ANDREW PARKER MORGAN

PERSONAL INFORMATION

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EDUCATION

2019–2023 Residency · Duke University Hospital
Internal medicine and pediatrics

2010–2019 MD · University of North Carolina at Chapel Hill
Dual-degree student in Medical Scientist Training Program (MSTP)

2012–2017 PhD · University of North Carolina at Chapel Hill
Curriculum in Bioinformatics & Computational Biology · Department of Genetics

2005–2009 BS · University of North Carolina at Chapel Hill
Biostatistics; biology · School of Public Health

HONORS AND AWARDS

2023 YT Chen Award, for excellence in patient care in pediatrics
James A Stockman Award, for contribution to resident education in pediatrics

2021 William Bell Award, for clinical diagnosis in pediatrics

2019 Isaac Hall Manning Award, for medical student scholarship and leadership

2017 Dean's Distinguished Dissertation Award, for best dissertation in biological sciences

2016 Terry Magnuson Award, for a senior student in Bioinformatics & Computational Biology curriculum

2015 Excellent student talk, 29th International Mammalian Genome Conference, Yokohama, Japan

2014 Pillsbury Award, best oral presentation in basic sciences, UNC Medical Student Research Day
Excellent student talk, 28th International Mammalian Genome Conference, Bar Harbor, Maine

2013 Best student talk, UNC Department of Genetics Scientific Retreat
Excellent student talk, 27th International Mammalian Genome Conference, Salamanca, Spain
Oxford Summer School in Computational Biology, invited participant (top 5% of applicants globally)

2009 Phi Beta Kappa, inductee
J.N. Couch Award, for excellence in plant biology research
Delta Omega Award, top undergraduate student in biostatistics

GRANTS AND FELLOWSHIPS

2014–2018 Ruth L. Kirschstein NRSA Inidividual Predoctoral Fellowship
National Institute of Mental Health F30MH103925
Sponsor: Fernando Pardo-Manuel de Villena, PhD

2012–2013 Bioinformatics & Computational Biology Training Grant
National Institute of General Medical Sciences T32GM067553
PI: Timothy Elston, PhD

2010–2011 Medical Scientist Training Program Training Grant
National Institute of General Medical Sciences T32GM008719
PI: Eugene Orringer, MD

SERVICE

2015– *Ad hoc* reviewer: *Genetics*, *G3*, *Scientific Data*, *Frontiers in Epidemiology*

2014–2016 Admissions committee, UNC Medical Scientist Training Program

2015–2016 Chief operating officer, UNC Student Health Action Coalition

2013–2015 Data and privacy officer, UNC Student Health Action Coalition

2012–2013 Medical (free) clinic director, UNC Student Health Action Coalition

TEACHING

2015 Systems Genetics Workshop, 29th IMGC, Yokohama, Japan
Guest lecture, graduate-level population genomics course (BCB 722)

2014 Academic coach (bioinformatics), UNC Initiative for Maximizing Student Diversity

2013 Teaching assistant for BCB 720: Principles of statistical modelling

PUBLICATIONS

2023 Jones K, **Morgan AP**, Whang A, Feeney CD (2023) Fever, rash and abdominal pain in a 12-year-old boy. *Pediatr Rev*, in press.

Siebert A, Brake, MA, Verbeek SC, Johnston AJ, **Morgan AP**, Cleuren AC, Jurek AM, Schneider CD, Germain DM, Battistuzzi FU, Zhu G, Miller DR, Johnsen JM, Pardo-Manuel de Villena F, Rondina MT, Westrick R (2023) Identification of genomic loci regulating platelet plasminogen activator inhibitor-1 in mice. *J Thromb Haemost*, in press. 10.1016/j.jtha.2023.06.018

Rao P, Jordan KA, Burrows H, **Morgan AP**, Beck Dallaghan GL, Zwemer E (2023) Association between in-training exam scores and clinical exposure during the COVID-19 pandemic. *Acad Pediatr*, in press. 10.1016/j.acap.2023.05.014

Morgan AP, DeRaddo JS, Atkins C, Campbell MJ (2023) Streptococcal endarteritis associated with severe aortic coarctation. *Prog Pediatr Cardiol* **70**: 101657. 10.1016/j.ppedcard.2023.101657

2022 **Morgan AP***, Hughes JJ*, Didion JP, Jolley WJ, Campbell KJ, Threadgill DW, Bonhomme F, Searle JB, Pardo-Manuel de Villena F (2022) Population structure and inbreeding in wild house mice (*Mus musculus*) at different geographic scales. *Heredity* **129**: 183–194. 10.1038/s41437-022-00551-z

2021 Brazeau NF, Mitchell CL, **Morgan AP**, Deutsch-Feldman M, Watson OJ, Thwai KL, Gelabert P, van Dorp L, Keeler CY, Waltmann A, Emch M, Gartner V, Redelings B, Wray GA, Mwandagalirwa MK, Tshefu AK, Likwela JL, Edwards JK, Verity R, Parr JB, Meshnick SR, Juliano JJ (2021) The epidemiology of *Plasmodium vivax* among adults in the Democratic Republic of the Congo. *Nat Commun* **12**: 4169. 10.1038/s41467-021-24216-3

Shrestha B, Shah Z, **Morgan AP**, Saingam P, Chaisatit C, Chaorattanakawee S, Praditpol C, Boonyalai N, Lertsethtakarn P, Wojnarski M, Deutsch-Feldman M, Adams M, Sea D, Chann S, Tyner SD, Lanteri CA, Spring MD, Saunders DL, Smith PL, Lon C, Gosi P, Sok S, Satharath P, Rekol H, Lek D, Vesely BA, Lin JT, Waters NC, Takala-Harrison S (2021) Distribution and Temporal Dynamics of Plasmodium falciparum Chloroquine Resistance Transporter Mutations Associated With Piperaquine Resistance in Northern Cambodia. *J Infect Dis* **224**: 1077–1085. 10.1093/infdis/jiab055

2020 Daughety MM, **Morgan AP**, Frost E, Kao C, Hwang J, Tobin R, Patel B, Fuller M, Welsby I, Ortel TL (2020) COVID-19 associated coagulopathy: Thrombosis, hemorrhage and mortality rates with an escalated-dose thromboprophylaxis strategy. *Thromb Res* **196**: 483–485. 10.1016/j.thromres.2020.10.004

Mukaj A, Pialek J, Fotopulosova V, **Morgan AP**, Odenthal-Hesse L, Parvanov ED, Forejt J (2020) *Prdm9* inter-subspecific interactions in hybrid male sterility of house mouse. *Mol Biol Evol* **37**: 3423-3438. 10.1093/molbev/msaa167

Verity R, Aydemir O, Brazeau NF, Watson OJ, Hathaway NJ, Mwandagalirwa MK, Marsh PW, Thwai K, Fulton T, Denton M, **Morgan AP**, Parr JB, Tumwebaze PK, Conrad M, Rosenthal PJ, Ishengoma DS, Ngondi J, Gutman J, Mulenga M, Norris DE, Moss WJ, Mensah BA, Myers-Hansen JL, Ghansah A, Tshefu AK, Ghani AC, Meshnick SR, Bailey JA, Juliano JJ (2020) The impact of antimalarial resistance on the genetic structure of *Plasmodium falciparum* in the DRC. *Nat Commun* **11**: 2107. 10.1038/s41467-020-15779-8

Morgan AP*, Brazeau NF*, Ngasala B, Mhamilawa LE, Denton M, Msellem M, Morris U, Filer DL, Aydemir O, Bailey JA, Parr JB, Martensson A, Bjorkman A, Juliano JJ (2020) Falciparum malaria from coastal Tanzania and Zanzibar remains highly connected despite effective control efforts on the archipelago. *Malaria J* **19**: 47. 10.1186/s12936-020-3137-8

2019 **Morgan AP**, Bell TA, Crowley JJ, Pardo-Manuel de Villena F (2019) Instability of the pseudoautosomal region in house mice. *Genetics* **212**: 469–487. 10.1534/genetics.119.302232

2017 **Morgan AP**, Pardo-Manuel de Villena F (2017) Sequence and structural diversity of mouse Y chromosomes. *Mol Biol Evol* **34**: 3186–3204. 10.1093/molbev/msx250

Rosshart SP, Vassallo BG, Angeletti D, Hutchinson DS, **Morgan AP**, Hickman HD, Ajami NJ, Petrosino JF, Pardo-Manuel de Villena F, Yewdell JW, Rehermann B (2017) Wild mouse gut microbiota promotes host fitness and improves disease resistance. *Cell* **171**: 1015–1028. 10.1016/j.cell.2017.09.016

Makhanova NA, **Morgan AP**, Kayashima Y, Makhanov M, Hiller S, Zhilicheva S, Xu L, Pardo-Manuel de Villena F, Maeda N (2017) Genetic architecture of atherosclerosis dissected by QTL analyses in three F2 intercrosses of apolipoprotein E-null mice on C57BL6/J, DBA/2J and 129S6/SvEvTac backgrounds. *PLoS One* **12**: e0182882. 10.1371/journal.pone.0182882

Gralinski LE, Menachery VD, **Morgan AP**, Totura A, Beall A, Kocher J, Plante J, Harrison-Shostak CD, Schäfer A, Pardo Manuel de Villena F, Ferris MT, Baric RS (2017) Allelic variation in mouse Ticam2 contributes to SARS-CoV pathogenesis. *G3* **7**: 1653–1663. 10.1534/g3.117.041434

Morgan AP, Gatti DM, Keane TM, Galante RJ, Pack AI, Mott R, Churchill GA, Pardo-Manuel de Villena F (2017) Structural variation shapes the landscape of meiotic recombination in mouse. *Genetics* **206**: 603–619. 10.1534/genetics.116.197988

Srivastava A*, **Morgan AP***, Najarian M*, Sarsani VK, Sigmon JS, Shorter JR, Kashfeen A, Giusti-Rodgriguez P, Ferris MT, Sullivan PF, Miller DR, Bell TA, McMillan L, Churchill GA, Pardo-Manuel de Villena F (2017) The genomes of the mouse Collaborative Cross. *Genetics* **206**: 537–556. 10.1534/genetics.116.198838

Shorter JR, Odet F, Aylor DL, Pan W, Kao CY, Fu CP, **Morgan AP**, Greenstein S, Bell TA, Stevans AM, Feathers RW, Patel S, Cates SE, Shaw GD, Ahmed S, Miller DR, Chesler EJ, McMillian L, OBrien DA, Pardo-Manuel de Villena F (2017) Male infertility is responsible for nearly half of the strain extinction observed in the Collaborative Cross. *Genetics***206**: 537–556. 10.1534/genetics.116.199596

2016

Morgan AP*, Didion JP*, Doran AG, Holt JM, McMillan L, Keane TM, Pardo-Manuel de Villena F (2016) Whole genome sequence of two wild-derived *Mus musculus domesticus* inbred strains, LEWES/EiJ and ZALENDE/EiJ, with different diploid numbers. *G3* **6**: 4211–4216. 10.1534/g3.116.034751

Chesler EJ, Gatti DM, **Morgan AP**, Strobel M, Trepanier L, Oberbeck D, McWeeney S, Hitzemann R, Ferris M, McMullan R, Clayshulte A, Bell TA, Pardo-Manuel de Villena F, Churchill GA (2016) Diversity Outbred Mice at 21: Maintaining allelic variation in the face of selection. *G3* **6**:3893–3902. 10.1534/g3.116.035527

Morgan AP, Holt JM, McMullan RC, Bell TA, Clayshulte AMF, Didion JP, Yadgary L, Thybert D, Odom DT, Flicek PW, McMillan L, Pardo-Manuel de Villena F (2016) The evolutionary fates of a large segmental duplication in mouse. *Genetics* **204**: 267–2885. 10.1534/genetics.116.191007

Didion JP*, **Morgan AP***, *...(39 others)...*, Pardo-Manuel de Villena F (2016) *R2d2* drives selfish sweeps in the house mouse. *Mol Biol Evol* **33**: 1381–1395. 10.1093/molbev/msw036

2015

Morgan AP (2015) `argyle`: an `R` package for analysis of Illumina genotyping arrays. *G3* **6**: 281–286. 10.1534/g3.115.023739

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 (2015) The Mouse Universal Genotyping Array: from substrains to subspecies. *G3* **6**: 263–279. 10.1534/g3.115.022087

Morgan AP, Welsh CE (2015) Informatics resources for the Collaborative Cross and related mouse populations [review]. *Mamm Genome* **26**: 521–539. 10.1007/s00335-015-9581-z

Didion JP, **Morgan AP**, *...(33 others)...*, Pardo-Manuel de Villena F. (2015) A multi-megabase copy number gain causes maternal transmission ratio distortion on mouse chromosome 2. *PLoS Genet* **11**: e1004850. 10.1371/journal.pgen.1004850

Crowley JJ, Zhabotynsky V, Sun W, *...(35 others)...*, **Morgan AP**, McMillan L, Sullivan PF, Pardo-Manuel de Villena F. (2015) Analyses of allele-specific gene expression in highly divergent mouse crosses identifies pervasive allelic imbalance. *Nat Genet* **47**: 353–360. 10.1038/ng.3222

2014

Morgan AP*, Crowley JJ*, Nonneman RJ, Quackenbush CR, Miller CN, Ryan AK, Bogue MA, Paredes SH, Yourstone S, Carroll IM, Kawula TH, Bower MA, Sartor RB, Sullivan PF (2014) The antipsychotic olanzapine interacts with the gut microbiome to cause weight gain in mouse. *PLoS One* **9**: e115225. 10.1371/journal.pone.0115225

Liu EY*, **Morgan AP***, Chesler EJ, Wang W, Churchill GA, Pardo-Manuel de Villena F (2014) High-resolution sex-specific linkage maps of the mouse reveal polarized distribution of crossovers in male germline. *Genetics* **197**: 91–106. 10.1534/genetics.114.161653

Rogala AR, **Morgan AP**, Christensen AM, Gooch TJ, Bell TA, Miller DR, Godfrey VL, Pardo-Manuel de Villena F (2014) The Collaborative Cross as a resource for modeling human disease: CC011/Unc, a new mouse model for spontaneous colitis. *Mamm Genome* **25**: 95-108. 10.1007/s00335-013-9499-2