CURRICULUM VITAE

PERSONAL INFORMATION

Martin T. Ferris, Ph.D.

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EDUCATION

- Postdoctoral Fellow, UNC-Chapel Hill, 2008-2013
- Ph.D., UNC-Chapel Hill, Chapel Hill NC, 2008, Biology
- B.S., University of Rochester, Rochester NY, 2002, Ecology and Evolutionary Biology

PROFESSIONAL EXPERIENCE AND EMPLOYMENT HISTORY

- Research Associate Professor 2021-present
- Associate Director, Systems Genetics Core Facility, University of North Carolina at Chapel Hill, July 2018-present
- Research Assistant Professor, Department of Genetics, University of North Carolina at Chapel Hill, April 2013 – present
- Member, Curriculum in Genetic and Molecular Biology, University of North Carolina, May 2014-present
- Member, Curriculum in Bioinformatics and Computational Biology, University of North Carolina, May 2014-present

HONORS AND AWARDS

2016   NIH early career reviewer, GHD study section

2012   UNC Office of Postdoctoral Affairs Service Award for Mentoring, 2012

2011   Travel Scholarship, Mouse Genetics 2011 Meeting, 2011

2011   UNC Office of Postdoctoral Affairs Service Award for Mentoring, 2011

2007   Tri-Beta Teaching Assistant Award, University of North Carolina, 2007

2004   Scholarship to attend NCSU Summer Institute in Statistical Genetics, 2004

1998-2002   Dean's List, The University of Rochester (3 semesters), 1998-2002

BIBLIOGRAPHY

BOOK CHAPTERS

3.   Bryant CD, **Ferris MT**, De Villena FPM, Damaj MI, Kumar V, Mulligan MK. Reduced complexity cross design for behavioral genetics In: Gerlai RT, editor. (ed) Molecular-genetic and statistical techniques for behavioral and neural research. 2018, pp.165–190.

2.   **Ferris MT**, Heise MT, and Baric RS. Host Genetics: It Is Not Just the Virus, Stupid. In Katze MG, Nathanson N editors. Viral Pathogenesis: From Basics to Systems Biology (3rd edition) 2016. Chapter 13.
https://doi.org/10.1016/B978-0-12-800964-2.00013-6

1.   **Ferris, M.T**. and M. T. Heise. 2014. Chapter 4: Quantitative Genetics in the Study of Virus-Induced Disease, in Advances in Virus Research, Elsevier, Oxford, United Kingdom. Volume 188. pp 193-227

REFERREED PAPERS
*Asterisk indicated Corresponding Author, underline indicates a trainee in my group

52.   Fay EJ, Balla KM, Roach SN, Shepherd FK, Putri DS, Wiggen TD, Goldstein SA, Pierson MJ, **Ferris MT**, Thefaine CE, Tucker A, Salnikov M, Cortez V, Compton SR, Kotenko SV, Hunter RC, Masopust D, Elde NC, Langlois RA. Natural rodent model of viral transmission reveals biological features of virus population dynamics. J Exp Med. 2022 Feb 7;219(2):e20211220. doi: 10.1084/jem.20211220. Epub 2021 Dec 27. PMID: 34958350

51.   Keele GR, Zhang T, Pham DT, Vincent M, Bell TA, Hock P, Shaw GD, Munger SC, deVillena FP, **Ferris MT**, Gygi SP, Churchill GA. Regulation of protein abundance in genetically diverse mouse populations. Cell Genomics 1(1) 100003 10/13/21 doi: 10.1016/j.xgen.2021.100003

50.   Graham JB, Swarts JL, Edwards KR, Voss KM, Green R, Jeng S, Miller DR, Mooney MA, McWeeney SK, **Ferris MT**, Pardo-Manuel de Villena F, Gale M Jr, Lund JM.Correlation of Regulatory T Cell Numbers with Disease Tolerance upon Virus Infection. Immunohorizons. 2021 Apr 23;5(4):157-169. doi: 10.4049/immunohorizons.2100009. PMID: 33893179

49.   Smeekens JM, Johnson-Weaver BT, Hinton AL, Azcarate-Peril MA, Moran TP, Immormino RM, Kesselring JR, Steinbach EC, Orgel KA, Staats HF, Burks AW, Mucha PJ, **Ferris MT**, Kulis MD. Fecal IgA, Antigen Absorption and Gut Microbiome Composition Are Associated With Food Antigen Sensitization in Genetically Susceptible Mice. Front Immunol. 2021 Jan 19, 11:599637.

48.   Graham JB, Swarts JL, Leist SR, Schäfer A, Menachery VD, Gralinski LE, Jeng S, Miller DR, Mooney MA, McWeeney SK, **Ferris MT**, Pardo-Manuel de Villena F, Heise MT, Baric RS, Lund JM. Baseline T cell immune phenotypes predict virologic and disease control upon SARS-CoV infection in Collaborative Cross mice. PLoS Pathog. 2021 Jan 29, 17(1).

47.   Sigmon JS, Blanchard MW, Baric RS, Bell TA, Brennan J, Brockmann GA, Burks AW, Calabrese JM, Caron KM, Cheney RE, Ciavatta D, Conlon F, Darr DB, Faber J, Franklin C, Gershon TR, Gralinski L, Gu B, Baines CH, Hagan RS, Heimsath EG, Heise MT, Hock P, Ideraabdullah F, Jennette JC, Kafri T, Kashfeen A, Kelada S, Kulis M, Kumar V, Linnertz C, Livraghi-Butrico A, Lloyd K, Loeser R, Lutz C, Lynch RM, Magnuson T, Matsushima GK, McMullan R, Miller D, Mohlke KL, Moy SS, Murphy C, Najarian M, O'Brien L, Palmer AA, Philpot BD, Randell S, Reinholdt L, Ren YY, Rockwood S, Rogala AR, Saraswatula A, Sasseti CM, Schisler JC, Schoenrock SA, Shaw G, Shorter JR, Smith CM, St. Pierre, CL, Tarantino LM, Threadgill DW, Valdar W, Vilen BJ, Wardwell K, Whitmire JK, Williams L, Zylka M, **Ferris MT***, McMillan L*, Pardo-Manuel de Villena F*. Content and performance of the MiniMUGA genotyping array, a new tool to improve rigor and reproducibility in mouse research. Genetics. 2020 Dec, 216(4):905-930.

46.   Noll KE, Whitmore AC, West A, McCarthy MK, Morrison CR, Plante KS, Hampton BK, Kollmus H, Pilzner C, Leist SR, Gralinski LE, Menachery VD, Schäfer A, Miller D, Shaw G, Mooney M, McWeeney S, Pardo-Manuel de Villena F, Schughart K, Morrison TE, Baric RS, **Ferris MT***, Heise MT*. Complex Genetic Architecture Underlies Regulation of Influenza-A-Virus-Specific Antibody Responses in the Collaborative Cross. Cell Rep 2020 Apr 28 31(4).

45.   Graham JB, Swarts JL, Menachery VD, Gralinski LE, Schafer A, Plante KS, Morrison CR, Voss KM, Green R, Choonoo G, Jeng S, Miller DR, Mooney MA,

McWeeney SK, **Ferris MT**, Pardo-Manuel de VIllena F, Gale M, Heise MT, Baric RS, Lund JM. Immune Predictors of Mortality After Ribonucleic Acid Virus Infection. J Infect Dis 2020 Mar 2 221(6)

44.   Smith CM, Proulx MK, Lai R, Kiritsy MC, Bell TA, Hock P, Pardo-Manuel de Villena F, **Ferris MT**, Baker RE, Behar SM, Sassetti CM. Functionally Overlapping Variants Control Tuberculosis Susceptibility in Collaborative Cross Mice. mBio 2019 Nov 26; 10(6)

43.   Noll KE, **Ferris MT**, Heise MT. The Collaborative Cross: A Systems Genetics Resource for Studying Host-Pathogen Interactions. Cell Host Microbe. 2019 Apr 10;25(4):484-498.

42.   Shorter JR, Najarian ML, Bell TA, Blanchard M, **Ferris MT**, Hock P, Kashfeen A, Kirchoff KE, Linnertz CL, Sigmon JS, Miller DR, McMillan L, Pardo-Manuel de Villena F. Whole Genome Sequencing and Progress Towards Full Inbreeding of the Mouse Collaborative Cross Population. G3 (Bethesda) 2019 Mar 11

41.   Orgel K, Smeekens JM, Ye P, Fotsch L, Guo R, Miller DR, Pardo-Manuel de Villena F, Burks AW, **Ferris MT***, Kulis MD*. Genetic diversity between mouse strains allows identification of the CC027/GeniUnc strain as an orally reactive model of peanut allergy. J Allergy Clin Immunol. 2019 Mar 143(3) 1027-1037.

40.   McMullan RC, **Ferris MT**, Bell TA, Menachery VD, Baric RS, Hua K, Pomp D, Smith-Ryan AE, de Villena FP. CC002.Unc females are mouse models of exercise-induced paradoxical fat responses. Physiol Rep. 2018 Jun 6(12)

39.   Maurizio PL, **Ferris MT**, Keele GR, Miller DR, Shaw GD, Whitmore AC, West A, Morrison CR, Noll KE, Plante KS, Cockrell AS, Threadgill DW, Pardo-Manuel de Villena F, Baric RS, Heise MT, Valdar W.Bayesian Diallel Analysis Reveals Mx1-Dependent and Mx1-Independent Effects on Response to Influenza A Virus in Mice. G3 (Bethesda) 2018 Feb 2; 8(2):427-445

38.   Graham JB, Swarts JL, Mooney M, Choonoo G, Jeng S, Miller DR, **Ferris MT**, McWeeney S, Lund JM. Extensive Homeostatic T Cell Phenotypic Variation within the Collaborative Cross. Cell Rep. 2017 Nov 21; 21(8):2313-2325

37.   Suwanmanee T#, **Ferris MT#**, Hu P, Gui T, Montgomery SA, Pardo-Manuel de Villena F, Kafri T. Towards personalized gene therapy; characterizing the host genetic control of lentiviral vector-mediated hepatic gene delivery. Mol Therap – Methods & Clinical Development. 2017 Apr 5; 5:83-92
#Both authors contributed equally to this work

36.   Srivastava A, Morgan AP, Najarian ML, Sarsani VK, Sigmon JS, Shorter JR, Kashfeen A, McMullan RC, Williams LH, Giusti-Rodríguez P, **Ferris MT**, Sullivan P, Hock P, Miller DR, Bell TA, McMillan L, Churchill GA, de Villena FP. The Genomes of The Collaborative Cross. GENETICS 2017 Jun; 206(2):537-556

35.   Gralinski LE, Menachery VD, Morgan AP, Totura AL, Beall A, Kocher J, Plante J, Harrison-Shostak DC, Schäfer A, Pardo-Manuel de Villena F, **Ferris MT**, Baric RS. Allelic variation in mouse Ticam2 contributes to SARS-CoV pathogenesis. G3 (Bethesda). 2017 Jun 7; 7(6):1653-1663.

34.   Green R, Wilkins C, Thomas S, Sekine A, Hendrick DM, Voss K, Ireton RC, Mooney M, Go JT, Choonoo G, Jeng S, de Villena FP, **Ferris MT**, McWeeney S, Gale M Jr. Oas1b-dependent Immune Transcriptional Profiles of West Nile Virus Infection in the Collaborative Cross. G3 (Bethesda)2017 Jun 7; 7(6):1665-1682

33.   The Collaborative Cross Resource for Systems Genetics Research of Infectious Diseases. Maurizio PL, **Ferris MT***. Methods Mol Biol. 2017;1488:579-596.

32.   RNA-Seq in the Collaborative Cross. Green R, Wilkins C, **Ferris MT**, Gale M Jr. Methods Mol Biol. 2017;1488:251-263.

31.   Transcriptional profiles of WNV neurovirulence in a genetically diverse Collaborative Cross population. Green R, Wilkins C, Thomas S, Sekine A, Ireton RC, **Ferris MT**, Hendrick DM, Voss K, Pardo-Manuel de Villena F, Baric RS, Heise MT, Gale M Jr. Genom Data. 2016 Oct 14;10:137-140.

30.   Identifying protective host gene expression signatures within the spleen during West Nile virus infection in the collaborative cross model. Green R, Wilkins C, Thomas S, Sekine A, Ireton RC, **Ferris MT**, Hendrick DM, Voss K, de Villena FP, Baric R, Heise M, Gale M Jr. Genom Data. 2016 Oct 14;10:114-117.

29.   A Mouse Model of Chronic West Nile Virus Disease. Graham JB, Swarts JL, Wilkins C, Thomas S, Green R, Sekine A, Voss KM, Ireton RC, Mooney M, Choonoo G, Miller DR, Treuting PM, Pardo Manuel de Villena F, **Ferris MT**, McWeeney S, Gale M Jr, Lund JM. PLoS Pathog. 2016 Nov 2;12(11):e1005996. doi: 10.1371/journal.ppat.1005996.

28.   Systems biology: A tool for charting the antiviral landscape. Bowen JR, **Ferris MT**, Suthar MS. Virus Res. 2016 Jan 12. pii: S0168-1702(16)30019-3.

27.   The Mouse Universal Genotyping Array: From Substrains to Subspecies. Morgan AP, Fu CP, Kao CY, Welsh CE, Didion JP, Yadgary L, Hyacinth L, **Ferris MT**, Bell TA, Miller DR, Giusti-Rodriguez P, Nonneman RJ, Cook KD, Whitmire JK, Gralinski

LE, Keller M, Attie AD, Churchill GA, Petkov P, Sullivan PF, Brennan JR, McMillan L, Pardo-Manuel de Villena F. G3 (Bethesda). 2015 Dec 18;6(2):263-79.

26.   γδ T Cells Play a Protective Role in Chikungunya Virus-Induced Disease. Long KM, **Ferris MT**, Whitmore AC, Montgomery SA, Thurlow LR, McGee CE, Rodriguez CA, Lim JK, Heise MT. J Virol. 2015 Oct 21;90(1):433-43.

25.   Genome Wide Identification of SARS-CoV Susceptibility Loci Using the Collaborative Cross. Gralinski LE, **Ferris MT**, Aylor DL, Whitmore AC, Green R, Frieman MB, Deming D, Menachery VD, Miller DR, Buus RJ, Bell TA, Churchill GA, Threadgill DW, Katze MG, McMillan L, Valdar W, Heise MT, Pardo-Manuel de Villena F, Baric RS. PLoS Genet. 2015 Oct 9;11(10) 2015 Oct.

24.   New Metrics for Evaluating Viral Respiratory Pathogenesis. Menachery VD, Gralinski LE, Baric RS, **Ferris MT***. PLoS One. 2015 Jun 26;10(6): eCollection 2015.

23.   Genetic diversity in the collaborative cross model recapitulates human west nile virus disease outcomes. Graham JB, Thomas S, Swarts J, McMillan AA, **Ferris MT**, Suthar MS, Treuting PM, Ireton R, Gale M Jr, Lund JM. MBio. 2015 May 5;6(3). pii: e00493-15. doi: 10.1128/mBio.00493-15.

22.   Lindesmith LC, **Ferris MT**, Mullan CW, Ferreira J, Debbink K, Swanstrom J, Richardson C, Goodwin RR, Baehner F, Mendelman PM, Bargatze RF, Baric RS. PLoS Med. 2015 Mar 24;12(3):e1001807. doi: 10.1371/journal.pmed.1001807. eCollection 2015 Mar.

21.   Rasmussen AL, Okumura A, **Ferris MT**, Green R, Feldmann F, Kelly SM, Scott DP, Safronetz D, Haddock E, LaCasse R, Thomas MJ, Sova P, Carter VS, Weiss JM, Miller DR, Shaw GD, Korth MJ, Heise MT, Baric RS, Pardo Manuel de Villena F, Feldmann H, and Katze MG. Host genetic diversity enables Ebola hemorrhagic fever pathogenesis and resistance. Science. Published online 30 October 2014 [DOI:10.1126/science.1259595]*

20.   Aevermann BD, Pickett BE, Kumar S, Klem EB, Agnihothram S, Askovich PS, Bankhead A, Bolles M, Carter V, Chang J, Clauss TRW, Dash P, Diercks AH, Eisfeld AJ, Ellis A, Fan S, **Ferris MT**, Gralinski LE, Green RR, Gritsenko MA, Hatta M, Heegel RA, Jacobs JM, Jeng S, Josset L, Kaiser SM, Kelly S, Law GL, Li C, Li J, Long C, Luna ML, Matzke M, McDermott J, Menachery V, Metz TO, Mitchell H, Monroe ME, Navarro G, Neumann G, Podyminogin RL, Purvine SO, Rosenberger CM, Sanders CJ, Schepmoes AA, Shukla AK, Sims A, Sova P, Tam VC, Tchitchek N, Thomas PG, Tilton SC, Totura A, Wang J, Webb-Robertson B, Wen J, Weiss JM, Yang F, Yount B, Zhang Q, McWeeney S, Smith RD, Waters KM, Kawaoka Y, Baric R, Aderem A, Katze MG, & Scheuermann RH. A comprehensive collection of systems biology data characterizing the host response to viral infection. Scientific Data 1, 2014 Oct 14

19.   Josset L, Tchitchek N, Gralinski LE, **Ferris MT**, Eisfeld AJ, Green RR, Thomas MJ, Tisoncik-Go J, Schroth GP, Kawaoka Y, Manuel de Villena FP, Baric RS, Heise MT, Peng X, Katze MG. Annotation of long non-coding RNAs expressed in Collaborative Cross founder mice in response to respiratory virus infection reveals a new class of interferon-stimulated transcripts. RNA Biol. 2014 Jun 12.

18.   Xiong H, Morrison J, **Ferris MT**, Gralinski LE, Whitmore AC, Green R, Thomas MJ, Tisoncik-Go J, Schroth GP, Pardo-Manuel de Villena F, Baric RS, Heise MT, Peng X, Katze MG. Genomic Profiling of Collaborative Cross Founder Mice Infected with Respiratory Viruses Reveals Novel Transcripts and Infection-Related Strain-Specific Gene and Isoform Expression. G3. 2014 Jun 5. PMC4132174

17.   Schafer A, Baric RS, **Ferris MT**. Systems approaches to coronavirus pathogenesis. Curr Opin Virol. 2014 May 16; 6C:61-69. PMC4076299

16.   Debbink K, Lindesmith LC, **Ferris MT**, Swanstrom J, Beltramello M, Corti D, Lanzavecchia A, Baric RS. Within Host Evolution Results in Antigenically Distinct GII.4 Noroviruses. J Virol. 2014 Mar 19. PMC4054459

15.   **Ferris MT**, Heise MT. Quantitative Genetics in the Study of Virus-Induced Disease. Advances in Virus Research. 2014;88:193-225.

14.   Mechanisms of SARS-CoV Induced Acute Lung Injury. Gralinski LE, Bankhead III A, Jeng S, Menachery VD, Proll S, Belisle SE, Matzke M, Webb-Robertson BM, Luna ML, Shukla AK, **Ferris MT**, Bolles M, Chang JH, Aicher LD, Waters KM, Smith RD, Metz TO, Law GL, Katze MG, McWeeney S, Baric, RS. *mBio.* 2013. doi:10.1128/mBio.00271-13.

13.   Specific mutations in H5N1 mainly impact the magnitude and velocity of the host response in mice. Tchitchek N, Eisfeld AJ, Tisoncik-Go J, Josset L, Gralinski LE, Bécavin C, Tilton SC, Webb-Robertson BJ, **Ferris MT**, Totura AL, Li C, Neumann G, Metz TO, Smith RD, Waters KM, Baric R, Kawaoka Y, Katze MG.BMC Syst Biol. 2013 Jul 29;7(1):69.

12.   Long KM, Whitmore AC, **Ferris MT**, Sempowski GD, McGee C, Trollinger B, Gunn B, Heise MT. Dendritic cell immunoreceptor regulates Chikungunya virus pathogenesis in mice. J. Virol 2013 May; 87(10):5697-5706. PMC3648201

11.   **Ferris MT**, Aylor DL, Bottomly D, Whitmore AC, Aicher LD, Bell TA, Bradel-Tretheway B, Bryan JT, Buus RJ, Gralinski LE, Haagmans BL, McMillan L, Miller DR, Rosenzweig E, Valdar W, Wang J, Churchill GA, Threadgill DW, McWeeney SK, Katze MG, deVillena FP, Baric RS, Heise MT. Modeling host genetic regulation of Influenza pathogenesis in the Collaborative Cross. PLOS Pathog. 2013 Feb 9(2). PMC3585141

10.   Wollish AC, **Ferris MT**, Blevins L, Loo Y, Gale M, Heise MT. An attenuating mutation in a neurovirlent Sindbis virus stain interacts with the IPS-1 signaling pathway in vivo. Virology, 2012 Oct 16. DOI: S0042-6822(12)00449-7.

9.   Bottomly D, **Ferris MT**, Aicher LD, Rosenzweig E, Whitmore A, Aylor DL, Haagmans BL, Gralinski LE, Bradel-Tretheway BG, Bryan JT, Threadgill DW, de Villena FP, Baric RS, Katze MG, Heise M, McWeeney SK. Expression quantitative trait Loci for extreme host response to influenza a in pre-collaborative cross mice. G3 2012 Feb; 2(2):213-221.

8.   Collaborative Cross Consortium. The genome architecture of the Collaborative Cross mouse genetic reference population. Gentics. 2012 Feb; 190(2): 389-401.

7.   Peng X, Gralinski L, **Ferris MT**, Frieman MB, Thomas MJ, Proll S, Korth MJ, Tisoncik JR, Heise M, Luo S, Schroth GP, Tumpey TM, Li C, Kawaoka Y, Baric RS, Katze MG. Integrative deep sequencing of the mouse lung transcriptome reveals differential expression of diverse classes of small RNAs in response to respiratory virus infection. MBio 2011 Nov 15; 2(6).

6.   Bolles M, Deming D, Long K, Agnihothram S, Whitmore A, **Ferris M**, Funkhouser W, Gralinski L, Totura A, Heise M, Baric RS. A Double-inactivated Severe Acute Respiratory Syndrome Coronavirus Vaccine Provides Incomplete Protection in Mice and Induces Increased Eosinophillic Proinflammatory Pulmonary response upon Challenge. J Virol 2011 85(23):12201-12215.

5.   Aylor DL, Valdar W, Foulds-Mathes W, Buus RJ, Verdugo RA, Baric RS, **Ferris MT**, Frelinger JA, Heise M, Frieman MB, Gralinski LE, Bell TA, Didion JD, Hua K, Nehrenberg DL, Powell CL, Steigerwalt J, Xie Y, Kelada SN, Collins FS, Yang IV, Schwartz DA, Branstetter LA, Chesler EJ, Miller DR, Spence J, Liu EY, McMillan L, Sarkar A, Wang J, Wang W, Zhang Q, Broman KW, Korstanje R, Durrant C, Mott R, Iraqi FA, Pomp D, Threadgill D, de Villena FP, Churchill GA. Genetic analysis of complex traits in the emerging Collaborative Cross. Genome Res. 2011. 21(8):1213-1222

4.   Sheahan T, Whitmore A, Long K, **Ferris M**, Rockx B, Funkhouser W, Donaldson E, Gralinski L, Collier M, Heise M, Davis N, Johnston R, Baric RS. Successful vaccination strategies that protect aged mice from lethal challenge from influenza virus and heterologous severe acutre respiratory syndrome coronavirus. Journal of Virology 2011. 85(1):217-230

3.   Peng X, Gralinski L, Armour CD, **Ferris MT**, Thomas MJ, Proll S, Dradel-Tretheway BG, Korth MJ, Castle JC, Biery MC, Bouzek HK, Haynor DR, Frieman MB, Heise M, Raymond CK, Baric RS, Katze MG. Unique signatures of long noncoding RNA expression in response to virus infection and altered innate immune signaling. MBio 2010: Oct 26 1(5)

2.   Rokyta DR, Beisel CT, Joyce P, **Ferris MT**, Burch CL, and Wichman HA. Beneficial fitness effects are not exponential for two viruses. Journal of Molecular Evolution 2008: 67(4): 368-376.

1.   **Ferris MT**, Joyce P, and Burch CL. 2007. High frequency of mutations that expand the host range of an RNA virus. Genetics 176: 1013-1022.

OTHER

7.   Schäfer A, Gralinski LE, Leist SR, <u>Hampton BK</u>, Mooney MA, Jensen KL, Graham RL, Agnihothram S, Jeng S, Chamberlin S, Bell TA, Scobey T, VanBlargan LA, Thackray LB, Hock P, Miller DR, Shaw GD, Diamond MS, de Villena FP, McWeeney SK, Heise MT, Menachery VD, **Ferris MT***, Baric RS*. Complex Genetic Regulation of SARS-CoV2 and SARS-like CoV Pathogenesis. BioRxiv 2021.05.14.444205

6.   <u>Hampton BK</u>, Jensen KL, Whitmore AC, Linnertz CL, Maurizio P, Miller DR, Morrison CR, <u>Noll KE</u>, Plante KS, Shaw GD, West A, Baric RS, de Villena, FP, Heise MT*, **Ferris MT***. Genetic regulation of homeostatic immune architecture in the lungs of Collaborative Cross mice. BioRxiv 2021.04.09.439180

5.   Biererle JM, Yao EJ, Goldstein SI, Scotellaro JL, Sena KD, Linnertz CD, Young EE, Peltz G, Emili A, **Ferris MT**, Bryant CD. Genetic basis of thermal nociceptive sensitivity and brain weight in a BALB/c reduced complexity cross. Accepted (1/22) Molecular Pain.

4.   Smith CM, Baker RE, Proulx MK, Mishra BB, Long JE, Prk SW, Lee H, Kiritsy MC, Bellerose MM, Olive AJ, Murphy KC, Papavinasasundaram K, Boehm FJ, Reames CJ, Meade RK, <u>Hampton BK</u>, Linnertz CL, Shaw GD, Hock P, Bell TA, Ehrt S, Schnappinger D, de Villena FP, **Ferris MT**, Ioerger TR, Sassetti CM. Host-pathogen genetic interactions underlie tuberculosis susceptibility in genetically diverse mice. Accepted eLife (2021/01)

3.   Plante JA, Plante KS, Gralinski LE, Beall A, **Ferris MT**, Bottomly D, Green R, McWeeney SK, Heise MT, Baric RS, Menachery VD. Mucin 4 Protects Female Mice from Coronavirus Pathogenesis BioRxiv 2022.02.19.957

2.   Mattocks MD, Plante KS, Fritsch EJ, Baric RS, **Ferris MT**, Heise MT, Lazear HM. Zika virus infection in Collaborative Cross mice. BioRxiv 695510

1.   Guest Editor, Host genetic regulation of immune-based and infectious diseases: Introduction to mammalian genome special issue: genetics of infectious disease. Ferris MT, Hood DW. Mamm Genome 2018 Aug 29(7-8): 365-366.

INVITED PRESENTATIONS

- B.A.A.G.s workshop "Genetic control of homeostasis in the Collaborative Cross mouse model", May 23rd, 2022

- NIAID Genetically Engineered Mouse Models to Accelerate HIV Vaccine Development Workshop "The Collaborative Cross as a resource for studying respiratory virus pathogenesis and immunity", March 31, 2021

- University of Vermont, Vermont Center for Immunobiology and Infectious Diseases "Genetic control of immune homeostasis in the Collaborative Cross mouse model", December 19, 2020

- Tectonic Plates, Alamance County's Science Café "CoVID and research: fast is slow and slow is fast", November 10, 2020

- NC RTP Lab Animal Medicine Residency Didactic program "Mouse Genetic Characterization, QC and Genetic Mapping", March 2, 2020

- Improving the Assembly of Genetically Diverse Mouse Genomes, Nov 11 2019, BioNano Genomics Informational Seminar; Lineberger Comprehensive Cancer Center

- Complex genetic regulation of gene therapy and immune homeostasis, Oct 1 2018, UNC Cell Biology and Physiology seminar series.

- Complex genetic regulation of gene therapy and immune homeostasis, April 8, 2019, Texas A&M University Genetics and Genomics Seminar series.

- Collaborative Cross Mouse Models, March 12, 2019, NC Academy of Laboratory Animal Medicine (seminar)

- 2017 The Scripps Research Institute "Genetic Regulation of Multiple Aspects of Host Immunity"

- 2016 Emory University "Lessons in Immunogenetics: Complex complexity"

- 2015 Complex Trait Consortium "Genetic Control of Extreme Influenza Disease"

- 2015 NIEHS, "Genetic Diversity in Ebola Response"

- 2014 Christopher Newport University, "Simple viruses causing complex diseases"

- 2014   Oregon Health Sciences University**, "**Systems genetics and viral pathogenesis: The Collaborative Cross model of host immune responses

- 2013   University of Massachusetts Medical School, "Systems approaches uncover novel host genetic regulation of respiratory pathogens"

- 2013   Saint Louis University, "Systems approaches uncover novel host genetic regulation of respiratory pathogens"

- 2010   Oregon Health Sciences University, "New insight into influenza pathogenesis using the Collaborative Cross."

- 2010   Rutgers University Department of Ecology, Evolution and Natural Resources Departmental Seminar "Dissecting the complex genetic architecture of virus-host interactions during influenza virus infection."

- 2009   UNC Department of Microbiology and Immunology Departmental Seminar "Complex host genetic contributions to influenza infection"

TEACHING RECORD

- Instructor, GNET645/BCB645: Quantitative Genetics of Complex Traits, University of North Carolina at Chapel Hill, Spring 2019-present (BCB crosslisting as of 2021)

- Lecturer: Host genetics of pathogenesis, MCRO640 Microbial Pathogenesis II, University of North Carolina, Spring 2008-2018

- UNC Biological and Biomedical Sciences Program student mentor. 2011-2012

- Teaching Assistant, Department of Biology, UNC-CH, Introduction to Evolution and Ecology; Evolutionary Mechanisms. 2002-2007

- Course Developer, BIOL842 "Teaching and Course Development," University of North Carolina, Chapel Hill. 2006

MENTORING/GRADUATE TRAINING

Graduate Students

Ellen Risemberg	2021-Present (Curriculum in Bioinformatics and Computational Biology [BCB]; Co-Mentored with Dr. Will Valdar)
Marta Cruz Cisneros	2019-Present (Curriculum in Genetics and Molecular Biology [GMB]; Co-Mentored with Dr. Mark Heise)
Brea Hampton	2017-Present (Curriculum in Genetics and Molecular Biology [GMB]; Student Co-Mentored with Dr. Mark Heise)
Kelsey Noll	2015-2020 (Microbiology & Immunology; Student Co-Mentored with Dr. Mark Heise)
	-Currently: Fellow at IMPACT Pharmaceuticals

Dissertation Committees

Richard Green	2022-Present	University of Washington, Advisors: Peter Tarczy-Hornoch, Michael Gale
Logan Whitehouse	2021-Present	BCB; Advisor: Dan Schreider (MTF is Committee chair)
Hang Su	2020-Present	BCB; Advisor: Leonard Mc Millan
John Sebastian Sigmon	2020-Present	Computer Science; Advisor: Leonard McMillan
Christiann Hill	2018-Present	Neuroscience; Advisor: Lisa Tarantino
Anwica Kashfeen	2020-2021	Computer Science; Advisor: Leonard McMillan
Yanwei Cai	2017-2020	BCB; Advisor: Will Valdar
Amelia Clayshulte	2015-2017	GMB; Advisor: Fernando Pardo-Manuel de Villena
Anne Beall	2014-2017	Microbiology and Immunology, Advisor: Ralph Baric
Heather Vincent	2014-2017	Microbiology and Immunology; Advisor, Nat Moorman

Faculty Mentoring

Johanna Smeekens, PhD 2022-present   Department of Pediatrics

Sam Wolff, PhD   2020-present   Department of Genetics

GRANTS

Active

- NIH R01AI57253. 9/25/2020-8/31/2025. Genetic Analysis of COVID-19 susceptibility and resistance determinants in the Collaborative Cross (PI: Dr. Mark Heise, PhD). $748,384. 5% effort, Co-Investigator.

- NIH U01DA050243. 9/1/2020-6/30/2025. A reduced complexity cross in BALB/C substrains to identify the genetic basis of oxycodone dependence phenotypes (PI: Dr. Camron Bryant, PhD, Boston University). $602,148. 5% effort, Co-Investigator.

- NIH R21DA052171. Rapid identification of cocaine sensitivity genes using a novel reduced complexity cross. Co-Investigator (PI. Dr. Lisa Tarantino, PhD). 2020-present

- NIH U01AI149644. Respiratory Virus Vaccine and Adjuvant Exploration. (PI: Dr. Ralph S Baric, PhD) Subcontract. $144,071 Directs. 2019-present

- NIH U42OD010924 A Carolina Center to Characterize and Maintain Mutant Mice. Co-Investigator (PI Dr. Terry Magnuson, PhD). 2020-present

- NIH P01AI132130. Systems Genetics of Tuberculosis. Co-Director, Core A (PI: Dr. Chris Sassetti, PhD UMass School of Medicine). $225,000 Directs. 2017-present

- NIH U19 AI100625. Systems Immunogenetics of Biodefense Pathogens in the Collaborative Cross. Co-Director Core B (PIs: Drs Mark T. Heise, Ralph S. Baric, PhD). $250,188 Directs. 2012-present

Completed

- NIH R01 HL128119. Lentiviral Vector-Based Gene Therapy and the Host Genetic Background. Co-Investigator (PI Dr. Tal Kafri, UNC). $127,516 Directs. 2015-2019

- NIH U19AI109761 CETR. Diagnostic and Prognostic Biomarkers for Viral Severe Lung Disease. Co-Investigator (PI: Ian Lipkin, Columbia Univ). 2014-2019

- NIH R01 ES024965. Gene-Environment Interactions with Ozone in Experimental Asthma. Co-Investigator (PI Dr. Samir Kelada, UNC) 2015-2018

- NIH R21 AI119933. Host Genetic Control of Chikungunya Virus-induced Arthritis. Co-Investigator (PI. Mark Heise). 2016-2018

- NIH R21 AI113485. Identifying host genetic determinants that regulate dendritic cell activation. Co-Investigator (PI Dr. Mehul Suthar, Emory University). 2015-2017

- NIH U54 Pacific Northwest Regional Center for Excellence in Biodefense and Emerging Infectious Diseases. Project 3.1: Systems Pathogenomics of Acute Respiratory Virus Infection (Co-Investigator). 2009-2014

- F32 NSRA Postdoctoral Fellowship AI084322-01 "Investigation host genetic polymorphisms contributing to influenza virus disease". 2011-2009

- NSF Doctoral Dissertation Improvement Grant DEB-0709823 "Characteristics of viral host niche evolution". 2007-2008

PROFESSIONAL SOCIETIES AND SERVICE

- Ad hoc reviewer American Institute of Biological Sciences 2/2022-present
- NIH Exploratory Data Science Methods and Algorithm Development Special Review Panel (ZAI1 SB-x(J1), 2021/10
- NIH Computational Models of Immunity Special Review Panel (11/2019)
- Member (2013-present, Chair of Nominations and Elections Committee (2019)) International Mammalian Genome Society
- Member (2015-present, GSA working group on Science Advocacy (2018)) Genetics Society of America
- NIH CSR Anonymization Study reviewer (2019)
- NIH GHD study section, Early Career Reviewer (2016)
- Graduate Student Admission, University of North Carolina at Chapel Hill, 'Q' committee 2016-2018
- Guest Editor, Mammalian Genomes 2016-2018
- Ad hoc NSF grant review, 2008-2010

- Ad hoc reviewer: PLoS Genetics, PLoS Pathogens, Genetics, G3, Nature Genetics, Journal of Pediatric Infectious Diseases, BMC Genetics, BMC

Genomics, PLoS Neglected Tropical Diseases, PLoS One, Journal of Infection and Public Health, FEMS Microbiology and Immunology, Trends in Microbiology, Pathogens and Disease, Frontiers Cellular and Infection Microbiology