POSTER LISTING

ESHG

EUROPEAN SOCIETY OF HUMAN GENETICS

EMPAG
EUROPEAN MEETING ON
PSYCHOSOCIAL ASPECTS OF GENETICS

European Human Genetics Conference

in conjunction with the

European Meeting on Psychosocial Aspects of Genetics

2014

Milan, Italy, May 31 – June 3, 2014

P17.59-S Improving power in family-based association of rare variants via wavelet-based test
Hui-Min WANG (Taipei, Taiwan)

P17.60-M Whole exome sequencing: Follow-up of a rare non-synonymous variant in GRHL3 in a German family with nonsyndromic orofacial cle ing
Anne BÖHMER (Bonn, Germany)

P17.61-S Novel mutations described in Saudi Arabia
Alaa EDREES (Jeddah, Saudi Arabia)

P17.62-M Contribution of SNPs (rs9939609 and rs8057044) and haplotypes of FTO gene to the genetic risk for obesity in children from Yucatan, Mexico
Lizbeth GONZALEZ-HERRERA (Merida, Mexico)

P17.63-S Molecular Analysis of TYR, OCA2, TYRP1 , SLC45A2 and GPR143 Genes in 158 Patients with Oculocutaneous and Ocular Albinism
Paola PRIMIGNANI (Milan, Italy)

P17.64-M Genetic landscape of populations along the Silk Road reveals a haplotype associated with hyposmia in Tajikistan's population
Massimo MEZZAVILLA (Trieste, Italy)

P17.65-S Targeting a gene network of ADAMTS genes contributing to pediatric stroke
Anika WITTEN (Muenster, Germany)

P17.66-M A genome-wide association study of Agreeableness suggests a novel association in the NAV2 gene in Korean women
Han-Na KIM (Seoul, Korea, Republic of)

P17.67-S New genetic matching methods for handling population stratification in genome-wide association studies
André LACOUR (Bonn, Germany)

P17.68-M The causal role of insulin-like growth factors and binding proteins in prostate cancer: a Mendelian randomization study
Carolina BONILLA (Bristol, United Kingdom)

P17.69-S Combining different sources of information to optimise genomic prediction of complex traits
Athina SPILIOPOULOU (Edinburgh, United Kingdom)

P17.70-M Technical issues of using Next Generation sequencing for rare-variant association
Carolien DE KOVEL (Utrecht, Netherlands)

P17.71-S A Script for Linkage Analysis of Rare variants
Irina ZORKOLTSEVA (Novosibirsk, Russian Federation)

P17.72-M Correcting for population substructure in rare variant - rare disease association studies
Na ZHU (Berlin, Germany)

P17.73-S Functional linear model for regional association analysis of rare genetic variants in family-based samples
Gulnara SVISHCHEVA (Novosibirsk, Russian Federation)

P17.74-M Genome wide inbreeding estimation within Lebanese communities using SNP arrays
Nadine JALKH (Beirut, Lebanon)

P17.75-S Population genomics analysis in whole genome sequencing of 152 rhesus macaques
Fuli YU (Houston, United States)

P17.76-M Association of five confirmed risk gene polymorphisms with Rheumatoid Arthritis in the Algerian population
Mostefa FODIL (Oran, Algeria)

P17.78-M How does this Arab Genome differ from other genome?
Ibrahim ALABDULKAREEM (Riyadh, Saudi Arabia)

P17.79-S Soluble CD40 ligand is regulated by membrane CD40 expression in platelet concentrates
Chaker ALOUI (Saint-Etienne, France)

P17.80-M Inferring rare disease risk variants based on exact probabilities of sharing by multiple affected relatives
Ingo RUCZINSKI (Baltimore, United States)

P17.81-S A Founder Effect for PPIB-associated recessive osteogenesis imperfecta in Acadian and Cajun Populations
Lauren CURRIE (Halifax, Canada)

P17.82-M Genetic survival modeling with large-scale population cohorts
Christian BENNER (Helsinki, Finland)

P17.83-S Genome- wide association analysis of swallowing symptoms related to dysphagia in a healthy older adult cohort
Alicja RAGINIS-ZBOROWSKA (Manchester, United Kingdom)

P17.85-S Investigation of hellenic families with microscopic hematuria reveals the frequency of collagen IV mutations and evidence for activation of the unfolded protein response
Louiza PAPAZACHARIOU (Nicosia, Cyprus)

P17.86-M Variation in BTBD9 gene is associated with Tourette syndrome in the Polish population
Mariusz BERDYNSKI (Warsaw, Poland)

P17.87-S The investigations of susceptibility genes/variants related to type 2 diabetes in Turkish
Hilal ARIKOGLU (Konya, Turkey)

P17.88-M The T allele of rs7903146 in TCF7L2 is associated with type 2 diabetes in Iranian: a large population-based cohort study
Mahdi SAFARPOUR (Tehran, Iran, Islamic Republic of)

P17.89-S The first genetic study of Type 2 Diabetes in the Cypriot population
Christina VOTSI (Nicosia, Cyprus)

P17.90-M The southern migration route: a supporting clue from aboriginal Vedda people of Sri Lanka
Lanka RANAWEERA (Ragama, Sri Lanka)

P17.91-S RNA-Sequencing reveals differential gene expression between visceral and subcutaneous adipose tissue in Greek women undergoing abdominal surgery
Efi KATSARELI (Kallithea, Athens, 17671, Greece)

P17.92-M Meta-analysis of Y chromosome haplogroups C, N and Q in Eurasian populations for the perspectives of proto-Bulgarian ancestry
Sena KARACHANAK (Sofia, Bulgaria)

P17.93-S Forensic parameters and allele frequency distribution of 15 autosomic STR loci in a Mestizo population from the State of Yucatan, Mexico
Javier SOSA-ESCALANTE (Merida, Mexico)

P17.94-M Retrospective analysis of live birth prevalence of children with Down syndrome in Denizli, Turkey
Ibrahim ACIKBAS (Denizli, Turkey)

P17.95-S Six novel loci associated with VEGF circulating levels identified by a meta-analysis of genome-wide association studies
Daniela RUGGIERO (Naples, Italy)*

Control/Tracking Number: 2014-A-1980-ESHG
Activity: ESHG Abstract
Current Date/Time: 6/10/2014 12:15:36 AM

A genome-wide association study of Agreeableness suggests a novel association in the NAV2 gene in Korean women

Author Block: **H. Kim**[1], S. Roh[1], B. Kim[1], H. Kim[1], H. Cho[1], N. Cho[2], C. Shin[3], J. Sung[4], H. Kim[1];
[1]Ewha Womans University, Seoul, Korea, Republic of, [2]Ajou University, Seoul, Korea, Republic of, [3]Korea University, Seoul, Korea, Republic of, [4]Seoul National University, Seoul, Korea, Republic of.

Abstract:
Data from genome-wide association (GWA) studies have been used to find the common variants of personality. In a previous study, we reported that neurotransmitters and the olfactory receptor 1A2 gene are associated with neuroticism in a cohort of young Korean women. However, many genetic variants that are highly associated with certain personality traits are still unknown. Here, we report on a meta-analysis of GWA data for personality in three cohorts samples (2045 individuals). All participants were of Korean ancestry. Personality traits were measured with the Revised Neuroticism-Extraversion-Openness Personality Inventory to assess five factors: Neuroticism, Extraversion, Agreeableness, Openness, and Conscientiousness. In either discovery stage, classical association analyses were performed under an additive model followed by meta-analysis using the weighted inverse variance method. We observed consistent direction of effect and significant association of the NAV2 gene and Agreeableness in either the discovery and combined stage (p=7.85×10-7, for meta-analysis). NAV2 gene involves in optic nerve development and sensory perception of smell and sound. We previously reported that the sensory system may play an important role in personality, and the present study leads to the same conclusion. The sensory system affects personality as a filter of the acceptance system, which may have an advantage to reconstruction.
This study was supported by a grant of the National Project for Personalized Genomic Medicine, Ministry for Health & Welfare, Republic of Korea (A111218).
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Topic (Complete): 17. Genetic epidemiology/Population genetics/Statistical methodology and evolutionary genetics
Keyword (Complete): Personality ; GWAS ; Agreeableness
Presentation Preference (Complete): Poster only
Awards - Fellowships (Complete):
YoungScientistAward: No
Application for Fellowship: No

Status: Complete

POCKET PROGRAMME AT A GLANCE

Saturday, May 31, 2014

Time	Gold Room	Space 3+4	Brown 3	Brown 1+2	Space 1	Space 2	Amber 3+4	Amber 7+8	Suite 5
10.30 – 12.00	ES1 The platelets planet: from diagnosis to therapy of inherited thrombocytopenias	ES2 Genetic prediction scores in common diseases: are they of any value?	ES3 What's new in Next Generation Sequencing?	ES4 DNA repair and genomic instability	WS01 Disease of the year: Rasopathies				
12.15 – 13.45	Lunch Break						EWS1 The impact of risk reducing surgery	CS01 Myriad Genetics Satellite	CS02 Personalis Satellite
14.00 – 14.30	Opening Welcome Addresses								
14.30 – 16.00	PL1 Opening Plenary Session						EPL1 Psychosocial issues in cancer genetics		
16.00 – 16.30	Vitamin Break								
16.30 – 18.00	PL2 What's New? Highlights Session						EPL2 Reproductive decision making		
18.00 – 18.30	Coffee Break								
18.30 – 20.00	C01 Prenatal testing	C02 Personalized medicine and pharmacogenomics	C03 Intellectual disability	C04 Cardiovascular disorders	C05 Genes and development 1	C06 Functional and computational genomics	EPL3 Genomic testing: psychosocial and ethical issues		
20.00 – 21.30	Opening Networking Mixer at the MCC								

Sunday, June 1, 2014

Time	Gold Room	Space 3+4	Brown 3	Brown 1+2	Space 1	Space 2	Amber 3+4	Amber 5+6	Amber 7+8	Suite 5
08.30 – 10.00	S01 Towards Genomic Personalised Medicine	S02 Functional genomics	S03 Neuronal Migration disorders	S04 Computational Analysis of Gene Networks	S05 Early development and preimplantation genetics	ES5 Mosaicism in human disease	EES 1 Responding to guilt and shame			
10.00 – 10.30	Coffee break / Poster viewing / Exhibition									
10.30 – 11.30	Poster viewing with presenters (poster numbers ending with "S")									
11.45 – 13.15	Poster viewing / Lunch break / Exhibition						EPL4 Family Dynamics (11.30-12.15)	CS3 Affymetrix Satellite	CS04 Life Technologies Satellite	CS05 BIOBASE Satellite
13.30 – 15.00	C07 Implementation of NGS in diagnostics	C08 Cancer genetics	C09 Common neurological disease	C10 Bone and skeletal patterning	C11 Statistical genetics	C12 Sensory disorders	EPL5 Access to genetic services and testing			
15.00 – 15.30	Vitamin break / Poster viewing / Exhibition									
15.30 – 17.00	WS02 Dysmorphology 1	WS03 ENSEMBL	WS04 Practical Bioinformatics: Whole exome sequence analysis	WS05 Quality assurance	WS06 Community genetics - Clinical Genetic Services in 2025	WS07 Preimplantation genetic diagnosis	EPL6 Facilitating communication about genetic information	CS06 PerkinElmer Satellite	CS07 Cartagenia Satellite	CS08 Multiplicom Satellite
17.00 – 17.30	Coffee break / Poster viewing / Exhibition									
17.30 – 19.00	S06 Risk perception and risk communication, joint with EMPAG	S07 Therapy for human genetic diseases	S08 Population genetics in a globalized world	S09 Advances and new challenges in genetics of cardiovascular diseases, joint with the Eur.Soc. of Cardiology	S10 New Mutational Mechanisms	ES6 How to be successful in rare disease gene identification				
19.00 – 20.30							ESHG Membership Meeting	CS09 AstraZeneca Satellite	CS10 Illumina Satellite	CS11 Natera Satellite

Monday, June 2, 2014

Time	Gold Room	Space 3+4	Brown 3	Brown 1+2	Space 1	Space 2	Amber 3+4	Amber 5+6	Amber 7+8	Suite 5
08.30 –	S11	S12	S13	S14	ES7					

	Rare copy number variants in common traits	Epigenetic basis of disease	Non-invasive prenatal testing, joint with EMPAG	Rapid genome diagnostics	From mutation identification to therapy					
10.00 – 10.30	Coffee break / Poster viewing / Exhibition									
10.30 – 11.30	Poster viewing with presenters (poster numbers ending with "M")									
11.45 – 13.15	Poster viewing / Lunch break / Exhibition							EPL7 Autonomy and consent (11.30-12.15)	CS12 Agilent Technologies Satellite	CS13 Abbott Molecular Satellite	CS14 LGC Satellite
13.30 – 15.00	C13 Innovation in genetic services	C14 Genetics of complex traits	C15 Novel genes in neurogenetic disorders	C16 Genes and development 2	C17 Metabolic and mitochondrial disorders			EPL8 Psychosocial issues in prenatal & preimplantation diagnosis			
15.00 – 15.30	Vitamin break / Poster removal / Exhibition										
15.30 – 17.00	WS08 Dysmorphology 2	WS09 Genome Browser UCSC	WS10 Analysis, interpretation and reporting of array data	WS11 Clinical Cancer Genetics Club	WS12 Preconception and prenatal screening	WS13 Next Generation Sequencing		EPL9 Lessons learned and new issues in predictive testing		CS15 Life Technologies Satellite	CS16 QIAGEN Satellite
17.00 – 17.30	Coffee break / Poster removal / Exhibition										
17.30 – 19.00	S15 Networks and pathways in genetic diseases	S16 The new RNA world	S17 Tumour heterogeneity	S18 A novel class of disease of lipid metabolism	S19 Three sequencing approaches in complex disease	ES8 Current developments in legal aspects of genetics: Untangling the law and what it means for you		EES 2 Qualitative and quantitative methods in psychosocial research			
19.00 – 20.30									CS17 BGI Satellite	CS18 Fluidigm Satellite	CS19 Roche Sequencing Satellite
20.30	Networking Party at the Old Fashion Club										

Tuesday, June 3, 2014

Time	Gold Room	Space 3+4	Brown 3	Brown 1+2	Space 1
09.00 – 10.30	PL3 ESHG-ASHG "Building Bridges Session": Debate: What IF... (Incidental Findings), an interactive Debate, joint with EMPAG				
10.30 – 11.00	Coffee break (Level 1 & 2)				
11.00 – 12.30	C18 Large scale genomics	C19 Internal organs	C20 Basic mechanisms in genetics	C21 Rasopathies and CDG	C22 Returning results: Ethical and legal issues, joint with EMPAG
12.30 – 13.30	Lunch Break (Level 1 & 2)				
13.30 – 14.15	PL4 Mendel Lecture				
14.15 – 15.45	PL5 Closing Plenary ESHG Award Lecture - ESHG Honorary Award - EJHG-NPG Awards - Young Investigator & Poster Awards - Closing				

Plenary Session | Symposium | Concurrent Session | Workshop | Educational Session | EMPAG Sessions | Corporate Satellite

POCKET SATELLITES

Saturday, May 31, 2014
SIGU High School Workshop
09:00 - 13:30 hrs, Space 2, Level 0

Sunday, June 1, 2014
Introduction to using Encode data for your analysis Workshop
11.30 - 13.00 hrs, Space 3+4, Level 0

Monday, June 2, 2014
Telegenetics in practice
12:15 - 13:15 hrs, Suite 3, Level 2

EUCID.net Satellite Meeting
12:30 - 13:15 hrs, Space 2, Level 0