# ICH GWAS Monthly Newsletter
# Issue 6 - May 2009


Due to impeding grant deadlines
the next ICH GWAS Conference Call scheduled for:

**Tuesday, May 19th 2009**
**10-11 am, Eastern USA time**


## WILL BE CANCELED

Dates for future ICH GWAS Conference Call
will be discussed at the ISGC Meeting in June

## In this issue:



**This is the sixth 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).**

# Recruitment Updates

## Sites recruiting prospectively as part of GOCHA

| Study site | Period | Warfarin | | Non Warfarin | | Total |
|---|---|---|---|---|---|---|
| | | Case | Control | Case | Control | |
| Mass General Hospital | February 2009 | 2 | 4 | 5 | - | **11** |
| | March 2009 | 1 | 2 | 5 | 0 | **8** |
| | April 2009 | 2 | 2 | 3 | 0 | **7** |
| University of Michigan | February 2009 | 1 | 2 | 1 | 1 | **5** |
| | March 2009 | - | 3 | 1 | 2 | **6** |
| | April 2009 | - | - | 1 | - | **1** |
| University of Virginia | February 2009 | - | - | - | - | **-** |
| | March 2009 | - | 2 | 2 | 25 | **29** |
| | April 2009 | - | - | 1 | 3 | **4** |
| Mayo Clinic - Jacksonville | February 2009 | - | - | 1 | - | **1** |
| | March 2009 | - | - | 2 | - | **2** |
| | April 2009 | - | - | 1 | - | **1** |
| University of Florida | February 2009 | - | - | - | - | **-** |
| | March 2009 | - | - | - | 1 | **1** |
| | April 2009 | - | - | 1 | - | **1** |
| Beth Israel Deaconess Medical Center | February 2009 | - | 5 | 1 | 1 | **7** |
| | March 2009 | - | - | 1 | 1 | **2** |
| | April 2009 | - | - | - | - | **-** |
| **Totals** | | **6** | **20** | **26** | **34** | **86** |

## 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 | Leuven | Belgium | Joining |
| Slowik | Agnieszka | Jagiellonian University, Krakow | Poland | Joined |
| Schmidt | Reinhold | Medical University Graz | Austria | Joined |
| Dichgans | Martin | 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 | | | | | |
| Lindgren | Arne | University Hospital, Lund | Sweden | 250 | 250 | |
| 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 | 185 | 270 | |
| Roquer | Jaume | Hospital del Mar | Spain | 200 | 200 | |
| Schmidt | Reinhold | Medical University Graz | Austria | 42 | 400 | |
| Slowik | Agnieszka | Jagiellonian University | Poland | 350 | 430 | **Yes** |

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: Article

Ioannidis JP, Thomas G, Daly MJ

**Validating, augmenting and refining genome-wide association signals.**

Nat Rev Genet. 2009 May;10(5):318-29

## ABSTRACT

Studies using genome-wide platforms have yielded an unprecedented number of promising signals of association between genomic variants and human traits. This Review addresses the steps required to validate, augment and refine such signals to identify underlying causal variants for well-defined phenotypes. These steps include: large-scale exact replication across both similar and diverse populations; fine mapping and resequencing; determination of the most informative markers and multiple independent informative loci; incorporation of functional information; and improved phenotype mapping of the implicated genetic effects. Even in cases for which replication proves that an effect exists, confident localization of the causal variant often remains elusive.