MELISSA R. MILLER

SUMMARY

Accomplished human geneticist with over 10 years of experience. My team is responsible for using human genetics, omics and clinical data to identify and prioritize most-promising novel targets across multiple cardiometabolic diseases (heart failure, obesity, and renal disease). I co-lead internal efforts to develop Pfizer's internal and external genetics strategy and chair multiple multi-pharma collaborations / public-private partnerships.

PROFESSIONAL EXPERIENCE

Pfizer, Research and Development, Internal Medicine Research 2014-current
Cambridge, MA 02139
Senior Director, Human Genetics 2023-current
Director, Human Genetics 2019-2023
Senior Manager, Human Genetics 2017-2019
Manager, Human Genetics 2014-2017

- Use human genetic, transcriptomics, epigenetic, proteomics data and other human data sources to identify and prioritize novel targets for cardiometabolic diseases
- Manage a team of computational geneticists who are responsible for target identification/prioritization as well as integration of new data types and methods into our internal genetic target discovery pipeline
- Developed genetic strategy for the Internal Medicine Research Unit, ensuring that genetic strategy and efforts are aligned with research unit disease area priorities.
- Co-lead efforts to develop Pfizer's internal and external genetics strategy including building internal genetics infrastructure and identifying and vetting promising external genetics collaborations
- Chair of two large external public private partnerships: UK Biobank Pharma Proteomics Project Consortium and the FNIH Accelerating Medicines Partnership – Common Metabolic Diseases
- Act as Pfizer lead on several pre-competitive industry collaborations and public private partnerships: UKB Biobank Exome Sequencing Consortium, and FNIH Accelerating Medicines Partnership-Type 2 Diabetes program

The Hospital for Sick Children, Genetics and Genome Biology 2012-2014
Toronto, ON, Canada
Post-Doctoral Research Fellow

- Conducted independent research to identify genetic variants of early pancreatic damage and early growth in cystic fibrosis.
- Interacted closely with a multi-disciplinary research team (physicians, molecular geneticists, and biostatisticians) in order to identify and understand genes that contribute to severity of cystic fibrosis.

- Assisted research team in operating multi-center research study, including recruiting study subjects, collecting blood and DNA samples, communicating with research coordinators, and reviewing/editing ethics protocols and operations documents.

EDUCATION

PhD University of Colorado, Denver Anschutz Medical College and Colorado School of Public Health — December 2011
Dissertation: *Role of the IKKβ/NF-κB inflammatory pathway, free fatty acids, adiposity, in insulin resistance in Hispanic Americans*
Advisor: Tasha E. Fingerlin

BA Biology, Pomona College, Claremont CA — May 2001

HONORS AND AWARDS

Fellowships

Post-Doctoral Fellowship, United States Cystic Fibrosis Foundation — 2013-2014
Post-Doctoral Fellowship, Canadian Institutes of Health Research — 2012-2014
Strategic Training in Advanced Genetic Epidemiology
Pre-Doctoral Fellowship, American Heart Association — 2010-2011
Pre-Doctoral Fellowship, Colorado Clinical and Translational Sciences Institute — 2008-2009

Honors

Delta Omega National Honorary Society in Public Health, Colorado Chapter — 2012
Outstanding Contribution by a Student, Colorado School of Public Health — 2012

PUBLICATIONS

Refereed Journal Articles

*denotes equal co-authorship

1. Klasfeld SJ, Knutson KA, **Miller MR**, Fauman EB, Berghout J, Kim HI. 2025. Common genetic modifiers influence cardiomyopathy susceptibility among the carriers of rare pathogenic variants. *Accepted to Human Genetics and Genomics Advances*.

2. Bollinger E, [et al (30 others) including **Miller MR**]. 2025. Restoration of branched chain amino acid catabolism improves renal function in preclinical cardiovascular-kidney-metabolic syndrome models. *Accepted to Kidney International*.

3. Costanzo MC, [et al (21 others) including **Miller MR**]. 2025. Accelerating Medicines Partnership in Type 2 Diabetes and Common Metabolic Diseases: Collaborating to maximize the value of genetic and genomic data. *Diabetes*.

doi.org/10.2337/db25-0042

4. Garnsey MR, [et al (41 others) including **Miller MR**]. 2024. Design and application of synthetic 17B-HSD13 substrates reveals preserved catalytic activity of protective human variants. *Nature Communications.*16(297)

5. Sun BB, Chiou C, [et al (49 others)], Szustakowski JD*, Gibson BW*, **Miller MR***, Whelan CD*. 2023. Plasma proteomics associations with genetics and health in the UK Biobank. *Nature*. 622(7982):329-338.

6. Smith KR, Wang W, **Miller MR**, Boucher M, Reynold JE, Daurio NA, Li D, Hirenallur-Shanthappa D, Ahn Y, Beebe DA, Kelly K, Ross TT, Bence KK, Wan M. 2023. GPAT1 deficiency in mice modulates NASH progression in a model-dependent manner *Cellular and Molecular Gastroenterology and Hepatology.* 17(2): 279-291.

7. Costanzo MC, [et al (56 others) including **Miller MR**]. 2023. The Type 2 Diabetes Knowledge Portal: An open access genetic resource dedicated to type 2 diabetes and related traits. 2023. *Cell Metabolism* 35(4):695-710.e6.

8. Iliodromiti S, McLaren J, Ghouri N, **Miller MR**, Dahlqvist Leinhard O, Linge J, Ballantyne, Platt J, Foster J, Hanvery S, Gujral UP, Kanaya A, Sattar N, Lumsden MA, Gill JMR. 2023. Liver, visceral, and subcutaneous fat in men and women of South Asian and white European descent: a systematic review and meta-analysis of new and published data. 2023. *Diabetologia* 66(1):44-56.

9. Karczewski KJ, [et al (42 others)], Davis JW*, Runz H*, **Miller MR***, Neale BM*. 2022. Systematic single-variant and gene-based association testing of thousands of phenotypes in 394,841 UK Biobank exomes. *Cell Genomics* 2(9):100168

10. Szustakowski JD, [et al (35 others) including **Miller MR**]. 2021. Advancing human genetics research and drug discovery through exome sequencing of the UK Biobank. *Nature Genetics* 53(7):942-948.

11. Linge J, Borga M, West J, Tuthill T, **Miller MR**, Dumitriu A, Thomas EL, Romu T, Tunon P, Bell JD, Dahlqvist Leinhard O. 2018. Body composition profiling in the UK Biobank Imaging Study. *Obesity* 26(11):1785-1795.

12. Winslow AR, Hyde CL, Wilk JB, Eriksson N, Cannon P, **Miller MR**, Hirst WD. 2018. Self-report data as a tool for subtype identification in genetically-defined Parkinson's Disease. *Scientific Reports* 28:8(1):12992

13. Jones AV, Tilley M, Gutteridge A, Hyde C, Nagle M, Ziemek D, Gorman D, Fauman EB, Chen X, **Miller MR**, Tian C, Hu Y, Hinds DA, Cox P, Scollen S. 2017. GWAS of self-reported mosquito bite size, itch intensity and attractiveness to mosquitos implicates immune-related predisposition loci. *Human Molecular*

Genetics 26(7):1391-1406.

14. **Miller MR**, Soave D, Li W, Gong J, Pace RG, Boëlle P-Y, Cutting GR, Drumm ML, Knowles MR, Sun L, Rommens JM, Accurso F, Durie PR, Corvol H, Levy H, Sontag MK, Strug LJ. 2014. Variants in Solute Carrier *SLC26A9* Modify Prenatal Exocrine Pancreatic Damage in Cystic Fibrosis. *Pediatric Research* 165(1152-7.e6).

15. Lamb MM, **Miller MR**, Seifert JA, Frederiksen B, Kroehl M, Rewers M, Norris JM. 2015. The effect of childhood cow's milk intake and HLA-DR genotype on risk of islet autoimmunity and type 1 diabetes: the diabetes autoimmunity study in the young (DAISY). *Pediatric Diabetes* 16(31-8).

16. Soave D, **Miller MR**, Keenan K, Li W, Gong J, Ip W, Accurso F, Sun L, Rommens JM, Sontag MK, Durie PR, Strug LJ. 2014. Evidence for a causal relationship between early exocrine pancreatic disease and cystic-fibrosis related diabetes: a Mendelian randomization study. *Diabetes* 63(2114-9).

17. Li W, Soave D, **Miller MR**, Keenan K, Lin F, Gong J, Chiang T, Stephenson A, Durie P, Rommens J, Sun L, Strug LJ. 2014. Unraveling the complex genetic model for cystic fibrosis: pleiotropic effects of gene modifiers on early CF-related morbidities. *Human Genetics* 133(151-61).

18. **Miller MR**, Pereira RI, Langefeld CD, Lorenzo C, Rotter JI, Chen Y-D, Bergman RN, Wagenknecht LE, Norris JM, Fingerlin TE. 2012. Levels of free fatty acids are associated with insulin resistance but do not explain the relationship between adiposity and insulin resistance in Hispanic Americans: The IRAS Family Study. *Journal of Clinical Endocrinology and Metabolism* 97(3285-91).

19. **Miller MR,** Sokol RJ, Narkewicz MR, Sontag MK. 2012. Pulmonary function in individuals with cystic fibrosis from the U.S. cystic fibrosis foundation registry who had undergone liver transplant. *Liver Transplatation 18(585-593).*

20. **Miller MR,** Yin X, Seifert J, Clare-Salzler M, Eisenbarth GS, Rewers M, Norris JM. 2010. Erythrocyte membrane omega-3 fatty acid levels and omega-3 fatty acid intake are not associated with conversion to type 1 diabetes in children with islet autoimmunity. The diabetes autoimmunity study in the young (DAISY). *Pediatric Diabetes* 12(669-675).

21. **Miller MR**, Seifert JA, Szabo N, Clare-Salzler M, Rewers M, Norris JN. 2010. Erythrocyte membrane fatty acid content in infants consuming formula supplemented with ARA and DHA: an observational study. *Maternal and Child Nutrition* 6(338-346).

22. Heerwagen MJR, **Miller MR**, Barbour LA, Friedman JE. 2010. Maternal obesity and fetal metabolic programming: a fertile epigenetic soil. *American Journal of*

Physiology-Regulatory, Integrative and Comparative Physiology 299: R711–R722.

23. Allen-Petersen BL[*], **Miller MR[*]**, Neville MC, Anderson SM, Nakayama KI, Reyland ME. 2009. Role of protein kinase Cdelta in mammary gland development and apoptosis. *Cell Death and Disease* 1(e17).

24. **Miller MR**, Zhang W, Sibbel SP, Langefeld CD, Bowden DW, Haffner SM, Bergman RN, Norris JM, Fingerlin TE. 2009. Variant in the 3' region of the IκBα gene associated with insulin resistance in Hispanic Americans: The IRAS Family Study. *Obesity 18(555-562).*

Conference Abstracts - Oral Presentations

1. **Miller MR**, Soave D, Li W, Chiang T, Gong J, Sun L, Rommens J, Accurso F, Durie P, Levy H, Sontag MK, Strug L. 2013. Genetic modifiers of prenatal exocrine pancreatic disease. North American Cystic Fibrosis Conference, Salt Lake City, Utah. Oral Presentation

2. **Miller MR**, Soave D, Li W, Gong J, Levy H, Corvol H, Cutting GR, Drumm M, Knowles M, Durie PR, Sun L, Rommens JM, Accurso F, Sontag MK, Strug L. 2014. Variant in the solute carrier *SLC26A9* modifies newborn weight and early weight gain in cystic fibrosis. North American Cystic Fibrosis Conference, Atlanta, Georgia. Oral Presentation.

INVITED PRESENTATIONS

Invited talks

1. Harnessing the power of genetics, proteomics and deep clinical phenotyping to identify targets for cardiovascular disease in UK Biobank. European Society of Cardiology. London, United Kingdom, September 2024.

2. Proteins speak louder than genes: exploring the world of pQTLs. UK Biobank 2023 Scientific Conference. London, United Kingdom, December 2023.

3. Harnessing the power of large-scale MRI with genetics data to drive therapeutic target identification and validation. International Society for Magnetic Resonance in Medicine Study Group Virtual Meting: Overview of Imaging-Informed Target Identification and CMR in Familial Cardiomyopathy in Clinical Trials, Virtual, March 2023.

4. Human genetics structure activity relationship (HGSAR): a novel methodology to link genotype-phenotype data to high throughput functional data to validate targets for human disease. International Common Disease Alliances Virtual Scientific Plenary. Virtual, March 2022.

5. Integrated approach to target identification and validation in common metabolic diseases. Paris NASH Meeting. Paris, France, September 2022.

6. Using human genetics to identify novel targets for NAFLD/NASH: opportunities and challenges. Hanson Wade 5th Annual NASH Drug Discovery Summit. Virtual, November 2021.

7. Using population-based biobanks to identify novel genetic targets for cachexia. 12th International Conference on cachexia, sarcopenia and muscle wasting. Berlin, Germany, December 2019.

8. Development of biomarkers for NASH. Spring 2018 Dan Morton Meeting of Boston Area Pathologists and Toxicologists. Boston, Massachusetts, April 2018.

9. Identifying a therapeutic target for cystic fibrosis-related diabetes: the role of the exocrine pancreas. Cardiovascular, Metabolic, and Endocrine Disease Genetics, Pfizer Inc. Cambridge, Massachusetts, July 2014.

10. Pulmonary function in individuals with cystic fibrosis from the U.S. cystic fibrosis foundation registry who had undergone liver transplant. Cystic Fibrosis Research Seminar at the Hospital for Sick Children. Toronto, Ontario, December 2011.

Invited panel discussions

1. Panelist: Past, present and future of the application of genetics and genomics to drug discovery and development. Industry-hosted session at American Society of Human Genetics, Washington, District of Columbia, November 2023.

2. Panelist: Advances in proteogenomics: how proteomics can complement genomic analyses. Genome Web Webinar, Virtual, April 2023.

3. Panelist: Drug discovery in 500,000 exomes: UK Biobank and the future of pharma. DNA Nexus Connect, San Francisco, California, October 2018.

SUPPORT

Completed Research Support

Predicting the Risk of CF-Related Diabetes from Birth, Miller13A0, (PI: M.R. Miller)
04/01/2013 – 03/31/2015
United States Cystic Fibrosis Foundation
Role, Post-Doctoral Fellow, PI

The overall goal of this project is to identify genetic modifiers of pancreatic damage in cystic fibrosis (CF) and to use genetic modifiers and biomarkers of pancreatic

damage to predict risk of development of CF-related diabetes.

Role of the IKKβ/NF-κB Inflammatory Pathway, Free Fatty Acids, Adiposity, and Insulin Resistance in Hispanics, 10PRE3430011, (PI: M.R. Miller)

07/01/2010 – 12/31/2011
American Heart Association
Role: Pre-Doctoral Trainee, PI

The overall goal of this project research was to further explore the mechanism by which inflammatory pathways influence insulin resistance by examining the relationships among adiposity, circulating FFAs and insulin sensitivity, and their relationship to genetic variants in genes in the IKKβ/NF-κB inflammatory pathway.