

News, Literature, and Events in Braingenethics

[View this email in your browser](#)

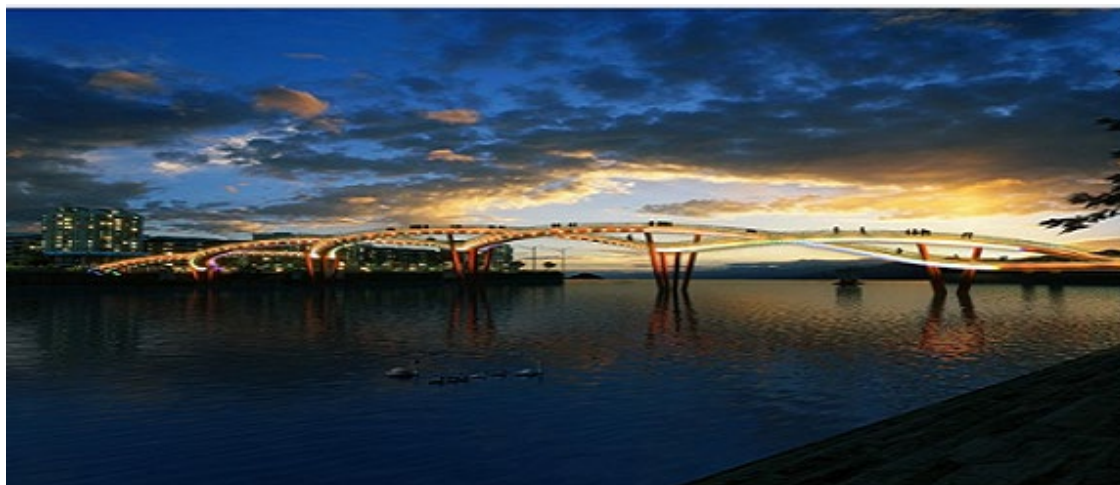


Braingenethics Update

Vol. 4, No. 5

June 2017

braingenethics.cumc.columbia.edu/



Genetics of Complex Traits

[An Expanded View of Complex Traits: From Polygenic to Omnigenic](#)

Evan A. Boyle et al.

In their “omnigenic” hypothesis of complex traits, the authors postulate that gene regulatory networks are sufficiently interconnected, such that

all genes expressed in disease-relevant cells are liable to affect the functions of core disease-related genes and that most heritability can be explained by effects on genes outside core pathways.

[What If \(Almost\) Every Gene Affects \(Almost\) Everything?](#)

Ed Yong

In the Media

[Schizophrenia Meta-Analysis Reveals Role for Rare, Damaging Variants](#)

GenomeWeb Staff Reporter

A new meta-analysis suggests that rare, damaging mutations may contribute to schizophrenia, both alongside and in the absence of intellectual disability.

- **More in** [Nature Genetics](#)

[Psychosis-Associated Mutations IDed in Brain-Expressed Gene](#)

GenomeWeb Staff Reporter

Using genotyping in a family with several individuals affected by schizophrenia, schizoaffective disorder, or psychotic bipolar disorder, researchers have found evidence that links some forms of psychosis to mutations on the end of the

Three Stanford scientists have proposed a provocative new way of thinking about genetic variants, and how they affect people's bodies and health. In the simplest terms, they're saying that most genes matter for most things.

[The Upside of Bad Genes](#)

Moises Velasquez-Manoff

If "bad" genes, albeit disease-causing, helped us survive in the past, is it wise to remove them from our genomes now? Instead of rewriting our genetic codes, a better approach might be to focus on and change the interplay between our genes and our environments.

[Computational Model Offers Clues to Missing Heritability for Complex Human Traits](#)

GenomeWeb Staff Reporter

A new computational model assesses the proportion of variation observed in a given phenotype that can be explained by the sum of known SNP contributors to that phenotype to help clarify complex trait heritability.

More In the Literature:

[Reevaluation of SNP Heritability in Complex Human Traits](#)

RNA-binding motif protein 12-coding gene RBM12.

- **More In the Literature:** [Truncating Mutations in RBM12 are Associated with Psychosis](#)

[Genetic Loci Linked to Brain Aging Features](#)

GenomeWeb Staff Reporter

A genome-wide association study of 1,163 individuals has shed light on DNA methylation signatures implicated in brain aging. These newly identified epigenetic aging-related loci with sites share some genetic overlap with loci previously linked to age-related macular degeneration and a range of metabolic, cognitive, inflammatory and psychiatric conditions.

[Genes Tied to Wasps Recognizing Faces](#)

Ashley P. Taylor

A new study has identified differential gene-expression and neuronal patterns involved in face and pattern recognition in multiple wasp species.

[Ancestry.com Denies Exploiting Users' DNA](#)

Harry Kretchmer

Direct-to-consumer genealogy company Ancestry.com has denied exploiting users' DNA, after a [blog post](#) criticized the company's "perpetual" licence to retain and use customers' genetic material.

[Is There Anything Grit Can't Do?](#)

Kay S. Hymowitz

University of Pennsylvania Psychology professor Angela Lee Duckworth discusses the power of grit and 'noncognitive skills' for success.

In the Literature

[Evaluation of a Web-based Decision Aid for People Considering the APOE Genetic Test for Alzheimer Risk](#)

Michael Ekstrat et al.

With the increasing interest in apolipoprotein E (APOE) genetic testing to estimate the risk of developing late-onset Alzheimer disease, new educational tools are needed to help people make the best decision for themselves about whether to

undergo this test. This study evaluated an online tool to assist in this decision process, finding it useful for education as well as facilitation of further discussions with health-care providers.

[Undermining Genetic Privacy? Employee Wellness Programs and the Law](#)

Kathy L. Hudson and Karen Pollitz

Genetic information is becoming ubiquitous in research and medicine, but a bill now moving through the House of Representatives would preempt key protections. Physicians, researchers, and the public need to be aware of it.

[Rare Copy Number Variants in NRXN1 and CNTN6 Increase Risk for Tourette Syndrome](#)

Alden Y. Huang et al.

Analyzing a sample of 2,434 Tourette Syndrome (TS) cases using SNP microarray data, this study identified two individual, genome-wide significant loci (NRXN1 deletions and CNTN6 duplications), each conferring a substantial increase in TS risk . Approximately 1% of TS cases carry one of these CNVs, indicating that rare structural variation contributes significantly to the genetic architecture of TS.

[ZNF804A: Insights from the First Genome-wide Significant Schizophrenia Gene](#)

Paul J. Harrison

Despite significant advances in genome-wide association studies of schizophrenia, the 2008 identification of ZNF804A gene remains valuable to the understanding of the disease and raises issues relevant to all GWAS studies in the field.

[Identification of Developmental and](#)



Race, Genomics and Intelligence

[There's Still No Good Reason to Believe Black-White IQ Differences Are Due to Genes](#)

Eric Turkheimer, Kathryn Paige Harden, Richard E. Nisbett

Psychologists have found no strong evidence to support a conclusion that the black-white IQ gap is even partially genetically determined, and instead believe that improving children's environments will improve their cognitive skills.

[What Both the Left and Right Get Wrong About Race](#)

Dalton Conley & Jason Fletcher
Genetic differences are a potential - but highly unlikely - explanation for national, racial, or ethnic differences in behavior and success. It is a good time to dispel myths about genetic variation - especially as it relates to race, IQ, and success - that are promoted by people on both sides of the aisle.

[Scientists are Finding More Genes Linked to IQ. This Doesn't Mean We Can Predict Intelligence](#)

Brian Resnick

[Behavioral Markers Associated with Genetic Abnormalities in Autism Spectrum Disorder](#)

Somer L. Bishop et al.

Limited progress has been made in identifying phenotype-genotype relationships in autism spectrum disorder (ASD). This study found that children with ASD and de novo mutations may exhibit a “muted” symptom profile with respect to social communication and language deficits relative to those with ASD with no identified genetic abnormalities.

[CSNK2B Splice Site Mutations in Patients Cause Intellectual Disability with or without Myoclonic Epilepsy](#)

Karine Poirier et al.

This exome screening study of two patients diagnosed with intellectual disability (ID) identified two de novo splice variants in the CSNK2B gene. This study adds knowledge to the increasingly growing list of causative and candidate genes in ID and epilepsy, and highlights CSNK2B as a new gene for neurodevelopmental disorders.

[Allostasis and the Epigenetics of Brain and Body Health Over the Life Course](#)

Bruce S. McEwen

Stressful experiences can precipitate major psychiatric disorders such as schizophrenia, bipolar illness, anxiety disorders, and major depression. This viewpoint article details how the brain and body influence one another over the course of psychiatric disorders with frequent multimorbidity.

[Sniekers et al.](#) has been hailed as an enormous success, but could be misused to make claims about racial superiority and differences between groups. Vox’s Brian Resnick discusses this issue with the study’s senior author, statistical geneticist Danielle Posthuma.

See our coverage of [Sniekers et al.](#) in last month’s [Braingenetics Update](#).

In the Literature, cont.

[Early Life Stress Confers Lifelong Stress Susceptibility in Mice via Ventral Tegmental Area OTX2](#)

Catherine J. Peña et al.

This study establishes a “two-hit” stress model in mice, wherein stress at a particular postnatal period increases susceptibility to adult stress, and causes long-lasting transcriptional alterations. This establishes a mechanism by which early life stress encodes lifelong susceptibility to stress.

[miR-183 Cluster Scales Mechanical Pain Sensitivity by Regulating Basal and Neuropathic Pain Genes](#)

Changgeng Peng

Nociception prevents tissue damage but can also facilitate chronic pain. This study identified that both basal mechanical and neuropathic pain are controlled by the microRNA-183 (miR-183) cluster in mice. This single microRNA cluster continuously scales acute noxious mechanical sensitivity in nociceptive neurons and suppresses neuropathic pain transduction in a specific, light-touch-sensitive neuronal type.

Upcoming Events

[NYU Nature Conference on Neurogenetics](#)

August 9-11, 2017

Kimmel Center for University Life, New York University, New York, NY, USA

This conference will facilitate interdisciplinary collaborations aimed at developing a more integrated understanding of how genes influence behavior, neuronal development and neurological disease.



Share



Tweet



Forward



+1

Click [here](#) to subscribe to our Braingenetics Update newsletter.



COLUMBIA UNIVERSITY
MEDICAL CENTER



The Hastings Center

Copyright © 2017 Center for Excellence in Ethical, Legal, and Social Implications of Psychiatric, Neurologic, and Behavioral Genetics, All rights reserved.

Our mailing address is:

The Hastings Center
21 Malcolm Gordon Rd.
Garrison, NY 10524

[unsubscribe from this list](#) [update subscription preferences](#)

This email was sent to ***|EMAIL|***

[why did I get this?](#) [unsubscribe from this list](#) [update subscription preferences](#)

|LIST:ADDRESSLINE|

|REWARDSI|