News, Literature, and Events in Braingenethics

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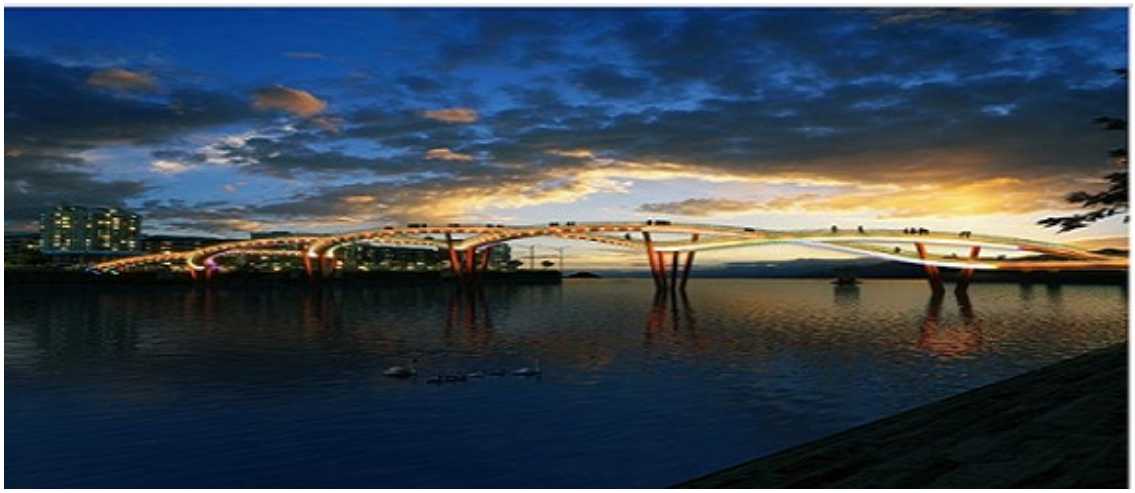

In the Literature

Genetics of Schizophrenia: Historical Insights and Prevailing Evidence
Joyve Van De Leemput et al.
In this review, the authors seek to synthesize perspectives from genetic and epigenetic literature on schizophrenia (SZ) through a qualitative review of risk factors and prevailing hypotheses. Based on the findings of previous genetic and epigenetic studies, as well as the continued development of new technologies to collect and interpret large-scale studies, they are left with a positive outlook for the future of efforts to clarify the molecular genetic mechanisms underlying SZ and other complex neuropsychiatric disorders.

Widespread Signatures of Positive

In The Media

Human Genome Editing: Science, Ethics, and Governance
National Academy of Science and National Academy of Medicine
In a new report, an expert committee considers important questions about the human application of genome editing.The report includes criteria that must be met before permitting clinical trials of heritable germline editing, conclusions on the need for public education and engagement, and seven general principles for the governance of human genome editing. Read more here.

Genomic Medicine Goes Mainstream
Joseph Conn

Selection in Common Risk Alleles Associated to Autism Spectrum Disorder

Renato Polimanti and Joel Gelernter

The systems genetics of psychiatric disorders may bear signatures of the innumerable evolutionary processes that make up the brain. Using data from the Psychiatric Genomics Consortium, the authors hypothesize that certain Autism Spectrum Disorder risk alleles were under positive selection during human evolution due to their involvement in neurogenesis and cognitive ability.

Targeted Sequencing Identifies 91 Neurodevelopmental-Disorder Risk Genes with Autism and Developmental-Disability Biases

Holly A. F. Stessman et al.

Gene-disruptive mutations contribute to the biology of neurodevelopmental disorders (NDDs), but most of the related pathogenic genes are not known. This study identified 25 genes with a bias for autism rather than intellectual disability, and highlighted a network of genes associated with high-functioning autism.

- **Read more:** Analyses Narrow In On ASD, Neurodevelopment-Related De Novo Mutations

Alzheimer Outlook Far From Bleak

Jeff Lyon

Last summer, deep disappointment befell the Alzheimer disease (AD) community when study results showed that the widely heralded experimental drug LMTX had failed to help AD patients. In November, another promising drug, Solanezumab, also dashed hopes. JAMA sat down with two prominent researchers on AD and discussed whether the picture really is as gloomy as some believe.

After decades of anticipation, some patients are now getting their DNA sequenced, seeing it matched against known genetically related conditions, and having their medication checked for genetic suitability.

NIH to Fund Research Into Genetics, Epigenetics of Substance Use Disorders

GenomeWeb Staff Reporter

The National Institutes of Health announced that it is seeking grant applications for projects that will use functional genetics and genomics to gain insights into the molecular underpinnings of substance use disorders (SUDs).

Happy Genes

GenomeWeb Staff Reporter

A list of variants linked to happiness published last year in Nature Genetics has grown from three to twenty, says Vrije Universiteit Amsterdan's Meike Bartels.

The Troubling Rise of the 'Genotocracy'

Amy Dockser Marcus

Imagine a world where dating services offer predictions about which combinations of genes are mostly likely to yield socially advantaged babies: a review of "The Genome Factor" by Dalton Conley and Jason Fletcher.

Genethics Literature

[Which Results to Return: Subjective Judgments in Selecting Medically Actionable Genes.]

Gabriel Lazaro-Munoz et al.

When identifying medically actionable genes appropriate for returning to patients, decision makers must expect and prepare to address such issues as the inevitability of subjective judgments, limited evidence about fundamental decision-making elements, the conceptual complexity of defining criteria, and the emergence of unplanned criteria during the gene selection process.

["They Just Want to Know" - Genetic Health Professionals' Beliefs About Why Parents Want to Know Their Child's Carrier Status.]

Danya F. Vears et al.

Genetic health professionals may be misattributing reasons to parents for desiring their child's genetic carrier status, and may be missing opportunities to assist parents with making decisions that are in line with the family's values and best interests.

[Whole Genome Sequencing in Children: Ethics, Choice and Deliberation]

Ainsley J. Newson

Appropriately implementing novel technologies involves critically

In the Literature, cont.

[Predicting Cognitive Executive Functioning with Polygenic Risk Scores for Psychiatric Disorders]

Chelsie E. Benca et al.

Because executive function (EF) deficits are associated with most psychiatric disorders, EFs have been proposed as an endophenotype for such disorders. This study found no evidence that EFs are better endophenotypes than currently used measures more similar to these disorders. However, larger sample sizes will be important in examining this relationship further.

[Genome-Wide Association Analyses of Sleep Disturbance Traits Identify New Loci and Highlight Shared Genetics With Neuropsychiatric and Metabolic Traits]

Jacqueline M. Lane et al.

Chronic sleep disturbances affect 25–30% of adults worldwide and are associated with cardiometabolic diseases, psychiatric disorders and all-cause mortality. This study discovered genetic loci associated with insomnia symptoms, and genetic correlations between longer sleep duration and schizophrenia risk.

[Heritability of Behavioral Problems in 7-Year Olds Based on Shared and Unique Aspects of Parental Views]

considering how and when to use them. The technology of next-generation DNA sequencing and its application in whole genome sequencing is a key example of where this 'how and when' problem arises.

Real-world Utility of Whole Exome Sequencing with Targeted Gene Analysis for Focal Epilepsy

Piero Perucca et al.

The clinical utility of next-generation sequencing remains to be determined in focal epilepsies, which account for 60% of all epilepsies and for which the importance of genetic factors is just beginning to emerge. This study found that whole exome sequencing with targeted gene analysis is an effective diagnostic and clinical decision-making tool for focal epilepsies with suspected genetic etiologies.

A Cross Species Study of Heterogeneity in Fear Extinction Learning in Relation to *FKBP5* Variation and Expression: Implications for the Acute Treatment of Posttraumatic Stress Disorder

Isaac R. Galatzer-Levy et al.

Posttraumatic stress disorder (PTSD) may be undergirded by deficits in fear extinction learning. These deficits may be due in part to genetic variation in the stress related gene *FKBP5*. Alteration of *FKBP5* mRNA expression is a plausible intervention for preventing PTSD development.

It's All in the Brain: A Review of Available Functional Genomic Annotations

Sarah A. Gagliano

This review summarizes the availability and accessibility of brain epigenetic and functional genomic data as a single

Iryna O. Fedko et al.

Parent assessments often form the backbone of child psychopathology studies, and maternal ratings are the most common metric used. Parents are not always in agreement on the behavior of their child, though, so adding paternal observations may provide additional information that increases a study's power.

Genetic and Environmental Sources of Implicit and Explicit Self-Esteem and Affect: Results from a Genetically Sensitive Multi-group Design

Stefan Stieger et al.

Researchers frequently utilize measures of implicit (i.e., automatic, spontaneous) evaluations. This study suggests that implicit and explicit evaluations of self-esteem and affect share a common genetic core, which aligns with the motivation and opportunity as determinants (MODE) model.

The Role of Genes and Environment in Degree of Partner Self-Similarity

James M. Sherlock et al.

The processes underlying romantic partner choice are remarkably complex and have been largely resistant to scientific explanation. One consistent finding is that, on average, members of romantic dyads tend to be more alike than would be expected by chance. This study revealed that very little of the variation in the tendency to assortatively mate across 14 traits was due to genetic effects (7%) or the shared environment.

The Influence of Genotype Information on Psychiatrists' Treatment Recommendations: More Experienced Clinicians Know Better What to Ignore

Alan McMichael et al.

A patient's genetic information may be used to predict their response to therapy;

resource. The paper is intended to allow investigators to easily access available brain annotations and incorporate this information into their research to inform the field of neuroscience.

such information, however, becomes redundant once a clinician knows the patient's actual response to treatment.Clinicians should be cautious about allowing a patient's genetic information to carry unnecessary weight in clinical decision making.

Upcoming Events

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.

Employment Opportunity at The Hastings Center

Rice Family Fellowship in Bioethics and the Humanities

The Hastings Center seeks applications for a 1-year, full-time fellowship position. Supported by the National Endowment for the Humanities (NEH) and private donors, The Hastings Center's new Humanities Research Initiative is now looking to award the inaugural Rice Family Fellowship in Bioethics and the Humanities. The successful candidate will be no more than 5 years beyond dissertation studies in the humanities and will show the potential to creatively and energetically contribute to the Initiative's theme this year: "The Gift and Weight of Genomic Knowledge."

The deadline for application is **March 3, 2017**. Apply here, read more here, and contact fellowship@thehastingscenter.org with any additional questions.

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