ICH GWAS Monthly Newsletter
Issue 9 - August 2009

In this issue:

Please do not forget to mark your calendars with the date for the next ICH GWAS Conference Call:

Tuesday, September 8th 2009
10-11 am, Eastern USA time

This is the ninth issue of the monthly newsletter for the ICH GWAS Study Group. This newsletter is meant to be a tool to keep investigators participating in the ICH GWAS updated on all aspects of this project, including phenotyping, genotyping, data analysis and logistics.

The newsletter will be sent out to participants on the 15th of each month (or nearest workday) as an email attachment from the Program Manager at the Coordinating Center.

If you want to add topics relevant to all investigators involved in the ICH GWAS to the next newsletter, or you'd like to give general feedback to the Newsletter Design Team please contact:
Lynelle Cortellini
(lcortellini@partners.org).

Currently Active ICH GWAS Sub-projects

This section of the ICH GWAS Newsletter will list all sub-project that have been proposed from Investigators. Contact information for each specific subproject will also be listed. Sub-project proposal for the ICH GWAS can be submitted for evaluation by all ICH GWAS Investigators that have already contributed samples. The ICH GWAS Sub-project proposal form can be obtained from the ICH GWAS section of the ISGC website or by contacting the Coordinating Center (see contact info for this topic).

Currently active Sub-Projects

ApoE Candidate Gene Study in ICH

Aims: Investigate the role of ApoE in ICH using a large-scale candidate-gene approach.

Current Status:

Genotyping has been completed on approximately 500 ICH cases and healthy controls.

Interim data analysis will be carried out and further genotyping performed in the next few months.

Requirements for Participation:

In silico ApoE genotype data or ICH samples eligible for ApoE genotyping.

Required phenotype data points are identical to the ICH GWAS minimal and additional requirements.

Contact: Jonathan Rosand, MD MSc
Massachusetts General Hospital
jrosand@partners.org

Consent Status in the determination of the phenotype spectrum in hemorrhagic stroke genetic research

Aims: Investigate the impact of consent status (self-consent, enrollment by proxy authorization, or waiver of consent because subject died prior to inclusion) in the ICH phenotypic spectrum in GOCHA / ICH GWAS

Current Status:

Currently available data was obtained from approximately 550 individuals (169 self-consented, 142 enrolled post mortem, and 239 enrolled via surrogate) from 7 sites. Analysis will be focused on preliminary comparisons among the 3 groups in relation to demographics (sex, race, age), risk factors, warfarin status, INR, and hemorrhage characteristics.

Requirements for Participation:

As discussed at the ICH GWAS Investigator Meeting in Munich, one group not currently represented in the data consists of eligible that declined participation. We anticipate being able to generate basic demographics on "refusers" from the MGH and UVA sites. If other individual sites have reasonably complete data on individuals who refused participation they are welcome to submit them for analysis.

Contact: Bradford B. Worrall, MD, MSc
University of Virginia Health System
bbw9r@virginia.edu

For further info on this topic please contact:
Lynelle Cortellini, M.Sc.
lcortellini@partners.org

Recruitment Updates

Sites recruiting prospectively as part of GOCHA

Study site	Period	Warfarin		Non Warfarin		Total
		Case	Control	Case	Control	
Mass General Hospital	May 2009	1	-	3	3	**7**
	June 2009	1	-	5	-	**6**
	July 2009	-	-	7	1	**8**
University of Michigan	May 2009	-	1	-	-	**1**
	June 2009	-	-	1	1	**2**
	July 2009	-	-	-	-	**-**
University of Virginia	May 2009	2	-	2	3	**7**
	June 2009	-	-	3	-	**3**
	July 2009	-	-	1	-	**1**
Mayo Clinic - Jacksonville	May 2009	-	-	1	3	**4**
	June 2009	-	-	2	1	**3**
	July 2009	-	-	-	1	**1**
University of Florida	May 2009	-	-	-	-	**-**
	June 2009	-	-	-	-	**-**
	July 2009	1	-	-	-	**1**
University of Washington	May 2009	-	-	-	-	**-**
	June 2009	-	-	-	-	**-**
	July 2009	1	-	-	-	**1**
Beth Israel Deaconess Medical Center	May 2009	-	-	-	-	**-**
	June 2009	-	-	1	-	**1**
	July 2009	-	-	-	-	**-**
Totals		**6**	**1**	**26**	**13**	**46**

Sites recruiting prospectively as part of ICH GWAS

Principal Investigator		Institution	Country of Origin	Status
Last Name	First Name			
Majersik	Jennifer	University of Utah	US	Joining
Thjis	Vincent	University Hospital Leuven	Belgium	Joining
Slowik	Agnieszka	Jagiellonian University, Krakow	Poland	Joined
Schmidt	Reinhold	Medical University Graz	Austria	Joined
Dichgans	Martin	Ludwig Maximilians University, Munich	Germany	Joined

Sites recruiting retrospectively as part of ICH GWAS

Principal Investigator		Institution	Country of Origin	Number of Cases	Number of Controls	Samples received by Genotyping Center
Last Name	First Name					
Dichgans	Martin	Munich	Germany	50	50	
Lindgren	Arne	University Hospital, Lund	Sweden	153	167	**Yes**
Macleod	Marie	University of Aberdeen	GB	40	40	
Markus	Hugh	St. George's, University of London	UK	200	200	
Melander	Olle	Malmo University Hospital	Sweden	100	300	
Montaner	Joan	Vall d'Hebron Hospital	Spain	169	176	**Yes**
Rothwell	Peter	Oxford	UK	40	40	
Roquer	Jaume	Hospital del Mar	Spain	200	200	
Schmidt	Reinhold	Medical University Graz	Austria	42	400	**Yes**
Slowik	Agnieszka	Jagiellonian University	Poland	224	420	**Yes**
Sudlow	Cathie	Western General, Edinburgh	GB	40	40	

Data presented in the table above are estimates of the number of samples each participating center has pledged to provide for the ICH GWAS. Actual numbers of samples analyzed will vary depending on DNA and phenotype quality.

For further info on this topic please contact:

Alessandro Biffi, M.D.

abiffi@partners.org

Spotlight: The Genomics of Common Diseases 2009

Wellcome Trust and Nature Genetics are proud to announce the third annual conference in this series of "The Genomics of Common Diseases," bringing together leading participants in this field.

The Genomics of Common Diseases 2009

September 23-26, 2009

Wellcome Trust Conference Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge, UK

The availability of whole-genome association studies and emerging "next-generation" sequencing technologies are redefining the genetic architecture of common diseases, revealing new susceptibility genes and offering new clues about mechanisms for a wide range of health disorders. The strategic focus of common disease genetics is progressing from the identification of susceptibility genes - with remarkable successes in the last two years - to understanding the extent to which rare and common variants explain inherited susceptibility to common diseases, to discovery of new disease mechanisms, and to pioneer and evaluate transfer of these advances through to potential clinical application.

The meeting will address the following topics:

- The state of the art in genome-wide association studies, across a range of common diseases, including whole genome sequencing
- Population genetics, statistics and evolution including common disease challenges in different populations, and biobanks
- Efforts to translate common disease genetics to the clinic and to the healthy population, incorporating pharmacogenomics, genomic profiling, utility of risk prediction, public health
- Genomics of common cancers and heritable cancer susceptibility
- Cell and animal models of common disease genetics
- The role of epigenomics in common diseases
- Ethical, legal and social implications of personal genetic information

For further info on this topic:

http://www.nature.com/natureconferences/gcd2009/index.html

Spotlight: Article

Gudbjartsson DF, Holm H, Gretarsdottir S. et al.

A sequence variant in ZFHX3 on 16q22 associates with atrial fibrillation and ischemic stroke

Nat Genet. 2009 Aug;41(8):876-8. Epub 2009 Jul

ABSTRACT

We expanded our genome-wide association study on atrial fibrillation (AF) in Iceland, which previously identified risk variants on 4q25, and tested the most significant associations in samples from Iceland, Norway and the United States. A variant in the ZFHX3 gene on chromosome 16q22, rs7193343-T, associated significantly with AF (odds ratio OR = 1.21, P = 1.4 x 10(-10)). This variant also associated with ischemic stroke (OR = 1.11, P = 0.00054) and cardioembolic stroke (OR = 1.22, P = 0.00021) in a combined analysis of five stroke samples.

Spotlight: Article

Boerwinkle E, Sinner MF, Dehghan A. et al.

Variants in ZFHX3 are associated with atrial fibrillation

in individuals of European ancestry.

Nat Genet. 2009 Aug;41(8):879-81. Epub 2009 Jul 13.

We conducted meta-analyses of genome-wide association studies for atrial fibrillation (AF) in participants from five community-based cohorts. Meta-analyses of 896 prevalent (15,768 referents) and 2,517 incident (21,337 referents) AF cases identified a new locus for AF (ZFHX3, rs2106261, risk ratio RR = 1.19; P = 2.3 x 10(-7)). We replicated this association in an independent cohort from the German AF Network (odds ratio = 1.44; P = 1.6 x 10(-11); combined RR = 1.25; combined P = 1.8 x 10(-15)).