



▪ Field Microbiology
▪ Name Cho, Yoon-shin
▪ Title Professor

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Education background

- 1996 – 2001 Major in Molecular Biology, University of Illinois (Doctor)
- 1993 – 1996 Major in Microbiology, University of Wisconsin, U.S. (Master)
- 1984 – 1986 Major in Biology, Sogang University (Master)
- 1980 – 1984 Major in Biology, Sogang University (Bachelor)

Major careers

- 2013 - present Leader of the BK21 Plus Business Team, Hallym University
- 2013 - present The Department of Biomedical Science, Hallym University
- 2013 - present Member of the Evaluation and Management Expert Committee of Healthcare Technology, Korea Centers for Disease Control and Prevention
- 2013 - present Member of the Review Committee of Materials and Resources Utilization, Korea Centers for Disease Control and Prevention
- 2012 - present Expert member of the Life Science Group, the National Research Foundation of Korea
- 2012 - present Leading Scientist of the Korean Academy of Science and Technology
- 2012 - 2013 Head professor of the Pre-Med Cooperative Major Course
- 2012 - present Professor of the Department of Biomedical Science, The College of Natural Sciences, Hallym University
- 2009 – 2011 Health Researcher of the Dielectric Center, the Korea National Institute of Health, the Korea Centers for Disease Control and Prevention
- 2006 – 2009 Chief researcher of the Dielectric Center, the Korea National Institute of Health, the Korea Centers for Disease Control and Prevention
- 2004 - 2006 Research Professor of the Department of Life Science, Hanyang University
- 2001 - 2004 Postdoctoral researcher of Medical School, University of Pennsylvania, U.S.
- 1989 - 1991 Full-time Assistant of the Department of Genetic Engineering, Hallym University

Studies & Books

Hsa-miR-10a-5p downregulation in mutant UQCRB-expressing cells promotes the cholesterol biosynthesis pathway. *Scientific Reports* Aug 17. 8:12407 (2018)

Nonsynonymous Variants in PAX4 and GLP1R are Associated with Type 2 Diabetes in an East Asian Population. *Diabetes* Sep. 67(9): 1892-1902 (2018)

Understanding the functional role of genistein in the bone differentiation in mouse osteoblastic cell line MC3T3-E1 by RNA-seq analysis. *Scientific Reports* Feb 19. 8(1): 3257 (2018)

Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. *Nature Genetics* Apr 1. 50(4): 559-571 (2018)

Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. *Plos Medicine* Sep 12. 14(9):e1002383 (2017)

A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. *Diabetes* Jul;66(7):2019-2032 (2017)

Association analyses of East Asian individuals and trans-ancestry analyses with European individuals reveal new loci associated with cholesterol and triglyceride levels. *Human Molecular Genetics* May 1, 26:1770-1784 (2017)

The genetic architecture of type 2 diabetes. *Nature* August 4. 536: 41-47 (2016)

Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. *Human Molecular Genetics* May 15 25(10):2070-2081 (2016)

Genome-wide association studies in the Japanese population identify seven novel loci for type 2 diabetes. *Nature Communications* Jan 28. 7:10531-10543 (2016)

Genome-wide association studies in East Asians identify new loci for waist-hip ratio and waist circumference. *Scientific Reports* 2016 Jan 20. 6:17958 (2016)

Genome-wide association study identified new susceptibility loci for polycystic ovary syndrome *Human Reproduction* Mar. 30(3): 723-731 (2015)

Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci *Human Molecular Genetics* Mar. 24(6): 1791-1800 (2015)

Genome-wide association meta-analysis identifies novel variants associated with fasting plasma glucose in East Asians *Diabetes* Jan. 64(1): 291-298 (2015)

Identification of three novel genetic variations associated with electrocardiographic traits (QRS duration and PR interval) in East Asians *Human Molecular Genetics* Dec. 23(24): 6659-6667 (2014)

Meta-analysis of genome-wide association studies in East Asian-ancestry populations identifies four new loci for body mass index *Human Molecular Genetics* Oct. 23(20): 5492-5504 (2014)

Rare variants in PPARG with decreased activity in adipocyte differentiation are associated with increased risk of type 2 diabetes *PNAS* Sep. 111(36):13127-13132 (2014)

Loss-of-function mutations in SLC30A8 protect against type 2 diabetes *Nature Genetics* April 46(4); 357-363 (2014)

Associations of genetic variants in/near BMI-associated genes with type 2 diabetes: A systematic meta-analysis *Clinical Endocrinology* Nov. 81(5): 702-710 (2014)

Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility *Nature Genetics* March 46(3): 234-244 (2014)

Genetic determinants of heel bone properties: genome-wide association meta-analysis and replication in the GEFOS/GENOMOS consortium Human Molecular Genetics June 23(11):3054-3068 (2014)

Sequence variants in SLC16A11 are a common risk factor for type 2 diabetes in Mexico Nature Feb 6;506(7486):97-101 (2014)

Genome-wide association study meta-analysis reveals transethnic replication of mean arterial and pulse pressure loci Hypertension Nov;62(5):853-859 (2013)

Identification of heart rate - associated loci and their effects on cardiac conduction and rhythm disorders Nature Genetics June; 45(6), 621-631 (2013)

Genome-wide association study identifies a novel locus contributing to type 2 diabetes susceptibility in Sikhs of Punjabi origin from India Diabetes May;62(5):1746-55 (2013)

Genetics of Type 2 Diabetes in East Asian Populations. Current Diabetes Reports December; 12, 686-696 (2012)

Meta-Analysis Identifies Multiple Loci Associated with Kidney Function-Related Traits in East Asian Populations. Nature Genetics July; 44, 904-909 (2012)

A Common Variant in SLC8A1 Is Associated with the Duration of the Electrocardiographic QT Interval. American Journal of Human Genetics July; 91, 180-184 (2012)

Meta-analysis identifies common variants associated with body mass index in east Asians. Nature Genetics March; 44, 307-311 (2012)

A Genome-Wide Association Study of Gestational Diabetes Mellitus in Korean Women. Diabetes February; 61, 531-541 (2012)

Meta-analysis of Genome-Wide Association Studies Identifies 8 New Loci for Type 2 Diabetes in East Asians. Nature Genetics January; 44, 67-72 (2012)

Large-Scale Genome-Wide Association Study in East Asians Identify New Genetic Loci Influencing Metabolic Traits. Nature Genetics October; 43, 990-995 (2011)

Genetic Variants in Novel Pathways Influence Blood Pressure and Cardiovascular Disease Risk. Nature October; 478, 103-109 (2011)

Meta-analysis of genome-wide association studies identifies common variants associated with blood pressure variation in east Asians. Nature Genetics June; 43, 531-538 (2011)

Biological, clinical and population relevance of 95 loci for blood lipids. Nature August; 466, 707-713 (2010)

Identification of New Genetic Risk Variants for Type 2 Diabetes. PLoS Genetics September; 6(9), e1001127 (2010)

A large scale genome-wide association study of Asian populations uncovers genetic factors influencing eight quantitative traits. Nature Genetics 41, 527-534 (2009)

I Others

- Genetic Research
- The Korea Genome Organization
- Korean Society for Biochemistry and Molecular Biology