News, Literature, and Events in Braingenethics

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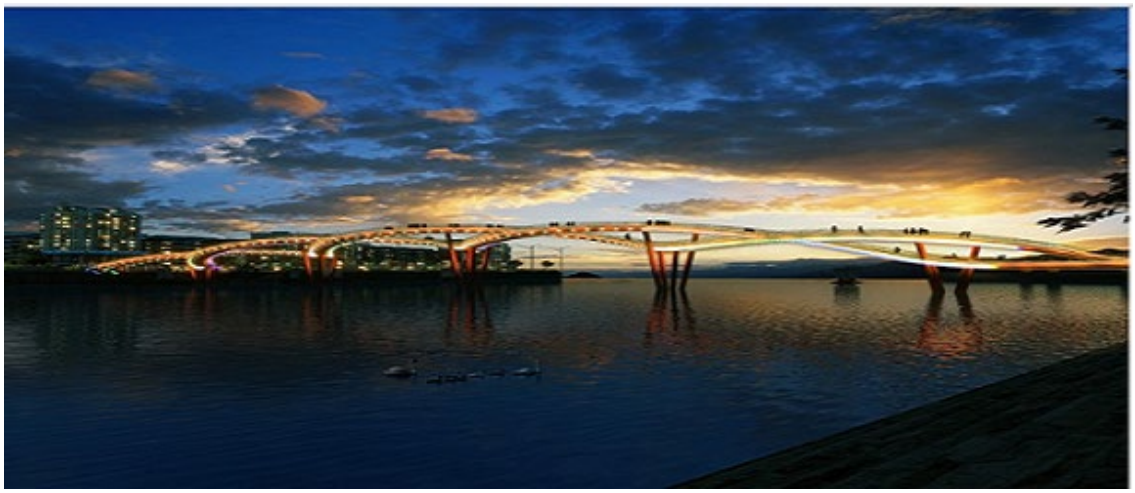

In the Literature

Genetic Ability, Wealth, and Financial Decision-Making

Daniel Barth et al.

Recent advances in behavioral genetics have enabled the discovery of genetic variants linked to a variety of economic outcomes, including education. This study demonstrates that the same genetic variants that predict educational attainment independently predict household wealth in the Health and Retirement Study (HRS). Their findings suggest that genetic factors that promote human capital accumulation contribute to wealth disparities not only through education and higher earnings, but also through their impact on the ability to process information and make good

In The Media

Autism Genes Conserved During Human Evolution to Make Us Smarter, Say Scientists

John von Radowitz

Researchers from Yale School of Medicine have identified strong positive evolutionary forces acting on variants that are associated with both autism spectrum disorder and intellectual achievement, possibly indicating why many genetic variants contributing to the disorder persist throughout society.

- Original study: Widespread Signatures of Positive Selection in Common Risk Alleles Associated to Autism Spectrum Disorder

financial decisions.

- Read more from GenomeWeb and Fortune.

Set in Stone or Ray of Hope: Parents' Beliefs About Cause and Prognosis After Genomic Testing of Children Diagnosed with ASD

Marian Reiff et al.

Limited information exists about how results from chromosomal microarray analysis (CMA) for autism spectrum disorders (ASD) influence parents' beliefs about etiology and prognosis. Through interviews with parents and children who received CMA results, the authors found that parents tended to incorporate their child's CMA results within their existing beliefs about the etiology of ASD, regardless of CMA result. However, parents' expectations for the future tended to differ depending on results.

Informed Consent

Christine Grady et al.

This multipart review provides an overview of innovative approaches to improving and expanding the informed consent process for researchers and participants, along with short essays covering specific areas of innovation

Meta-assessment of Bias in Science

Daniele Fanelli et al.

To analyze biases and reproducibility issues in research, this study probed for multiple bias-related patterns in a large random sample of meta-analyses taken from all disciplines. While small, early, highly cited studies were likely to overestimate effects, very little evidence of biases exists overall.

Genethics Literature

Psychiatric Disorder Sequencing Project Adds 10x Genomics Tech for Phasing, Structural Variant ID

Monica Heger

The InPSYght project is about halfway towards its goal of sequencing 10,000 whole genomes in order to study schizophrenia and bipolar disorder, as well as to increase the amount of genomic data available from individuals of African ancestry.

Understanding the Roots of Human Musicality

Catherine Offord

Researchers from MIT and Brandeis University are using multiple methods to study the origins of humans' capacity to perceive and produce music. Their results contribute to an enduring debate of the biological and cultural influences on humans' musicality.

- See past work on the The Genetics of Music Accomplishment: Evidence for Gene–Environment Correlation and Interaction.

African Ancestry-Specific Variant Linked to Increased BMI, Obesity

GenomeWeb Staff Reporter

In a new study, a National Human Genome Research Institute-led team conducted a genome-wide association study for body-mass index on some 1,570 people from West Africa and found a novel variant within the *SEMA4D* gene, which has a role in immune response and other processes. They also found that higher serum levels of the protein *SEMA4D* were linked to increased obesity risk.

[Opposition Grows to 'Workplace Wellness' Bill That Would Scale Back Genetic Privacy]

Sharon Begley

A bill currently going through Congress would eliminate the Genetic Information Nondiscrimination Act's genetic privacy protections from workplace wellness programs, potentially allowing employers to require that employees undergo genetic testing and disclose their results.

[This Company Wants to Analyze Your Saliva — To Try to Predict When You'll Die]

Rebecca Robbins

GWG Life, a company that buys life insurance policies from people who don't want or can't afford them anymore, has started requiring its clients to submit a saliva sample. The company analyzes patterns of DNA methylation with hopes of better predicting their clients' life spans, despite doubts regarding the predictive value of DNA methylation signatures.

[Evolving Policy with Science]

R. Alta Charo and Richard O. Hynes

The co-chairs of the National Academy of Science's Human Genome Editing Committee comment on United States policy governing heritable human germline modification, and discuss their committee's report on human gene editing. The authors note that, under strict regulations, clinical trials for heritable editing may eventually be permissible for parents hoping to prevent serious diseases in their children.

- Original Study: Genome-wide Analysis identifies an african-specific variant in SEMA4D associated with body mass index

In the Literature, cont.

[Autism Gene *Ube3a* and Seizures Impair Sociability by Repressing VTA Cbln1]

Vaishnav Krishnan et al.

Maternally inherited 15q11-13 chromosomal triplications cause a frequent and highly penetrant type of autism. This *in vivo* mouse genetics study suggests that gene and seizure interactions in ventral tegmental area (VTA) glutamatergic neurons impair sociability by downregulating the synapse organizer Cbln1, a key node in the expanding protein interaction network of autism genes.

[Depression and Genetic Causal Attribution of Epilepsy in Multiplex Epilepsy Families]

Shawn T. Sorge et al.

Little is known about how epilepsy patients and their relatives will respond to genetic attributions of epilepsy, despite increased emphasis on genetic components of the disease. Through a

- Read the NAS' Report on Human Genome Editing, as featured in Volume 4 Issue 1 of Braingenethics.

Adding Protective Genetic Variants to Clinical Reporting of Genomic Screening Results

Marci L.B. Schwartz et al.

As the availability of sequence data from healthy individuals increases, the authors consider the clinical use, required levels of evidence and medical relevance of "protective" variants in human disease. To maximize the utility of protective variants, the authors argue that concerted efforts are needed to develop standards for the classification and reporting of such variants for precision medicine.

HudsonAlpha's 'Elective Genome' for Healthy Individuals Adds to Emerging Field

Julia Karow

The HudsonAlpha Institute for Biotechnology has launched an 'elective genome' test for healthy individuals, called Insight Genome, that also allows participants to enroll in a clinical research study of genetic risks for common diseases. Insight Genome is self-paid, costs approximately $7,000, and has a turnaround time of about 90 days. The cost includes a clinical whole-genome sequencing test, a separate pharmacogenetic test, and pre- as well as post-test visits with physicians and genetic counselors.

Korean Startup 3billion Focuses on Rare Disease Community With DTC Exome Screening Test

Julia Karow

Korean startup 3billion is getting

survey of multiplex epilepsy families, the authors found that depression is associated with perceived likelihood of carrying an epilepsy-related mutation, specifically among individuals without epilepsy in families containing multiple affected individuals. This association should be considered when addressing mental health issues in such families.

Traumatic Brain Injury Induces Genome-Wide Transcriptomic, Methylomic, and Network Perturbations in Brain and Blood Predicting Neurological Disorders

Qingying Meng et al.

This study utilized modern systems biology in a rodent model of concussive injury to understand the impact of traumatic brain injury (TBI) on fundamental aspects of gene regulation, which have the potential to drive or alter the course of the TBI pathology. The study found that concussive brain injury reprograms genes which could lead to predispositions to neurological and psychiatric disorders, and that genomic information from peripheral leukocytes has the potential to predict TBI pathogenesis in the brain.

Diagnostic Yield and Novel Candidate Genes by Exome Sequencing in 152 Consanguineous Families With Neurodevelopmental Disorders

Miriam S. Reuter et al.

The study aimed to promote the identification of neurodevelopmental disease genes and provide an overview of the diagnostic yield of exome sequencing in consanguineous families. Because of the possibility of identifying treatable diseases or the coexistence of several disease-causing variants, the authors recommend using exome sequencing as a first-line diagnostic approach in consanguineous families with neurodevelopmental disorders. The study

ready to offer a direct-to-consumer (DTC) genomic rare disease screening test to patients in the United States. While strict regulations on DTC in Korea forbid the company from offering its service at home, less rigorous regulations allow 3billion to focus on the US market.

Out Now: Behavioral Genetics: 7th Edition

Behavioral Genetics, 7th edition introduces students to the field's underlying principles, defining experiments, ongoing controversies, and most recent discoveries. The text outlines heredity, it's DNA basis, the methods used to discover genetic influence on behavior and identify specific genes, what is known about genetic influence on cognitive ability, psychopathology, substance abuse, personality, health psychology, and aging, and future steps in the field.

The Alu Neurodegeneration Hypothesis: A Primate-specific Mechanism for Neuronal Transcription Noise, Mitochondrial Dysfunction, and Manifestation of Neurodegenerative Disease

Peter A. Larsen et al.

This study provides evidence of enriched Alu retrotransposons in mitochondrial genes, and postulates that Alus can disrupt mitochondrial populations in neurons, thereby setting the stage for progressive neurologic dysfunction. This Alu neurodegeneration hypothesis is compatible with past research and offers a plausible mechanism for the disruption of neuronal mitochondrial homeostasis, ultimately cascading into neurodegenerative diseases such

also identified 52 novel candidate genes that are awaiting confirmation in independent families.

Understanding Psychiatric Disorders in People With 22q11.2 Deletion and Duplication

James C. Harris

Microdeletions and microduplications on chromosome 22 at the 22q11.2 locus are associated with increased risk of developing a wide range of cognitive and psychiatric disorders. The most frequent microdeletion syndrome in the general population is the hemizygous microdeletion 22q11.2 deletion syndrome, while a smaller percentage of affected individuals have shorter contiguous gene deletions in the same region. Several genes linked to psychiatric disorder are in the deletion region.

Factors Related to Genetic Testing in Adults At Risk for Huntington Disease: The Prospective Huntington At-Risk Observational Study (PHAROS)

Kimberly A. Quaid et al.

The PHAROS study is a unique observational study of 1001 individuals at risk for Huntington disease (HD) who had not been previously tested for HD and had no plans to do so. Within the cohort, baseline behavioral scores, especially apathy, were more strongly associated with later genetic testing than motor and chorea scores. Following genetic testing, subject's experiences of depression varied based on the number of cytosine–adenine–guanine repeats in the Huntingtin gene.

Further Evidence for Genetic Variation at the Serotonin Transporter Gene *SLC6A4* Contributing Toward Anxiety.

Andreas J. Forstner et al.

Social anxiety disorder (SAD) is a common and heritable psychiatric

as Alzheimer's disease.

- Read more in the media here.

Whole Genome Sequencing Resource Identifies 18 New Candidate Genes for Autism Spectrum Disorder

Ryan K.C. Yuen et al.

The authors of this study performed whole-genome sequencing of families with autism spectrum disorder (ASD) to build a resource for subcategorizing the phenotypes and underlying genetic factors involved. The paper provides access to an online database of 5,205 sequences from families with ASD and their clinical information, and identifies 18 new candidate ASD-risk genes.

disorder, for which only a few candidate genes have been implicated so far. The study investigated single-nucleotide polymorphisms (SNPs) associated with other psychiatric disorders, finding evidence for an involvement of the serotonin transporter gene *SLC6A4* in the etiology of anxiety-related traits. Variation at the genome-wide associated bipolar disorder locus *ANK3* might also influence anxiety-related personality traits.

Upcoming Events

April Seminar on Ethical, Legal and Social Implications of Genetics

Monday, April 24th, 2017, 12:00 pm, Sergievsky Center Room PH19-201, Columbia University Medical Center

This month's speaker is Julia Wynn, MS, CGC, a Senior Genetic Counselor and Clinical Research Manager at Columbia University Medical Center. Ms. Wynn's talk is titled *Consenting, educating and disclosing results from genomic sequencing: A genetic counselor's perspective*.

2017 Annual CEER Conference: Ethical Tangles in Neurodegenerative Disease Research: Targeting Participants at Genetic Risk

Monday, April 3, 2017, 8:30 am - 1 pm, Alumni Auditorium, Neurological Institute, Columbia University Medical Center

This conference will discuss major current studies aimed at treatment and prevention of neurodegenerative disorders and the ethical dilemmas raised by the use of genetics in their design.**The conference is free to attend**. To register, please email cangiam@nyspi.columbia.edu.

2017 Genomics and Society: Expanding the ELSI Universe (The 4th ELSI Congress)

June 5, 2017, The Jackson Laboratory for Genomic Medicine and UConn Health, Farmington, CT

This is the latest in a series of major conferences for ELSI researchers and others interested in the ethical, legal, and social implications of genomic research.

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