Curriculum Vitae

Name Hong-Hee Won

Education

2007-2011 Ph.D. in Bio and Brain Engineering, KAIST, South Korea

2002-2004 M.S. in Computer Science, Yonsei University, South Korea

1998-2002 B.S. in Computer Science, Yonsei University, South Korea

Professional Experience

2016-Pres. Assistant Professor, SAIHST, Sungkyunkwan University, South Korea

2012-2015 Research Fellow, Massachusetts General Hospital, Harvard Medical School and Broad Institute of MIT and Harvard, USA

2004-2012 Research Scientist, Samsung Biomedical Research Institute and Samsung Medical Center

2002-2004 Researcher and Teaching Assistant, Soft Computing Laboratory, Yonsei University

2001-2002 Undergraduate Research Assistant, Soft Computing Laboratory, Yonsei University

Selected Publications (*equal contribution)

2016 Exome Aggregation Consortium (2016). Analysis of protein-coding genetic variation in 60,706 humans. ***Nature*** (Accepted).

*Khera A, ****Won HH***, *Peloso GM, et al. (2016). Diagnostic yield of sequencing familial hypercholesterolemia genes in severe hypercholesterolemia. ***Journal of the American college of cardiology JACC*** 67(22), 2578-89.

Stitziel NO, Stirrups KE, Masca NGD, Erdmann J, Ferrario PG, König IR, Weeke PE, Webb TR, Auer PL, Schick UM, Lu Y, Zhang H, Dube MP, Goel A, Farrall M, Peloso GM, **Won HH**, et al. (2016) Coding variation in ANGPTL4, LPL, and SVEP1 and the risk of coronary disease. ***New England journal of medicine NEJM*** 374(12), 1134-44.

2015 **Won HH**, Natarajan P, Dobbyn A, et al. (2015). Disproportionate contributions of select genomic compartments and cell types to genetic risk for coronary artery disease. ***PloS genetics*** doi:10.1371/journal.pgen.1005622.

*Nikpay M, *Goel A, ****Won HH***, et al. (2015). A comprehensive 1000 Genomes-based GWAS meta-analysis of coronary artery disease. ***Nature genetics*** 47(10), 1121-30.

*Kim J, ****Won HH***, Kim Y, et al. (2015). Breakpoint mapping by whole genome sequencing identifies PTH2R gene disruption in a patient with midline craniosynostosis and a de novo balanced chromosomal rearrangement. ***Journal of medical genetics*** 52(10), 706-9. (Featured on the Cover page)

Thormaehlen AS, Schuberth C, **Won HH**, et al. (2015). Systematic cell-based phenotyping of missense alleles empowers rare variant association studies: a case for *LDLR* and myocardial infarction. ***PloS genetics*** 11(2), e1004855.

*Do R, *Stitziel NO, ****Won HH***, et al. (2015). Exome sequencing identifies rare *LDLR* and *APOA5* alleles conferring risk for myocardial infarction. ***Nature*** 518, 102-106.

Covered by **Nature Reviews Cardiology** (Mutations in *APOA5* or *LDLR* increase risk of

myocardial infarction).

2014 *Stitziel NO, **<u>*Won HH</u>**, et al. (2014). Inactivating mutations in *NPC1L1* and protection from coronary heart disease. ***New England journal of medicine NEJM*** 371(22), 2072-2082.

Covered by **Nature News** (Drug trial supports importance of low cholesterol to treat heart disease), **Nature Reviews Cardiology** (NPC1L1 mutations lower CHD risk), **MIT Technology Review** (The Search for Exceptional Genomes), **the New York Times** (Study Finds Alternative to Anti-Cholesterol Drug), **the Boston Globe** (Flawed gene protects against heart disease), **BBC** (Gene error 'reduces heart attack and cholesterol risk'), **the Washington Post** (Rare Mutation Mimicked by Merck's Pill Zetia Slashes Heart Risk), **Forbes** (Newly Identified Gene Mutations Act Like A Lifetime Of Treatment With Merck Cholesterol Drug).

*Tada H, **<u>*Won HH</u>**, et al. (2014). Multiple associated variants increase the heritability explained for plasma lipids and coronary artery disease. ***Circulation: cardiovascular genetics*** 7(5), 583-587.

*Lim SW, **<u>*Won HH</u>**, *Kim H, et al. (2014). Genetic prediction of antidepressant drug response and nonresponse in korean patients. ***PloS one*** 9(9), e107098.

2013 **<u>Won HH</u>**, Kim JW, and Lee D (2013). A Bayesian ensemble approach with a disease gene network predicts damaging effects of missense variants of human cancers. ***Human genetics*** 132, 15-27.

*Kim HJ, **<u>*Won HH</u>**, Park KJ, et al. (2013). SNP linkage analysis and whole exome sequencing identify a novel POU4F3 mutation in autosomal dominant late-onset nonsyndromic hearing loss (DFNA15). ***PloS one*** 8(11), e79063.

<u>Won HH</u>, Myung W, et al. (2013). Predicting national suicide numbers with social media data. ***PloS one*** 8(4), e61809.

2012 **<u>Won HH</u>**, Lee J, Park JO, et al. (2012). Polymorphic markers associated with severe oxaliplatin-induced, chronic peripheral neuropathy in colon cancer patients. ***Cancer*** 118, 2828-2836.

<u>Won HH</u>, Kim SR, Bang OY, et al. (2012). Differentially expressed genes in human peripheral blood as potential markers for statin response. ***Journal of molecular medicine*** 90, 201-211.

*Ahn MJ, **<u>*Won HH</u>**, Lee J, et al. (2012). The 18p11.22 locus is associated with never smoker non-small cell lung cancer susceptibility in Korean populations. ***Human genetics*** 131, 365-372.

2011 Shrif NE, **<u>Won HH</u>**, Lee ST, et al. (2011). Evaluation of the effects of VKORC1 polymorphisms and haplotypes, CYP2C9 genotypes, and clinical factors on warfarin response in Sudanese patients. ***European journal of clinical pharmacology*** 67, 1119-1130.

*Kim DH, *Lee ST, **<u>*Won HH</u>**, et al. (2011). A genome-wide association study identifies novel loci associated with susceptibility to chronic myeloid leukemia. ***Blood*** 117, 6906-6911.

2010 **<u>Won HH</u>**, Kim JW, Kim MJ, et al. (2010). Interleukin 10 polymorphisms differentially influence the risk of gastric cancer in East Asians and Caucasians. ***Cytokine*** 51, 73-77.

2009 **<u>Won HH</u>**, Park I, Lee E, Kim JW, and Lee D (2009). Comparative analysis of the JAK/STAT signaling through erythropoietin receptor and thrombopoietin receptor using a systems approach. ***BMC bioinformatics*** 10 Suppl 1, S53.

<u>*Won HH</u>, *Lee S, Jang E, et al. (2009). A genome-wide scan for the Sasang constitution in a Korean family suggests significant linkage at chromosomes 8q11.22-23 and 11q22.1-3. ***Journal of alternative and complementary medicine*** 15, 765-769.

*Kim KK, ***Won HH**, Cho SS, et al. (2009). Comparison of identical single nucleotide polymorphisms genotyped by the GeneChip Targeted Genotyping 25K, Affymetrix 500K and Illumina 550K platforms. ***Genomics*** 94, 89-93.

Hong KS, **Won HH**, Cho EY, et al. (2009). Genome-widely significant evidence of linkage of schizophrenia to chromosomes 2p24.3 and 6q27 in an SNP-Based analysis of Korean families. ***American journal of medical genetics Part B, Neuropsychiatric genetics*** 150b, 647-652.

2008 **Won HH**, Kim MJ, Kim S, and Kim JW (2008). EnsemPro: an ensemble approach to predicting transcription start sites in human genomic DNA sequences. ***Genomics*** 91, 259-266.

Won HH**, *Kim HJ, Lee KA, and Kim JW (2008). Cataloging coding sequence variations in human genome databases. ***PloS one 3, e3575.

2007 *Nam MH, ***Won HH**, Lee KA, and Kim JW (2007). Effectiveness of in silico tagSNP selection methods: virtual analysis of the genotypes of pharmacogenetic genes. ***Pharmacogenomics*** 8, 1347-1357.

Kim HJ, Sohn KM, Shy ME, Krajewski KM, Hwang M, Park JH, Jang SY, **Won HH**, et al. (2007). Mutations in *PRPS1*, which encodes the phosphoribosyl pyrophosphate synthetase enzyme critical for nucleotide biosynthesis, cause hereditary peripheral neuropathy with hearing loss and optic neuropathy (cmtx5). ***American journal of human genetics*** 81, 552-558.

2003 **Won HH**, Cho SB (2003). Neural networks for bio-informatics applications-neural network ensemble with negatively correlated features for cancer classification. ***Lecture notes in computer science*** 2714, 1143-1150.

Cho SB, **Won HH** (2003). Machine learning in DNA microarray analysis for cancer classification. ***Proceedings of the first Asia-Pacific bioinformatics conference*** 19, 189-198.

Selected Talks

2015 New England Bioscience Society 23rd Annual Conference, Boston, USA. Human gene knockouts and myocardial infarction.

2015 Annual Retreat, Center for Human Genetic Research, Massachusetts General Hospital, Boston, USA. Rare coding variants, LDL cholesterol, and coronary heart disease.

2014 The American Heart Association (AHA), Chicago, USA. Contribution of rare mutations in Mendelian hypercholesterolemia genes to risk for premature coronary artery disease in the population.

2014 Annual Retreat, Cardiovascular Research Center, Massachusetts General Hospital, Boston, USA. Inactivating mutations in *NPC1L1* and protection from coronary heart disease.

2009 The Asia Pacific Bioinformatics Conference (APBC), Beijing, China. Comparative analysis of JAK/STAT signaling through erythropoietin receptor and thrombopoietin receptor using systems approach.

Patents

2014 Kim DK, Kim JW, Myung WJ, **Won HH**. SUICIDE PREDICTION METHOD AND DEVICE USING SOCIAL DATA. Korean Patent (#1013855620000)

2012 Kim JW, Kim DH, Lee ST, **Won HH**. METHOD FOR PREDICTING A RISK OF CHRONIC MYELOID LEUKEMIA, AND DIAGNOSIS KIT USING SAME. WO (#2012150818)

2011 Kim JW, Kim DH, Lee ST, **Won HH**. Method for predicting chronic myeloid leukemia risk and kit for diagnosing chronic myeloid leukemia risk thereof. Korean Patent application (#10-2011-0041690)

Awards and Honors

2015-2016	American Heart Association: Founders Affiliate Postdoctoral Fellowship, Percentile Rank: 1%
2015	NEBS Alumni in Korea Research Fellow Award
2015	Trainee Winner for the Best Paper, Center for Human Genetic Research, Massachusetts General Hospital
2008-2011	Encouraging Prize from Samsung Biomedical Research Institute Research Award
2007-2010	General Scholarship of KAIST from Samsung Biomedical Research Institute
2003	IEEE Neural Networks Society 2003 Student Travel Grant
2002-2004	Scholarship from The Graduate School of Yonsei University
1998-2002	Scholarship from Yonsei University