frequent in PD than in controls. The strength of this study is the congruent finding of these three highly associated phenotypes that could not be isolated in regression analysis. Spurious association regarding PD and BI should be considered due to multiple testing since only HA passed in permuted adjusted analysis.

EFHC2 may be associated with anxiety by interfering in fear process related to amygdale function. Pillay et al (2007) showed that PD patients produced more activation of amygdale than controls in response to fearful faces using fMRI. However, the SNP found in this association study was not the same and neither it is in linkage disequilibrium ($LOD < 0.5$) with the one that has been reported to be associated with fear recognition in Turner Syndrome (Weiss et al., 2007). *EFHC2* is a candidate to be involved in neural circuits; however its role in fear circuits has not been properly understood.

Our results should be interpreted in light of some limitations. Most importantly, the small sample size means that our analyses may be subject to Type II error. Besides this, the possibility of spurious association must be considered. Finally, p values were corrected only by permutation and not for the three phenotypes evaluated with Bonferroni's correction.

Regardless the small sample size and the unknown RNA expression implications of polymorphisms in this gene, the association described between *EFHC2* and anxiety, if replicated, has potential implication in elucidating a possible neurobiological path of fear.

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Table 1. Allelic Association between individual SNPs in EFHC2 with Behavioral Inhibition and Harm Avoidance

SNP Characteristic					Behavioral Inhibition				Harm Avoidance			
SNP	Role	Allele Change	MAF	HWE p	B	r ²	p-value (asymptotic)	p-value corrected	β	r ²	p-value (asymptotic)	p-value corrected
rs287779	Intron	A/G	0.24	0.54	-0.059	0.005	0.267	0.849	-0.237	<0.001	0.690	0.999
rs12557505	Intron	A/T	0.10	0.70	0.066	0.002	0.410	0.961	0.888	0.004	0.309	0.894
rs12014680	Intron	A/G	0.18	0.47	0.081	0.006	0.210	0.761	1.091	0.009	0.119	0.536
rs2208592	Exon	G/T	0.12	0.53	0.151	0.015	0.055	0.301	1.154	0.007	0.178	0.698
rs7055196	Intron	A/G	0.18	0.48	0.089	0.007	0.170	0.681	0.032	<0.001	0.964	1.000
rs17146914	Exon	C/T	0.09	1	0.204	0.019	0.031*	0.184	1.232	0.005	0.236	0.800
rs1562875	Intron	A/T	0.08	1	0.206	0.021	0.022*	0.137	2.798	0.031	0.005*	0.032*
rs5906930	Promoter	C/G	0.40	0.54	0.011	<0.001	0.814	1.000	-0.206	<0.001	0.694	0.999

Abbreviations: SNP, Single Nucleotide Polymorphism; EFHC2, EF-hand domain containing 2; MAF, Minimal allele frequency; HWE, Hardy-Weinberg equilibrium; β, regression coefficient; r² regression r-squared; p, Wald-test asymptomatic p-value.

Statistic tests: Wald test;

Note: **Bold** indicates minor allele. * indicates p<0.05.

**Artigo 4 – *CREB1* as a predictor of long term response to
cognitive-behavior therapy for pharmacotherapy-resistant panic
disorder patients**

Carolina Blaya¹, Priya Moorjani², Elizeth Heldt¹, Giovanni A. Salum¹, Sandra
Leistner-Segal¹, Roy H. Perlis², Jordan W. Smoller², Gisele G. Manfro^{1*}

Submetido no *Genes, Brain and Behavior*

Abstract

OBJECTIVES: While numerous studies have investigated the role of genetic variation in predicting response to psychotropic medications, none have examined whether genes influence response to Cognitive Behavior Therapy (CBT). The aim of this study was to evaluate the role of variants in 7 genes previously implicated in the etiology or treatment of anxiety: *BDNF*, *CREB1*, *RGS2*, *CRHR1*, *SLC6A4*, *HTR2A*, *HTR1A* and response to CBT in pharmacological-resistant panic disorder (PD) patients.

METHODS: Seventy-four Caucasian patients with PD resistant to antidepressant treatment received group CBT for 4 months. Baseline illness severity was assessed using the Clinical Global Impression (CGI) scale, and treatment response was indexed by change in CGI at the end of treatment and at 1-year follow-up. Additionally, the remission criteria (CGI \leq 2 and no panic attack) were also evaluated. We examined single nucleotide polymorphisms (SNPs) using either known functional variants or tag SNPs within each gene and 10 kb flanking sequence which yielded a total of 47 SNPs. For *SLC6A4*, we examined the 5HTTLPR promoter variation including the embedded SNP (rs25531). Genes were screened using a set-based test in PLINK followed by single marker association tests for genes that reached gene-wide significance.

RESULTS: In the set-based test, *CREB1* achieved gene-wide significant association with improvement at 1-year follow-up (empirical p-value = 0.016). Out of the 5 *CREB1* single markers SNPs, two showed nominally significant

associations (rs7594560, p-value 0.003 and rs2253206, p-value 0.021), that did not remain significant after 10,000 permutations. In the haplotype analysis, we identified one haplotype significantly associated with 1-year response ($p=0.0002$). We did not observe experiment-wide association between CBT outcome and the remaining genes for either acute or 1-year response or remission.

CONCLUSION: Although limited by small sample size, these results provide preliminary evidence that variations in *CREB1* may be related to long-term CBT response among pharmacological-resistant patients with PD.

Introduction

Cognitive-behavioral therapy (CBT) has been established as an effective treatment for panic disorder (PD), and may be superior to pharmacotherapy for maintaining long-term treatment gains (Gould *et al.*, 1995). Despite the consistent evidence for the efficacy of CBT (Gould *et al.*, 1995, Otto & Deveney, 2005), many patients fail to respond to treatment. The nature of factors that underlie these individual differences in treatment response are not well understood (Gould *et al.*, 1995, Rosenbaum *et al.*, 1996).

The burgeoning field of pharmacogenetics has provided evidence that specific genetic variants may explain differential response and toxicity to medication treatment. Previous research has shown that individual response to pharmacotherapy in major depression (Kim *et al.*, 2006, Kraft *et al.*, 2005, McMahon *et al.*, 2006), schizophrenia (Wang *et al.*, 2007), generalized social anxiety disorder (Stein *et al.*, 2006), and other psychiatric disorders may be related to genetic variation. However, no study has evaluated the role of these genetic markers in panic disorder patients and CBT response.

The biological mechanism by which CBT exerts its therapeutic effect is still unknown. However, Linden (2006) proposed similarities in the biological mechanisms of psycho- and pharmacotherapy. Neuroimage studies have shown regional metabolic changes with psychotherapy that are similar to pharmacological treatment in patients with major depression (Brody *et al.*, 2001, Martin *et al.*, 2001) and anxiety disorders including obsessive compulsive

disorder (Baxter *et al.*, 1992, Schwartz *et al.*, 1996) and specific phobias (Paquette *et al.*, 2003). Hence, genes implicated in etiology and pharmacological treatments of anxiety disorders are plausible candidates to be evaluated in the CBT response for PD.

PD has been associated with polymorphisms in serotonin receptor 1A (HTR1A) (Broocks *et al.*, 2003), serotonin receptor 2A (HTR2A) (Maron *et al.*, 2005) and regulator of G-protein signalling 2 (RGS2) (Leygraf *et al.*, 2006) in humans. Animal models have shown that anxiety is related to cAMP responsive-element binding protein (CREB1) (Blendy, 2006), corticotropin-releasing hormone receptor (CRHR1) (Timpl *et al.*, 1998) and brain derived neurotrophic factor (BDNF) (Chen *et al.*, 2006). Regarding response to pharmacological treatment, Perna *et al.* showed that paroxetine treatment response in PD is related to the serotonin transporter gene (SLC6A4) (Perna *et al.*, 2005).

The aim of this study was to evaluate the association between CBT response in PD patients resistant to previous pharmacological treatment and variants in 7 genes previously implicated in the etiology or treatment of anxiety: BDNF, CREB1, RGS2, CRHR1, SLC6A4, HTR2A, HTR1A.

Methods

We examined the role of these genes in a cohort of PD patients treated in an open study of CBT with one year of naturalistic follow-up. Participants were recruited from the Anxiety Outpatient Clinic at the Hospital de Clínicas de Porto

Alegre from 1998 to 2006. All participants were referred to be treated with cognitive behavioral group therapy (CBGT) as an augmentation strategy after resistant pharmacological treatment i.e. patients had to have residual symptoms of PD such as panic attacks, anticipatory anxiety and phobic avoidance despite being on stable dose of medication for at least 4 months. Patients were advised not to change pharmacological treatment during CBT. CBGT was an adaptation of the procedures manualized (Otto *et al.*, 1996) and sessions are described detailed elsewhere (Heldt *et al.*, 2003). Patients were treated in one of the twelve groups (with a mean of 7 patients per group) offering 12-sessions of treatment over 4 months. Blood was collected from participants for DNA extraction during 2005 to 2006 after written informed consent. Institutional review board approval was obtained from the ethics committee (Number 04-272).

The inclusion criteria were as follows: (1) PD with or without agoraphobia, according to DSM-IV diagnostic criteria (Heldt *et al.*, 2003); (2) at least eighteen years old; (3) Clinical Global Impressions (CGI) ≥ 3 despite being on a stable dose of medications for at least 4 months (selective serotonin reuptake inhibitor, tricyclic antidepressant or venlafaxine, with or without benzodiazepines). Patients with mental retardation, dementia or other organic brain syndrome, psychotic disorders and disabling chronic disease were excluded. Patients with comorbidities common to PD were included in the study provided that the symptoms were not clinically more prominent than the PD symptoms.

Of the 110 patients that entered the treatment protocol, DNA was collected from 91 subjects. Only 82 Caucasians patients were included in order to minimize confusion due to population stratification. Ethnicity was defined based on phenotypic characteristics (Zembrzuski *et al.*, 2006) and ethnic background. Eight individuals with genotyping call rates less than 90% were excluded resulting on 74 patients included in the analysis. Figure 1 displays how the analytic sample was selected. The sample was predominantly female (79.7%), with a mean age of 39.51 (SD=11.26) years, mean age of PD onset of 29.83 (SD=10.47) years, and median PD duration of 8 year (P25=3 to P75=11). Patients included had been on pharmacological treatment for a median of 2 years (p25=1 to p75=4) before starting the CBGT. Five patients spontaneously stop their medication during the acute treatment, and eighteen patients stop it during the follow-up period. Thirteen patients (72%) that stop the medication were in remission in the 1-year follow-up.

The Mini International Neuropsychiatry Interview (MINI) - Brazilian version (Amorim, 2000) was used to confirm the PD diagnosis and establish comorbidity diagnoses. A semi-structured interview was used to access sociodemographic data and clinical history. Comorbidities included agoraphobia (90.54%), generalized anxiety disorder (33.78%), major depression (25.68%), social anxiety disorder (18.92%), and dysthymia (14.86%).

The Clinical Global Impressions scale (CGI) (Guy, 1976) and Panic Inventory (PI) (Heldt *et al.*, 2003) were used to access severity at baseline, after

the 12th session, and 1 year post treatment. At study entry, ratings were completed by the clinicians running the group blinded to genotype. Outcome ratings at the end of the treatment and at follow-up evaluations were completed by trained clinicians who did not participate in the group therapy or knew the results of the baseline ratings and the genotyping.

Two end-points were evaluated in this study: acute treatment (at the end of 12-session therapy) and one-year follow-up. Treatment response was defined by change in CGI score at each endpoint relative to baseline; and remission was defined as the absence panic attacks and CGI \leq 2. Since this sample is composed by resistant patients, the 1-year endpoint could be a most adequate moment to evaluate CBT outcome because some patients could need more time to recover (Heldt *et al.*, 2006).

Genotyping was performed for HapMap single nucleotide polymorphisms (SNPs) selected within each gene and 10kb flanking region. For the CREB1 gene, SNPs were selected based on previous studies (Perlis *et al.*, 2007b, Perlis *et al.*, 2007c). For SLC6A4 we examined functional polymorphism including the embedded SNP (rs25531). For BDNF we examined functional Val66Met polymorphism. The Tagger program (De Bakker *et al.*, 2005) (<http://www.broad.mit.edu/mpg/tagger/>) was used to identify tag SNPs with a minor allele frequency of greater than 5% and minimum r^2 of 0.8. A total of 47 SNPs were thus selected for genotyping using mass spectrometry as previously described (Sklar *et al.*, 2002).

Genotyping of the polymorphism in the promoter of the serotonin transporter (5-HTTLPR) was performed with the following protocol - Genomic DNA (1.4 ng) was amplified in a of 7 μ l reaction using KlenTaq DNA Polymerase (0.2 U), the proprietary KlenTaq Buffer (1X), dNTPs (200 μ M each), 5% glycerol, Betaine (1 M) and the marker specific primers (0.2 μ M). Amplification was performed with thirteen cycles of denaturation for 30 seconds at 93°C, annealing for 30 seconds beginning at 61.5°C and dropped 0.5° C every cycle and primer extension at 72°C for 30 second, followed by 37 cycles of denaturation for 30 seconds at 93°C, annealing for 30 seconds at 55° C and primer extension at 72°C for 30; 72°C for 1 hour. The amplified product (1 μ l) was combined with size standard (LIZ-250) before being analyzed on an ABI-3730. The long allele appears as a product of about 412 while the short allele shows a band at about 370. The genotype of the SNP embedded in the 5-HTTLPR (Wendland *et al.*, 2006) (rs25531) was assayed by digesting the PCR product with the restriction enzyme, *MspI* (Hu *et al.*, 2006). This 10 μ l reaction contains 2 μ l of the PCR product, 1 μ l of 10X restriction buffer (New England Biolabs), 1 μ l of *MspI* enzyme and 6 μ l of water. The reaction was incubated at 37°C for 1 hour. The digested product (1 μ l) was then combined with size standard (LIZ-250) before being analyzed on an ABI-3730. Post-digestion, the long allele with the A SNP allele appears as a product of about 320, the presence of the G SNP allele is indicated by the presence of a band at 148, while the short allele shows a band

at about 277. The final genotype was determined from the information from the analysis of both the digested and undigested PCR product.

In addition, markers were retained only if they met the following quality control criteria: (1) >90% genotype call rate; (2) minor allele frequency (MAF) >5%; (3) Hardy Weinberg equilibrium $P > 0.001$. Three duplicates were assessed in the experiment with 100% concordance. After applying these quality control filters, 42 SNPs were retained for the association analysis.

For an initial analysis, we screened each gene using the set-based test in PLINK (Purcell *et al.*, 2007) (<http://pngu.mgh.harvard.edu/purcell/plink/>) followed by single marker association tests for genes that reached gene-wide significance. The set-based test is based on calculating the average test statistic for the best three SNPs per gene region, and evaluating the significance of these set-statistics by permutation (10,000). Gene-wide accounts for multiple comparison within the gene, whereas experiment-wide significance accounts for multiple comparisons, controlling for the 42 polymorphisms evaluated by permutation. Haplotype analysis was performed for genes that reached the gene-wide significance. Haplotype analysis was corrected for number of haplotypes observed (minor allele frequencies [MAF] < .01) with Bonferroni's correction. The overall level of significance adopted was $\alpha=0.05$.

Results

Patients who provided DNA were generally similar to the full sample treated with CBGT. Since the DNA sample collection began after CBGT

longitudinal study initiation, those providing DNA samples were the ones in follow-up. However, there were no differences between baseline characteristics, outcome measures or co adjuvant treatments of patients included and those who did not provide blood sample (n=19).

A set-based test was performed with delta CGI and remission at acute treatment and 1-year follow-up. No association was found with the set-based test in remission at both end-points and neither for delta-CGI after acute-treatment. On the other hand, for the delta-CGI 1-year follow-up, a gene-wide association was found in *CREB1* (Table 1). Single marker tests of 5 *CREB1* tag SNPs (Figure 2) showed two nominally significant associations (Table 2), which did not remain significant after 10,000 permutations. In light of previous studies indicating sex-specific effects of *CREB1* (Perlis *et al.*, 2007a, Perlis *et al.*, 2007b), we also tested for sex-related heterogeneity. No interaction was found in the gene-by-sex analysis (data not shown).

In the haplotype analysis, Hap4 was significantly associated with delta-CGI evaluated at 1-year ($p=0.0002$) that remained significant after Bonferroni's correction, and two haplotypes were associated with worse response, but this association did not remain significant after Bonferroni's correction (Table 2).

Discussion

This is the first study that evaluates the role of genetic markers in CBT response. Two SNPs in *CREB1* were nominally associated with improvement at

1 year follow-up treatment. *CREB1* is a nuclear transcription factor that mediates the effects of cAMP on gene expression (Montminy *et al.*, 1990) and has been previously related to anger and antidepressant-emergent suicidal ideation in depressed patients (Perlis *et al.*, 2007b, Perlis *et al.*, 2007c).

By what mechanism might *CREB1* influence response to CBT? One possibility is that *CREB1* mediate anger, a domain associated with impulsivity, aggressive and goal-directed behaviors (Lara & Akiskal, 2006). Recently, Lara & Akiskal (2006) have proposed a bidimensional model based on fear and anger traits which conceive mood, behavior and personality concomitantly. Interestingly, Perlis *et al.* (2007b) found an association between a haplotype and anger that is similar to the one found to be associated with PD improvement. Anger would be associated with disinhibited exploration and low perception of cues of danger (Lara & Akiskal, 2006), and probably facilitate exposition in CBT for PD. Moreover anxiety and stress is related to the “flight or fight response” (Mcewen, 2007) and PD patients who fight (anger) could have better improvement as compared to those that flight (fear). Besides, *CREB1* is also related to memory – an important hallmark for CBT (Garakani *et al.*, 2006). The connection between *CREB1* and long-term memory was established in several organisms (Garakani *et al.*, 2006), however the mechanisms that underlie the ability of *CREB1* to facilitate memory are not completely understood (Carlezon *et al.*, 2005). *CREB1* activity in the amygdale serves as a molecular switch for the formation of long-term memory in fear conditioning in rats (Josselyn *et al.*, 2001).

The association between *CREB1* and CBT response might be mediated through personal characteristics as well as through memory modulation that can interfere in desensitization and exposure during the follow up treatment period.

The association with *CREB1* was found only in 1-year follow-up. Although outcomes cannot be attributed unequivocally to CBGT, the likelihood that our results are due to non-specific factors or time are unlikely given the history of chronicity of the illness (median duration of the disease was 8 years) and inadequate response to open pharmacotherapy for this sample (median 2 years of pharmacotherapy before starting CBT). Besides, it is also unlikely that this association is due to modification in medication status, since almost 30% of those who were in remission have spontaneously stopped their medication. It is possible that due to patient's severity, they need more time to perform the exposure exercise and that is the reason why we found the association only in follow-up period. Another possibility is *CREB1* influence some characteristics toward "fight response", that could be related to anger. These personal characteristics would become more important to patients' recover in follow-up period, when exercise depends on their own motivation and not on the therapist.

There was no significant association between the remaining genes (*BDNF*, *SLC6A4*, *RGS2*, and *CRHR1*) and CBT response. We examined these genes in light of prior evidence that they may contribute to anxiety-related or treatment response phenotypes. For example, serum *BDNF* level has been related to CBT response in a sample of PD (Kobayashi *et al.*, 2005). *SLC6A4*

and other genes in the serotonin pathway (Broocks *et al.*, 2003) (Stahl, 1998) have been implicated in PD, although results have been inconclusive (Blaya *et al.*, 2007, Maron *et al.*, 2004, Perna *et al.*, 2005). A recent study (Leygraf *et al.*, 2006) reported association between four SNPs in *RGS2* and PD. Finally, extrahypothalamic CRH systems mediate a broad range of behavioral stress and anxiety responses (Heinrichs & Koob, 2004) and the CRH receptor 1 (*CRHR1*) is implicated in anxiogenic CRH actions (Contarino *et al.*, 1999, Muller & Wurst, 2004). We found no evidence that these loci are associated with response to CBGT for PD, although the small sample size examined here does not allow us to exclude a role for these genes.

Our results should be interpreted in light of some limitations. Most importantly, the small sample size means that our analyses may be subject to Type II error. Besides this, the association was found only in the follow-up period with the empirical p value and not after 10,000 permutations. The possible confounding due to population stratification in Brazilian was addressed by restricting our analyses to Caucasian subjects (Zembrzuski *et al.*, 2006), therefore these findings are restricted to this population. Gene's selection was performed in a no-systematic search, and association previously related to PD was not evaluated (Deckert *et al.*, 1999, Domschke *et al.*, 2003). Additionally, our finding could be restricted only to pharmacological resistant PD. Finally, the *CREB* polymorphisms examined here were chosen to tag genetic variation across the gene but are not known to have direct functional effects.

In sum, this study is the first analysis of genetic influences on response to CBT. We observed preliminary evidence that variants in *CREB1*, a gene implicated in the biological basis of anger, anxiety and memory, are associated with CBT outcome at 1 year. Clearly, additional larger studies are needed to further define the effect of *CREB1*, if any, on CBT response. However, if replicated, these findings may have implications for elucidating the neurobiology of CBT and identifying a potential subgroup of PD patients more likely to improve with this treatment modality.

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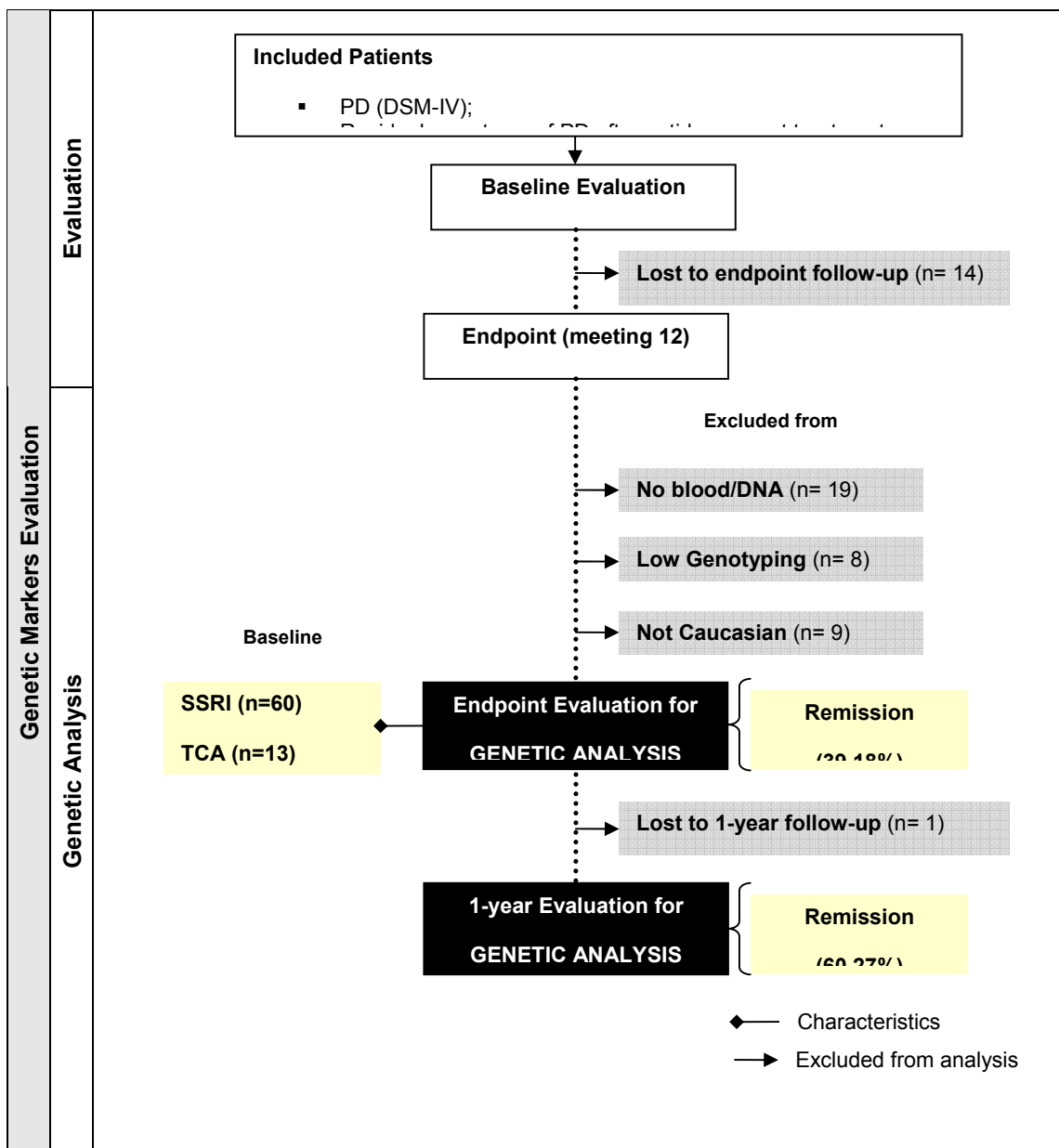


Figure 1. Flowchart of patients treated at CBGT that were included in genetic analysis and their characteristics.

Abbreviations: SSRI, Selective serotonin reuptake inhibitor; TCA, Tricyclic Antidepressant.

Table 1 Set-based test for the association between Polymorphisms (PMs) and Delta-CGI (Baseline CGI – 1-year CGI) at 1-year follow-up (n=73)

Set	PMs in the Set	PMs	T-value	Empirical p-value 0	Empirical p-value 1	Empirical p-value 2
BDNF	P1	rs6265	0.006	1	1	1
CREB	P1	rs7594560	9.961	0.013	0.020	0.111
	P2	rs2253206	7.765	0.009	0.013	0.079
	P3	rs1862952	5.839	0.011	0.016	0.098
CRHR1	P1	rs9892359	1.316	0.915	0.931	1
	P2	rs17690314	1.13	0.917	0.932	1
	P3	rs242944	0.867	0.941	0.953	1
HTR1A	P1	rs6295	0.0381	0.995	0.996	1
	P2	rs4521432	0.0238	0.995	0.995	1
	P3	rs6449693	0.0159	0.995	0.995	1
HTR2A	P1	rs6313	0.789	0.472	0.485	0.994
	P2	rs6311	0.621	0.441	0.455	0.988
RGS2	P1	rs2746073	0.723	0.867	0.886	1
	P2	rs3856223	0.720	0.827	0.850	1
	P3	rs10921267	0.689	0.796	0.820	1
SLC6A4	P1	Biallelic	0.802	0.380	0.380	0.979
SLC6A4	P1	Triallelic	0.079	0.805	0.805	1

A multi-marker set-based test implemented in PLINK was used for the analysis of all the genes. Sets that have gene-wide association p-value ($p < 0.05$) are shown in bold. In each set, P1 is the best PMs associated with the outcome; P2 is the second one and P3 is the third one. Maximum computed permutations were 10000.

Empirical p-value P_0: p-value for average chi-square without correction.

Empirical p-value P_1: p-value corrected for all tests within this gene.

Empirical p-value P_2: p-value corrected for all tests within the experiment.

Abbreviations: PMs, Polymorphisms; CGI, Clinical Global Impression; BDNF, Brain Derived Neurotrophic Factor; CREB, cAMP responsive-element binding protein; RGS2, regulator of G-protein signalling g; CRHR1, corticotropin-releasing hormone receptor; HTR2A, Serotonin receptor 2A; HTR1A, Serotonin receptor 1A; SLC6A4, Serotonin transporter gene.

Table 2 Association between individual SNP and Haplotype in CREB gene and delta-CGI at 1-year follow-up (n=73)

SNP	rs1862952	rs2253206	rs7569963	rs7594560	rs4675690	Frequency	β	R ²	Wald (t)	p-value (asymptotic)	p-value corrected
Hap1	A	A	A	T	T	0.01	0.798	0.006	0.681	0.498	>0.999
Hap2	T	G	G	T	T	0.02	-0.452	0.004	-0.550	0.584	>0.999
Hap3	A	A	G	T	T	0.09	-0.435	0.019	-1.176	0.244	>0.999
Hap4	A	G	G	C	T	0.09	1.111	0.171	3.832	0.0002	0.002
Hap5	A	G	G	T	T	0.18	-0.036	<0.001	-0.124	0.902	>0.999
Hap6	T	A	A	T	C	0.06	0.017	<0.001	0.042	0.967	>0.999
Hap7	A	A	A	T	C	0.19	-0.067	<0.001	-0.256	0.799	>0.999
Hap8	T	A	G	T	C	0.02	-1.985	0.086	-2.592	0.012	0.12
Hap9	A	A	G	T	C	0.04	-1.695	0.080	-2.484	0.015	0.15
Hap10	A	G	G	T	C	0.29	0.061	<0.001	0.240	0.811	>0.999
HWE	1	0.34	0.76	0.14	0.47						
Allele change	A/T	A/G	A/G	C/T	C/T						
Minor allele	T	A	A	C	T						
MAF	0.11	0.43	0.26	0.10	0.40						
β	-0.439	-0.478	-0.016	0.873	0.282						
SE	0.311	0.203	0.230	0.277	0.208						
R ²	0.027	0.073	<0.001	0.123	0.025						
Wald (t)	-1.410	-2.360	-0.068	3.156	1.358						
p-value (asymptotic)	0.163	0.021	0.946	0.002	0.179						
p-value (empirical, corrected)	>0.999	0.998	>0.999	0.929	>0.999						

Abbreviations: CGI, Clinical Global Impression; CREB, cAMP responsive-element binding protein; SNP, Single Nucleotide Polymorphism; HWE- Hardy Weinberg Equilibrium p value; MAF,

Minimal Allele Frequency; β , regression coefficient; r² regression r-squared. **Bold** means p<0.05.

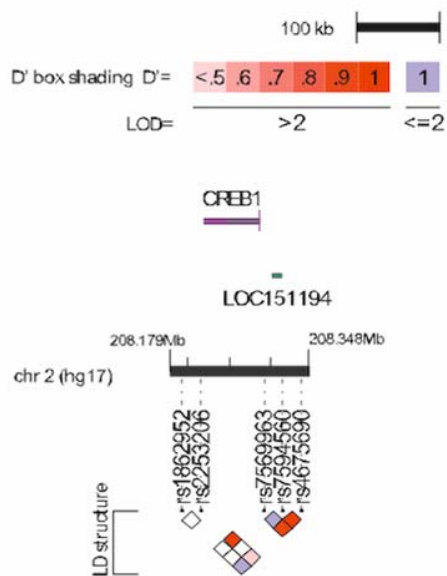


Figure 2. Location of single nucleotide polymorphisms (SNPs) that span the CREB1 gene. LOD indicates logarithmic odds; Chr, chromosome; Hg 17, Human Genome Sequence 17 (Single Nucleotide Polymorphisms database, National Center for Biotechnology Information, build 35, May 2004); LD, linkage disequilibrium; and Mb, megabases.

14. Considerações finais

Dentre os diversos fatores etiológicos envolvidos no TP, a vulnerabilidade genética está bem estabelecida como um fator de risco, uma vez que a herdabilidade para esse transtorno é de 28 (14) a 43% (10). No entanto, os estudos com genes candidatos não demonstraram resultados muito consistentes.

O gene transportador da serotonina, que é um gene candidato natural para ser investigado nos Transtornos de Ansiedade devido a sua associação aos Transtornos de Humor (71) e ao temperamento de evitação de danos (75), não foi associado ao TP em diversos estudos prévios. Alguns autores freqüentemente argumentam que a ausência de associação nos estudos em genética pode ser por falta de poder dos estudos, pois se espera um efeito muito pequeno para um único polimorfismo conferir risco a um transtorno. No entanto, no estudo 1 pode-se constatar com a meta-análise a ausência de associação do polimorfismo 5-HTTLPR com o Transtorno do Pânico (RC=0,91, IC95% 0,80 a 1,03, p=0,14). Três subanálises foram realizadas nessa meta-análise divididas por etnia, qualidade do grupo controle e comorbidade com Agorafobia, e também não foi identificada nenhuma associação com esse gene. Entretanto, o tamanho amostral incluído nesse estudo foi de cerca de 1000 pacientes com TP, justificando então a realização de outros estudos para vir a identificar um possível efeito do gene no TP com menor magnitude. Além disso, nenhum estudo havia avaliado o *5-HTTLPR* na sua forma trialélica no TP.

Realizamos então o estudo 2 com um dos objetivos de avaliar o 5-*HTTLPR* na forma bialélica e trialélica no TP e, assim como na meta-análise, não encontramos qualquer associação. O diferencial desse estudo foi que ele contemplou a medida de interação do gene com traumas na infância. Ao contrário do que ocorreu na depressão (71), não encontramos qualquer interação do gene-ambiente. Esses resultados devem ser considerados com cautela, pois esse é o primeiro estudo no TP que avaliou esse tipo de interação. Um estudo prévio encontrou associação entre abuso emocional ou abuso físico e sensibilidade à ansiedade (193), um fenótipo intermediário que está intimamente ligado ao TP. Diante desses achados é possível levantar algumas hipóteses. A primeira é de que nosso estudo não possui poder suficiente para identificar a interação do 5-*HTTLPR* com trauma, uma vez que foram incluídos apenas 232 sujeitos. Curiosamente, o achado de Stein *et al* (193) foi descrito em apenas 150 sujeitos, mas como o fenótipo avaliado era uma medida contínua, e não dicotômica como no nosso estudo, é possível que esse tamanho amostral tenha sido suficiente.

Outra hipótese é de que a interação gene-ambiente com o 5-*HTTLPR* ocorre apenas para um aspecto ligado ao TP – a sensibilidade à ansiedade – e não ao transtorno como um todo. Isso fundamenta a pesquisa de fenótipos intermediários, que possivelmente são mais adequados para os estudos de associação em comparação com a nosologia psiquiátrica proposta pelo DSM-IV (1). No estudo 2 optou-se por não avaliar fenótipos intermediários, uma vez que

o número excessivo de testes implicaria uma correção ainda maior do valor p . Determinamos uma única medida para cada covariável avaliada na interação (pai protetor, mãe protetora e trauma), mas como foram testados 8 marcadores, o número de testes já nos pareceu excessivo para incluir também os fenótipos intermediários. Nossa abordagem difere da adotada por Stein *et al* (193) que foi utilizar duas subescalas do CTQ, ao invés de avaliar uma medida mais global, em dois fenótipos intermediários: neuroticismo e sensibilidade à ansiedade. Apesar de realizar 12 testes (sensibilidade à ansiedade, escala de sintomas físicos da sensibilidade à ansiedade e neuroticismo para a forma bialélica e trialélica e duas covariáveis, abuso emocional e físico), os autores não fizeram correção para múltiplos testes. Baseado nos achados dos estudos 1 e 2, concluímos que o *5-HTTLPR* não apresenta um papel maior na genética do TP nem mesmo quando considerada sua forma trialélica ou a interação com trauma, apesar de existir evidência de influenciar fenótipos intermediários associados à ansiedade.

Outros genes foram também pesquisados, e naturalmente os receptores da serotonina *HTR1A* e *HTR2A* são genes candidatos. Um polimorfismo do *HTR1A* havia sido associado previamente ao TP, mas com resultados contraditórios (88, 95). No nosso achado replicamos a associação do alelo G do polimorfismo localizado no promotor (rs6295) com TP e identificamos outros 2 SNPs do *HTR1A* associados ao TP. Os alelos de menor frequência desses polimorfismos constituem um haplótipo de risco para o TP, enquanto que os

alelos complementares conferem proteção ao transtorno. As associações encontradas com o *HTR1A* não sofreram interação com nenhuma medida ambiental avaliada no nosso estudo. Possivelmente, estudos de meta-análise poderão avaliar qual a real contribuição desse gene.

Já o *HTR2A* havia sido associado ao TP em 2 estudos independentes (12, 95), mas esse achado não foi replicado em 2 outros estudos (88, 96). No nosso estudo não identificamos associação entre esse gene e o TP. No entanto, quando considerada a interação com pais pouco superprotetores e muito afetivos, a presença de alelo T em dois polimorfismos do *HTR2A* conferiu proteção ao TP. Esse achado replica parcialmente o que foi recentemente reportado para a Depressão por Jokela *et al* (196). Ansiedade e Depressão são comorbidades freqüentes, e alguns autores sugerem que ambas compartilham fatores de risco comuns (218). Apesar de o achado prévio ter sido descrito com mães e o nosso com pais, os achados nos parecem congruentes, pois existe uma contribuição diferente para o cuidado materno e paterno dentro de cada cultura (21). Parece também que variações no *HTR2A* influenciam o indivíduo a aproveitar o suporte do ambiente familiar (podendo ser tanto o pai, quanto à mãe) para evitar o desenvolvimento tanto de Ansiedade quanto Depressão.

Além de replicar associações com genes previamente associados ao TP, essa tese sugere que o *EFHC2* está associado ao TP e a dois fenótipos intermediários associados à ansiedade (comportamento inibido e temperamento evitador de dano). A força desse achado está na congruência da associação

com esses três fenótipos. O *EFHC2* havia sido previamente associado à percepção do medo (180), levando então ao desenvolvimento do nosso estudo 3. Caso esse achado seja replicado, possivelmente poderá contribuir para a compreensão do neurocircuito do medo.

Já o estudo 4 propõe pela primeira vez avaliar a influência de variações gênicas na resposta à Terapia Cognitivo-Comportamental. Nesse estudo avaliamos variações no *5-HTTLPR*, *HTR1A*, *HTR2A*, *BDNF*, *CREB1*, *RGS2* e *CRHR1* e encontramos que variações no *CREB1* estavam associadas à melhor resposta à TCC. O *CREB1* havia sido previamente associado à raiva, e na análise de haplótipos encontramos que o haplótipo associado à raiva foi também associado com a melhor resposta à TCC. A ansiedade está associada à resposta de “luta ou fuga”, e nosso estudo sugere que aqueles pacientes que lutam (raiva) respondem melhor à TCC que os que fogem (medo).

Por fim, essa tese versa sobre alguns aspectos relacionados ao TP, abrangendo desde a revisão sistemática da literatura, até estudos de associação, de interação gene-ambiente e de resposta à TCC. Esses estudos estão de acordo com a proposta de estudos para o século 21 (219), incluindo a pesquisa de vários genes e análise de múltiplos loci. Como perspectiva futura, essa linha de pesquisa será ampliada, com o aumento do tamanho amostral, a pesquisa de novos genes candidatos, a avaliação de outros fenótipos intermediários e a análise de interação gene-ambiente e gene-gene na busca de um melhor entendimento da genética do TP.

15. Anexo A: Termo de Consentimento Informado

Termo de Consentimento Informado para Pacientes

Estamos realizando uma pesquisa sobre a influência genética na evolução de pacientes com Transtorno do Pânico. A causa do Transtorno do Pânico é multifatorial, ou seja, existem alguns fatores genéticos e ambientais que predispõe à doença. O objetivo desse estudo é verificar se existe alguma predisposição genética que influencie no modo como os indivíduos lidam com os estressores ambientais. A avaliação constará de uma entrevista psiquiátrica e um exame de sangue que identificará alguns genes que são associados a ansiedade. O tratamento será escolhido de acordo com as indicações clínicas e desejo do paciente, podendo ser farmacológico ou psicoterápico. Os pacientes serão reavaliados clinicamente anualmente e inquiridos quanto a estressores ambientais no ano anterior à entrevista. A não participação do estudo não acarretará em nenhum prejuízo no seu atendimento no HCPA.

Eu fui informado dos objetivos acima descritos e da justificativa para qual estão sendo utilizadas as escalas de forma clara e detalhada. Sei que poderei solicitar novos esclarecimentos e que, a qualquer momento, terei liberdade de retirar meu consentimento da participação da pesquisa, sem prejudicar meu atendimento no HCPA.

O (a) pesquisador(a) certificou-me de que as informações por mim fornecidas terão caráter confidencial e no caso de divulgação serão sem identificação e unicamente para fins de pesquisa.

Porto Alegre, de de

Assinatura do paciente

Assinatura do pesquisador

Contato com pesquisadora: Carolina Blaya – Fone: 3316 82 72

Pesquisador Responsável: Gisele Gus Manfro

Adendo ao Termo de Consentimento Informado para Pacientes

Estamos realizando uma pesquisa sobre a influência genética na evolução de pacientes com Transtorno do Pânico que você já está participando conforme Consentimento prévio. Atualmente estamos desenvolvendo uma parceria com uma Universidade do exterior que dispõe de maior tecnologia para o estudo desses fatores genéticos. Com essa parceria, iremos avaliar um outro fator genético que vem sendo relacionado ao Transtorno do Pânico. Esses estudos serão desenvolvidos em parceria entre o nosso grupo de pesquisa e essa instituição do Exterior.

Eu fui informado dos objetivos acima descritos e da justificativa para qual minha amostra será enviada para o exterior e concordo.

Como existem estudos novos na área da genética a cada ano, o seu sangue poderá ser armazenado para futuras pesquisas. No entanto, a cada nova pesquisa, os pesquisadores entrarão em contato com você para obter um novo consentimento informado.

Concordo com o armazenamento do material biológico () sim

() não

O (a) pesquisador(a) certificou-me de que as informações por mim fornecidas terão caráter confidencial e no caso de divulgação serão sem identificação e unicamente para fins de pesquisa.

Porto Alegre, de de

Assinatura do paciente

Assinatura do pesquisador

Contato com pesquisadora: Carolina Blaya – Fone: 2101 82 72

Pesquisador Responsável: Gisele Gus Manfro

Termo de Consentimento Informado para os Controles

Estamos realizando um banco de dados genéticos de indivíduos sem patologia psiquiátrica. Sabe-se que a etiologia dos transtornos psiquiátricos é multifatorial, ou seja, existem alguns fatores genéticos e ambientais que predispõe às doenças. O objetivo desse estudo é estabelecer um banco de dados genéticos de indivíduos normais para que possa ser utilizado como controle nas pesquisas psiquiátricas. A avaliação constará de uma entrevista psiquiátrica e um exame de sangue que identificará alguns genes que estão sendo estudados nos transtornos psiquiátricos. Se for identificado algum problema psiquiátrico, você será encaminhado para tratamento. O anonimato dos dados será garantido através de um banco de códigos, ou seja, os seus dados não serão identificados pelo seu nome, e sim por um número. A não participação do estudo não acarretará em nenhum prejuízo no seu trabalho no HCPA.

Eu fui informado dos objetivos acima descritos e da justificativa para qual serão utilizados os dados de forma clara e detalhada. Sei que poderei solicitar novos esclarecimentos e que, a qualquer momento, terei liberdade de retirar meu consentimento da participação da pesquisa, sem prejudicar meu trabalho no HCPA. O (a) pesquisador(a) certificou-me de que as informações por mim fornecidas terão caráter confidencial e no caso de divulgação serão sem identificação e unicamente para fins de pesquisa.

Porto Alegre, de de

Assinatura do paciente

Assinatura do pesquisador

Pesquisadora: Carolina Blaya – Fone: 2101 82 72 - 3333 40 78

Pesquisador Responsável: Gisele Gus Manfro

Adendo ao Termo de Consentimento Informado para Controles

Conforme consentimento informado prévio, você faz parte de um banco de controles de patologia psiquiátrica. Estamos realizando uma pesquisa sobre a influencia genética no Transtorno do Pânico, para verificar se os pacientes com esse transtorno possuem alguma variação no material genético. Para isso, precisamos comparar os resultados dos pacientes com um grupo controle.

Eu.....fui informado dos objetivos acima descritos e concordo que avaliem marcadores genéticos na minha amostra do meu material genético.

Como existem estudos novos na área de genética a cada ano, o seu material genético poderá ser armazenado para futuras pesquisas. No entanto, a cada nova pesquisa, os pesquisadores entrarão em contato com você para obter um novo consentimento informado.

Concordo com o armazenamento do material biológico () sim

() não

O pesquisador(a) certificou-me de que as informações por mim fornecidas terão caráter confidencial e no caso de divulgação serão sem a identificação e unicamente para fins de pesquisa.

Porto Alegre, de de

Assinatura do paciente

Assinatura do pesquisador

Contato com pesquisadora – Carolina Blaya – Fone 2101 82 72

Pesquisador Responsável – Gisele Gus Manfro

16. Anexo B: Produção científica durante o período do doutorado

Com o objetivo de aumentar a amostra de pacientes com TP para os estudos de associação em genética, foi desenvolvido um ensaio clínico aberto com Milnaciprano. Esse estudo resultou em uma publicação em anexo nessa tese.



The efficacy of milnacipran in panic disorder: an open trial

Carolina Blaya, Ana Carolina Seganfredo, Marina Dornelles, Mariana Torres, Angela Paludo, Elizeth Heldt and Gisele Gus Manfro

The aim of this study is to evaluate the efficacy of milnacipran in the acute treatment of patients with panic disorder. Thirty-one patients who met *Diagnostic and Statistical Manual of Mental Disorders-IV* criteria for panic disorder with or without agoraphobia were included in the study. Patients were initially treated with milnacipran 25 mg twice daily and then 50 mg twice daily until the 10th week. The treatment outcome and panic disorder severity were determined by the Panic Disorder Severity Scale, Panic Inventory, Clinical Global Impression and Hamilton Anxiety Scale, all of which were applied during every evaluation interview. Quality of life (WHOQOL-bref) was evaluated at baseline and at the end of the study. Missing data were handled by using the last observation carried forward for all participants who had taken at least one dose of study medication. Intention-to-treat was used in the analyses. Pharmacological treatment resulted in a clinically and statistically significant mean reduction in all severity measures. Remission (Clinical Global Impression ≤ 2) was obtained in 58.1% of the sample. Regarding WHOQOL, we found a significant improvement ($P < 0.05$) across

treatment in all the domains studied. Although results may be influenced by the open design of this pilot study and by the small sample size, our findings suggest that milnacipran may be effective for the treatment of panic disorder and justify further research. *Int Clin Psychopharmacol* 00:000–000 © 2007 Lippincott Williams & Wilkins.

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Keywords: efficacy, milnacipran, open-trial, panic disorder

Post-Graduate Program in Medical Sciences: Psychiatry, Federal University of Rio Grande do Sul and Anxiety Disorders Program, Clinical Hospital of Porto Alegre, Porto Alegre, Brazil.

Correspondence to: Dr Gisele Gus Manfro, MD, PhD, Universidade Federal do Rio Grande do Sul, Ramiro Barcelos, 2350, Lúcia Manoel Gonzaga, 630/11, 90470-280, Porto Alegre, RS, Brazil
Tel: +55 51 33309272; fax: +55 51 3333 4078;
email: gmanfro@portoweb.com.br

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Introduction

Panic disorder (PD) is characterized by panic attacks, which are recurrent and followed by anticipatory anxiety and phobic avoidance (Association, 1994). This disorder usually has a chronic course, complicated by agoraphobia, impairing participants' quality of life (Candilis *et al.*, 1999; Mendlowicz and Stein, 2000).

The lifetime prevalence of PD is between 1.5 and 3.5% and is two to three times more frequent in women, usually beginning in young adulthood (Kessler *et al.*, 1994).

Serotonergic dysfunction is present in PD (Inada *et al.*, 2003). Panic patients have a decrease in this neurotransmitter in some cerebral regions (Versiani *et al.*, 2002). In addition, the response shown by panic patients when treated with selective serotonin reuptake inhibitors (SSRIs) and the worsening when using serotonergic agonist have corroborated this serotonergic dysfunction hypothesis (Versiani *et al.*, 2002; Inada *et al.*, 2003). Nowadays the SSRI are the most commonly used medication for PD (Bakker *et al.*, 2002; Baldwin *et al.*, 2005).

There is also a considerable body of evidence to implicate norepinephrine in the pathophysiology of PD. Indeed,

the locus coeruleus, which contains the highest concentration of norepinephrine cell bodies in the brain, is known to be involved in mediating fear and anxiety responses (Chamey, 1998; Coplan and Lydiard, 1998). Studies in patients with PD using agents with some degree of selectivity for the noradrenergic system have shown efficacy. Lofepamine, a norepinephrine selective tricyclic antidepressant (TCA), was shown to be at least as effective as clomipramine in reducing both the symptoms and the number of panic attacks experienced by patients (Fahy *et al.*, 1992). On the other hand, desipramine, which is also mainly selective on norepinephrine reuptake, was less effective than clomipramine in a double-blind crossover trial (Sasson *et al.*, 1999). Reboxetine, a selective norepinephrine reuptake inhibitor, has significantly improved the clinical profile of patients with PD (Versiani *et al.*, 2002), but maprotiline had almost no effect in PD (Den Boer and Westenberg, 1988).

It has been suggested that there may be an imbalance between norepinephrine and serotonin systems leading to heterogeneity in PD. Thus, one group of patients may experience panic as a result of dysfunction of the norepinephrine system, and others as a result of dysfunction on the serotonin system (Versiani *et al.*, 2002). Alternatively, dysfunction at the level of a

downstream pathway common to both the serotonin and norepinephrine (SNRI) systems may be responsible, and therefore agents acting on either system specifically could be effective. Venlafaxine, a dual-action drug that selectively inhibits the reuptake of SNRI, has been shown to be effective in PD (Pollack *et al.*, 1996) and is considered by some authors as a first line treatment for PD (Baldwin *et al.*, 2005).

Milnacipran is SNRI that generally has similar efficacy to TCAs and SSRI in the acute and long-term treatment of depression (Spencer and Wilde, 1998). Unlike the TCA, however, and owing to its singular chemical structure, which is directly associated to an inhibitory action at norepinephrine and serotonin neuronal reuptake systems, milnacipran shows no relevant affinity to other neurotransmitter receptors (postsynaptic adrenergic, muscarinic and histamine receptors). Therefore, this new antidepressant has a potential tolerance profile superior to that of the TCA, with a reduced propensity to produce undesirable antimuscarinic effects.

The pharmacokinetic profile of milnacipran is characterized by rapid absorption, high bioavailability, low protein binding and rapid elimination. This gives milnacipran certain pharmacokinetic advantages, such as low inter-individual variation in plasma levels, low potential for drug interactions and limited impact on hepatic cytochrome P450 systems (Puzzo *et al.*, 2002). When comparing milnacipran to venlafaxine and mirtazapin, which were proved to be efficient in the PD treatment (Pollack *et al.*, 1996; Sarchiapone *et al.*, 2003; Manfro and Blaya, 2004), it was found that venlafaxine and mirtazapin in lower doses have a predominantly serotonergic action, contrasting with the predominantly serotonergic and noradrenergic action of milnacipran.

Recent studies in animal models have raised the idea that milnacipran may be effective in anxiety disorders (Bouin *et al.*, 2005; Moajen *et al.*, 2006). No open or controlled trials, however, evaluating the efficacy of milnacipran in the treatment of patients with PD exist. Although controlled trials are trustworthy to assure efficacy of a medication, they can only be justified after open trials are performed.

The aim of the present study was to determine the efficacy and effectiveness of milnacipran in the acute treatment of patients with PD with or without agoraphobia.

Method

Study design

Milnacipran was administered in an open 10-week trial using a flexible dosing design. All participants, after 1 week of placebo, started on a regimen of milnacipran

25 mg twice daily. This dose was increased to 50 mg twice daily, when tolerated. The decision to increase or decrease a participant's dose was based on the treating psychiatrist's judgment of clinical response assessed by the rating scales and the absence of side effects. No other psychotropic drug or psychotherapy treatment was allowed during this trial. All patients gave their informed consent. The study was approved by the local ethical committee (number 04-225).

Study procedures

Participants in the study were recruited from clinical referrals and local media advertisements. Patients referred to the study were prescreened by an interview to determine eligibility and willingness to participate. Screening included a clinical interview, which was confirmed with the structured clinical interview Mini International Neuropsychiatric Interview – Portuguese version 5.0. (Amarim, 2000). Patients who met the inclusion criteria and agreed to participate in the study were eligible to the study.

Patient selection

Inclusion criteria

Outpatients from 18–65 years old who met *Diagnostic and Statistical Manual of Mental Disorders-IV* criteria for primary diagnosis of PD were eligible for the study. Patients should have presented at least 1 panic attack a week in the 4 weeks before entering in the study and at least 1 complete attack in the week before the study. Patients with comorbidity with mild major depression or anxiety disorders could be included if their major symptoms were related to PD. Patients should have Hamilton Anxiety (HAM-A) score above 18 and Hamilton Depression (HAM-D) below 18, be in good clinical condition, and be using safe contraceptive methods. Patients with previous pharmacological treatment could be enrolled in the study after a wash-out of three half-lives. Patients with panic attacks and Clinical Global Impression (CGI) above 2 after 1-week placebo treatment were to be included in this trial.

Exclusion criteria

Individuals were excluded if they had (i) comorbidities involving any psychotic disorder, bipolar disorder, mental retardation or any neurological disease; (ii) alcohol or drugs dependence or abuse during the previous 6 months; (iii) any history of hypersensitivity to milnacipran; (iv) Current cognitive-behavioral or psychodynamic treatment for PD (individual or group); (v) patients with other anxiety or mood disorders whose symptoms were more severe than those of PD; (vi) patients with suicide risk in the 6 months before the study; (vii) patients taking psychotropic medications in the 4 weeks before the study and whose interruption was not recommended; (viii) patients who were currently breastfeeding, pregnant or unwilling or unable to take adequate contraceptive

precautions; (ix) patients with a HAM-D score equal to or above 18.

Assessment

The CGI determines the global severity of the disease according to the frequency and intensity of panic attacks, level of anticipatory anxiety, level of phobic avoidance, a decrease in quality of life as well as the environmental maladaptation to the disorder. Its scores vary from 1 (normal, not ill) to 7 (extremely ill) (Guy, 1976).

The Panic Inventory is an instrument that characterizes panic attacks as spontaneous, situational, complete or incomplete. It also characterizes their intensity, duration and frequency, and the severity of the agoraphobia and the anticipatory anxiety.

The Hamilton Anxiety scale (HAM-A) (Hamilton, 1959) quantifies anxiety through its 14 items and scores vary from 0 to 4, according to severity. The Hamilton Depression (Hamilton, 1969) scale evaluates the severity of depressive symptoms (17 items). Participants with scores < 7 are normal, 7–17 are mild, 18–24 are moderate and > 25 are severe.

The Panic Disorder Severity Scale (Shear *et al.*, 1997) is composed of seven items with five alternatives that evaluate frequency and intensity of panic attacks, anticipatory anxiety, phobic avoidance, physical avoidance, and professional and social impairment.

The WHOQOL-*bref* evaluates quality of life. It is a self-applied instrument composed of 26 items that evaluate four domains of quality of life (physical, psychological, social relationships and environmental) (Anonymous, 1998; Fleck *et al.*, 2000).

Efficacy evaluation

The primary efficacy variables were the CGI scores, which were assessed at weeks 1, 2, 4, 6, 8 and 10.

Secondary variables included scores on HAM-A, Panic Disorder Severity Scale, Panic Inventory and WHOQOL-*bref*. All severity scales were assessed at weeks 1, 2, 4, 6, 8 and 10. The WHOQOL-*bref* was assessed at baseline and at week 10.

Remission was defined as CGI < 2 (Rapaport *et al.*, 2001) and improvement was defined according to decrease of 50% on the severity scales.

Safety measure

Side effects were assessed by spontaneous report and by a brief checklist of those commonly associated with SNRI. The checklist comprised 24 items. Each item was scored on a 4-point scale, with higher scores indicating greater

distress (0 = none, 1 = mild, 2 = moderate, 3 = severe). The checklist was completed at each session, including the first and the second interviews (baseline and after 1-week of placebo, respectively).

Statistical analysis

Missing data were handled by using the last observation carried forward for all participants who had taken at least one dose of the study medication. On the quality of life analysis, only patients who had completed the protocol were included. Participants who dropped out during the placebo run-in were excluded from the analyses ($n = 5$). Changes in baseline scores on the outcome measures were analyzed with either a paired-samples *t*-test or a repeated-measures analysis of variances. Categorical data were compared using χ^2 test (with Yates correction) and Fisher's exact test; Levene's test and Kolmogorov-Smirnov test were used for normality and homogeneity of variances. Effect size for treatment outcome was calculated with the Cohen formula ($ES = (M_1 - M_2) / \sqrt{SD_1^2 + SD_2^2} - 2 \times r \times SD_1 \times SD_2$). All analyses were conducted using the Statistical Package for the Social Sciences 14.0 version for Windows and all statistical tests were two-tailed with $\alpha = 0.05$.

Results

A flow diagram of the patients in the study is presented in Fig. 1. Out of a total of 77 screened PD patients, 37 patients were treated with 1 week of placebo treatment. One patient was excluded owing to response to placebo and five patients were excluded owing to intolerance to placebo side effects. Thirty-one patients (10 male, mean age 37 + 12 years) were finally eligible for the study and were included in the intention-to-treat efficacy analyses and safety population. Two patients withdrew from the study owing to non-compliance and one patient had a clinical intercurrent and was not able to remain in the study. The mean drop-out time was 6 weeks (range 2–8 weeks). The mean milnacipran dosage was 91 mg which was achieved by week 4.

Efficacy measures

Table 1 depicts treatment outcome measures on all severity scales. Fifteen patients (48.4%) became free of panic attacks after the treatment. Pharmacological treatment resulted in a clinically and statistically significant mean reduction in all severity measures. Remission (CGI ≤ 2) was obtained in 18 patients (58.1% of the sample). When using a stricter criterion of remission (CGI < 2 and no panic attacks) (Heldt *et al.*, 2003), 14 patients (45.2%) achieved this criterion. Improvement (i.e. decrease higher than 50% of initial symptoms) was obtained in 14 patients (45.2%) when using the Hamilton Anxiety scale, 19 patients (61.3%) when using the agoraphobia measure and 18 patients (58.1%) when using the anticipatory anxiety measure.

Regarding WHOQOL, we found a significant improvement ($P < 0.05$) across treatment in all domains studied (Table 2).

The analysis of the remission predictors resulted in no significant effect related to mean age, age of onset, sex, baseline severity or mean milnacipran dose (χ^2 and independent t -test, $P = NS$).

Safety measures

No unexpected adverse effects occurred. Most of the treatment-emergent adverse events reported during the study were mild in severity. Table 3 lists the most commonly reported treatment-emergent adverse-effects, that is, reported by at least 5% of the treated patients. Only four patients had severe side effects (two had dysuria, one had nausea and one had constipation). After a dose decrease, such effects became mild and all the patients remained in the study.

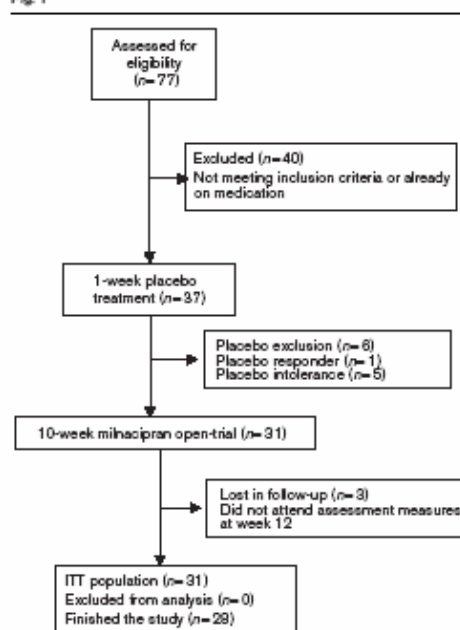
Discussion

This open trial provides preliminary evidence that milnacipran may be efficacious and well tolerated for the treatment of PD. Patients had improvement in all efficacy measures and 58% of the participants were in remission by the end of the 10-week trial. A statistically significant improvement in CGI was observed from the fourth week of treatment, and the improvement continued progressively until the end of the study. Furthermore, the drop-out numbers during milnacipran open-trial were in agreement with data found in literature (Kimura *et al.*, 2002) and were below those which were found in the placebo week. The drop-out numbers seen in our study were below those reported with TCAs and SSRI (Bakker *et al.*, 2002).

In general, milnacipran was well tolerated in this group of participants. Only four patients had serious side effects, which were easily controlled with dose decrease. Side effects, such as constipation and dry mouth, were primarily related to the anticholinergic properties of milnacipran. We also found a high incidence of dysuria which is consistent with previous reports on milnacipran (Puech *et al.*, 1997). This effect can be explained by the facilitation of sympathetic neurotransmission caused by norepinephrine reuptake inhibition in the periphery (Deakin and Darsun, 2002).

It is interesting to emphasize the effect size found with milnacipran in anticipatory anxiety which was above 2.0 (see Table 1). On the other hand, only 48% of the patients became free of panic attacks after milnacipran treatment, a result that differs from a meta-analysis (Bakker *et al.*, 2002) that reported that 60% of patients treated with TCA and 55% with SSRI became free of

Fig. 1



Flowchart of patients' progress through the phases of the study. ITT, intention-to-treat.

Table 1 Treatment outcome measures on severity scales

	Baseline mean (SD)	Week 1 mean (SD)	Week 2 mean (SD)	Week 4 mean (SD)	Week 6 mean (SD)	Week 8 mean (SD)	Week 10 mean (SD)	F(8,180)	P	Effect size ^a
PDSS	15.97 (3.43) ^b	12.84 (4.40) ^b	11.03 (5.55) ^b	8.42 (5.01) ^b	6.48 (4.82) ^b	4.81 (4.37) ^b	4.90 (4.85) ^b	59.782	<0.001	1.71
Hamilton Anxiety	24.29 (7.70) ^b	19.74 (7.00) ^b	17.61 (7.73) ^b	14.81 (7.12) ^b	12.87 (6.14) ^b	11.97 (7.07) ^b	11.42 (8.32) ^b	30.534	<0.001	1.08
Agoraphobia	7.39 (2.88) ^b	6.77 (2.99) ^b	5.94 (3.73) ^b	5.35 (3.29) ^b	4.03 (3.97) ^b	3.61 (3.77) ^b	3.2 (3.4) ^b	13.952	<0.001	1.08
Anticipatory anxiety	8.65 (2.19) ^b	8.81 (1.16) ^b	7.92 (3.16) ^b	6.13 (3.23) ^b	5.26 (3.16) ^b	4.39 (3.74) ^b	3.87 (3.04) ^b	18.772	<0.001	2.14
CGI	4.39 (0.88) ^b	3.97 (0.83) ^b	3.61 (0.91) ^b	3.19 (0.91) ^b	2.77 (0.84) ^b	2.61 (0.71) ^b	2.35 (0.87) ^b	44.098	<0.001	1.89

CGI, clinical global impression; PDSS, panic Disorder Severity Scale.

^aEffect size was calculated based on t -test between week 1 and week 10.

^bEqual letters means did not differ in Bonferroni adjustment.

Table 2 Changes in quality of life after milnacipran treatment

	Baseline mean (SD)	Week 10 mean (SD)	<i>t</i>	df.	<i>P</i>	Effect size
Physical domain	47.8 (18.7)	67.3 (19.4)	-5.90	27	<0.001	1.02
Psychological domain	46.3 (16.0)	62.8 (18.0)	-6.59	27	<0.001	0.92
Social domain	56.8 (21.8)	65.8 (17.5)	-3.17	27	0.004	0.45
Environmental domain	49.4 (14.3)	58.4 (13.0)	-3.88	27	0.001	0.63
General Quality of life	52.7 (17.5)	62.5 (18.0)	-2.92	27	0.007	0.55

*Paired *t*-test.

Table 3 Most common treatment-emergent adverse events (new or worsened symptoms)

Adverse event	Frequency (%)
Constipation ^b	18 (58.1)
Hot flashes	18 (58.1)
Nausea ^b	18 (58.1)
Anxiety	18 (58.1)
Dyspepsia	17 (54.8)
Tiredness	16 (51.6)
Agitation	16 (51.6)
Sweating	15 (48.4)
Headache	15 (48.4)
Abdominal pain	13 (41.9)
Nervousness	13 (41.9)
Dry mouth	14 (45.2)
Sexual dysfunction	12 (38.7)
Insomnia	12 (38.7)
Somnolence	12 (38.7)
Palpitation	12 (38.7)
Erectile dysfunction ^a	4 (40.0)
Dizziness	11 (35.5)
Decreased libido	10 (32.3)
Ejaculation impairment ^a	3 (30.0)
Tremor	9 (29.0)
Vomiting	7 (22.6)
Dysuria ^b	4 (12.9)
Anorgasmia	5 (16.1)

^aOn the basis of the number of men.^bPatient had severe side effects and had to decrease medication dosage.

panic attacks. Studies in rodents (Moret *et al.*, 1985) and humans (Vaishnavi *et al.*, 2004) showed that milnacipran preferentially blocks the uptake of norepinephrine when compared with serotonin by approximately 2:1. Perhaps the lower activity of milnacipran in serotonin is what led to this intermediate result in panic attacks which is close to some placebo reports (Rapaport *et al.*, 2000). The norepinephrine action may have led to a better response in anticipatory anxiety. These findings provide data that may contribute to elucidate the role of neurotransmitters in different clinical aspects of PD.

Quality of life has been a new valuable variable used in clinical trials to evaluate response (Rapaport *et al.*, 2000). Some studies suggested that quality of life in patients with PD is as impaired as that for patients with major depression, and worse than in other chronic diseases such as hypertension, type 2 diabetes, chronic obstructive pulmonary disease and osteoarthritis (Candilis *et al.*, 1999). That is the reason why changes in this measure are an important outcome for clinical studies in PD,

potentially capturing changes associated with active treatment compared with placebo (Rapaport *et al.*, 2000). Our study provides evidence that milnacipran is effective in improving quality of life of patients with PD despite having a small improvement in panic attacks. This is in accordance with a previous study which suggested that symptoms in anticipatory anxiety and avoidance appear to be more important than episodic panic attacks in affecting quality of life (Heldt *et al.*, 2006).

The analysis of remission predictors did not show any variable related to this outcome. This data differ from a previous study with sertraline in which age of onset and severity were predictors of treatment outcome (unpublished data). Maybe the small sample size of this open trial has not enabled the identification of the usual predictors of treatment response.

The major limitations of this study are the small number of patients, the absence of a placebo control group and of randomization procedures, all of which limited the generalizability of these findings. In addition, an extension to 12 or more weeks could have resulted in further improvement in the partial responders.

Despite the limitations common to all open-label studies, the results of this trial suggest that milnacipran may be an effective short-term treatment for PD. Findings from this study, however, suggest that a more rigorous randomized, double-blind, placebo-controlled trial to assess the efficacy of milnacipran in the treatment of PD is justified.

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