Curriculum Vitae

Eun Pyo Hong, Ph.D

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Hallym University College of Medicine,
Chuncheon, Korea.
Field1:Genomic Epidemiologist
Field2:Bioinformatics
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EDUCATION

- 2012.09. - 2017.8. Ph.D in Medical Genetics, Hallym University, Chuncheon, South Korea
- 2009.03. - 2012.8. MS in Medical Genetics, Hallym University, Chuncheon, South Korea
- 2002.03. - 2006.2. BS in Informatics & Statistics, Hallym University, Chuncheon, South Korea

WORK EXPERIENCE

- 2021.05. – Present. Seiner Researcher, Institute of New Frontier Research, Hallym University College of Medicine, Chuncheon 24252, Korea.
- 2019.03. – 2021.04. Postdoctoral Scholar and member, Medical and Population Genetics Program, Broad Institute of M.I.T and Harvard, Cambridge MA 02142, USA.
- 2018.01. – 2021.04. Postdoctoral Fellow, Department of Neurology, Harvard Medical School, Boston MA 02115, USA
- 2018.01. – 2021.04. Research Fellow, Molecular Neurogenetics Unit, Center for Genomic Medicine, Massachusetts General Hospital, Boston, MA 02114, USA.
- 2016.08. - 2017.11. Researcher, Institute of Natural Medicine, Hallym University College of Medicine, Chuncheon, Gangwon-do 24252, South Korea
- 2016.08. - 2017.11. Co-researcher, Dpt. of Medical Genetics, Hallym University College of Medicine, Chuncheon, Gangwon-do 24252, South Korea
- 2014.03. - Present. Co-researcher and member, Pan-Cancer Analysis of Whole Genome (PCAWG) Project - Germline Cancer Genome Analysis (Working Group 8)
- 2009.03. - 2016.07. Research Assistant, Dpt. of Medical Genetics, Hallym University College of Medicine, Chuncheon, Gangwon-do 24252, South Korea
- 2008.08. - 2009.02. Apprentice in Dpt. of Medical Genetics, Hallym University College of Medicine, Chuncheon, Gangwon-do 24252, South Korea

RSEARCH PROJECTS (In South Korea)

- 2017.06.01. - 2017.12.31. Development of prediction modeling methods for lung cancer using genomic big data (NRF No. 2017R1D1A1B03029833)
- 2014.11.01. - 2017.07.31. Development of multifactorial liability threshold model to predict the risk of nephropathy in patients with type 2 diabetes mellitus (NRF No. 2014R1A1A3053168; HRF No. HRF-201403-015).
- 2014.03.01. - 2017.02.26. Personalized Genome Medicine 21 Project (PGM21 Project No. A111218-GM07).
- 2014.03.01. - 2015.02.26. Risk prediction of the development of tuberculosis in Korea
- 2013.02.28. - 2013.12.27. Simulation study for early warning model using linear mixed model and construction for early warning system contents based on Korean genome information (NRF No. 2013E7300300).
- 2009.09.01. - 2012.08.31. Gene-environment interaction for aging-related traits (NRF No. 2009-0090837; HRF No. HRF-G2012-5).

NRF. The National Research Foundation, Republic of Korea
HRF, HallymUniversity Research Fund, Republic of Korea

OTHER EXPERIENCE

- 2017. 07. 21 - 22. Lab Lecturer, “Lab: 1) Genetic-based Survival Analysis and 2) Next Generation Sequencing Analysis” in 12th Asian Institute in Statistical Genetics and Genomics. Korea Genome Organization, South Korea.
- 2016. 07. 20 - 21. Lab Lecturer, “Lab: 1) Genetic-based Survival Analysis and 2) Next Generation Sequencing Analysis” in 11th Asian Institute in Statistical Genetics and Genomics. Korea Genome Organization, South Korea.
- 2015. 07. 15 - 16. Lab Lecturer, “Lab: Next Generation Sequencing Analysis” in 10th Asian Institute in Statistical Genetics and Genomics. Korea Genome Organization, South Korea.

PROGRAMMING, ANALYSIS & COMMON SKILL

O/S and Language Applications

- O/S application: Linux-Ubuntu/Centos (Middle level)
- Program language: Python language (Middle level, e.g., make a script to handle and perform a large-scale genomic dataset)

Analysis Skills

- For cancer genomes: Variant calling & Sequencing data analysis
  Germline Variation Study, Exome-Wide Association Study, RNA-seq Analysis
  Cancer WGS/WES data: PCAWG project driven from ICGC and TCGA consortiums
- For neurodegenerative disease: RNA sequencing (~2k brain tissues, PsychENCODE), single-cell RNA sequencing for genomic base editing (finding off-target effects, Human iPSC), allele-specific expression analysis, whole-exome sequencing etc.
- Candidate gene study, GWAS, and Meta-analysis
  Population-based Study (Case-control, Cohort) on Human Complex Traits
- Gene-Gene & Gene-Environment interaction analysis

- Survival analysis (follow-up data, cohort study)
- Analysis of genetic/non-genetic disease risk predictions

S/W and Others Application Skills

- Web Server Management/Construction, development, for example, https://cegeme.partners.org/gem.euro.9k [Ref1, 2]
- Statistical S/W: R, STATA, SKAT, PLINK, PLINK/SEQ, GCTA, GATK, etc.
- Web database application: DAVID, PubMed, dbSNP, etc.

SPECIAL AWARD

- Bioinformatics Analysis Award: "*Risk prediction for NK-AML using Whole Exome Sequencing*", Published in 2013, Genomics & Informatics, Korea Genome Organization & Personalized Genomic Medicine21, Feb. 2013.
- Most Cited Paper Award: "*Sample Size and Statistical Power Calculation in Genetic Association Studies*". Published in 2012, Genomics & Informatics, Korea Genome Organization, Feb. 2015.

THESIS

- MS. degree: Impact of gene-environment interactions on high sensitivity C-reactive protein levels in Koreans: Hallym Aging Study
- Ph.D. degree: A risk assessment study on type 2 diabetes and diabetic cardiovascular disease using multiple genetic and environmental risk factors in Koreans

PUBLICATION (REFERENCE)

1. Kim BJ, **Hong EP**, Youn DH, Jeon JP; First Korean Stroke Genetics Association Research. Genome-Wide Association Study of the Relationship Between Matrix Metalloproteinases and Intracranial Aneurysms. J Clin Neurol. 2022 Feb 14. doi: 10.3988/jcn.2022.18.e6. Online ahead of print.
2. **Hong EP**, Youn DH, Kim BJ, Ahn JH, Park JJ, Rhim JK, Jeon JP. Fine-mapping of intracranial aneurysm susceptibility based on a genome-wide association study. Sci Rep. 2022 Feb 17;12(1):2717.
3. Gaastra B, Alexander S, Bakker MK, Bhagat H, Bijlenga P, Blackburn S, Collins MK, Doré S, Griessenauer C, Hendrix P, **Hong EP**, Hostettler IC, Houlden H, IIhara K, Jeon JP, Kim BJ, Kumar M, Morel S, Nyquist P, Ren D, Ruigrok YM, Werring D, Galea I, Bulters D, Tapper W. Genome-Wide Association Study of Clinical Outcome After Aneurysmal Subarachnoid Haemorrhage: Protocol. Transl Stroke Res. 2022 Jan 6. doi: 10.1007/s12975-021-00978-2. Online ahead of print.
4. Youn DH, Kim BJ, **Hong EP**, Jeon JP; first Korean Stroke Genetics Association Research. Bioinformatics Analysis of Autophagy and Mitophagy Markers Associated with Delayed Cerebral Ischemia Following Subarachnoid Hemorrhage. J Korean Neurosurg Soc. 2021 Dec 23. doi: 10.3340/jkns.2021.0169. Online ahead of print.
5. **Hong EP**, Chao MJ, Jones L, Holmans P, Kwak S, Orth M, Monckton DG, Loing JD, Wheeler VC, MacDonald ME, Gusella JF, Lee JM. Association analysis of chromosome X

modifiers of Huntington's Disease. 2021;10(3):367-375. doi: 10.3233/JHD-210485.
6. **Hong EP**, MacDonald ME, Wheeler V, Jones L, Holmans P, Orth Michael, Monckton DG, Long JD, Kwak S, Gusella JF, and Lee JM. Huntington's Disease Pathogenesis: Two Sequential Components. Journal of Huntington's Disease. 10 (2021) 35–51. DOI: 10.3233/JHD-200427.
7. **Hong EP**, Heo SG, Park JW. The Liability Threshold Model for Predicting the Risk of Cardiovascular Disease in Patients with Type 2 Diabetes: A Multi-Cohort Study of Korean Adults. Metabolites. 2021 Jan;11(1):E6.
8. Bailey MH et al.; PCAWG Consortium. Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. Nat Commun. 2020 Sep 21;11(1):4748.
9. Li CH, Prokopec SD, Sun RX, Yousif F, Schmitz, PCAWG Tumour Subtypes and Clinical Translation, Paul C. Boutros, and PCAWG Consortium. Sex differences in oncogenic mutational processes. Nat Commun. 2020 Aug 28;11(1):4330.
10. Kim KH, **Hong EP**, Shin JW, Chao MJ, Loupe J, Gillis T, et al. Genetic and Functional Analyses Point to FAN1 as the Source of Multiple Huntington Disease Modifier Effects. Am J Hum Genet. 2020 Jul 2;107(1):96-110.
11. The ICGC/TCGA Pan-Cancer Analysis of Whole Genomes Consortium. Pan-cancer analysis of whole genomes. Nature. 2020 Feb 5;578:82-93.
12. Genetic Modifiers of Huntington's Disease (GeM-HD) Consortium: Ellis et al. Genetic risk underlying psychiatric and cognitive symptoms in Huntington's Disease. Biol Psychiatry. 2020 May 1;87(9):857-865.
13. Genetic Modifiers of Huntington's Disease (GeM-HD) Consortium. CAG Repeat Not Polyglutamine Length Determines Timing of Huntington's Disease Onset. Cell. 2019 Aug 8;178(4):887-900.e14.
14. **Hong EP**, Kim BJ, Yang JS, Choi JH, Kang SH, Cho YJ, Jeon JP. Association of endothelin receptor type A with intracranial aneurysm in 20,609 East Asians: An updated meta-analysis. World Neurosurg. 2019 Jul 9. pii: S1878-8750(19)31886-8.
15. Kim BJ, Kim YM, Hong EP, Jeon JP, Yang JS, Choi HJ, Kang SH, Cho YJ. Correlation between altered DNA methylation of intergenic regions of ITPR3 and development of delayed cerebral ischemia in subarachnoid hemorrhage patients. World Neurosurg. 2019 Jun 24. pii: S1878-8750(19)31665-1.
16. Jeon JP, Kim SE, Chai LC, Hong EP, Yang SJ, Kang HS, Cho JY, Choi JH. Seizure incidence of angiogram-negative subarachnoid hemorrhage: An updated meta-analysis. Clin Neurol Neurosurg. 2020 May;83(5):466-470.
17. **Hong EP**, Kim BJ, Jeon JP*, Yang JS, Choi HJ, Kang SH, Cho YJ. Genome-wide association between the 2q33.1 locus and intracranial aneurysm susceptibility: An updated meta-analysis including 18,019 individuals. J Clin Med. 2019 May 16;8(5). pii: E692.
18. Kim CH, Rhim JK, Ahn JH, Park JJ, Moon JU, **Hong EP**, Kim MR, Kim SG, Lee SH, Jeong JH, Choi SW, Jeon JP*. Machine learning application for rupture risk assessment in small-sized intracranial aneurysm. J Clin Med. 2019 May 15;8(5). pii: E683.
19. **Hong EP**, Kim BJ, Cho SS, Yang JS, Choi JH, Kang HS, Jeon JP. Genomic Variations in Susceptibility to Intracranial Aneurysm in the Korean Population. J Clin Med. 2019;8(2):275.
20. Kim SE, **Hong EP**, Kim HC, Lee SU, Jeon JP. Ultrasonographic optic nerve sheath

diameter to detect increased intracranial pressure in adults: a meta-analysis. Acta Radiol. 2019 Feb;60(2):221-229.
21. Lee SU, **Hong EP**, Kim BJ, Kim SE, Jeon JP. Delayed Cerebral Ischemia and Vasospasm After Spontaneous Angiogram-Negative Subarachnoid Hemorrhage: An Updated Meta-Analysis. World Neurosurg. 2018 Jul;115:e558-e569.
22. **Hong EP**, Kim BJ, Jeon JP, Kim SE, Kim CH, Choi HJ. Association of SOX17 gene polymorphisms with intracranial aneurysm in East-Asian populations. World Neurosurg. 2018 Feb;110:e823-e829.
23. Jeon JP, **Hong EP**, Kim JE, Ha EJ, Cho WS, Son YJ, Bang JS, Oh CW. Genetic risk assessment of Elastin gene polymorphisms with intracranial aneurysm in Koreans. Neurol Med Chir (Tokyo). 2018 Jan 15;58(1):17-22.
24. **Hong EP**, Rhee KH, Kim DH, Park JW. Identification of pleiotropic genetic variants affecting osteoporosis risk in a Korean elderly cohort. J Bone Miner Metab. 2019 Jan;37(1):43-52.
25. **Hong EP**, Jeon JP, Kim SE, Yang JS, Choi HJ, Kang SH, Cho YJ. A novel association between Lysyl oxidase (LOX) gene polymorphisms and intracranial aneurysm in the Korean population: a preliminary study. Yonsei Med J. 2017;58(5):1006-1011.
26. **Hong EP**, Go MJ, Kim HL, Park JW. Risk Prediction of Pulmonary Tuberculosis Using Genetic and Conventional Risk Factors in Adult Korean Population. PLoS One. 2017 Mar 29;12(3):e0174642.
27. **Hong EP**, Kim DH, Park JW. Interactions of genetic and non-genetic factors on plasma hs-CRP concentration in a Korean community-based cohort study. Genes & Genomics. 2015 Mar;37(3):231–239.
28. **Hong EP**, Kim DH, Suh JG, Park JW. Effect of interactions between genetic polymorphisms and cigarette smoking on plasma triglyceride levels in elderly Koreans: The Hallym Aging Study. Genes & Genomics. 2015 Feb 37(2):173-181.
29. **Hong EP**, Kim DH, Suh JG, Park JW. Genetic risk assessment for cardiovascular disease with seven genes associated with plasma C-reactive protein concentrations in Asian populations. Hypertens Res. 2014 Jul;37(7):692-8.
30. Heo SG, **Hong EP**, Park JW. Genetic Risk Prediction for Normal-Karyotype Acute Myeloid Leukemia Using Whole Exome Sequencing. Genomics Inform. 2013;11(1):46-51.
31. **Hong EP**, Kim DH, Suh JG, Park JW. Analyses of Longitudinal Effects of Gene-Environment Interactions on Plasma C-reactive Protein Levels: The Hallym Aging Study. Genes & Genomics. 2013;35(1):131-139.
32. **Hong EP**, Park JW. Sample Size and Statistical Power Calculation in Genetic Association Studies. Genomics Inform. 2012;10(2):117-122.

ACKNOWLEDGMENTS IN PUBLICATION

1. Heo et al. Identification of somatic mutations using whole-exome sequencing in Korean patients with acute myeloid leukemia. BMC Med Genet. 2017 (Eun Pyo Hong in Acknowledgements: contribution to the evaluation of the functional importance of the gene mutations).

PUBLICATIONS IN PREPARATION (OR UNDER REVIEW)

1. **Hong EP** et al. A study of genome-wide interactions mediated via BOLL and EDNRA polymorphisms in intracranial aneurysm. J Kor Neuro Soci. 2022 Jul (under review).

ABSTRACT LIST IN ACARDEMIC CONFERENCE

1. Hong EP et al. Statistical power and sample size in genetic association studies using case-control and case-parent study designs. Korean Society of Epidemiology. 2010 Nov 22. South Korea (Poster Presenter: Eun Pyo Hong).
2. Hong EP et al. Analysis of gene-environment interaction for plasma CRP level in a Korean cohort, American Society of Human Genetics. 2011 Oct 11. Canada (Poster Presenter: Eun Pyo Hong).
3. Hong EP et al. Interactions of genetic and non-genetic factors on plasma hs-CRP concentration: Hallym Aging Study. Federation Meeting of Korean Basic Medical Scientists. 2013 Apr 26. South Korea (Poster Presenter: Eun Pyo Hong).
4. Hong EP et al. Genome-wide linear mixed model to estimate heritability for type 2 diabetes mellitus in Koreans. Korea Genome Organization. 2013 Sep 5. South Korea (Poster Presenter: Eun Pyo Hong).
5. Hong EP et al. Risk prediction of type 2 diabetes based on liability threshold model. Clinical Genomics & Informatics. 2013 Dec 4. Portugal (Poster Presenter: Ji Wan Park).
6. Hong EP et al. Risk assessment of chronic kidney disease based on linear mixed models in Korean populations. European Society of Human Genetics. 2014 May 31. Italy (Poster Presenter: Ji Wan Park).
7. Hong EP et al. Exome-wide association study and risk assessment of lung squamous cell carcinoma using cording variants in Korean men. 10th International Cancer Genome Consortium Scientific Workshop. 2015 Feb. Italy (Abstract only, Participant: Ji Wan Park).
8. Hong EP et al. Genome-wide linear mixed model and risk assessment for cardiovascular disease in Koreans. Korea Genome Organization. 2015 Feb 4. South Korea (Poster Presenter: Eun Pyo Hong).
9. Hong EP et al. Differences in Genotype Frequencies of Cancer Susceptibility Variants between Cancer Patients and Controls in Multi-Ethnic Populations. 11th International Cancer Genome Consortium Scientific Workshop. 2015 Dec. India (Abstract only, Participant: Ji Wan Park).
10. Hong EP et al. Risk prediction of pulmonary tuberculosis using genetic and conventional risk factors. Korea Genome Organization. 2016 Feb 1. South Korea (Poster Presenter: Eun Pyo Hong).
11. Hong EP, Kim HL, PCAWG-8, PCAWG-3, Park JW. A genome-wide association study of hepatocellular carcinoma using whole genome sequencing. 13th International Cancer Genome Consortium Scientific Workshop. 2017 June 12-14. Korea (Poster Presenter: Ji Wan Park).
12. Hong EP et al. Analysis of the X Chromosome for Modifiers of Huntington's Disease Age-at-Onset. American Society of Human Genetics. 2019 Oct 15-19. Huston, TX, USA (Poster Presenter: Eun Pyo Hong).

LIST OF PATENTS

08/27/2021
10-2021-011368#(#: 3-8) Matrix metalloproteinase (MMP) biomarkers contributing to the diagnosis of intracranial aneurysm Jeon JP(55);Kim BJ(15);Youn DH(15);Hong EP(15) Aug 27 (2021)

10-2021-0113683: matrix metalloproteinase (MMP) 13 biomarker contributing to the diagnosis of intracranial aneurysm
10-2021-0113684: rs1555322 contributing to the diagnosis of intracranial aneurysm
10-2021-0113685: rs2425024 contributing to the diagnosis of intracranial aneurysm
10-2021-0113686: rs6119593 contributing to the diagnosis of intracranial aneurysm
10-2021-0113687: rs11642206 contributing to the diagnosis of intracranial aneurysm
10-2021-0113688: rs16938619 contributing to the diagnosis of intracranial aneurysm

09/14/2021
10-2021-0122235 Dignosis method of Stroke using single nuecleotide polymorphism (SNP) markers Jeon JP(40);Hong EP(30);Kim BJ(15);Youn DH(15) Sept 14 (2021)

02/03/2022
10-2022-001415# (#: 3-8) Single nuecleotide polymorphim (SNP) markers composition for diagnosing cerebral aneurysm and method of use thereof Jeon JP(40);Hong EP(30);Kim BJ(15);Youn DH(15) Feb 3 (2022)

10-2022-0014153 rs7779989 marker composition for diagnosing cerebral aneurysm and method of use thereof
10-2022-0014154 rs3120004 marker composition for diagnosing cerebral aneurysm and method of use thereof
10-2022-0014155 rs1522095 marker composition for diagnosing cerebral aneurysm and method of use thereof
10-2022-0014156 rs12935558 marker composition for diagnosing cerebral aneurysm and method of use thereof
10-2022-0154157 rs3826442 marker composition for diagnosing cerebral aneurysm and method of use thereof
10-2022-0014158 rs2440154 marker composition for diagnosing cerebral aneurysm and method of use thereof