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News, literature, and events on the ethical, social, and legal implications of psychiatric, neurologic, and behavioral genetics.

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Braingenethics Update

Vol. 2, No. 7 September 2015
braingenethics.cumc.columbia.edu/

Upcoming Seminar on Ethical, Legal and Social Implications of Genetics:

"Looping Genomes: Diagnostic Expansion and the Genetic Makeup of the Autism Population"

Gil Eyal, PhD
Professor and Chair
Department of Sociology
Columbia University

Monday, October 12, 2015
12:00-1:00pm
Board Room #6601
New York State Psychiatric Institute
1051 Riverside Drive
New York, NY 10032

"The Genetics of Intelligence: Ethics and the Conduct of Trustworthy Research"
Edited by Erik Parens and Paul S. Appelbaum

A Special Report Published as a Supplement to the September-October 2015 issue of the *Hastings Center Report*

Contributors:
James Tabery, Sarah S. Richardson, Dorothy Roberts, Jonathan A. Plucker, Amy L. Shelton, Matt McGue, Irving Gottesman, Eric Turkheimer, Kathryn Asbury, Aaron Panofsky, Shawneequa L. Callier, Vence L. Bonham, Josephine Johnston, Mohini P. Banerjee, Gail Geller, Elaine Hansen, Stuart

In the Literature

Genetic causal attribution of epilepsy and its implications for felt stigma
Maya Sabatello et al.

Research in other disorders suggests that genetic causal attribution of epilepsy might be associated with increased stigma. In a self-administered survey-based study, the researchers investigated this hypothesis in a unique sample of families containing multiple individuals with epilepsy. They conclude that felt stigma may be increased in people with epilepsy who believe epilepsy in the family has a genetic cause, emphasizing the need for sensitive communication about genetics.

Neurogenethics: An emerging discipline at the intersection of ethics, neuroscience, and genomics
Turhan Canli

Ethical, legal, and social implications (ELSI) research in genetics ("genethics") has been focused on traditional concerns in bioethics, such as privacy and informed consent. However, ELSI research in neuroscience ("neuroethics") has focused on concerns related to notions of personhood, such as free will or cognitive enhancement. Novel questions have emerged with the confluence of these two lines of research. Here, Canli calls this area of ethics inquiry "neurogenethics" and anticipates research questions related to genome editing and gene therapy, optogenetics, memory manipulation, genomic identity, and online communities.

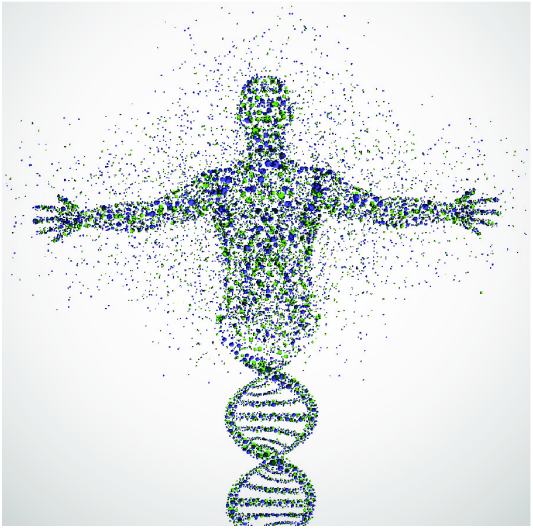
The ethics weathervane
Bartha Knoppers and Ruth Chadwick

Gluck, Erik Parens, and Paul S. Appelbaum

Commentary

1193 to 4
Robert Resta

An ethical dilemma emerges when genetic counselors encounter a fetus that has been diagnosed with Down syndrome: on the one hand, counselors advocate for the rights of women faced with reproductive decisions and, on the other hand, they support the rights of the disabled. Here, Resta reviews the literature--or lack thereof--examining the benefits of prenatal genetic testing related to Downs.



Brain correlates of the interaction between 5-HTTLPR and psychosocial stress mediating attention deficit hyperactivity disorder severity
Dennis van der Meer et al.

This study provides insight into the

This past decade has witnessed the emergence of six new, interconnected areas of ethical consensus and emphasis for policy in genomics: governance, security, empowerment, transparency, the right not to know, and globalization. The globalization of genomic research warrants an approach to governance policies grounded in human rights. A human rights approach activates the ethical principles underpinning genomic research. It lends force to the right of all citizens to benefit from scientific progress, and to the right of all scientists to be recognized for their contributions.

Understanding and predicting suicidality using a combined genomic and clinical risk assessment approach
Alexander Niculescu et al.

The authors of this study have developed blood tests using RNA biomarkers and questionnaire instruments in the form of an app that can predict with approximately 92 percent accuracy which patients being treated for bipolar disorder and other psychiatric illnesses will begin thinking of suicide, or attempt it.

MicroRNA and posttranscriptional dysregulation in psychiatry
Michael Geaghan and Murray J. Cairns

MicroRNAs are involved in regulating the expression of many different genes simultaneously, and are emerging as prospective regulators in the pathophysiology of psychiatric disease. Evidence suggests that there is a strong association of miRNA genes and their targets with a broad range of psychiatric conditions. This review explores biological pathways that may be instrumental in ADHD, and how social stress may play a crucial role in altering risk for psychopathology. The authors ask if the same short ("s" - allele) that reportedly makes carriers more vulnerable to depression when faced with adverse events also has predictive value for ADHD under the same stimuli. This study, which reports a strong possible correlation, was conducted in such a way as to bolster confidence in its ability to be replicated.

Whole genome sequencing provides insight into the genetics of major depressive disorder
Britt Drögemöller

To understand the genetics of major depressive disorder (MDD), the CONVERGE consortium used whole-genome sequencing to overview genetic variation in a large cohort of homogenous patients (11,670 Han Chinese women). Two potentially illuminating single nucleotide polymorphisms (SNPs) were identified and compared to data from a previous Psychiatric Genetics Consortium (PGC) MDD genome-wide association study. Examination of the PGC data failed to identify significant associations for these two genetic variants. This study does suggest the utility of whole genome sequencing and large well-characterized cohorts of subjects for future genetic studies of MDD.

Holocaust exposure induced intergenerational effects on FKBP5

ways in which miRNA dysregulation and dysfunction can be linked with schizophrenia, bipolar disorder, major depressive disorder, and autism spectrum disorders, and miRNA's potential biomarker or therapeutic potential for these disorders.

Antisocial behavior and polymorphisms in the oxytocin receptor gene: findings in two independent samples
Hovey et al.

Are SNPs in the OXT receptor gene associated with the expression of antisocial behavior? Researchers genotyped samples from two twin studies and concluded that the rs7632287 and rs4564970 polymorphisms in OXTR may independently influence antisocial behavior in adolescent boys. Further examination based on this evidence will be will be crucial to understanding how aberrant social behavior arises, and would support the OXT receptor as one potential target in the treatment of aggressive antisocial behavior.

Heritability of individual psychotic experiences captured by common genetic variants in a community sample of adolescents
Dominika Sieradzka et al.

Psychotic experiences are common amongst adolescents in the general population. This paper examines the extent to which common genetic variants account for some of these episodes, and finds that common genetic variants appear to play a role in the etiology of some adolescent psychotic experience, but that further research is necessary on larger sample sizes with a MAF-stratified approach.

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methylation
Rachel Yehuda et al.

Holocaust exposure had an effect on methylation within the gene encoding for FK506 binding protein 5 (FKBP5) that was observed in exposed parents as well in their offspring. The findings of this study suggest the possibility of site specificity to environmental influences, as sites in bins 3 and 2 were differentially associated with parental trauma and the offspring's own childhood trauma, respectively. This is the first demonstration of transmission of preconception parental trauma to a child associated with epigenetic changes in both generations, providing a potential insight into how severe psychological trauma can have intergenerational effects.

Clinically useful genetic markers of antidepressant response: How do we get there from here?
Francis J. McMahon

Predicting who will respond to an antidepressant—and who will not—remains an urgent but unfulfilled need in psychiatry. Clinical indicators of response have a long history, but probably have low predictive value. This state of affairs has fueled an energetic search for biomarkers. In this month's issue of the *American Journal of Psychiatry*, Schatzberg et al. report that common genetic markers in ABCB1 provide some information about which patients are most likely to respond to certain selective serotonin reuptake inhibitors.

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To contribute a news item, an academic article, or an event on the ethical, legal, and social implications of psychiatric, neurological, and behavioral genetics research please email us.

FTO obesity variant circuitry and adipocyte browning in humans
Melina Claussnitzer et al.

The strongest common genetic contributor to extreme obesity discovered so far is a variant found in an intron of the FTO gene. Variations in this untranslated region of the gene have been tied to differences in body mass and a risk of obesity. The authors suggest that the answer is not in regions of the brain that control appetite, but in the progenitor cells that produce white and beige fat. The risk variant is part of a larger genetic circuit that determines whether bodies burn or store fat. This discovery may yield new approaches to intervene in obesity with treatments designed to change the way fat cells handle calories.

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