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Research Interests

Bioinformatics, genomics, pharmacogenomics, genetics, multiomics integration, respiratory diseases, opensource tool development

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

- 2021-present Department of Biostatistics, Epidemiology, and Informatics, Institutes of Biomedical Informatics, University of Pennsylvania Research Associate Supervisor: Dr. Blanca E Himes
- 2016-2021 Department of Biostatistics, Epidemiology, and Informatics, Institutes of Biomedical Informatics, University of Pennsylvania Postdoctoral Researcher in Biomedical Informatics Mentor: Dr. Blanca E Himes

Selected Peer-reviewed Publications

* indicates co-first authored papers

Multiomics Integration

1. Kan M, Diwadkar AR, Shuai H, Joo J, Wang AL, Ong MS, Sordillo JE, et al. Multiomics analysis identifies BIRC3 as a novel glucocorticoid response-associated gene. J Allergy Clin Immunol. 2022

Jun;149(6):1981-1991.

- 2. Kan M, Sun M, Jiang X, Diwadkar AR, Parikh V, Cao G, Gebski E, Jester W, Lan B, Panettieri RA Jr, Koziol-White C, Lu Q, Himes BE. CEBPD modulates the airway smooth muscle transcriptomic response to glucocorticoids. Respir Res. 2022 Jul 28;23(1):193.
- 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.

Open-source tools and their applications

- 4. Kan M, Diwadkar AR, Saxena S, Shuai H, Joo J, Himes BE. REALGAR: a web app of integrated respiratory omics data. Bioinformatics. 2022 Sep 15;38(18):4442-4445.
- 5. 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 2018 Student Paper Award.
- 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
- 7. Xu Y, Zhang Y, García-Cañaveras JC, Guo L, **Kan M**, Yu S, Blair IA, Rabinowitz JD, Yang X. Chaperone-mediated autophagy regulates the pluripotency of embryonic stem cells. Science. 2020 Jul 24;369(6502):397-403.
- 8. 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.

Asthma genetics and pharmacogenetics

- 9. Joo J, Mak ACY Mak, Xiao S, Sleiman PM, Hu D, Huntsman S, Eng C, **Kan M**, Diwakar AR, et al. Genome-wide association study in minority children with asthma implicates DNAH5 in bronchodilator responsiveness. Sci Rep. 2022 Jul 22;12(1):12514.
- 10. 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.
- 11. 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.

NHLBI Exome Sequencing Project (ESP)

- 12. 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.
- 13. 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.

Cancer genomics and epigenomics

14. 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.

15. 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.

De novo genome sequencing

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

Genetic and epigenetic association studies

- 17. 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.
- 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.
- 19. 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.
- 20. 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.
- 21. 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.
- 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.

Review

- 23. Kan M, Himes BE. Insights into Glucocorticoid Responses Derived from Omics Studies. Pharmacol Ther. 2021 Feb;218:107674.
- 24. Kan M, Shumyatcher M, Himes B. Using omics approaches to understand pulmonary diseases. Respir Res. 2017 18(1):149.

Book Chapter

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.

Complete List of Published Work in MyBibliography

https://www.ncbi.nlm.nih.gov/sites/myncbi/1NEHhRomJXK5j/bibliography/48466198/public/?sortby=pubD ate&sdirection=descending

Invited Talks

2021 American Thoracic Society, Mini Symposium: Omics in Asthma and COPD (Virtual)

Multi-Omics Analysis Identifies a Novel Glucocorticoid Response-Associated Locus Near BIRC3

2020 American Thoracic Society, Newman Stephens Memorial Mini Symposium: a Legacy of Science and Success (Virtual) *CEBPD Influences the Airway Smooth Muscle Transcriptomic Response to TNFα and Budesonide Exposure*

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

Conference Abstracts

2022 American Society of Human Genetics Annual Meeting, San Francisco, CA *Genome-Wide Analysis of SARS-CoV-2 Variants in the United States*

2021 American Society of Human Genetics Annual Meeting (Virtual) Multi-omics analysis identifies a novel glucocorticoid response-associated locus near BIRC3

ACE2 and TMPRSS2 gene expression changes are not associated with cigarette smoke and glucocorticoid exposure

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

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

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.*

Open-Source Tools

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

Teaching

2018-2021 Guest Lecturer. Data Science for Biomedical Informatics (BMIN503), University of Pennsylvania, Philadelphia

Lecture(s): 1) Gene expression data analysis: microarray and RNA-Seq and 2) Functional enrichment analysis.

2020-2022 Guest Lecturer. Introduction to Biomedical Informatics (BMIN 501), University of Pennsylvania, Philadelphia

Lecture(s): Introduction to bioinformatics

2021-2023 Guest Lecturer. Genetic Epidemiology (EPID 575), University of Pennsylvania, Philadelphia Lecture(s): Community Resources for Genetic Studies

Lectures by Invitation

2021 Instructor. A Practical, Hands-on Introduction to Genomic Analysis in Pulmonary Medicine (Postgraduate Course 7), American Thoracic Society (Virtual) Lecture(s): RNA-Seq: Alignment, QC, and Analysis

Memberships

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

Journal and Conference Reviewer

AMIA Annual Symposium Proceedings AMIA Joint Summits on Translational Science Scientific Reports Pediatric Pulmonology