

ANDREW PARKER MORGAN

PERSONAL INFORMATION

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EDUCATION

2019– 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

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 Individual 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 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

- 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*, in press.
- 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, Tshetu 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](https://doi.org/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](https://doi.org/10.1093/infdis/jiab055)
- 2020 Daugherty 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](https://doi.org/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**: 167. [10.1093/molbev/msaa167](https://doi.org/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, Tshetu 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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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, Rehmann B (2017) Wild mouse gut microbiota promotes host fitness and improves disease resistance. *Cell* **171**: 1015–1028. [10.1016/j.cell.2017.09.016](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/10.1534/genetics.116.197988)
- Srivastava A*, **Morgan AP***, Najarian M*, Sarsani VK, Sigmon JS, Shorter JR, Kashfeen A, Giusti-Rodriguez 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](https://doi.org/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, McMillan L, O'Brien 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](https://doi.org/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 ZALLENDE/EiJ, with different diploid numbers. *G3* **6**: 4211–4216. [10.1534/g3.116.034751](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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: CCo11/Unc, a new mouse model for spontaneous colitis. *Mamm Genome* **25**: 95–108. [10.1007/s00335-013-9499-2](https://doi.org/10.1007/s00335-013-9499-2)