ICH GWAS Monthly Newsletter
Issue 7 - June 2009

In this issue:

This is the seventh 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	March 2009	1	2	5	0	**8**
	April 2009	3	0	9	7	**19**
	May 2009	1	0	3	3	**7**
University of Michigan	March 2009	-	3	1	2	**6**
	April 2009	-	-	1	-	**1**
	May 2009	-	1	-	-	**1**
University of Virginia	March 2009	-	2	2	25	**29**
	April 2009	-	-	1	3	**4**
	May 2009	2	-	2	3	**7**
Mayo Clinic - Jacksonville	March 2009	-	-	2	-	**2**
	April 2009	-	-	1	-	**1**
	May 2009	-	-	1	3	**4**
University of Florida	March 2009	-	-	-	1	**1**
	April 2009	-	-	1	-	**1**
	May 2009	-	-	-	-	**-**
Beth Israel Deaconess Medical Center	March 2009	-	-	1	1	**2**
	April 2009	-	-	-	-	**-**
	May 2009	-	-	-	-	**-**
Totals		**7**	**8**	**30**	**48**	**93**

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	**Yes**
Slowik	Agnieszka	Jagiellonian University	Poland	282	420	**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:

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Spotlight: Article

Newton-Cheh C. et al, Global BPGen Consortium

Genome-wide association study identifies eight loci associated with blood pressure.

Nat Genet. 2009 May; Epub ahead of print

ABSTRACT

Elevated blood pressure is a common, heritable cause of cardiovascular disease worldwide. To date, identification of common genetic variants influencing blood pressure has proven challenging. We tested 2.5 million genotyped and imputed SNPs for association with systolic and diastolic blood pressure in 34,433 subjects of European ancestry from the Global BPgen consortium and followed up findings with direct genotyping (N </= 71,225 European ancestry, N </= 12,889 Indian Asian ancestry) and in silico comparison (CHARGE consortium, N = 29,136). We identified association between systolic or diastolic blood pressure and common variants in eight regions near the CYP17A1 (P = 7 x 10(-24)), CYP1A2 (P = 1 x 10(-23)), FGF5 (P = 1 x 10(-21)), SH2B3 (P = 3 x 10(-18)), MTHFR (P = 2 x 10(-13)), c10orf107 (P = 1 x 10(-9)), ZNF652 (P = 5 x 10(-9)) and PLCD3 (P = 1 x 10(-8)) genes. All variants associated with continuous blood pressure were associated with dichotomous hypertension. These associations between common variants and blood pressure and hypertension offer mechanistic insights into the regulation of blood pressure and may point to novel targets for interventions to prevent cardiovascular disease.

Spotlight: Article

Levy D.. et al, CHARGE Consortium

Genome-wide association study of blood pressure and hypertension.

Nat Genet. 2009 May; Epub ahead of print

ABSTRACT

Blood pressure is a major cardiovascular disease risk factor. To date, few variants associated with interindividual blood pressure variation have been identified and replicated. Here we report results of a genome-wide association study of systolic (SBP) and diastolic (DBP) blood pressure and hypertension in the CHARGE Consortium (n = 29,136), identifying 13 SNPs for SBP, 20 for DBP and 10 for hypertension at P < 4 x 10(-7). The top ten loci for SBP and DBP were incorporated into a risk score; mean BP and prevalence of hypertension increased in relation to the number of risk alleles carried. When ten CHARGE SNPs for each trait were included in a joint meta-analysis with the Global BPgen Consortium (n = 34,433), four CHARGE loci attained genome-wide significance (P < 5 x 10(-8)) for SBP (ATP2B1, CYP17A1, PLEKHA7, SH2B3), six for DBP (ATP2B1, CACNB2, CSK-ULK3, SH2B3, TBX3-TBX5, ULK4) and one for hypertension (ATP2B1). Identifying genes associated with blood pressure advances our understanding of blood pressure regulation and highlights potential drug targets for the prevention or treatment of hypertension.