CURRICULUM VITAE

PERSONAL INFORMATION

Name: Samir N. P. Kelada
Work address: Campus Box 7264, 120 Mason Farm Road, Chapel Hill, NC 27514
                  Phone: 919-962-2148
Email address: samir_kelada@med.unc.edu

EDUCATION

Post-doctoral Research Fellow, National Human Genome Research Institute   2006–2012
    National Institutes of Health, Bethesda, MD
    Laboratory of Dr. Francis Collins

Ph.D. in Environmental Health/Toxicology, University of Washington, Seattle WA   2006

M.P.H. in Environmental Health and Certificate in Public Health Genetics   2000
    University of Michigan, Ann Arbor, MI

B.S. in Biological Chemistry University of Michigan Ann Arbor, MI   1997

PROFESSIONAL EXPERIENCE

Associate Professor, Department of Genetics   2018-present
    University of North Carolina, Chapel Hill, NC

Assistant Professor, Department of Genetics   2012-2018
    University of North Carolina, Chapel Hill, NC

University of North Carolina Affiliations
    Member, Marsico Lung Institute   2012-present
    Faculty, Curriculum in Genetics & Molecular Biology   2012-present
    Faculty, Curriculum in Toxicology   2012-present
    Faculty, Curriculum in Bioinformatics & Computational Biology   2012-present

HONORS AND AWARDS

NIEHS Outstanding New Environmental Scientist Award   2015
Joy Cappel Young Investigator Award, Rockland Immunochemicals   2014
University of North Carolina Junior Faculty Development Award   2013
NIH Fellows Award for Research Excellence   2011
Thomas L. Petty Travel Award, Aspen Lung Conference   2010
Graduate Student of the Year, Department of Environmental and Occupational
Health Sciences, University of Washington   2005
Pre-doctoral Training grant fellowship, Environmental Toxicology & Pathology
    University of Washington (NIEHS funded training grant)   2001-2006
Magnuson Health Sciences Scholar, University of Washington   2003-2004
Graduate Student Scholarship, University of Michigan School of Public Health   1999

BIBLIOGRAPHY

Book Chapters

1. Checkoway H., Lundin J. I., **Kelada S. N**., 2011 Neurodegenerative diseases. In: *Molecular Epidemiology: Principles and Practices. IARC Scientific Publication No. 163*, Lyon, France, pp. 407–419.

2. **Kelada S. N**., Eaton D. L., Wang S. S., Rothman N. R., Khoury, 2004 Applications of Human Genome Epidemiology to Environmental Health. In: Khoury MJ, Little J, Burke W (Eds.), *Human Genome Epidemiology: A scientific foundation for using genetic information to improve health and prevent disease*, Oxford University Press, New York, pp. 145–167.

3. **Kelada S. N.**, Checkoway H., Costa L. G., 2006 Neurodegenerative Diseases. In: Costa LG, Eaton DL (Eds.), *Gene-Environment Interactions: Fundamentals of Ecogenetics*, John Wiley & Sons, Ltd., Hoboken, NJ, pp. 253–270.

Refereed Original Research Articles

1. Smith G.J., Tovar A., McFadden K. M., Kanke M., Wang Y., Deshane J., Sethupathy P., **Kelada S. N. P**. Ozone-induced changes in the murine lung extracellular vesicle small RNA landscape. Physiolologic Reports. 2021, *in press*.

2. Smith G.J., Tovar A., McFadden K. M., Moran T. P., Wagner J. G., Harkema J. R., **Kelada S. N. P**. A Murine Model of Ozone-Induced Non-atopic Asthma from the Collaborative Cross. The American Journal of Respiratory Cellular Molecular Biology. 2021, *in press*.

3. Crouse W. L., **Kelada S. N. P.,** Valdar W., Inferring the Allelic Series at QTL in Multiparental Populations. Genetics 2020; 216(4): 957-983.

4. Laudermilk L. T., Tovar A., Homstad A. K., Thomas J. M., Mcfadden K. M., Tune M. K., Cowley D. O., Mock J. R., Folami Ideraabdullah, **Kelada S. N. P**., Baseline and innate immune response characterization of a *Zfp30* knockout mouse strain. Mamm. Genome **31**: 2020; 205–213.

5. Tovar A., Smith G., Thomas J., Harkema J., **Kelada S.N.P.**, Transcriptional profiling of the murine airway response to acute ozone exposure. Toxicol. Sci. 2019: 1–17.

6. Keele G, Crouse W, **Kelada SNP**, Valdar W. Determinants of QTL mapping power in the realized Collaborative Cross. Genes|Genomes|Genetics 2019. g3.400194.

7. Smith GS, Walsh W, Higuchi M, **Kelada SNP.** Development of a large-scale computer-controlled ozone inhalation exposure system for rodents. Inhalation Toxicology 2019;1-12.

8. Tsai Y, Parker JS, Yang IV, **Kelada SN**. Meta-analysis of Airway Epithelia Gene Expression in Asthma. European Respiratory Journal 2018*;* 51(5):1701962.

9. Laudermilk LT, Thomas JT, **Kelada SN**. Differential regulation of *Zfp30* expression in murine airway epithelia through altered binding of ZFP148 to rs51434084. Genes | Genomes | Genetics 2018; 8(2):687-693.

10. Gomez JC, Dang H, Kanke M, Hagan RS, Mock JR, **Kelada SN**, Sethupathy P, Doerschuk CM. Predicted effects of observed changes in the mRNA and microRNA transcriptome of lung neutrophils during *S. pneumoniae* pneumonia in mice. Scientific Reports 2017; 7:11258.

11. Donoghue LJ*, Livraghi-Butrico A*, McFadden KM, Thomas JM, Chen G, Grubb BR, O'Neal WK, Boucher RC, **Kelada SN**. Identification of *trans* protein QTL for secreted airway mucins in mice and a causal role for *Bpifb1*. Genetics 2017; 207:801-812.

12. **Kelada SN**. Plethysmography Phenotype QTL in Mice Before and After Allergen Sensitization and Challenge. Genes | Genomes | Genetics 2016; 6(9):2857-2865.

13. Rutledge H, Baran-Gale J, Chessler EJ, Churchill GA, Pardo-Manuel de Villena F, Sethupathy P*, **Kelada SN***. Identification of microRNAs Associated with Allergic Airway Disease Using a Genetically Diverse Mouse Population. BMC Genomics 2015: 25;16(1):633.

14. Rutledge H, Aylor DL, Carpenter DE, Peck BCE, Chines P, Ostrowski LE, Chessler EJ, Churchill GA, Pardo-Manuel de Villena F, **Kelada SN**. Genetic Regulation of *Zfp30*, CXCL1, and Neutrophilic in Mouse Lung. Genetics, 2014;198(2): 735-745.

15. Collins AL, Kim Y, Bloom RJ, **Kelada SN**, Sethupathy P, Sullivan PF. Transcriptional targets of the schizophrenia risk gene miR-137. Translational Psychiatry 2014;4:e404.

16. **Kelada SN**, Carpenter DE, Aylor DL, Chines P, Rutledge H, Chessler EJ, Churchill GA, Pardo-Manuel de Villena F, Schwartz DA, Collins FS. Integrative Genetic Analysis of Allergic Inflammation in the Murine Lung. The American Journal of Respiratory Cellular Molecular Biology 2014;51(3):436-445.

17. **Kelada S***, Sethupathy P*, Okoye IS*, Kistasis E, Czieso S, White S.D., Chou D, Martens C, Ricklefs SM, Virtaneva K, Sturdevant DE, Porcella SF, Belkaid Y, Wynn TA, Wilson MS. miR-182 and miR-10a are key regulators of Treg function during Th2 and Th1-associated inflammation. PLoS Pathogens 2013; 9(6):e1003451. *co-first author.

18. **Kelada SN***, Aylor DA*, Peck B, Ryan JF, Miller D, Chesler E, Threadgill DW, Pardo-Manuel de Villena F, Churchill GA, Collins FS. Genetic Analysis of Hematological Parameters in Incipient Lines of the Collaborative Cross Mice. Genes | Genomes | Genetics 2012; 2(2); 157-165. * co-first author

19. Bobb JF, Scharfstein DO, Daniels MJ, Collins FS, **Kelada S**. Multiple Imputation of Missing Phenotype Data for QTL Mapping. Statistical Applications in Genetics and Molecular Biology 2011; 10(1): Article 29.

20. **Kelada SN**, Wilson MS, Tavarez U, Borate B, Whitehead GS, Maruoka S, Roy MG, Olive M, Carpenter DE, Brass DM, Wynn TA, Cook DN, Evans CM, Schwartz DA, Collins FS. Strain-Dependent Genomic Factors Affect Allergen-Induced Airway Hyper-responsiveness in Mice. The American Journal of Respiratory Cellular Molecular Biology 2011; 45(4):817-24.

21. Aylor DL, Valdar W, Foulds-Mathes W, Buus RJ, Verdugo R, Baric RS, Ferris M, Frelinger JA, Heise M, Frieman M, Gralinski L, Bell T, Didion JD, Hua K, Nehrenberg D, Powell C, Steigerwalt J, Xie Y, **Kelada SN**, Collins FS, Yang IV, Schwartz DA, Branstetter LA, Chesler EJ, Miller DR, Spence J, Liu E, McMillan L, Sarkar A, Wang J, Wang W, Zhang Q, Broman KW, Korstanje R, Durrant C, Mott R, Iraqi F, Pomp D, Threadgill DW, Pardo-Manuel de Villena F, Churchill GA. Genetic Analysis of Complex Traits in the Emerging Collaborative Cross. Genome Research 2011; 21(8): 1213-22.

22. **Kelada SN**, Checkoway H, Kardia SLR, Carlson CS, Costa-Mallen P, Eaton DL, Firestone JA, Swanson PD, Franklin GM, Longstreth WT Jr., Smith-Weller T, Afsharinejad Z, Costa LG. 5′ and 3′ Region Variability in the Dopamine Transporter Gene (*SLC6A3*), Pesticide Exposure and Parkinson's Disease Risk: a hypothesis generating study. Human Molecular Genetics 2006; 15(20): 3055-62.

23. **Kelada SN**, Costa-Mallen P, Checkoway H, Carlson CS, Smith-Weller T, Franklin GM, Swanson PD, Longstreth WT Jr., Afsharinejad Z, Costa LG. Dopamine Transporter (*SLC6A3*) 5' Region Haplotypes Significantly Affect Transcriptional Activity *In Vitro* but are not Associated with Parkinson's Disease. Pharmacogenetics and Genomics 2005;15:659-68.

24. Costa-Mallen P, **Kelada SN**, Costa LG, Checkoway H. Characterization of the in vitro transcriptional activity of polymorphic alleles of the human monoamine oxidase-B gene. Neuroscience Letters 2005; 383: 171-5.

25. Costa-Mallen P, Afsharinejad Z, **Kelada SN**, Costa LG, Franklin GM, Swanson PD, Longstreth WT Jr, Viernes HM, Farin FM, Smith-Weller T, Checkoway H. DNA sequence analysis of monoamine oxidase B gene coding and promoter regions in Parkinson's disease cases and unrelated controls. Movement Disorders 2004; 1: 76-83.

26. **Kelada SN**, Costa-Mallen P, Checkoway H, Furlong CE, Jarvik GP, Viernes HA, Marin FM, Smith-Weller T, Franklin GM, Swanson PD, Longstreth WT Jr., Costa LG. Paraoxonase 1 promoter and coding region polymorphisms in Parkinson's disease. Journal of Neurology Neurosurgery and Psychiatry 2003; 74: 546-7.

27. **Kelada SN**, Stapleton PL, Farin FM, Bammler TK, Eaton DL, Smith-Weller T, Franklin GM, Swanson PD, Longstreth WT Jr., Checkoway H. Glutathione S-transferase M1, T1, and P1 Polymorphisms and Parkinson's Disease. Neuroscience Letters 2003; 337:5-8.

28. **Kelada SN**, Costa-Mallen P, Costa LG, Smith-Weller T, Franklin GM, Swanson PD, Longstreth WT Jr., Checkoway H. Gender Difference in the Interaction of Smoking and

Monoamine Oxidase B Intron 13 Genotype in Parkinson's Disease. Neurotoxicology 2002; 23:515-9.

29. **Kelada SN**, Kardia SLR, Walker AH, Wein AJ, Malkowicz SB, Rebbeck TR. The Glutathione S-Transferase-μ (GSTM1) and -θ (GSTT1) Genotypes in the Etiology of Prostate Cancer: Gene-Environment Interactions with Smoking. Cancer Epidemiology, Biomarkers and Prevention 2000; 9(12):1329-34.

Manuscripts under review

1. Tovar et al. Integrative phenotypic and genomic analyses reveal mouse strain-dependent responses to acute ozone exposure and their associations with airway macrophage transcriptional activity. Submitted to American Journal of Physiology-*Lung Cellular and Molecular Physiology*.

2. Tovar et al. A locus on chromosome 15 contributes to acute ozone-induced lung injury in Collaborative Cross mice. Submitted to American Journal of Respiratory Cellular Molecular Biology.

Review articles

1. **Kelada SN**, Eaton DL, Wang SS, Rothman NR, Khoury MJ. The role of genetic polymorphisms in environmental health. Environmental Health Perspectives 2003; 111: 1055-64.

2. **Kelada SN**, Shelton E, Kaufmann RB, Khoury MJ. δ-Aminolevulinic Acid Dehydratase (ALAD) Genotype and Lead Toxicity: A HuGE Review. American Journal of Epidemiology 2001; 154(1):1-13.

Oral Presentations

Invited Oral Presentations:
University of North Carolina, Marsico Lung Institute, May 2021 (Virtual)
University of Washington Center for Lung Biology, November 2020 (Virtual)
North Carolina State University, Program in Toxicology, September 2019
University of Alabama School of Medicine, Division of Pulmonary and Critical Care Medicine, January 2020
Gordon Research Conference, Cilia, Mucus & Mucociliary Interactions, Barga, Italy, February 2019.
NIEHS Outstanding New Environmental Scientist Symposium, Research Triangle Park, NC, May 2018.
Center for Excellence in Environmental Toxicology, University of Pennsylvania, Philadelphia, PA, November 2017.
NIEHS Annual Core Center Meeting. Atlanta, GA, June 2017.
Lung Biology Seminar Series, University of Rochester, Rochester, NY, March 2017.
NIEHS Environmental Health Science Fest. Durham, NC, December 2016.
Groningen Research Institute for Asthma and COPD Seminar Series, Groningen Medical Center. Groningen, The Netherlands. November 2016.

NIEHS Outstanding New Environmental Scientist Symposium, Research Triangle Park, NC, May 2016.
Respiratory Research Initiative Jaqua Foundation Seminar, Michigan State University, East Lansing, MI April 2016.
Cardiovascular Disease Group Seminar, University of North Carolina, Chapel Hill, NC, October 2015.
Genetics and Environmental Mutagenesis Society Meeting, Research Triangle Park, NC, April 2015.
Toxicology Program Seminar, North Carolina State University, Raleigh, NC, April 21, 2015.
National Health and Environmental Effects Research Division Seminar Series, EPA, Research Triangle Park, NC, September 30, 2014.
Center for Lung Biology Seminar, University of Washington, Seattle, WA, July 2014.
Laboratory of Respiratory Biology Seminar, NIEHS, Research Triangle Park, NC, November 2012.

Additional Oral Presentations at Conferences:
International Mammalian Genome Conference, San Juan, Puerto Rico, October 2018
Complex Trait Community, Memphis, TN, June 2017
From Pathway Biology to Precision Therapeutics, Keystone Symposia Conference, February Keystone, CO, 2017
Society of Toxicology, Baltimore, MD, March 2017
Complex Trait Consortium 2015. Portland, OR, June 2015
Gordon Research Conference on Cilia, Mucus & Mucociliary Interactions, Galveston, TX, February 2015
American Society of Human Genetics, Boston, MA, October 2013
International Mammalian Genome Conference, Salamanca, Spain, September 2013
Gordon Research Conference on Quantitative Genetics and Genomics, Galveston, TX, February 2011
Aspen Lung Conference, Aspen, CO, June 2010
International Mammalian Genome Conference, Prague, Czech Republic, October 2008

Published Meeting Abstracts (underlined names denote trainees in my lab; unless otherwise noted, abstracts were presented in poster format)

1. **Kelada SN**, Li Y, van Buren E, Ford AA, Radicioni G, O'Neal WK, Ortega VE, Prescott G. Woodruff, Eugene R. Bleecker, Boucher RC, and Kesimer M. Genome-Wide Association Study of Sputum Mucin Concentrations in The Subpopulations and Intermediate Outcomes in COPD Study (SPIROMICS). American Thoracic Society International Conference, Dallas, TX, May 2019.

2. Tovar A, Smith G, Thomas JM, McFadden K, **Kelada SN**. Investigating Susceptibility to Ozone-Induced Lung Inflammation and Injury Using the Collaborative Cross Mouse Genetic Reference Population. American Thoracic Society International Conference, Dallas, TX, May 2019. Oral presentation

3. Smith GJ, Tovar A, Kanke M, Sethupathy P, **Kelada SN**. Airway Transcriptomic Responses to Ozone: Altered Extracellular Vesicle MicroRNA and Alveolar Macrophage mRNA Expression Profiles. Society of Toxicology Annual Meeting, Baltimore, MD, March 2019.

4. Crouse W, **Kelada S**, Valdar W. "Tree-based Inference of Multiallelism via Bayesian Regression." Gordon Research Seminar on Quantitative Genetics and Genomics, Lucca, Italy, February 2019. Oral presentation

5. Tovar A, Speen A, Jaspers I, Purvis J, Furey T, **Kelada SN**. Dynamics of Alveolar Macrophage Transcriptional Regulation Following Sterile Inflammation. Cold Spring Harbor Meeting on Systems Immunology, Cold Spring Harbor Labs, March 2019.

6. Tovar A, Smith G, Thomas JM, McFadden K, **Kelada SN**. Exploring Mouse Strain-by-Exposure Interactions in Pulmonary and Systemic Inflammatory Responses to the Air Pollutant Ozone. International Mammalian Genome Society Conference, Rio Mar, Puerto Rico, November 2018.

7. Donoghue LJ, Patterson MS, McFadden K, Thomas JM, Tovar AE, Parker JS, **Kelada SNP**. Pairing Systems Genetics and Longitudinal Analyses to Identify Regulators of Complex Lung Phenotypes. International Mammalian Genome Conference, Rio Mar, Puerto Rico, Nov 2018. Oral Presentation.

8. Tovar A, Smith G, Thomas JM, McFadden K, **Kelada SN**. Murine Strain Differences in Neutrophil Recruitment and Lung Injury Following Acute Ozone Exposure. North Carolina Society of Toxicology Annual Meeting, NIEHS, October 2018.

9. Smith GJ, Sethupathy P, **Kelada SN**. Ozone exposure alters murine airway extracellular vesicle microRNA profiles. North Carolina Regional Chapter, Society of Toxicology Meeting, Research Triangle Park, October 2018.

10. Tovar A, Smith G, Thomas JM, McFadden K, **Kelada SN**. Using a Systems Genetics Approach to Interrogate Alveolar Macrophage Contributions to Ozone Responses. Duke University BioCoRE Symposium, Durham, NC, July 2018.

11. Smith GJ, Sethupathy P, **Kelada SN**. Ozone exposure increases extracellular vesicles in the murine respiratory tract. Early Stage Investigator Presentation, NIEHS P30 Core Centers Meeting, Davis, CA, July 2018. Oral Presentation

12. Donoghue LJ, Livraghi-Butrico A, Thomas JM, McFadden K, O'Neal WK, Grubb BR, Doerschuk CM, Boucher RC, **Kelada SNP**. Genetic Analysis of Major Secreted Airway Mucins in Reveals a Novel Regulator of MUC5B. FASEB Conference – The Lung Epithelium in Health and Disease, Olean, NY. July 2018. Oral Presentation.

13. Crouse W, **Kelada S**, Valdar W. "Tree-based Inference of Multiallelism via Bayesian Regression." Population, Evolutionary and Quantitative Genetics Conference, Madison, WI, June 2018.

14. <u>Smith GJ</u>, **Kelada SN**. Ozone Exposure Increases Exosome-sized Vesicles In Murine Bronchoalveolar Lavage Fluid. Society of Toxicology Annual Meeting, San Antonio, TX, March 2018.

15. <u>Tovar A</u>, Speen A, Moran T, Jaspers I, **Kelada SN**. Characterization of the murine alveolar macrophage response to *in vitro* ozone exposure. Society of Toxicology, San Antonio, TX, March 2018.

16. <u>Laudermilk LT</u>, Thomas JM, **Kelada SN.** Identification of a Causal Variant and Mechanism for a Lung eQTL Related to Neutrophil Chemotaxis. Mammalian Genetics and Genomics: From Molecular Mechanisms to Translational Applications (hosted by the European Molecular Biology Laboratory and the International Mammalian Genome Society, Heidelberg, Germany), October 2017.

17. <u>Smith GJ</u>, **Kelada SN**. Development of a feedback-controlled ozone inhalation exposure system for large-scale in vivo studies in rodents. North Carolina Regional Chapter Meeting, Society of Toxicology, Research Triangle Park, October 2017.

18. <u>Crouse W</u>, Kelada S, Valdar W. Tree-based Inference of Multiallelism via Bayesian Regression. Complex Trait Community Meeting, Memphis, TN, June 2017. (Oral presentation)

19. **Kelada SN**, <u>Donoghue LJ</u>, Livraghi-Butrico A, Crouse W, Thomas JM, McFadden K, Kim Y, Valdar W, O'Neal WK, Boucher RC. Genetic Analysis of Allergen-Induced Secreted Mucins Identifies *Bpifb1* as a Regulator of MUC5B in the Airway. American Thoracic Society, Washington, D.C., May 2017.

20. <u>Donoghue LJ</u>, Livraghi-Butrico A, Crouse W, Thomas JM, McFadden K, Kim Y, Valdar W, O'Neal WK, Boucher RC, **Kelada SN**. Quantitative Genetic Analysis of Major Secreted Mucin Glycoproteins in a Mouse Model of Asthma. Asthma: Pathways and Therapeutics (Keystone Conference), Keystone, CO, February 2017.

21. <u>Crouse W</u>, **Kelada S,** Valdar W. Bayesian Inference of the Allelic Series at Quantitative Trait Loci in Multiparent Populations. Gordon Research Conference on Quantitative Genetics and Genomics, Galveston, TX, February 2017.

22. <u>Laudermilk LT</u>, **Kelada SN**. Interrogating the Regulation and Function of *Zfp30*. The Allied Genetics Conference (Genetics Society of America), Orlando, FL, July 2016.

23. **Kelada SN**, <u>Donoghue LJ</u>, Livraghi-Butrico A, Thomas JM, McFadden K, O'Neal WK, Boucher RC. Quantitative Genetic Analysis of MUC5AC and MUC5B in a Mouse Model of Asthma. The Allied Genetics Conference (Genetics Society of America), Orlando, FL, July 2016.

24. <u>Donoghue LJ</u>, Livraghi-Butrico A, Crouse W, Thomas JM, McFadden K, Kim Y, Valdar W, O'Neal WK, Boucher RC, **Kelada SN**. Quantitative Genetic Analysis of the Major Secreted Mucins. International Conference on Quantitative Genetics, Madison, WI, June 2016.

25. <u>Crouse W</u>, **Kelada S,** Valdar W. Bayesian Inference of the Allelic Series at Quantitative Trait Loci in Multiparent Populations. International Conference on Quantitative Genetics 5, Madison, WI, June 2016.

26. **Kelada SN**, <u>Donoghue LJ</u>, Livraghi-Butrico A, Thomas JM, McFadden K, O'Neal WK, Boucher RC. Quantitative Genetic Analysis of MUC5AC and MUC5B in a Mouse Model of Asthma. American Thoracic Society, San Francisco, CA, May 2016.

27. **Kelada SN.** Identifying Genetic Predictors of Response to Respiratory Toxicants Using the Collaborative Cross Mouse Genetic Reference Population. Poster Presentation, Society of Toxicology, March 2016, New Orleans, LA.

28. <u>Crouse W</u>, Valdar W, Kelada, S. Efficient Detection of Trans-eQTL in Incipient Lines of the Collaborative Cross. Complex Trait Community Meeting, Portland, OR, June 2015.

29. Livraghi-Butrico A, Wilkinson KJ, Volmer AS, Miller DR, Shaw GD, Grubb BR, **Kelada SN**, Pardo-Manuel de Villena F, Boucher, RC, O'Neal WK. Development of a Mouse Model of Spontaneous Bronchiectasis. American Thoracic Society International Conference, Denver, CO, May 2015.

30. <u>Crouse W</u>, Valdar W, **Kelada, S**. Efficient Detection of Trans-eQTL in Incipient Lines of the Collaborative Cross. Population-Based Rodent Resources for Environmental Health Sciences Meeting, Durham, NC, March 2015.

31. Sethupathy P, Miller D, Chesler E, Churchill G, Pardo Manuel de Villena F, **Kelada SN**. Gene Expression Modules Associated with Allergen-Induced Airway Inflammation in Mice. Keystone Meeting on Asthma and COPD, Santa Fe, NM, February 2013.

32. **Kelada SN**, Carpenter D, Tavarez U, Chessler E, Miller D, Threadgill D, Churchill G, Pardo Manuel de Villena F, Schwartz DA, Collins FS. Gene Expression Modules Associated with Allergen-Induced Airway Inflammation in Mice. American Thoracic Society, San Francisco, CA, May 2012.

33. **Kelada SN**, Carpenter D, Aylor D, Tavarez U, Kubalanza K, Buus R, Chessler E, Miller D, Threadgill D, Churchill G, Pardo Manuel de Villena F, Schwartz DA, Collins FS. Use of Pre-Collaborative Cross Mice to Characterize the Genomics of Allergen Response in the Lung. Mouse Genetics (hosted by the International Mammalian Genome Conference), Washington, DC, May 2011.

34. **Kelada SN**, Carpenter D, Aylor D, Tavarez U, Kubalanza K, Buus R, Chessler E, Miller D, Threadgill D, Churchill G, Pardo Manuel de Villena F, Schwartz DA, Collins FS. Genetic Susceptibility to Allergen-Induced Airway Inflammation in Mice. American Thoracic Society, Denver, CO, May 2011.

35. **Kelada SN**, Aylor D, Chessler E, Miller D, Threadgill D, Churchill G, Pardo Manuel de Villena F, Collins FS. QTL Mapping of Blood Cell Phenotypes in PreCC Mice. International Mammalian Genome Conference, San Diego, CA, October 2009.

36. **Kelada SN**, Kubalanza K, Tavarez U, Whitehead G, Schwartz DA, Collins FS. Strain-dependent Dissociation of Airway Hyper-responsiveness from Inflammation in a Mouse Model of Asthma. Aspen Lung Conference, Aspen, CO, June 2009.

37. **Kelada SN**, Brass DM, Maruoka S, Schwartz DA, Collins FS. Detecting Loci That Confer Susceptibility to Dust Mite-Induced Asthma Using a Combined In Vivo and In Silico Approach. American Society of Human Genetics, San Diego, CA, October 2007.

38. **Kelada SN**, Costa-Mallen P, Checkoway H, Carlson CS, Smith-Weller T, Franklin GM, Swanson PD, Longstreth WT Jr., Afsharinejad Z, Costa LG. Dopamine Transporter (*SLC6A3*) 5' Region Haplotypes Significantly Affect Transcriptional Activity *In Vitro* but are not Associated with Parkinson's Disease. Society for Neuroscience, Washington, D.C., 2005.

39. **Kelada SN**, Costa-Mallen P, Checkoway H, Costa LG. Multiple 5' Region Polymorphisms in the Dopamine Transporter Gene (*SLC6A3*). Neurotoxicology, Honolulu, HI, 2004.

40. **Kelada SN**, Costa-Mallen P, Checkoway H, Costa LG. Exploration of Alternative Splicing of Monoamine Oxidase-B Transcripts by the Intron 13 Polymorphism. Society of Toxicology. Salt Lake City, UT, 2003.

41. Costa-Mallen P, Afsharinejad Z, **Kelada SN**, Viernes HM, Srinouanprachanh S, Farin FM, Costa L, Checkoway H. DNA sequence analysis of monoamine oxidase B gene coding and promoter regions in Parkinson's disease cases and controls. 10th International Amine Oxidase Workshop, Istanbul, Turkey, 2002.

42. **Kelada SN**, Costa-Mallen P, Costa LG, Smith-Weller T, Franklin GM, Swanson PD, Longstreth WT Jr., Checkoway H. Gender Difference in the Interaction of Smoking and Monoamine Oxidase B Intron 13 Genotype in Parkinson's Disease. Neurotoxicology Colorado Springs, CO, 2001.

TEACHING RECORD

Courses

Course Co-Director, Genetics 647: Human Genetics and Genomics, Graduate students, 13 contact hours, 2015-present. Lecturer, 2.5 contact hours, 2013-2015.

Course Co-Director, Genetics 702: Genetics & Molecular Biology Student Seminar Series, 2014-2015. 14 contact hours.

Course Instructor, Biological & Biomedical Sciences Program 901, 902: First Year Group, Gradate Students, 2017-2021, 37.5 contact hours. Course co-instructor, 2016-2017, 18.75 contact hours. First Year Group Mentor, 2013-2015, 10 contact hours.

Lecturer, Bioinformatics & Computatonal Biology 722: Population Genomics, Graduate students, 2013-2015. 1.25 contact hours.

Lecturer, Toxicology 442: Biochemical Toxicology, Graduate and undergraduate students, 2014-2021. 1.25 contact hours.

<u>Post-doctoral Fellow Advisor</u>
Gregory J. Smith, PhD, Toxicology	2016-2021

<u>Graduate Student Thesis Advisor</u>
Moran Nalesnik, Ph.D. student, Toxicology & Environmental Medicine	2020-present
Lauren Donoghue, Ph.D. student, Genetics & Molecular Biology	2016-2021
Adelaide Tovar, Ph.D. student, Genetics & Molecular Biology	2016-2021
Wesley Crouse, Ph.D. student, Bioinformatics & Computational Biology, co-mentored with Dr. Will Valdar	2015-2020
Luke Laudermilk, Ph.D., Genetics & Molecular Biology	2014-2019

<u>Graduate Rotation Advisory</u>
Nicole Kramer (2019), Syed Masood (2018), Adelaide Tovar (2016), Lauren Donoghue (2016), Wesley Crouse (2015), Luke Laudermilk (2014), Amanda Raimer (2014), Rachel McMullan (2014), Phillip Clapp (2014), Bryan Quach (2013)

<u>Graduate Student Thesis Advisory Committees</u>
Victoria Parsons, Genetics & Molecular Biology	2020-
Sonja Mihailovic, Genetics & Molecular Biology	2020-
Taylor Tibbs, Microbiology & Immunology	2020-
Jessica Jimenez, Ph.D. student, Toxicology and Environmental Medicine	2020-
Sarah Brotman, Ph.D. student, Genetics & Molecular Biology	2019-
Hannah Perrin, Ph.D. student, Genetics & Molecular Biology	2019-
Kyle Martin, Ph.D. student, Toxicology and Environmental Medicine	2019-
Alexia Perryman, Ph.D. student, Toxicology and Environmental Medicine	2018-
Brea Hampton, Ph.D. student, Genetics & Molecular Biology	2017-
Yanwei Cai, Ph.D. student, Bioinformatics & Computational Biology	2017-2020
Gregory Keele, Ph.D. student, Bioinformatics & Computational Biology	2016-2018
Alisha Coffey, Ph.D. student, Genetics & Molecular Biology	2016-2018
Michelle Engle, Ph.D. student, Genetics & Molecular Biology	2016-2018
Adam Speen, Ph.D. student, Toxicology	2016-2018
Bryan Quach, Ph.D. student, Bioinformatics & Computational Biology	2016-2017
Kathie Sun, MPH student, Environmental Sciences and Engineering	2016

<u>Awards to Trainees</u>
Wesley Crouse, NIGMS T32 Bioinformatics and Computational Biology Training Grant fellow, 2015-2016

Lauren Donoghue, NIH/NHLBI F31 Graduate Trainee Fellowship, 2017; NIGMS T32 Genetics Training Grant fellow, 2016-2017; Travel Scholarship, Keystone Conference - Asthma Pathways and Therapeutics, 2017; Honorable Mention - Graduate Research Fellowship Program, National Science Foundation, 2017; 1st Place Best Graduate Student Poster Award, UNC Women in Science Symposium, 2017; 3rd Place Best Graduate Student Poster Award, Visiting Pulmonary Scholars Symposium, 2017; Outstanding Oral Presentation Award, 32nd International Mammalian Genome Conference, November 2018; Lorraine Flaherty Award, 32nd International Mammalian Genome Conference; Jo Rae Wright Outstanding Young Investigator of the Year Award, FASEB Lung Epithelium in Health and Disease Conference, July 2018.

Lucas Laudermilk, International Mammalian Genome Society Travel Award, 2016 and 2017; Outstanding Research Poster Award, International Mammalian Genome Society, 2017; Outstanding Research Poster Award, The Allied Genetics Conference, 2016.

Morgan Nalesnik, NIEHS T32 Toxicology Training Grant fellow, 2020-2021; Outstanding Oral Presentation, 2021 Toxicology & Environmental Medicine Curriculum Retreat

Gregory Smith, Ph.D., NIEHS T32 Training grant fellow, 2016-present; Gabriel L. Plaa Education Award, Mechanisms Specialty Section, Society of Toxicology, 2017; Leon and Bertha Golberg Fellowship in Toxicology, Curriculum in Toxicology, University of North Carolina, September 2018; President's Award for Research Competition (2nd Place), North Carolina Society of Toxicology, October 2018; Postdoctoral Poster Award (1st Place), Curriculum in Toxicology, University of North Carolina, June 2018; Pilot Project Award, Center for Environmental Health and Susceptibility, University of North Carolina, April 2017.

Adelaide Tovar, University of Washington Department of Biostatistics Summer Institute in Statistical Genetics Scholarship, April 2019; American Thoracic Society Environmental, Occupational, and Population Health Assembly Abstract Award, April 2019; American Thoracic Society Minority Trainee Development Scholarship, March 2019;UNC Graduate School Travel Award, March 2019; International Mammalian Genome Society Graduate Student Travel Scholarship, September 2018.

GRANTS
<u>Active</u>
1R21AI162084-01   5/19/2021-4/30/2023   13% effort
NIH/NIAID   275,000 direct costs
A new mouse model of severe asthma
Role: PI

1R21ES032089 A1   7/1/2021-6/30/2023   10% effort
NIH/NIEHS $275,000 direct costs
A Murine Gene-by-Ozone Interaction Model of Non-atopic Asthma
Role: PI

U19 AI100625 (MPI:Heise/Baric)   09/01/12-8/31/22   5% effort
NIH/NIAID
Systems Immunogenetics of Biodefense Pathogens in the Collaborative Cross
Role: Co-Investigator on Project 2

UNC Center for Environmental Health & Susceptiblity Pilot Grant, 4/1/21-3/31/22
$25,000   0% effort
Understanding Adaptation to Ozone Using Single Cell Genomics
Role: PI

UNC School of Medicine Emerging Challenges in Biomedical Research Grant, 2/20/20 -
8/19/21
$50,000   0% effort
A Mouse Genetics Approach to Understand E-cigarette or Vaping Associated Lung Injury
Role: co-PI

Pending
R01 ES033629-01   12/01/2021-11/30/2026   25% effort
NIH/NIEHS $2,489,678 total direct costs
Discovery and Validation of Gene-Environment Interactions with Ozone in Human Airway
Epithelial Cells
Role: co-PI

Completed
UNC School of Medicine   10/1/2021   0% effort
Bridge Funding $50,000

1R01ES024965-S1 (Kelada)   7/1/2016-10/31/2019   0% effort
NIH/NIEHS $153,247 total direct costs
Administrative Supplement to Gene-Environment Interactions with Ozone in Experimental
Asthma
Role: Sponsor and mentor

1R01ES024965-01 (Kelada)   01/05/2015 – 10/31/2019   50% effort
NIH/NIEHS $1,688,962 total direct costs
Gene-Environment Interactions with Ozone in Experimental Asthma
Role: PI

1R01HL122711-01A1 (Kelada)   08/15/2015 – 05/31/2019   25% effort
NIH/NHLBI $1,259,437 total direct costs
Systems-level transcriptomic analysis of mouse models of allergic airway disease
Role: PI

PROFESSIONAL SERVICE

Service to Discipline

Reviewer, Grants
NIH Systemic Injury by Environmental Exposure Study Section, Ad Hoc Member, 2018, 2021
UK Medical Research Council, Ad Hoc Member, 2018 and 2019
NIH/National Institute of Allergy and Infectious Disease Study section for Asthma and Allergic Diseases Cooperative Research Centers (U19), 2017
NIH Center for Scientific Review Special Emphasis Panel on Epidemiology of Environmental Exposures, Metabolism, and Kidney, Lung, and Infectious Disease, 2017
Health Effects Institute, Health Effects of Air Pollution Proposals, 2016

Reviewer, Journals
American Journal of Respiratory Cellular and Molecular Biology, BMC Genomics, BMC Pulmonary Medicine, Clinical and Experimental Allergy, Environmental Health Perspectives, Genes|Genomes|Genetics, Journal of Allergy & Clinical Immunology, Journal of Clinical Investigation, Immunogenetics, Pharmacogenetics and Genomics, Toxicological Sciences

Service within UNC-Chapel Hill
Department of Genetics Computational Biology Faculty Search, 2021
Department of Genetics Diversity Committee, 2020-present
Department of Genetics Strategic Hiring Committee, 2019
Creativity Hub Reviewer, 2018-2019
Department of Genetics Space Committee, 2017-2018
Curriculum in Genetics & Molecular Biology Executive Committee, 2018-present
Curriculum in Toxicology & Environmental Medicine Executive Committee, 2018-2021
Deparment of Genetics Systems Immunology Faculty Search Committee, 2017
BBSP Graduate Admissions Committee for Bioinformatics & Computational Biology, 2016
School of Medicine Committee on Human Resources, 2014

Memberships in Professional Societies
Society of Toxicology, 2014-present
Genetics Society of America, 2014-present
American Thoracic Society, 2009-present
International Mammalian Genome Society, 2008-present

Research Statement
My long-standing research interest has been in gene-environment interactions (GxE) with environmental health hazards. My motivation stems from the desire to understand inter-individual variation in response to exposures associated with disease, and my training in both toxicology and genetics allows me to marry these two disciplines. My lab's research is focused on the identification of GxE that affect the development of common airway diseases like asthma and COPD, with the mindset that identifying GxE provides an important means to gain information about mechanisms underlying the association between exposure (e.g., to air pollution) and disease.

Our work to date has heavily relied upon use of genetically diverse mice as a model system to detect GxE, the logic being that by controlling the exposure side of the equation in these experiments, we can illuminate novel genetic signals which can then be examined in human studies. To that end, we have worked heavily with the Collaborative Cross (CC), a relatively new mouse genetics reference population that features abundant genetic variation in format of inbred lines. We have exposed CC lines to the common indoor allergen house dust mite, which is linked to onset and exacerbation of allergic asthma, and the secondary air pollutant ozone, which has also been linked the development of asthma. Using this type of approach, we have identified genes that regulate key aspects of response to allergen and ozone. This includes identification of the gene *Bpifb1* as a regulator of mucus levels in the lung after allergen exposure, and more recently a region on mouse chromosome 15 containing three genes (*Angpt1*, *Rspo2*, and *Oxr1*) that affects the degree of lung injury caused by ozone exposure. The results of these studies have been used to guide experiments and/or data analysis of human data; as an example, we are currently conducting an association analysis of genetic variants (SNPs) in ANGPT1, RSPO2, and OXR1 in subjects exposed to ozone at UNC (through the Center for Environmental Medicine, Asthma, and Lung Biology).

As part of this work, we have put considerable effort into developing statistical methods for analysis of Collaborative Cross data (in collaboration with Dr. William Valdar). This includes a detailed description of statistical power for QTL mapping studies in the CC (published in 2019) and an important study describing a novel statistical approach to infer the allelic series at QTL in multi-parental populations such as the Collaborative Cross and Diversity Outbred populations. These research products have enabled other researchers to more effectively use the Collaborative Cross, as well as other multi-parental populations, and analyze their data more rigorously.

A second emphasis of our recent work has been on developing and utilizing inhalation exposure systems to enable precise studies with rodents. In 2019, we built a state-of-the-art ozone exposure facility to facilitate large-scale studies in mice. This new facility makes UNC one of the few places in the country where controlled ozone exposure studies can be conducted in both humans (through the Center for Environmental Medicine, Asthma and Lung Biology) and rodents, allowing for cross-species comparisons. We are currently building an e-cigarette exposure system that we expect will be utilized by multiple labs on campus.
My vision for the future of the Kelada Lab is that we both continue to exploit the strengths of genetic reference populations like the Collaborative Cross and Diversity Outbred for GxE discovery and also expand our toolkit for GxE discovery and validation using human studies and human *in vitro* models. With respect to the latter goal, we have developed ambitious but feasible plans. First, we will compile and analyze data from multiple studies of ozone response in humans to enable a genome-wide association study. Second, we have begun to utilize primary human bronchial epithelial cells to study ozone response *in vitro*, and are working with Dr. Scott Randell (Director of the Marsico Lung Institute's Tissue Procurement and Cell Culture Core) to enable large scale studies with hundreds of donors so that we can identify QTL for ozone response.

TEACHING STATEMENT
My teaching activities span three different contexts, two in the classroom environment and one in the laboratory.

<u>Human Genetics and Genomics (GNET 647)</u>
I co-direct and lead the class by presenting lectures covering fundamental and cutting-edge topics in human genetics. To engage and involve students more directly, I lead a group discussion on evaluating causality for particular genetic variants in disease by evaluating recent research papers. This strategy requires students to examine the robustness of study findings, particularly by critiquing a weak paper, and to evaluate how researchers frame their arguments scientifically and persuasively. Student pairs also present recent papers on human genetics topics covered in the course; this strategy requires students to apply their understanding of human genetics principles and methods and to critique the authors' presentation and interpretation. I guide the students in the process of developing their ability to understand and critique the primary literature, and to apply fundamental concepts in human genetics to their own research.

<u>First Year Group (BBSP 901-902)</u>
Whereas GNET 647 is a typical didactic course, the course content of BBSP 901-902 is about professional skills development. The course has 3 foci: communication in scientific arenas, research ethics (i.e., the responsible conduct of research), and mentorship. Collectively, these three sets of topics address fundamental aspects of research and training. I personally value that we as educators at UNC stress these areas of training because they are critical, often undervalued in conventional curricula, and set the stage for successful careers for our students.

<u>Laboratory Teaching/Mentorship</u>
I mentor Ph.D. students, post-doctoral fellows and technical staff through daily interactions in the laboratory. My mentorship practice in this setting is based on two main ideas: (1) sharing my enthusiasm for learning and exploration in the laboratory, and (2) preparing trainees by exposing them to all aspects of the research endeavor so that they are aware of what a research intensive involves. In addition to stressing principles of rigor and reproducibility in data generation and analysis, I focus on developing strong communication skills (oral and written) because I know that this is often a make-or-break issue for scientists. I also require each trainee to generate an Individual Development Plan, which we review and revise annually based on the trainee's development and evolving future goals. Finally, I strive to incorporate diversity into my laboratory. I currently have one graduate and one under-graduate student from under-represented minorities in the sciences. Academically, I mentor trainees in three curricula, namely Genetics & Molecular Biology, Toxicology, and Bioinformatics & Computational Biology. These two aspects of diversity enhance my laboratory's training environment by providing collaborative and unique learning experiences that will benefit trainees throughout their careers.