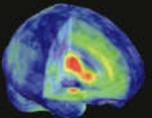


IV Seminário de Prevenção do Suicídio no Espírito Santo: resiliência em situações de suicídio, fatores de risco e proteção

Vitória 23 e 24 de setembro de 2016

Humberto Corrêa
Professor Titular de Psiquiatria da UFMG
Presidente da ABEPS
Presidente da ASULAC

Como			Somos?	
	A Genética	Quem		
Por que	E Nós	História de Vida	Interagem:	
			para produzir	
				Risco ou proteção ao suicídio.

Conflitos de Interesse

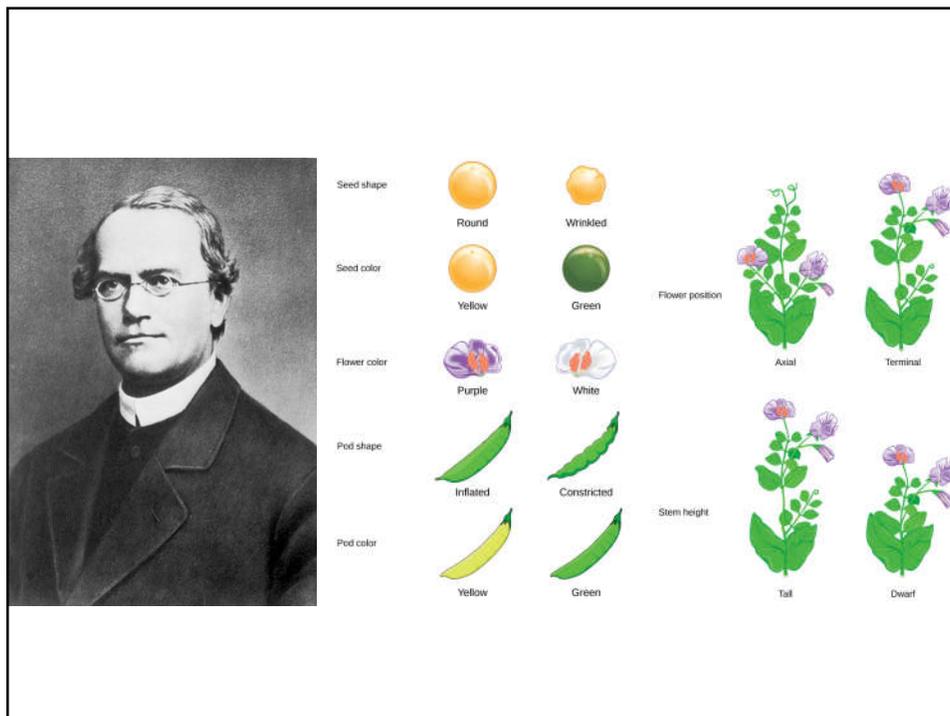
Considerando o disposto nas resoluções do Conselho Federal de Medicina (CFM n° 1.595/00 de 18/05/2000) e da Agência Nacional de Vigilância Sanitária (ANVISA n° 102/2000 de 30/11/2000), DECLARAMOS que:

Financiamento para pesquisa:

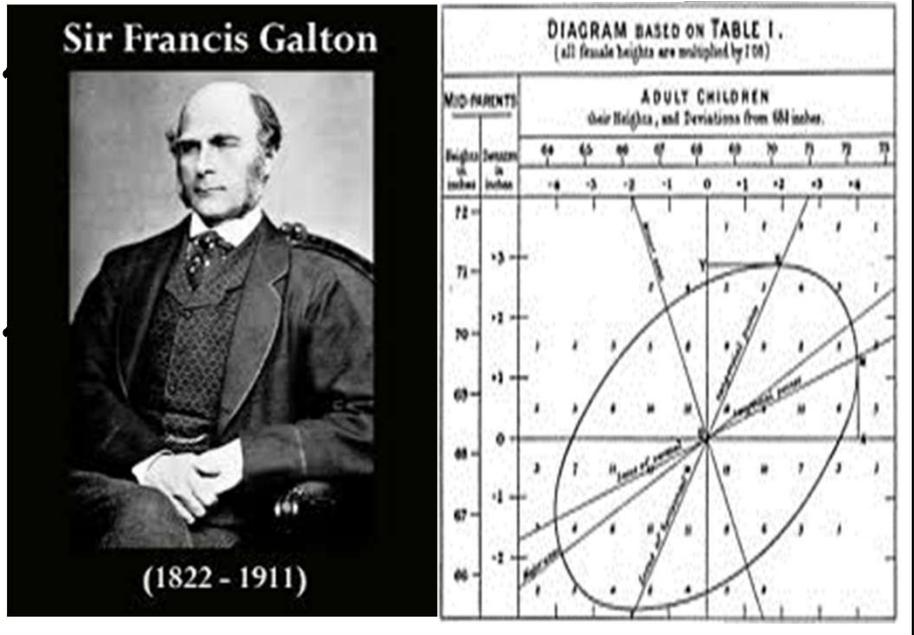
CNPq
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Bolsas Individuais:

Pesquisador Nível I
do CNPq
Pesquisador
Mineiro-FAPEMIG



Sir Francis Galton





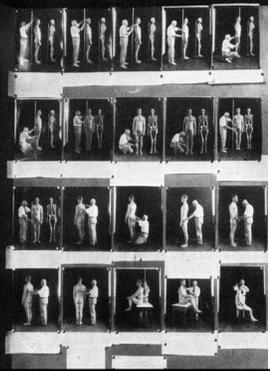


EUGENICS

EUGENICS IS THE SELF DIRECTION OF HUMAN EVOLUTION

LIKE A TREE EUGENICS DRAWS ITS MATERIALS FROM MANY SOURCES AND ORGANIZES THEM INTO AN HARMONIOUS ENTITY.



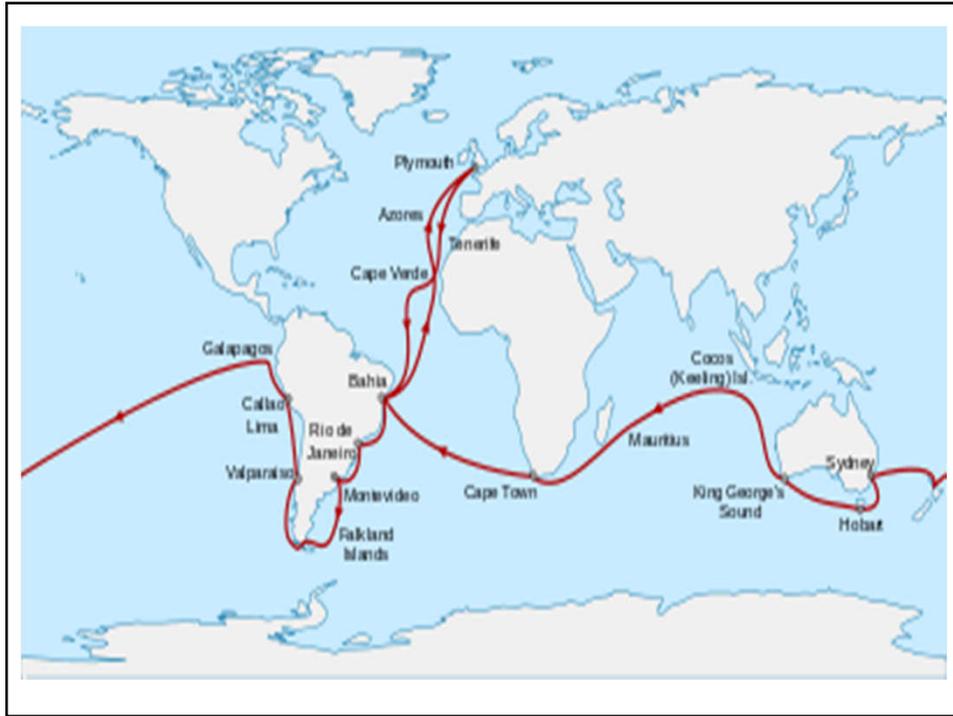


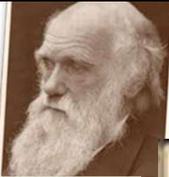


Qualitativer Bevölkerungsabstieg
bei zu schwacher Fortpflanzung der höherwertigen



So würde es kommen, wenn Minderwertige 4 Kinder und höherwertige 2 Kinder haben.





C. Darwin





1



4



2



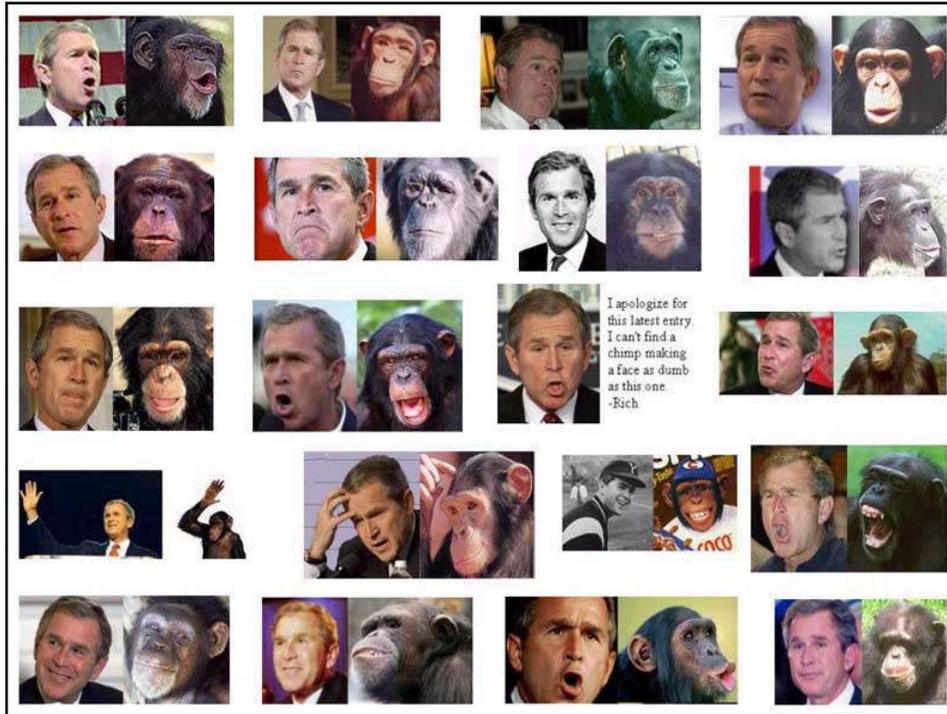
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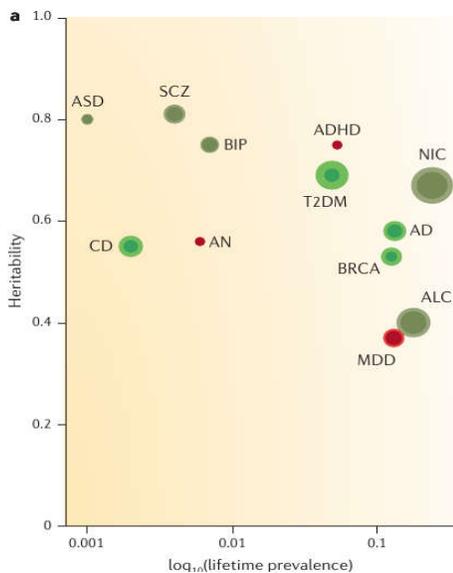
3



6



Herdabilidade das doenças psiquiátricas



ASD: transtornos do espectro autista
 AD: Alzheimer
 ADHD: Transtorno do deficit de atenção e hiperatividade
 AN: Anorexia nervosa
 ALC: Dependência ao álcool
 BIP: Transtorno Bipolar
 BRCA: Cancer de mama
 CD: Doença de Crohn
 MDD: Transtorno depressivo maior
 NIC: Dependência de nicotina
 SCZ: Esquizofrenia
 T2DM: Diabetes tipo II

Sullivan et al, 2012. Genetic architectures of psychiatric disorders: the emerging picture and its implications. *Nature*

Estudos de Genética Epidemiológica

Estudos de Família

Estudos de Gêmeos

Estudos de Adoção

Suicídio é parcialmente geneticamente determinado. Contribuição da genética seria de cerca de 50%.

no. 4356 April 25, 1953

NATURE

737

equipment, and to Dr. G. E. R. Deacon and the captain and officers of R.R.S. *Discovery II* for their part in making the observations.

*Young, F. B., Gornall, H., and Jervis, W., *Phil. Mag.*, **45**, 149 (1952).

*Logan, H., M. S., *Mem. Nat. Bur. Geol. Surv., Geophys. Rept.*, **8**, 256 (1952).

*Von Arz, W. S., *Wied. Abh. Preuss. Akad. Wiss., Physik. Math. Kl.*, **11**, 11 (1954).

*Kron, V. W., *Arch. Mikr. Techn. Anat. Pathol.*, **2**(11) (1945).

MOLECULAR STRUCTURE OF NUCLEIC ACIDS

A Structure for Deoxyribose Nucleic Acid

WE wish to suggest a structure for the salt of deoxyribose nucleic acid (D.N.A.). This structure has novel features which are of considerable biological interest.

A structure for nucleic acids has already been proposed by Pauling and Corey¹. They kindly made their manuscript available to us for advance publication. Their model consists of two intertwined chains, with the phosphates near the fibre axis, and the bases on the outside. In our opinion, this structure is unsatisfactory for two reasons:

(1) We believe that the material which gives the X-ray diagram is the salt, not the free acid. Without the acidic hydrogen atoms it is not clear what forces would hold the structure together, especially as the negatively charged phosphates near the axis will repel each other. (2) Some of the van der Waals distances appear to be too small.

Another three-chain structure has also been suggested by Fraser (in the press). In his model the phosphates are on the outside and the bases on the inside, linked together by hydrogen bonds. This structure as described is rather ill-defined, and for this reason we shall not comment on it.

We wish to put forward a radically different structure for the salt of deoxyribose nucleic acid. This structure has two helical chains each coiled round the same axis (see diagram). We have made the usual chemical assumptions, namely, that each chain consists of phosphate ester groups joining β-D-deoxy-ribofuranose residues with 3',5' linkages. The two chains (but not their bases) are related by a dyad perpendicular to the fibre axis. Both chains follow right-handed helices, but owing to the dyad the sequences of the atoms in the two chains run in opposite directions. Each chain loosely resembles Furberg's model No. 1; that is, the bases are on the inside of the helix and the phosphates on the outside. The configuration of the sugar and the atoms near it is close to Furberg's 'standard configuration', the sugar being roughly perpendicular to the attached base. There



The figure is a schematic diagram of the proposed DNA structure. It shows two intertwined helical chains around a common vertical axis, which is labeled as the fibre axis. The chains are right-handed helices. The diagram illustrates the arrangement of phosphate groups and deoxyribose sugar residues, with hydrogen bonds between the bases of the two chains. A vertical line indicates the fibre axis.

is a residue on each chain every 3.4 Å, in the z-direction. We have assumed an angle of 36° between adjacent residues in the same chain, so that the structure repeats after 10 residues on each chain, that is, after 34 Å. The distance of a phosphorus atom from the fibre axis is 10 Å. As the phosphates are on the outside, cations have easy access to them. The structure is an open one, and its water content is rather high. At lower water contents we would expect the bases to tilt so that the structure could become more compact.

The novel feature of the structure is the manner in which the two chains are held together by the purine and pyrimidine bases. The planes of the bases are perpendicular to the fibre axis. They are joined together in pairs, a single base from one chain being hydrogen-bonded to a single base from the other chain, so that the two lie side by side with identical x-coordinates. One of the pair must be a purine and the other a pyrimidine for bonding to occur. The hydrogen bonds are made as follows: purine position 1 to pyrimidine position 1; purine position 6 to pyrimidine position 6.

If it is assumed that the bases only occur in the structure in the most plausible tautomeric forms (that is, with the keto rather than the enol configurations) it is found that only specific pairs of bases can bond together. These pairs are: adenine (purine) with thymine (pyrimidine), and guanine (purine) with cytosine (pyrimidine).

In other words, if an adenine forms one member of a pair, the other must be thymine; similarly for guanine and cytosine. The sequence of bases on a single chain does not appear to be restricted in any way. However, if only specific pairs of bases can be formed, it follows that the sequence of bases on one chain is given, then the sequence on the other chain is automatically determined. It is found that the ratio of the amounts of adenine to thymine, and the ratio of guanine to cytosine, are always very nearly unity for deoxyribose nucleic acid.

It has been found experimentally that the ratio of the amounts of adenine to thymine, and the ratio of guanine to cytosine, are always very nearly unity for deoxyribose nucleic acid.

It is probably impossible to build this structure with a ribose sugar in place of the deoxyribose, as the extra oxygen atoms would make too close a van der Waals contact.

The previously published X-ray data^{2,3} on deoxyribose nucleic acid are insufficient for a rigorous test of our structure. So far as we can tell, it is roughly compatible with the experimental data, but it must be regarded as unproved until it has been checked against more exact results. Some of these are given in the following communications. We were not aware of the details of the results presented there when we devised our structure, which rests mainly though not entirely on published experimental data and stereochemical arguments.

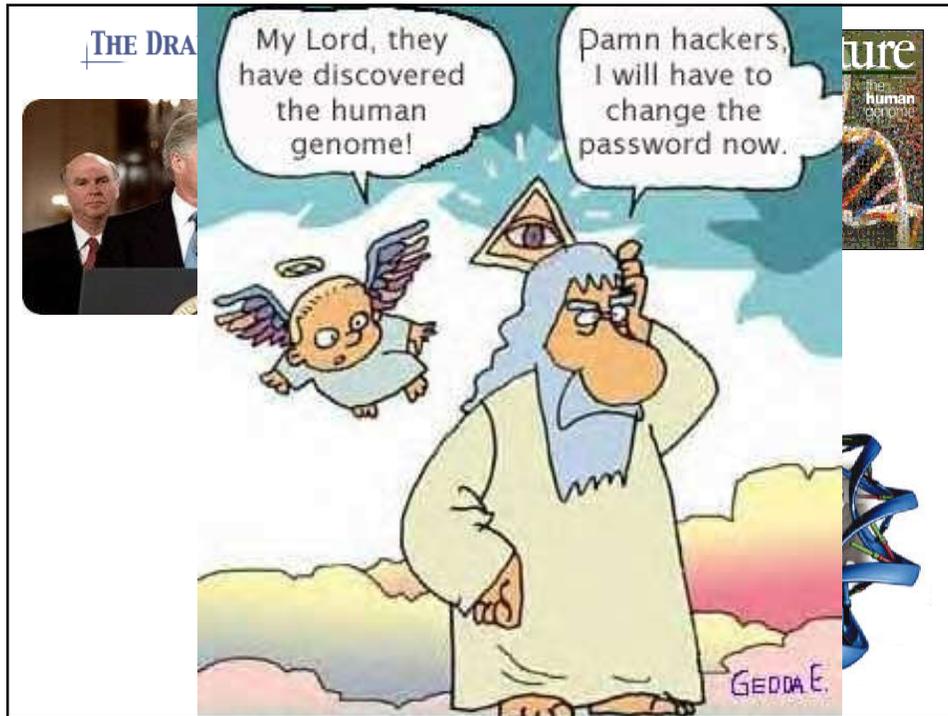
It has not escaped our notice that the specific pairing we have postulated immediately suggests a possible copying mechanism for the genetic material. Full details of the structure, including the conditions assumed in building it, together with a set of co-ordinates for the atoms, will be published elsewhere.

We are much indebted to Dr. Jerry Donohue for constant advice and criticism, especially on inter-atomic distances. We have also been stimulated by a knowledge of the general nature of the unpublished experimental results and ideas of Dr. M. H. F. Wilkins, Dr. R. E. Franklin and their co-workers at



"We wish to suggest a structure for the salt of [DNA]."

This structure has novel features which are of considerable biological interest."



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NEWSFOCUS



Gene Tests for Psychiatric Risk Polarize Researchers

A small California company is the first to venture into psychiatric gene testing. But is the science ready?

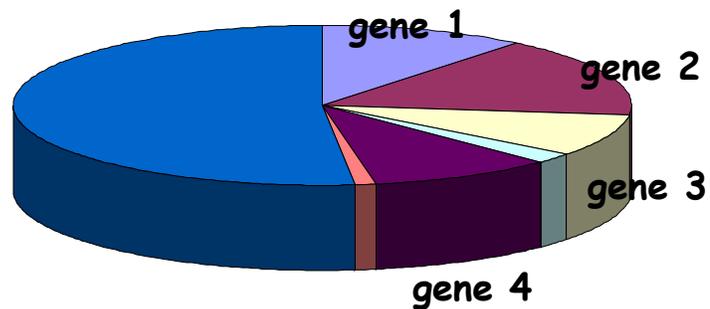


Players in the Psychiatric Gene-Testing Business

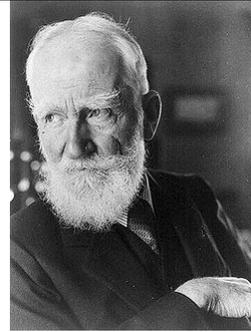
Company	Test available	Disease	Type of test	Number of genes
NeuroMark	mid-2008	Major depression	Risk of suicidality from antidepressants	4
Psynomics	now	Bipolar disorder	Diagnosis and response to antidepressants	2*
SureGene	mid-2009	Schizophrenia	Risk of psychosis and response to antipsychotics	6

* Psynomics plans to add five more genes early this year.

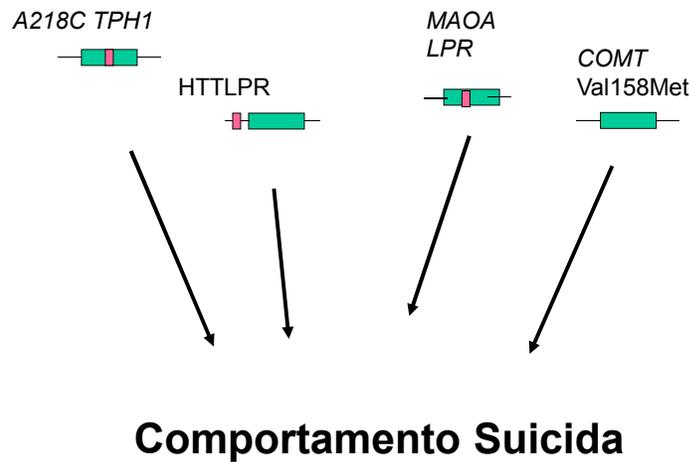
Quais são os 04 genes da suicidabilidade??

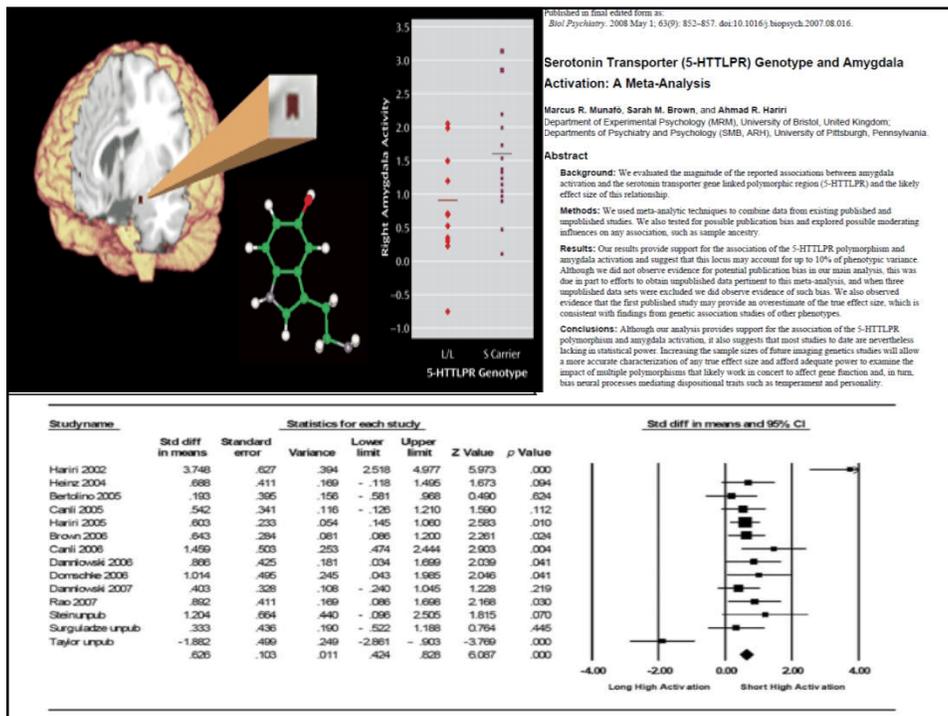
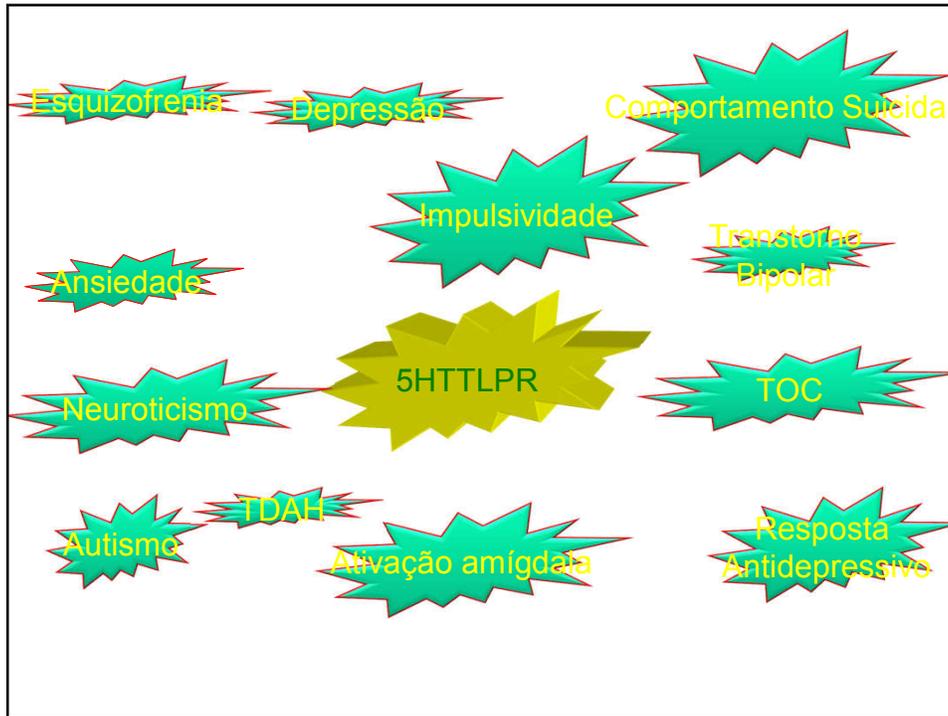


"Para todo problema complexo, existe uma solução clara, simples...

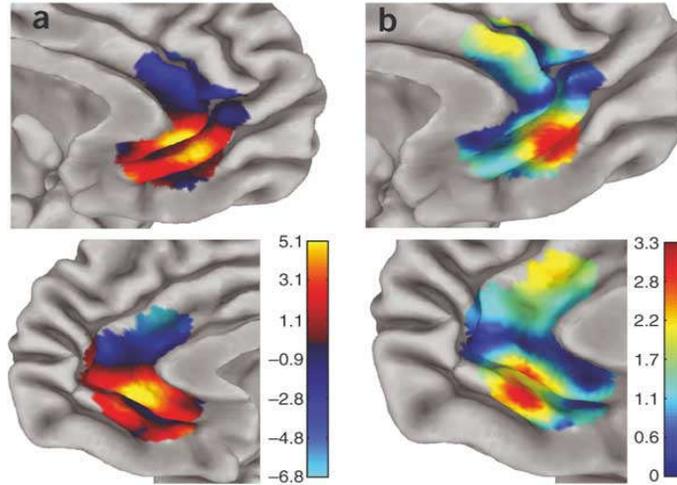


e errada."

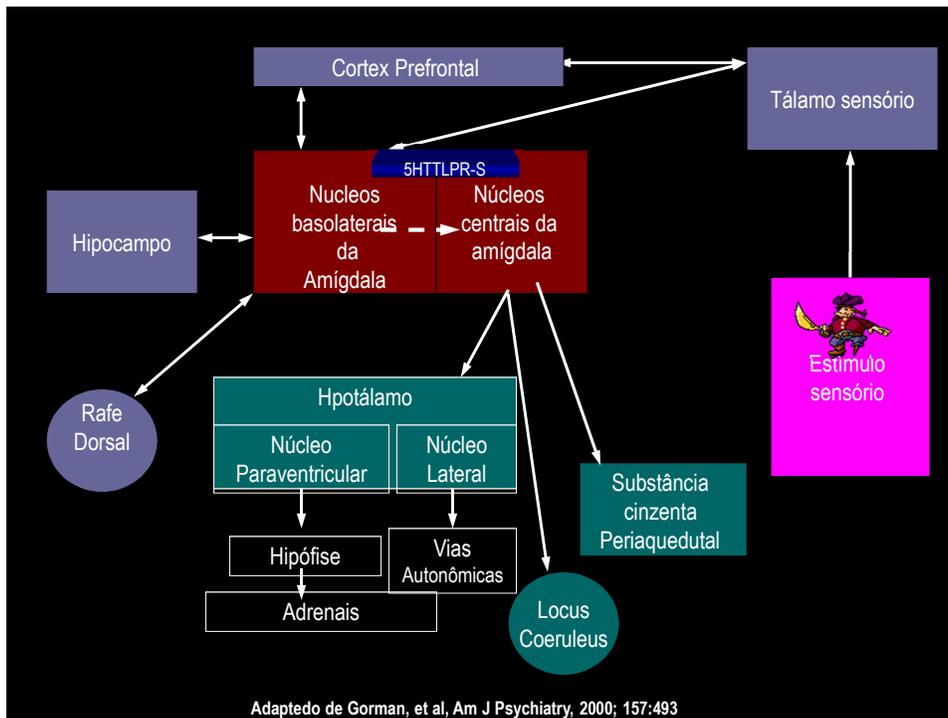




Nature Neuroscience 8, 828 - 834 (2005) 5-HTTLPR polymorphism impacts human cingulate-amygdala interactions: a genetic susceptibility mechanism for depression
Lukas Pezawas et al.



Integridade dessa via córtico-amígdala seria comprometida em portadores do alelo S resultando em perda da integração e regulação inibitória da Amígdala.



Adaptado de Gorman, et al, Am J Psychiatry, 2000; 157:493

HPA Axis Reactivity: A Mechanism Underlying the Associations Among 5-HTTLPR, Stress, and Depression

Ian H. Gotlib, Jutta Joormann, Kelly L. Minor, and Joachim Hallmayer

Background: Recent evidence indicates that individuals who are homozygous for the short (s) allele in the promoter region of the serotonin transporter gene have higher rates of depression and other psychiatric disorders as a function of exposure to increasing levels of stressful life events than do individuals who have one or two copies of the long (l) allele. Despite the reliability of this association, the mechanism by which this polymorphism confers risk for psychopathology in the presence of stress is not understood. This study was designed to examine the formulation that individuals who are homozygous for the s allele are characterized by a greater biological reactivity to stress than are their counterparts who have one or two copies of the l allele.

Methods: Girls at high ($n = 25$) and low ($n = 42$) risk for depression by virtue of the presence or absence of a family history of this disorder were genotyped and exposed to a standardized laboratory stress task. Cortisol levels were assessed before the stressor, after the stressor, and during an extended recovery period.

Results: Girls who were homozygous for the s allele produced higher and more prolonged levels of cortisol in response to the stressor than did girls with an l allele.

Conclusions: These findings indicate that the 5-HTTLPR polymorphism is associated with biological stress reactivity, which may increase susceptibility to depression in the face of stressful life events.

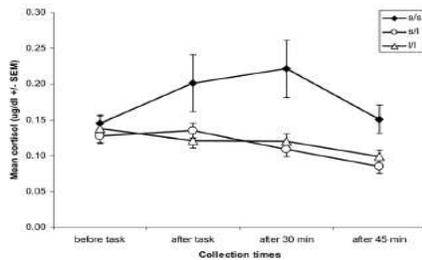


Figure 1. Stress reactivity by genotype.

of measurements (31), $F(2,63) = 4.26$, $p < .05$, reflecting the elevated cortisol production in response to stress in daughters who were homozygous for the s allele.⁷

Genetic Variation in Brain-Derived Neurotrophic Factor Is Associated with Serotonin Transporter but Not Serotonin-1A Receptor Availability in Men

Susanne Henningsson, Jacqueline Borg, Johan Lundberg, Jessica Bah, Mats Lindström, Erik Ryding, Hristina Jovanovic, Tomoyuki Saijo, Makoto Inoue, Ingmar Rosén, Lil Traskman-Bendz, Lars Farde, and Elias Eriksson

Background: The serotonergic system, including the serotonin transporter (5-HTT), which is the target of many antidepressants, seems to be influenced by brain-derived neurotrophic factor (BDNF).

Methods: Positron emission tomography (PET) was used to address, in 25 and 53 healthy volunteers, respectively, the possible association between six polymorphisms in the gene encoding BDNF and the availability of two proteins expressed by serotonergic neurons: the 5-HTT, measured with the radioligand [¹¹C]MADAM, and the serotonin-1A (5-HT1A) receptor, measured with [¹¹C]WAY-100635.

Results: Several single nucleotide polymorphisms were associated with [¹¹C]MADAM binding potential (BP) in most brain regions, male carriers of the valine/valine genotype of the Val66Met polymorphism displaying higher availability. Effect sizes ranged from a 50% to a threefold increase. In contrast, there was no association for [¹¹C]WAY-100635 BP. The observation that BDNF polymorphisms were associated with 5-HTT availability could be partly replicated in an independent population comprising nine male suicide attempters and nine matched control subjects, in which transporter availability had been measured with single photon emission computed tomography with [¹²⁵I]-9-CIT as ligand.

Conclusions: Our results suggest that genetic variation in BDNF influences 5-HTT but not 5-HT1A receptor density in the human brain.

Key Words: BDNF, imaging, PET, serotonin, serotonin transporter, and synaptic localization, exerts its effects via another receptor, p75NTR (21,23).

BIOL PSYCHIATRY 2009;66:477-485
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Influence of Life Stress on Depression: Moderation by a Polymorphism in the 5-HTT Gene

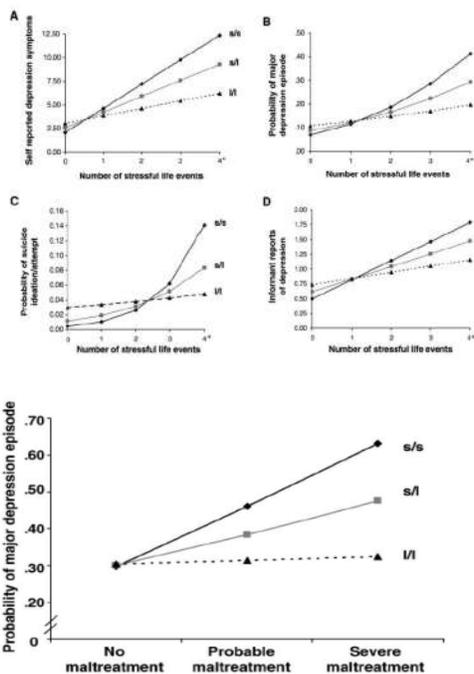
Avshalom Caspi,^{1,2} Karen Sugden,¹ Terrie E. Moffitt,^{1,2*} Alan Taylor,¹ Ian W. Craig,¹ Honalee Harrington,² Joseph McClay,¹ Jonathan Mill,¹ Judy Martin,³ Antony Braithwaite,⁴ Richie Poulton³

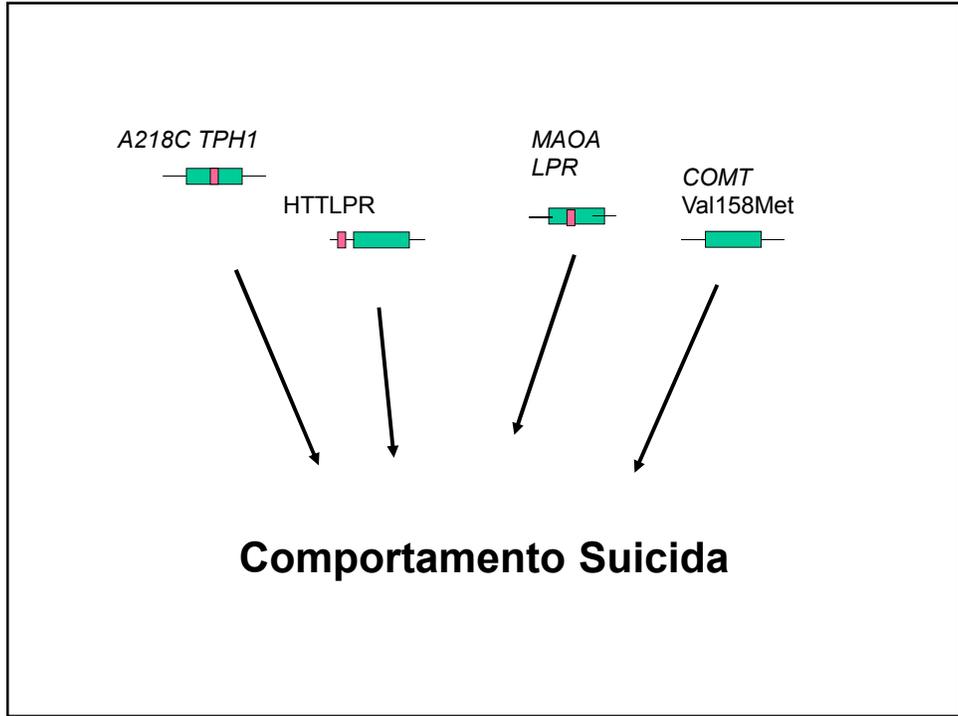
In a prospective-longitudinal study of a representative birth cohort, we tested why stressful experiences lead to depression in some people but not in others. A functional polymorphism in the promoter region of the serotonin transporter (5-HTT) gene was found to moderate the influence of stressful life events on depression. Individuals with one or two copies of the short allele of the 5-HTT promoter polymorphism exhibited more depressive symptoms, diagnosable depression, and suicidality in relation to stressful life events than individuals homozygous for the long allele. This epidemiological study thus provides evidence of a gene-by-environment interaction, in which an individual's response to environmental insults is moderated by his or her genetic makeup.

Depression is among the top five leading causes of disability and disease burden throughout the world (1). Across the life span, stressful life events that involve threat, loss, humiliation, or defeat influence the onset and course of depression (2-5). However, not all people who encounter a stressful life experience succumb to its depressogenic effect. Diathesis-stress theories of depression predict that individuals' sensitivity to stressful events depends on their genetic makeup (6, 7). Behavioral genetics research supports this prediction, documenting that the risk of depression after a stressful event is elevated among people who are at high genetic risk and diminished among those at low genetic risk (8). However, whether specific genes exacerbate or buffer the effect of stressful life events on depression is unknown. In this study, a functional polymorphism in the pro-

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REPORTS





Published online: July 4, 2015

Epigenetic Dysregulation in the Prefrontal Cortex of Suicide Completers

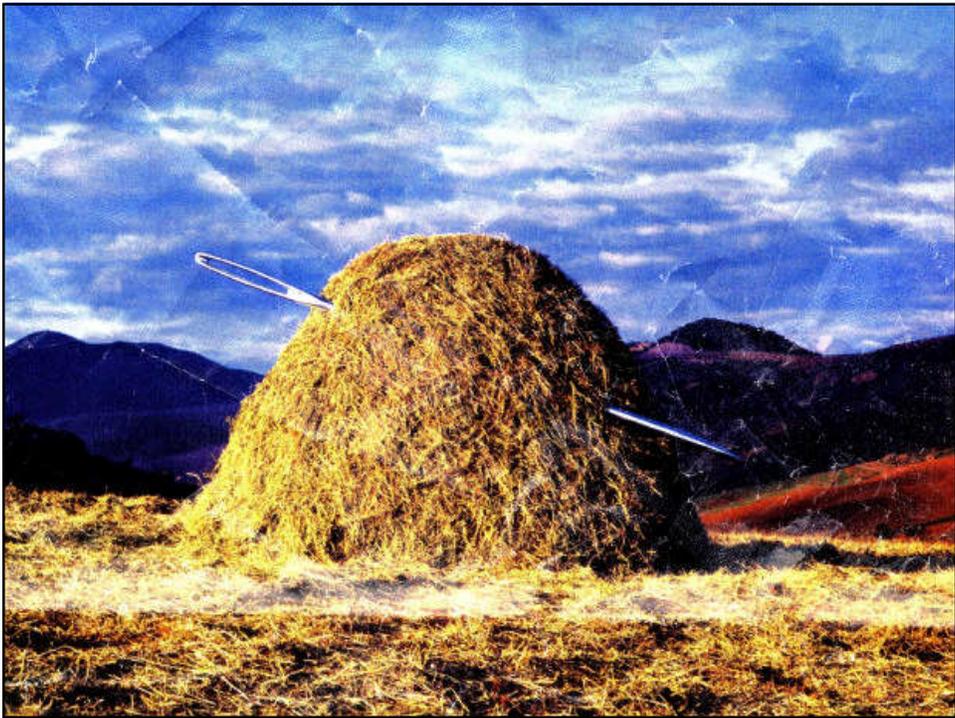
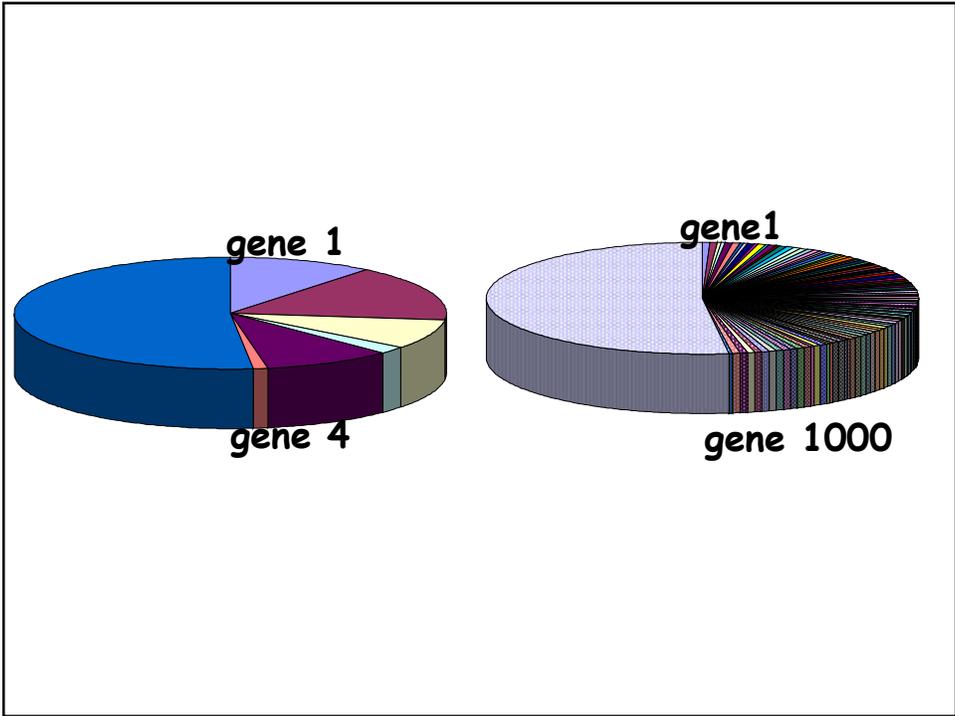
Eberhard Schneider^a Nady El Hajj^a Fabian Müller^b Bianca Navarro^c Thomas Haaf^a

^aInstitute of Human Genetics, University of Würzburg, Würzburg, ^bMax Planck Institute for Informatics, Saarbrücken, and ^cInstitute of Legal Medicine, University Medical Center, Mainz, Germany

Table 2. Suicide candidate genes that have been replicated in genetic association, brain expression and methylation studies, respectively

Gene ^a	Genetic association	DNA methylation	Expression	Gene ^a	Genetic association	DNA methylation	Expression	Gene ^a	Genetic association	DNA methylation	Expression
<i>ABAT</i>			X	<i>HTR2A</i>	X		X	<i>RPL19</i>			X
<i>AC004507.1</i>	X			<i>HTR2C</i>	X		X	<i>RPS6KA1</i>		X	X
<i>ACCN3</i>	X			<i>HTRA1</i>			X	<i>S100A10</i>	X		X
<i>ADCT8</i>	X			<i>IFNG</i>		X		<i>S100B</i>			X
<i>AMD1</i>		X	X	<i>ILDR2</i>		X		<i>SCD3</i>			X
<i>APLP2</i>			X	<i>ITPR1</i>			X	<i>SFRS5</i>		X	X
<i>ACPF4</i>		X	X	<i>KCNIL2</i>		X		<i>SGK2</i>			X
<i>ARG2</i>		X	X	<i>KLHL34</i>		X		<i>SLC1A2</i>			X
<i>ARVCF</i>		X	X	<i>KRT37</i>		X		<i>SLC1A3</i>			X
<i>ASB3</i>		X	X	<i>LASS2</i>		X		<i>SLC6A4</i>	X		X
<i>ATP1B2</i>			X	<i>LEPR</i>			X	<i>SLC14A1</i>		X	X
<i>ATPSY0A1</i>			X	<i>LRMS1</i>	X		X	<i>SMOX</i>			X
<i>BDNF</i>	X	X	X	<i>LOC100129652</i>			X	<i>SMS</i>			X
<i>BTG1</i>			X	<i>LOC440917</i>			X	<i>SNAP25</i>			X
<i>C10orf120</i>		X	X	<i>MAPKAP1</i>	X		X	<i>SNORA68</i>		X	X
<i>C10orf1</i>		X	X	<i>MARCKS</i>		X	X	<i>SNORD31</i>		X	X
<i>C10orf45</i>		X	X	<i>MCRS1</i>	X		X	<i>SNORD50B</i>		X	X
<i>C10orf71</i>		X	X	<i>MBP</i>		X	X	<i>SNORD114-14</i>		X	X
<i>CD6</i>			X	<i>MEI</i>			X	<i>SNORD115-7</i>		X	X
<i>CENPF</i>		X	X	<i>MIR10B</i>		X	X	<i>SNORD115-22</i>		X	X
<i>CLRC12B</i>		X	X	<i>MIR555</i>		X	X	<i>SNP1</i>			X
<i>COMT</i>	X		X	<i>MOG</i>		X	X	<i>SOX9</i>			X
<i>CREB</i>			X	<i>MSI1</i>		X	X	<i>SPTBN1</i>	X		X
<i>CRHR2</i>	X		X	<i>MSMP</i>		X	X	<i>SSAT</i>		X	X
<i>CTNNB1</i>			X	<i>NME1-NME2</i>		X	X	<i>SST</i>		X	X
<i>DEDD</i>		X		<i>PHC1B</i>		X	X	<i>SYN2</i>		X	X
<i>DLEC1</i>		X	X	<i>NTRK2</i>		X	X	<i>SYNE2</i>		X	X
<i>DTNA</i>		X	X	<i>NRX1</i>		X	X	<i>SYNP2</i>		X	X
<i>DYRK2</i>		X	X	<i>OR13G1</i>		X	X	<i>SYNP2L</i>		X	X
<i>ECHDC1</i>		X	X	<i>PCHL2</i>		X	X	<i>SYPL1</i>		X	X
<i>EZR</i>		X	X	<i>PCTP</i>		X	X	<i>TAF5L</i>			X
<i>F10</i>		X	X	<i>PHACTR3</i>		X	X	<i>TFPT</i>			X
<i>FAM49B</i>		X	X	<i>PHC1B</i>		X	X	<i>TGM7</i>			X
<i>FAM96A</i>		X	X	<i>PKM2</i>		X	X	<i>TGOLN2</i>	X		X
<i>GABRR2</i>			X	<i>PCP2</i>		X	X	<i>TPRS36</i>		X	X
<i>GABRA1</i>			X	<i>PLSCR4</i>		X	X	<i>TNFA</i>	X		X
<i>GABRR1</i>			X	<i>PMP1</i>		X	X	<i>TOP1</i>			X
<i>GATM</i>			X	<i>PMP22</i>		X	X	<i>TPH1</i>	X		X
<i>GJA1</i>	X		X	<i>PNMAL2</i>		X	X	<i>TPH2</i>	X		X
<i>GLUL</i>			X	<i>PCMP</i>		X	X	<i>TSPL1</i>			X
<i>GP5</i>		X	X	<i>PRK3</i>		X	X	<i>UBC</i>			X
<i>GRM4B</i>		X	X	<i>PRKCI</i>		X	X	<i>UGT1A9</i>		X	X
<i>GPR133</i>		X	X	<i>PRR40A</i>		X	X	<i>USP25</i>		X	X
<i>GRI2</i>			X	<i>PTDSS1</i>		X	X	<i>USP2X</i>		X	X
<i>GSK3B</i>	X		X	<i>PTN</i>		X	X	<i>VAMP3</i>		X	X
<i>H3F3B</i>		X	X	<i>PTP4A2</i>		X	X	<i>VAV3</i>		X	X
<i>HIST2H2AB</i>		X	X	<i>RAB31</i>	X		X	<i>VTG1</i>		X	X
<i>HOMER2</i>		X	X	<i>RAC1</i>		X	X	<i>YWHAE</i>		X	X
<i>HSD17B6</i>			X	<i>RFT1</i>		X	X	<i>ZNF185</i>		X	X
<i>HTR1A</i>	X		X	<i>RIMS1</i>		X	X	<i>ZNF259</i>		X	X
<i>HTR1B</i>	X		X	<i>RNF6</i>		X	X	<i>ZNF546</i>		X	X
				<i>RPL13A</i>		X	X				X

* Genes highlighted in bold belong to the top 1,000 DMRs.



SCIENTIFIC CORRESPONDENCE

Association of the serotonin transporter promoter polymorphism with suicidal behavior

Molecular Psychiatry (2003) 0, 1–2. doi:10.1038/sj.mp.4001381

is important because a significant degree of past suicidal behavior may not be recorded during routine clinical assessment.⁴ Furthermore, we evaluated, for the most lethal lifetime suicide attempt; the lethality, using the Lethality Rating Scale (LRS), scored 0–8,^{7,2} with a score of 3 or greater as a cutoff point; the intention with the Suicide Intent Scale (SIS);⁸ and the methods, classified as nonviolent (drug overdose) or violent (cutting beyond a superficial scratch, jumping from a height, shooting, hanging).

$P=0.001$). In S-carriers, LL-carriers as reference, the odds ratio were 2.34 (95% CI (1.32–4.15)), 2.44 (95% CI (0.93–6.53)) and 3.97 (95% CI(1.37–11.91)), respectively, to number of suicide attempts, lethality greater than 2 and violent suicide attempt.

AC Campi-Azevedo^{1,2}, W Bason³, LA De Marco^{1,2}, MA Romano-Silva^{1,2,3,4} and H Correa^{1,2,3,4}
¹Laboratório de Farmacogenética, ICB, Universidade Federal de Minas Gerais, Belo Horizonte-MG, Brazil; ²Departamento de Farmacologia, ICB, Universidade Federal de Minas Gerais, Belo Horizonte-MG, Brazil; ³Departamento de Morfologia, ICB, Universidade Federal de Minas Gerais, Belo Horizonte-MG, Brazil; ⁴Grupo de

SCIENTIFIC CORRESPONDENCE

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AC Campi-Azevedo^{1,2}, W Bason³, LA De Marco^{1,2}, MA Romano-Silva^{1,2,3,4} and H Correa^{1,2,3,4}
¹Laboratório de Farmacogenética, ICB, Universidade Federal de Minas Gerais, Belo Horizonte-MG, Brazil; ²Departamento de Farmacologia, ICB, Universidade Federal de Minas Gerais, Belo Horizonte-MG, Brazil; ³Departamento de Morfologia, ICB, Universidade Federal de Minas Gerais, Belo Horizonte-MG, Brazil; ⁴Grupo de Pesquisa em Neuropsiquiatria Clínica e Molecular, Universidade Federal de Minas Gerais, Belo Horizonte-MG, Brazil

Correspondence should be addressed to Professor H Correa, Departamento de Neurologia-ICB, Universidade Federal de Minas Gerais, Av. Antônio Carlos 662, 31220-004 Belo Horizonte-MG, Brazil.
E-mail: hcorrea@icb.ufmg.br

Investigation of A218C tryptophan hydroxylase polymorphism: association with familial suicide behavior and proband's suicide attempt characteristics

W Bason¹, LA De Marco¹, H Correa¹, MA Romano-Silva¹ and AC Campi-Azevedo¹

1 Laboratório de Farmacogenética, Instituto de Ciências Biológicas, Universidade Federal de Minas Gerais, Av. Antônio Carlos 662, 31220-004 Belo Horizonte-MG, Brazil

Background: The serotonin transporter (5-HTT) gene has been associated with suicidal behavior. The aim of this study was to investigate the association of the A218C polymorphism of the tryptophan hydroxylase 2 (TPH2) gene with suicidal behavior and suicidal attempt characteristics in a sample of 100 bipolar patients.

Method: The TPH2 gene was genotyped in 100 bipolar patients and 100 healthy controls. The association of the A218C polymorphism with suicidal behavior and suicidal attempt characteristics was investigated using logistic regression analysis.

Results: The TPH2 gene was genotyped in 100 bipolar patients and 100 healthy controls. The association of the A218C polymorphism with suicidal behavior and suicidal attempt characteristics was investigated using logistic regression analysis.

Conclusion: The TPH2 gene was genotyped in 100 bipolar patients and 100 healthy controls. The association of the A218C polymorphism with suicidal behavior and suicidal attempt characteristics was investigated using logistic regression analysis.

Keywords: TPH2, bipolar disorder, suicidal behavior, suicidal attempt characteristics

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Journal of Affective Disorders 100 (2003) 201–208

Research paper

The 5-HTTLPR polymorphism, impulsivity and suicide behavior in euthymic bipolar patients

Leandro Fernandes Malloy-Diniz^{1,2,3}, Fernando Silva Neves^{3,4}, Paulo Henrique Paiva de Moraes^{3,4}, Luiz Armando De Marco^{3,4}, Marco Aurélio Romano-Silva^{3,4}, Maria-Delise Krebs³, Humberto Correa^{3,4}

¹Departamento de Psiquiatria, Universidade Federal de Minas Gerais, Avenida Antônio Carlos 662, Belo Horizonte, Minas Gerais, Brazil; ²Departamento de Neurologia, Universidade Federal de Minas Gerais, Avenida Antônio Carlos 662, Belo Horizonte, Minas Gerais, Brazil; ³Departamento de Farmacologia, Universidade Federal de Minas Gerais, Avenida Antônio Carlos 662, Belo Horizonte, Minas Gerais, Brazil; ⁴Grupo de Pesquisa em Neuropsiquiatria Clínica e Molecular, Universidade Federal de Minas Gerais, Avenida Antônio Carlos 662, Belo Horizonte, Minas Gerais, Brazil

Brief Research Communication
Is the 5-HTTLPR Polymorphism Associated With Bipolar Disorder or With Suicidal Behavior of Bipolar Disorder Patients?

F.S. Neves¹, G. Silveira², M.A. Romano-Silva¹, L. Malloy-Diniz¹, A.A. Ferreira¹, L. De Marco³ and H. Correa^{1,2,3,4}

¹Laboratório de Farmacogenética, Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil; ²Departamento de Farmacologia, Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil; ³Departamento de Morfologia, Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil; ⁴Grupo de Pesquisa em Neuropsiquiatria Clínica e Molecular, Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil

Association study of serotonin 2A receptor (5-HT2A) gene with schizophrenia and suicidal behavior using systematic meta-analysis
Doree Li^{1,2,3}, Yan Duan^{3,4}, Lin He^{3,4}

Background: The serotonin 2A receptor (5-HT2A) gene has been associated with schizophrenia and suicidal behavior. The aim of this study was to investigate the association of the 5-HT2A gene with schizophrenia and suicidal behavior using systematic meta-analysis.

Method: The 5-HT2A gene was genotyped in 100 bipolar patients and 100 healthy controls. The association of the 5-HT2A gene with suicidal behavior and suicidal attempt characteristics was investigated using logistic regression analysis.

Results: The 5-HT2A gene was genotyped in 100 bipolar patients and 100 healthy controls. The association of the 5-HT2A gene with suicidal behavior and suicidal attempt characteristics was investigated using logistic regression analysis.

Conclusion: The 5-HT2A gene was genotyped in 100 bipolar patients and 100 healthy controls. The association of the 5-HT2A gene with suicidal behavior and suicidal attempt characteristics was investigated using logistic regression analysis.

Keywords: 5-HT2A, bipolar disorder, suicidal behavior, suicidal attempt characteristics

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Journal of Affective Disorders 100 (2003) 201–208

Research paper

Genetic variations in FOXO3A are associated with Bipolar Disorder with conferring vulnerability for suicidal behavior

Luiz Alexandre V. Magnó¹, Carolina V.M. Santana¹, Erika K. Sacramento¹, Vinícius R. Bezerra¹, Marcus V. Cardoso¹, Luiz Mauro-da-Silva¹, Fernando S. Neves¹, Dora M. Miranda¹, Luiz A. De Marco¹, Humberto Correa¹, Marco A. Romano-Silva¹

¹Laboratório de Farmacogenética, Universidade Federal de Minas Gerais, Avenida Antônio Carlos 662, Belo Horizonte, Minas Gerais, Brazil; ²Departamento de Farmacologia, Universidade Federal de Minas Gerais, Avenida Antônio Carlos 662, Belo Horizonte, Minas Gerais, Brazil; ³Departamento de Morfologia, Universidade Federal de Minas Gerais, Avenida Antônio Carlos 662, Belo Horizonte, Minas Gerais, Brazil; ⁴Grupo de Pesquisa em Neuropsiquiatria Clínica e Molecular, Universidade Federal de Minas Gerais, Avenida Antônio Carlos 662, Belo Horizonte, Minas Gerais, Brazil



EPIGENETICS

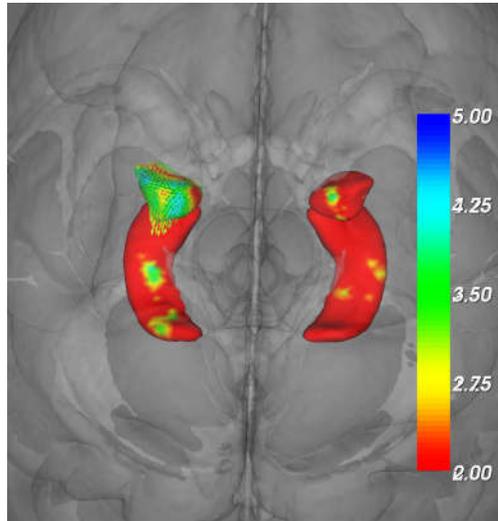
Tales of adversity

Genetic studies of people conceived during famine reveals that prenatal malnutrition lingers long after the event.

S 20 | NATURE | VOL 468 | 23/30 DECEMBER 2010

Fetal exposure to maternal cortisol is associated with child brain development

- **Altas concentrações de cortisol na gestação são associadas com maiores volumes do corpo amigdalóide e mais problemas psiquiátricos futuros.**
- A magnitude do aumento é substancial: 1 SD de aumento no cortisol materno associado com 6.4% de aumento.



Buss et al., *Proceedings of the National Academy of Science*, 2012, 109, E1312-1319

ARTICLES

COMT + Materna

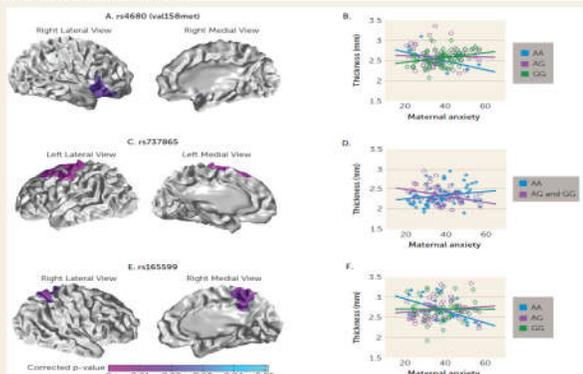
Anqi Qiu, Ph.D., T Birit F.P. Broekman, Marielle V. Fortier,

Objective: Explore complex genetic variation in particular, the COMT gene located on chromosome 22, which is involved in dopamine signaling in the brain, and stress-related gene and their interaction with antenatal maternal anxiety.

Method: A total of 1,000 children underwent MRI shortly after birth. Neonatal cortical morphology was characterized using cortical thickness. Antenatal maternal anxiety was assessed using the State-Trait Anxiety Inventory at week 26 of pregnancy.

Results: Individual COMT SNPs (val158met, rs737865, and rs165599) modulated the association between antenatal maternal anxiety and the prefrontal and parietal cortical

FIGURE 2. Statistical Maps of Interactive Effects of Antenatal Maternal Anxiety and Individual Single-Nucleotide Polymorphisms (SNPs) on Cortical Thickness in Neonates*



Conclusions: These results suggest that the association between maternal anxiety and in utero neurodevelopment is modified through complex genetic variation in COMT. Such genetic moderation may explain, in part, the variation in phenotypic outcomes in offspring associated with maternal emotional well-being.

Am J Psychiatry 2015; 172:163–172; doi: 10.1176/appi.ajp.2014.14030313

maternal anxiety

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expression of COMT in the prefrontal cortex and amygdala. Antenatal maternal anxiety was associated with increased amygdala volume and decreased prefrontal cortex volume in offspring.

Adult total *BDNF* mRNA (exon IX)

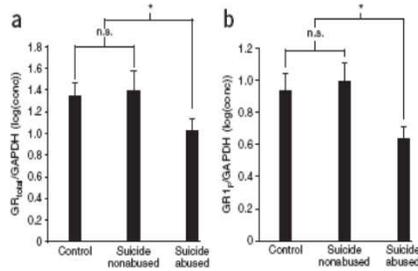
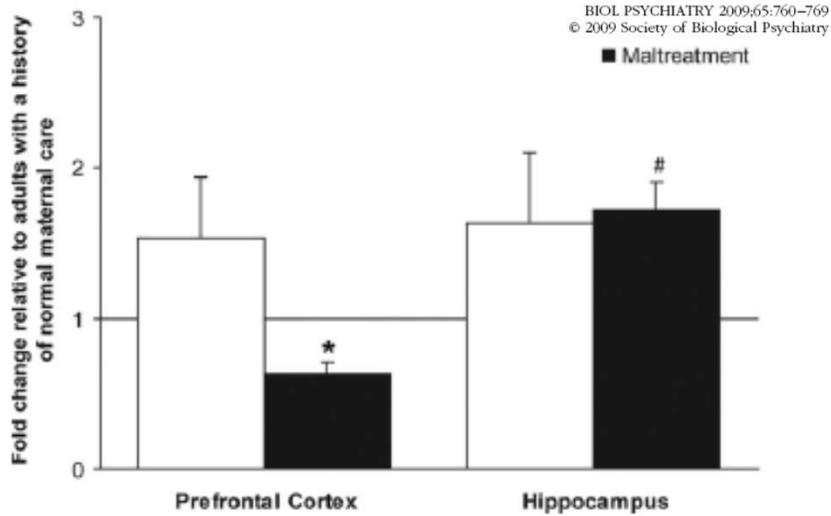
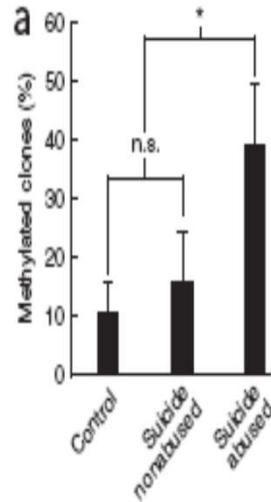


Figure 1 Hippocampal glucocorticoid receptor expression. (a,b) Mean \pm s.e.m. expression levels of total glucocorticoid receptor (GR) mRNA (a) and glucocorticoid receptor 1 β (GR1 β) in 12 suicide victims with a history of childhood abuse, 12 nonabused suicide victims and 12 control subjects (b). Outliers excluded from analysis included $n = 2$ control subjects, $n = 1$ suicide victims with a history of childhood abuse for glucocorticoid receptor 1 β and an additional $n = 1$ suicide victim with a history of childhood abuse, and $n = 3$ nonabused suicide victims for overall levels of glucocorticoid receptor. * indicates $P < 0.05$; n.s. indicates not statistically significant.



ved.

Alternative Splicing, Methylation State, and Expression Profile of Tropomyosin-Related Kinase B in the Frontal Cortex of Suicide Completers

Carl Ernst, MSc; Vessilina Deleva, MSc; Xiaoming Deng, MD; Adolfo Sequiera, PhD; Amanda Pomaranski, BS; Tim Klempan, PhD; Neil Ernst, MSc; Romi Quirion, PhD; Alain Gratton, PhD; Moshe Sczyf, PhD; Gustavo Turecki, MD, PhD

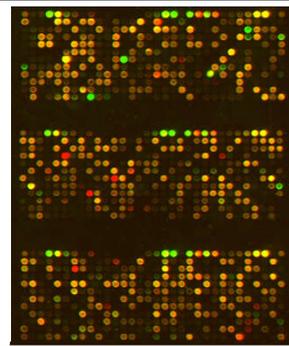
Context: Although most of the effort to understand the neurobiology of depressive states and suicide has focused on neuronal processes, recent studies suggest that astroglial dysfunction may play an important role. A truncated variant of the tropomyosin-related kinase B (TrkB-T1) is expressed in astrocytes, and brain-derived neurotrophic factor–TrkB signaling has been linked to mood disorders.

Objectives: To test the hypothesis that TrkB-T1 expression is downregulated in suicide completers and that this downregulation is mediated by an epigenetic process.

Design: Postmortem case-control study.

periments were performed to control for drug and alcohol effects. Genetic and epigenetic studies were performed by means of direct sequencing and bisulfite mapping.

Results: We found that 10 of 28 suicide completers (36%) demonstrated significant decreases in different probe sets specific to TrkB-T1 in Brodmann areas 8 and 9. These findings were generalizable to other frontal regions but not to the cerebellum. The decrease in TrkB expression was specific to the T1 splice variant. Our results were not accounted for by substance comorbidity or by reduction in astrocyte number. We found no effect of genetic variation in a 2500-base pair promoter region or at telomeric CpG islands. However, we observed an effect of



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PMID: 23010000

Global Brain Gene Expression Analysis Links Glutamatergic and GABAergic Alterations to Suicide and Major Depression

Adolfo Sequiera¹, Firoza Mamdani¹, Carl Ernst¹, Marquis P. Vawter², William E. Bunney³, Veronique Labelle¹, Sonia Belal¹, Tim Klempan¹, Alain Gratton¹, Chwoki Benkhalif¹, Guy A. Rouleau¹, Naguib Mechawar¹, Gustavo Turecki¹

¹McGill Gaze de la Santé, Douglas Mental Health University Institute, McGill University, Montreal, Quebec, Canada; ²Shirley Winters Haskin, West Virginia University, Martinsburg, West Virginia, USA; ³Centre de Recherche en Neurosciences, Université de Montréal, Montreal, Quebec, Canada; ⁴Department of Psychiatry and Human Behavior, School of Medicine, University of California Davis, Davis, California, United States of America

Abstract

Background: Most studies investigating the neurobiology of depression and suicide have focused on the serotonergic system. While it seems clear that serotonergic alterations play a role in the pathogenesis of these major public health problems, dysfunction in additional neurotransmitter systems and other molecular alterations may also be implicated. Microarray expression studies are excellent screening tools to generate hypotheses about additional molecular processes that may be at play. In this study we investigated brain regions that are known to be implicated in the neurobiology of suicide and major depression in order to represent viable global molecular alterations.

Methodology/Principal Findings: We performed gene expression analysis using the HG-U133B chip in 17 cortical and subcortical brain regions from suicides with and without major depression and controls. Total mRNA levels were analyzed using 602 brain samples isolated from 30 male subjects, including 26 suicide cases and 13 controls, diagnosed by means of psychological autopsies. Independent brain samples from 24 subjects and animal studies were used to control for the potential confounding effects of comorbidity with alcohol. Using a Gene Ontology analysis as our starting point, we observed molecular pathways that may be involved in depression and suicide, and performed follow-up analyses on these possible targets. Methodology: Annotated gene expression measures from microarrays, Gene Set Enrichment for global ontological profiling, and semi-quantitative RT-PCR. We observed the highest number of suicide specific alterations in prefrontal cortex areas and hippocampus. Our results revealed alterations of synaptic neurotransmission and intracellular signaling. Among these, Glutamate (GLU) and GABAergic related genes were globally altered. Semi-quantitative RT-PCR results investigating expression of GLU and GABA receptor subunit genes were consistent with microarray data.

Conclusions/Significance: The observed results represent the first overview of global expression changes in brains of suicide victims with and without major depression and suggest a global brain alteration of GLU and GABA receptor subunit genes in these conditions.

ARTICLE IN PRESS

ARCHIVAL REPORT

Characterization of QKI Gene Expression, Genetics, and Epigenetics in Suicide Victims with Major Depressive Disorder

Timothy A. Klempan, Carl Ernst, Vessilina Deleva, Benoit Labonte, and Gustavo Turecki

Background: A number of studies have suggested deficits in myelination and glial gene expression in different psychiatric disorders. We examined the brain expression and genetic/epigenetic regulation of QKI, an oligodendrocyte-specific RNA binding protein important for cell development and myelination.

Methods: The microarray-based expression of QKI was evaluated in cortical and subcortical brain regions from suicide victims with a diagnosis of major depression ($n = 16$) and control subjects ($n = 13$). These findings were also assessed with a real-time (quantitative polymerase chain reaction [qPCR]) approach, with QKI protein levels evaluated through immunoblotting. Identification of a QKI promoter sequence was then used to examine genetic and epigenetic variation at the QKI locus.

Results: The messenger RNA (mRNA) levels of multiple transcripts of QKI were evaluated on Affymetrix microarrays, revealing significant reductions in 11 cortical regions and the hippocampus and amygdala of suicide victims compared with control subjects. Microarray findings were confirmed by qPCR, and reduced expression of QKI protein was identified in orbitofrontal cortex. Analysis of promoter variation and methylation state in a subset of individuals did not identify differences at the genetic or epigenetic level between depressed suicide victims and control subjects.

Conclusions: The observation of consistent reductions in multiple isoforms of QKI mRNA in depressed suicide victims supports the growing body of evidence for a role of myelination-related deficits in the etiology of psychiatric disorders. A specific role of QKI in this process is implied by its reduced expression and known interactions with genes involved in oligodendrocyte determination; however, QKI gene variation responsible for these changes remains to be identified.

Brief report

Increased DNA methylation in the suicide brain

Fatemeh Haghghi, PhD; Yurong Xin, PhD; Benjamin Chanrion, PhD; Anne H. O'Donnell, MD, PhD; Yongchao Ge, PhD; Andrew J. Dwork, MD; Victoria Arango, PhD; J. John Mann, MD



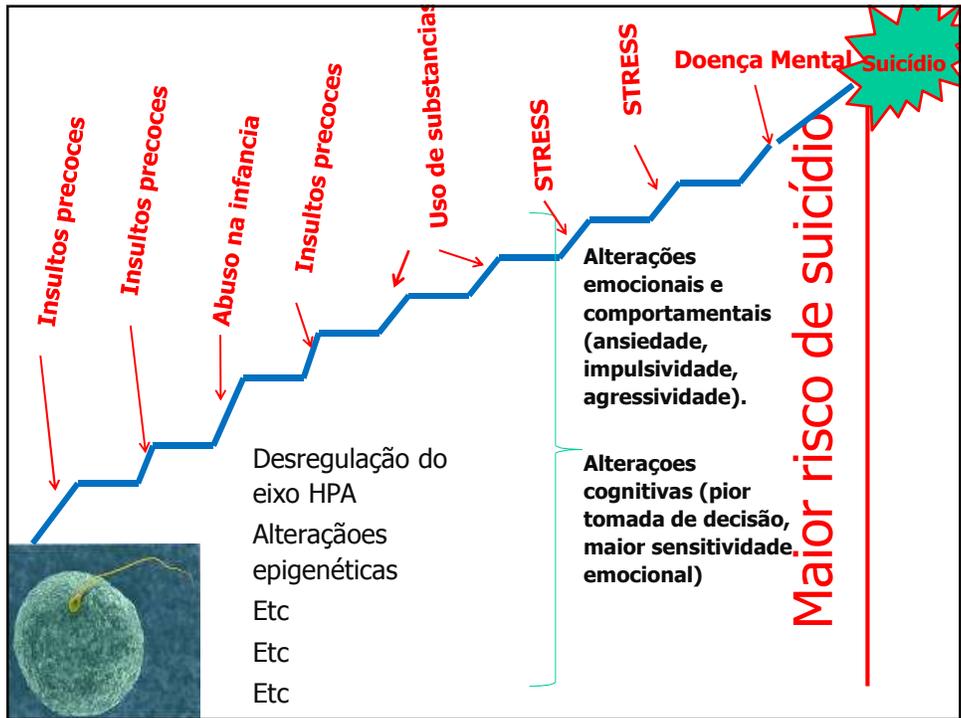
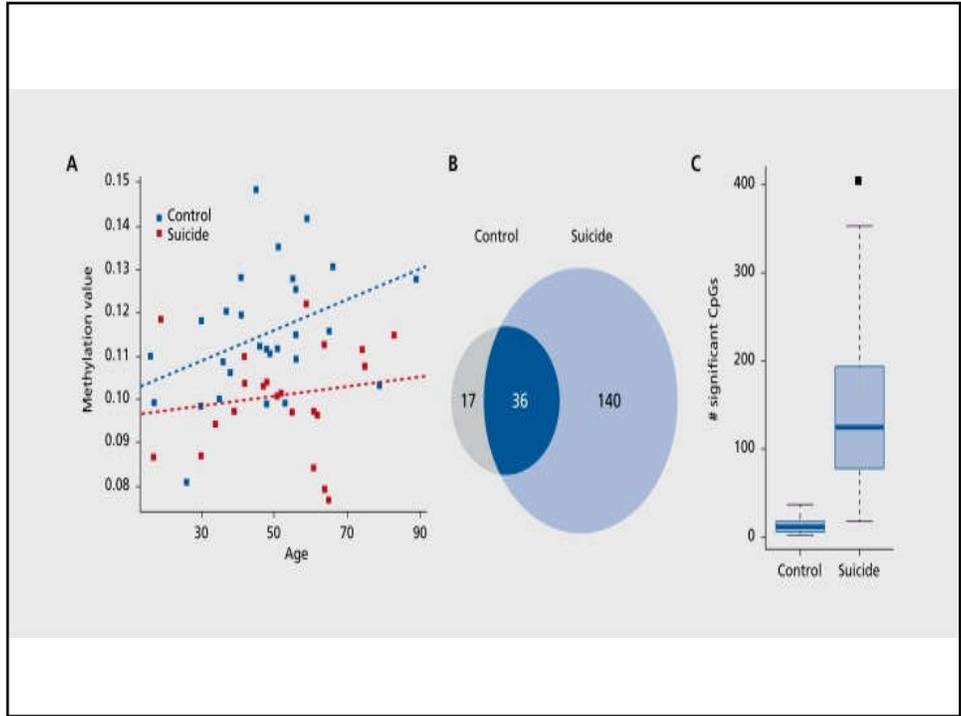
Clinical studies find that childhood adversity and stressful life events in adulthood increase the risk for major depression and for suicide. The predispositions to either major depression or suicide are thought to depend on genetic risk factors or epigenetic effects. We investigated DNA methylation signatures postmortem in brains of suicides with diagnosis of major depressive disorder. DNA methylation levels were determined at single C-phosphate-G (CpG) resolution sites within ventral prefrontal cortex of 53 suicides and nonpsychiatric controls, aged 16 to 89 years. We found that DNA methylation increases throughout the lifespan. Suicides showed an 8-fold greater number of methylated CpG sites relative to controls ($P < 2 \times 10^{-9}$), with greater DNA methylation changes over and above the increased methylation observed in normal aging. This increased DNA methylation may be a significant contributor to the neuropathology and psychopathology

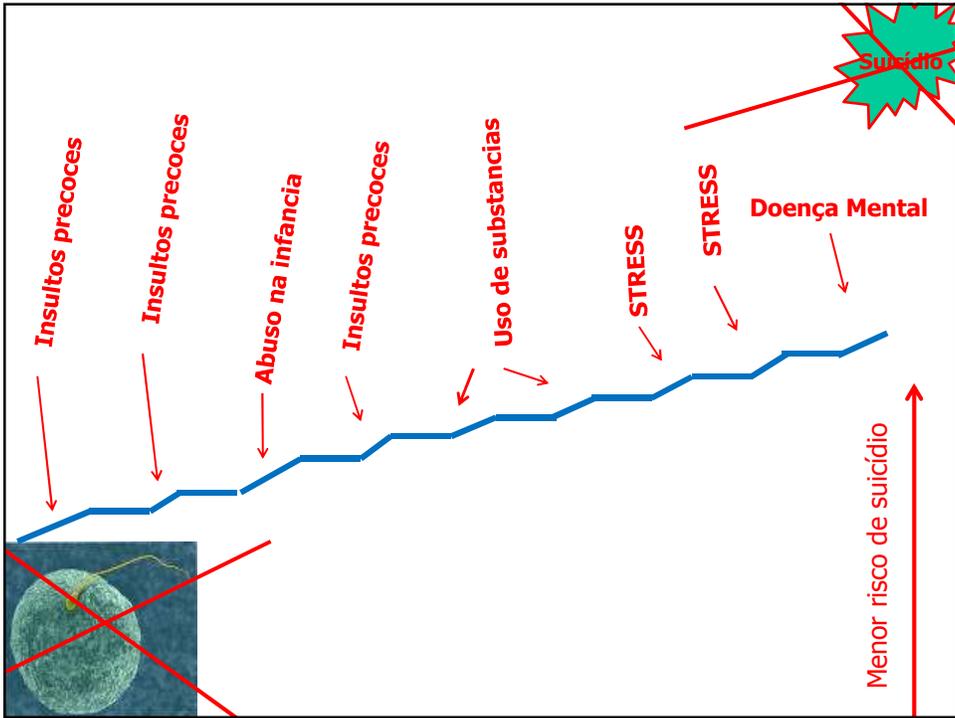
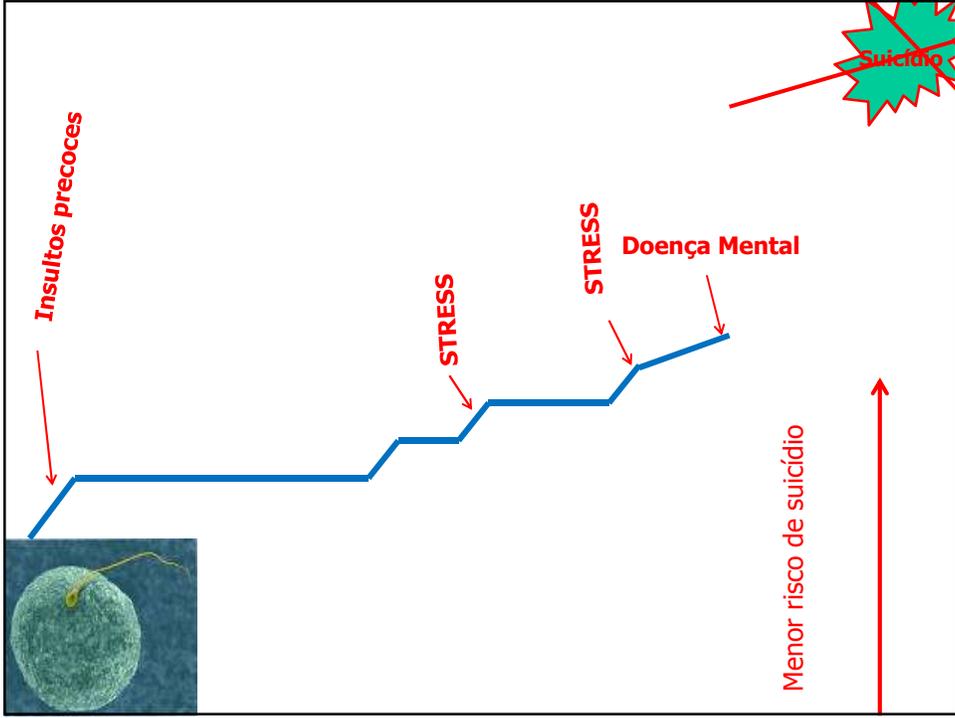
Introduction

The World Health Organization estimates that nearly 1 million people die from suicide yearly (World Health Organization figures, 2012). Psychological autopsies find that about 90% of suicides in Western nations have a psychiatric illness at the time of suicide.¹ Of those, about 60% are suffering from a mood disorder. Suicide risk is influenced by a wide range of factors. Although some genetic risk factors have been identified, environmental events such as childhood adversity or repeated exposure to life-threatening situations typical in war and active combat have also been reported to contribute to the increased risk of suicidal behavior.² Exposure to stress can confer lasting biological and behavioral effects, such as altered responses to stress, throughout the lifespan, and as such these effects may be mediated by epigenetic factors like DNA methylation.

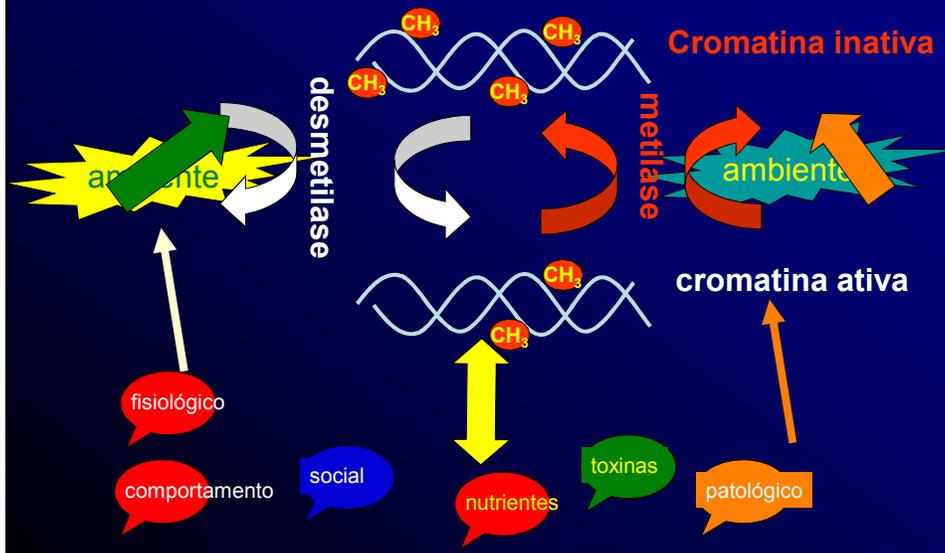
Keywords: aging; depression; DNA methylation; epigenetics; mood disorder; suicide

Author affiliations: James J. Peters Veterans Affairs Medical Center; Fishberg Department of Neuroscience, Mount Sinai School of Medicine (Fatemeh Haghghi); Department of Psychiatry, Division of Molecular Imaging and Neuropathology, New York State Psychiatric Institute, Columbia University (Fatemeh Haghghi); Yurong Xin, Benjamin Chanrion, Anne H. O'Donnell, Andrew J. Dwork, Victoria Arango, J. John Mann; Depart-





Hipótese: O padrão de metilação resulta de um equilíbrio entre as atividades da metilase e desmetilase.



Journal of Clinical Pharmacy and Therapeutics

Journal of Clinical Pharmacy and Therapeutics (2011)

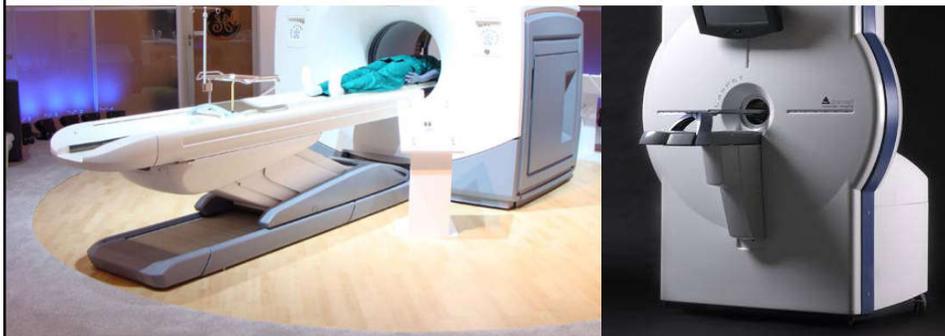
doi:10.1111/j.1365-2710.2011.01301.x

COMMENTARY

Psychotherapy as an epigenetic 'drug': psychiatric therapeutics target symptoms linked to malfunctioning brain circuits with psychotherapy as well as with drugs

S. M. Stahl*† MD PhD

*Department of Psychiatry, University of California San Diego, San Diego, CA, USA and †Department of Psychiatry, University of Cambridge, Cambridge, UK





Obrigado pela Atenção