Mengyuan Kan, Ph.D.

Postdoctoral Researcher

Biomedical Informatics, University of Pennsylvania

423 Blockley Hall, 423 Guardian Drive, Philadelphia, PA 19104

Tel (O): 215-573-4248

mengykan@pennmedicine.upenn.edu; mengyuankan@gmail.com

Personal website: http://mengyuankan.github.io/

Research Summary

Specialized in genetics and bioinformatics, I utilize state-of-the-art computational approaches to leverage large-scale omics data and identify genetics and genomics factors behind complex diseases with the goal to translate these results into clinical insights. In my current research, I use asthma as a disease model and investigate cell type-specific gene expression signatures and asthma drug-induced transcription factor binding by integrating a wide range of omics data to advance our understanding of cell type-specific mechanisms underlying asthma and asthma-related drug responsiveness. Meanwhile, I develop open-source informatics pipelines that automate reproducible analysis of publicly available omics data and a cloud-based app that facilitates wet-lab researchers to visualize and access to analysis-ready omics results.

Education

2009-2015 Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, Shanghai, China
Ph.D. in Genetics
Mentor: Dr. Lin He

2011-2013 Center for Statistical Genetics, Baylor College of Medicine
Visiting Ph.D. Student in Statistical Genetics
Mentor: Dr. Suzanne M Leal

2005-2009 East China University of Science and Technology, Shanghai, China
B.S in Biological Science

Employment

2016-present Department of Biostatistics, Epidemiology, and Informatics,
Institutes of Biomedical Informatics, University of Pennsylvania
Postdoctoral Researcher in Biomedical Informatics
Mentor: Dr. Blanca E Himes

2015 Shanghai Ninth People's Hospital Affiliated to Shanghai Jiao Tong University Medical School, Shanghai, China
Assistant Investigator in Cancer Genetics and Genomics

2014 Cloud Health Genomics Ltd, Shanghai, China
Bioinformatics Analyst Intern

Other Trainings

2019 NHGRI Genome Sequencing Program (GSP)-NHLBI Trans-Omics for Precision Medicine (TOPMed) Analysis Workshop, University of Michigan, Ann Arbor, MI
2017 Causal Inference and Big Data Summer Institute, University of Pennsylvania, Philadelphia, PA
2015 Genetic Counseling Training Program, Fudan University, Shanghai, China
2014 HiSeq X Ten: Best Practices in High Volume Sequencing, Illumina Inc, Shanghai, China
2012 Advanced Gene Mapping Course, Rockefeller University, New York City, NY

Teaching

2018-2020 Gene expression data analysis: Microarray and RNA-Seq.
2020 Functional enrichment analysis.
Data science for Biomedical Informatics (BMIN503 / EPID600).
University of Pennsylvania, Philadelphia
Guest Lecturer

Open-Source Tools

RAVED (https://github.com/HimesGroup/raved) - Reproducible Analysis and Validation of Expression Data
Brocade (https://github.com/HimesGroup/brocade) - Reproducible Analysis of ChIP-Seq Data
REALGAR (http://realgar.org/) - Reducing Associations by Linking Genes And omics Results

Conference Presentations

Oral Presentations
2018 American Medical Informatics Association Annual Symposia, San Francisco, CA
Integration of Transcriptomic Data Identifies Global and Cell-Specific Asthma-Related Gene Expression Signatures (Student Paper Award Finalist)

Poster Presentations
2020 American Society of Human Genetics Annual Meeting (Virtual)
Multi-omics analysis identifies a novel glucocorticoid response-associated locus near BIRC3

2020 American Thoracic Society Annual Meeting (Virtual)
CEBPD Influences the Airway Smooth Muscle Transcriptomic Response to TNFα and Budesonide Exposure

2019 American Thoracic Society Annual Meeting, Dallas, TX
Airway Smooth Muscle-Specific Transcriptomic Signatures of Glucocorticoid Exposure in Asthma and Non-Asthma Donors

2014 American Society of Human Genetics Annual Meeting, San Diego, CA
High-resolution characterization of a leiomyoma on mayer-rokitansky-kuster-hauser syndrome.

2013 American Society of Human Genetics Annual Meeting, San Francisco, CA
Detecting rare variant associations with waist-to-hip ratio in NHLBI-ESP female cohorts.

Publications

*** indicates co-first authored papers**

Integrative omics study of asthma and drug response using asthma as a disease model

1. **Kan M**, Himes BE. Insights into Glucocorticoid Responses Derived from Omics Studies. Pharmacol Ther **[Accepted]**
2. Diwadkar AR, **Kan M**, Himes BE. Facilitating Analysis of Publicly Available ChIP-Seq Data for Integrative Studies. AMIA Annu Symp Proc. 2020 Mar 4;2019:371-379. **Received AMIA 2019 Distinguished Paper Award**
3. **Kan M**, Koziol-White C, Shumyatcher M, Johnson M, Jester W, Panettieri RA Jr, Himes BE. Airway Smooth Muscle-Specific Transcriptomic Signatures of Glucocorticoid Exposure. Am J Respir Cell Mol Biol. 2019 61(1):110-120.
4. **Kan M**, Shumyatcher M, Diwadkar AR, Soliman G, Himes BE. Integration of Transcriptomic Data Identifies Global and Cell-Specific Asthma-Related Gene Expression Signatures. AMIA Annu Symp Proc. 2018 Dec 5;2018:1338-1347. **Finalist of AMIA Student Paper Award.**
5. **Kan M**, Shumyatcher M, Himes B. Using omics approaches to understand pulmonary diseases. Respir Res. 2017 18(1):149.

Asthma genetics and pharmacogenetics

6. Panganiban R, Sun M, Dahlin A, Park H, **Kan M**, Himes BE, et al. A functional splicing variant associated with decreased asthma risk abolishes the ability of gasdermin B (GSMDB) to induce epithelial cell pyroptosis. J Allergy Clin Immunol. 2018 142(5):1469-1478.
7. Dahlin A, Sordillo JE, Ziniti J, Iribarren C, Lu M, Weiss ST, Tantisira KG, Lu Q, **Kan M**, Himes BE, et al. Large-scale, multiethnic genome-wide association study identifies novel loci contributing to asthma susceptibility in adults. J Allergy Clin Immunol 2019 143(4):1633-1635.
8. **Kan M**, Himes BE. Genetics and Pharmacogenetics of Asthma. Precision Therapy in Pulmonary, Critical Care and Sleep Medicine. Gomez JL, Himes BE, Kaminski N (eds). 1st ed. Springer, New York, NY. 2020. Chapter 3: 25-37p.

Applications of developed omics data analysis pipeline

9. Y Xu, Y Zhang, JC García-Cañaveras, L Guo, **M Kan**, S Yu, IA Blair, JD Rabinowitz, X Yang. Chaperone-mediated autophagy regulates the pluripotency of embryonic stem cells. Science. 2020 Jul 24;369(6502):397-403.
10. Balamuth F, Alpern ER, **Kan M**, Shumyatcher M, Hayes K, Lautenbach E, Himes BE. Gene Expression Profiles Differentiate Viral from Bacterial Source Pathogen in Children with Suspected Sepsis in the Emergency Department. Ann Emerg Med. 2020 Jun;75(6):744-754.

NHLBI-ESP: rare variant association with complex diseases

11. **Kan M**, Auer PL, Wang GT, Bucasas KL, Hooker S, Rodriguez A, Li B, Ellis J, Cupples LA, Chen YD, et al. Rare variant associations with waist-to-hip ratio in European-American and African-American women from the NHLBI-Exome Sequencing Project. Eur J Hum Genet. 2016 24(8):1181-7.
12. He Z, O'Roak BJ, Smith JD, Wang G, Hooker S, Santos-Cortez RL, Li B, **Kan M**, Krumm N, Nickerson DA, et al. Rare-variant extensions of the transmission disequilibrium test: application to autism exome sequence data. Am J Hum Genet. 2014 94:33-46.

NHLBI-ESP Consortium Publication:

13. Rosenthal EA et al. Rare loss of function variants in candidate genes and risk of colorectal cancer. Hum Genet. 2018 137(10):795-806.

14. Auer PL et al. Rare and Coding Region Genetic Variants Associated With Risk of Ischemic Stroke: The NHLBI Exome Sequence Project. JAMA Neurol. 2015 72:781-788, 2015.
15. Do R et al. Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. Nature. 2015 518:102-106.
16. Tabor HK et al. Pathogenic variants for Mendelian and complex traits in exomes of 6,517 European and African Americans: implications for the return of incidental results. Am J Hum Genet 95:183-193, 2014.
17. Lange LA et al. Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. Am J Hum Genet. 2014 94:233-245.
18. Rosenthal EA et al. Joint linkage and association analysis with exome sequence data implicates SLC25A40 in hypertriglyceridemia. Am J Hum Genet. 2013 93:1035-1045.
19. Guo DC et al. Recurrent gain-of-function mutation in PRKG1 causes thoracic aortic aneurysms and acute aortic dissections. Am J Hum Genet. 2013 93:398-404.
20. Johnsen JM et al. Common and rare von Willebrand factor (VWF) coding variants, VWF levels, and factor VIII levels in African Americans: the NHLBI Exome Sequencing Project. Blood. 2013 122:590-597.
21. Norton N et al. Exome sequencing and genome-wide linkage analysis in 17 families illustrate the complex contribution of TTN truncating variants to dilated cardiomyopathy. Circ Cardiovasc Genet. 2013 6:144-153.
22. Fu W et al. Analysis of 6,515 exomes reveals the recent origin of most human protein-coding variants. Nature. 2013 493:216-220.
23. Boileau C et al. TGFB2 mutations cause familial thoracic aortic aneurysms and dissections associated with mild systemic features of Marfan syndrome. Nat Genet. 2012 44:916-921.
24. Emond MJ et al. Exome sequencing of extreme phenotypes identifies DCTN4 as a modifier of chronic Pseudomonas aeruginosa infection in cystic fibrosis. Nat Genet. 2012 44:886-889.

Cancer genomics and epigenomics

25. Zhang L, **Kan M***, Zhang M, Yu S, Xie H, Gu Z, Wang H, Zhao S, Zhou G, Song H, Zheng C. Multiregion sequencing reveals intratumor heterogeneity of driver mutations in TP53-driven non-small cell lung cancer. Int J Cancer. 2017 140(1):103-10.
26. Liu F, Zhou Y, Zhou D, **Kan M**, Niu X, Zhang Z, Zhang D, Tao L, He L, Zhang L, Liu Y. Whole DNA methylome profiling in lung cancer cells before and after epithelial-to-mesenchymal transition. Diagnosis Pathology. 2014 9:66.

Next generation sequencing application

27. Wu C, Zhang D, **Kan M***, Lv Z, Zhu A, et al. The draft genome of the large yellow croaker reveals well-developed innate immunity. Nat Commun. 2014 5:5227.

Genetic and epigenetic factors associated with complex diseases in Chinese population

28. Weng X, Liu F, Zhang H, **Kan M**, Wang T, Dong M, Liu Y. Genome-wide DNA methylation profiling in infants born to gestational diabetes mellitus. Diabetes Res Clin Pract. 2018 142:10-18.
29. Weng X, Zhang H, **Kan M***, Ye J, Liu F, et al. Leukocyte telomere length is associated with advanced age-related macular degeneration in the Han Chinese population. 2015. Exp Gerontol 69:36-40.
30. Weng X, Zhang H, Ye J, **Kan M**, Liu F et al. Hypermethylated Epidermal growth factor receptor (EGFR) promoter is associated with gastric cancer. 2015 Sci Rep 5:10154.
31. **Kan M**, Weng X, Wang T, Liu F, Ye J, et al. No evidence of association between variant rs2075650 in lipid metabolism-related locus APOE/TOMM40 and advanced age-related macular degeneration in Han Chinese population. Exp Biol Med (Maywood). 2015 240:230-234.
32. **Kan M**, Liu F, Weng X, Ye J, Wang T, et al. Association study of newly identified age-related macular degeneration susceptible loci SOD2, MBP, and C8orf42 in Han Chinese population. Diagn Pathol. 2014 9:73.
33. Qian D, **Kan M***, Weng X, Huang Y, Zhou C, et al. Common variant rs10033900 near the complement factor I gene is associated with age-related macular degeneration risk in Han Chinese population. Eur J Hum Genet. 2014 22:1417-1419.

34. Weng X, Zhou D, Liu F, Zhang H, Ye J, Zhang Z, Zhang D, Wang Y, Tao L, Cao L, **Kan M** et al. DNA methylation profiling in the thalamus and hippocampus of postnatal malnourished mice, including effects related to long-term potentiation. BMC Neurosci. 2014 15:31.
35. Niu X, Li H, Chen Z, Liu Y, **Kan M** et al. A study of ethnic differences in TGFbeta1 gene polymorphisms and effects on the risk of radiation pneumonitis in non-small-cell lung cancer. J Thorac Oncol. 2012 7:1668-1675.
36. Tao L, Zhang Z, Chen Z, Zhou D, Li W, Kan M et al. A Common variant near the melanocortin 4 receptor is associated with low-density lipoprotein cholesterol and total cholesterol in the Chinese Han population. Mol Biol Rep. 2012 39:6487-6493.
37. Shen Q, Zhao X, Yu L, Zhang Z, Zhou D, **Kan M** et al. Association of leukocyte telomere length with type 2 diabetes in mainland Chinese populations. 2012 J Clin Endocrinol Metab 97:1371-1374.
38. Zheng Y, **Kan M***, Yu L, Niu X, Zhou D, He L, Lu S, Liu Y. GPC5 rs2352028 polymorphism and risk of lung cancer in Han Chinese. 2012 Cancer Invest 30:13-19.
39. Chen G, Zhou D, Zhang Z, Kan M, Zhang D et al. Genetic variants in IFIH1 play opposite roles in the pathogenesis of psoriasis and chronic periodontitis. Int J Immunogenet. 2012 39:137-143.
40. Zhang Z, Tao L, Chen Z, Zhou D, **Kan M** et al. Association of genetic loci with blood lipids in the Chinese population. 2011 PLoS One 6:e27305.
41. Shen Q, Zhang Z, Yu L, Cao L, Zhou D, Kan M et al. Common variants near TERC are associated with leukocyte telomere length in the Chinese Han population. Eur J Hum Genet. 2011 19:721-723.
42. **Kan MY**, Zhou DZ, Zhang D, Zhang Z, Chen Z, et al. Two susceptible diabetogenic variants near/in MTNR1B are associated with fasting plasma glucose in a Han Chinese cohort. Diabet Med. 2010 27:598-602.
43. Zhou DZ, Liu Y, Zhang D, Liu SM, Yu L, Yang YF, Zhao T, Chen Z, **Kan MY** et al. Variations in/nearby genes coding for JAZF1, TSPAN8/LGR5 and HHEX-IDE and risk of type 2 diabetes in Han Chinese. J Hum Genet. 2010 55:810-815.

Complete List of Published Work in MyBibliography
https://www.ncbi.nlm.nih.gov/sites/myncbi/1NEHhRomJXK5j/bibliography/48466198/public/?sort=date&direction=ascending

Professional Activities

Journal Referee
BMJ Open Diabetes Research & Care
Cell Biology and Toxicology
Oncotarget
Scientific Reports
The Journal of Clinical Psychiatry

Membership
American Medical Informatics Association (AMIA)
American Society of Human Genetics (ASHG)
American Thoracic Society (ATS)