Simons VIP Connect Family Gathering
19-21 July 2013

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News: Clinics unroll genome tests for disorders

SFARIgene
An annotated list of candidate genes for autism

SFARIbase
Access to data and biological materials from the SSC

SFARIwiki
A wiki of autism-related scientific terms

News & Opinion

Toolbox

Bright light
Researchers have found a new way to light up proteins in living cells, revealing neuronal connections.

Blog

Pseudo prevalence
Autism rates rose steeply in three regions of eastern Canada, but only some of that increase is genuine.

Microbe mash
Introducing gut bacteria to germ-free mice increases their social interactions, but mainly with familiar mice.

Mosaic mutations
A new software tool detects chromosomal alterations present in only a subset of cells in the body.

Conference News

Girl power
Girls with autism carry more mutations than boys do, and show greater differences in brain activity.

Statin rescue
Defects in cholesterol metabolism may influence the severity of Rett syndrome, a rare genetic disorder.

Workshop report

Online research
This workshop report explores the use of online tools to collect data from individuals with autism.
Investigator-Initiated Grant Programs

• ~100 Laboratories
• Annual Request for Applications
• Research and Pilot Awards

- Gene discovery
- Molecular mechanisms
- Cognitive and behavioral neuroscience
- Experimental therapeutics and biomarkers
SFARI Programs and Resources

- Simons Simplex Collection (SSC)
- **Simons Variation in Individuals Project (Simons VIP)**
- SFARI Gene
- Distribution and characterization of mouse models
Are there medical, cognitive, brain and behavioral characteristics shared by genetically well defined groups that can inform and improve treatment and quality of life?
Simons Variation in Individuals Project (Simons VIP): A Genetics-First Approach to Studying Autism Spectrum and Related Neurodevelopmental Disorders

The Simons VIP Consortium

We describe a project aimed at studying a large number of individuals (~200) with specific recurrent genetic variations (deletion or duplication of segment 16p11.2) that increase the risk of developing autism spectrum (ASD) and other developmental disorders. The genetics-first approach augmented by web-based recruitment, multisite collaboration and calibration, and robust data-sharing policies could be adopted by other groups studying neuropsychiatric disorders to accelerate the pace of research.

Journal of MEDICAL GENETICS

Copy-number variation

A 600 kb deletion syndrome at 16p11.2 leads to energy imbalance and neuropsychiatric disorders

Analysis of Simons VIP Biospecimens Request for Applications

Analysis of Simons VIP Biospecimens Request for Applications (closed)

This RFA is closed. To download a PDF version of this announcement, click here. To view the FAQ for this RFA, click here.

SFARI mission

The mission of the Simons Foundation Autism Research Initiative (SFARI) is to improve the diagnosis and treatment of autism spectrum disorders by funding innovative research of the highest quality and relevance.

Objective of this award

The Simons Variation in Individuals Project (Simons VIP) comprises a large cohort of individuals with a deletion or duplication of chromosomal segment 10p11.2 (approximately 100 deletion and 100 duplication carriers). A wealth of phenotypic (behavioral, neurological and neuroimaging) data has been collected from these individuals and their families. The data collected so far emphasize significant phenotypic variability: About 20% of deletion and duplication carriers meet strict criteria for an autism diagnosis; many other carriers have other neuropsychiatric diagnoses, including a high rate of language difficulties.

We anticipate that further analyses of biospecimens collected from the individuals in the Simons VIP will help explain some of the heterogeneity in phenotype.

This RFA seeks proposals that take advantage of the unique combination of biospecimens and rich phenotypic information collected by the Simons VIP. Although SFARI is open to many different approaches, we will likely give priority to those that aim to accomplish a comprehensive characterization of RNA expression differences and correlate such expression patterns with phenotypes. Furthering the ability to include genomic analysis would be an additional strength. The data produced in this effort will be made available to the research community with minimum delay and thus will be a valuable resource for all researchers.
http://en.wikipedia.org/wiki/Christopher_Columbus
Levels of investigation