

# ANDREW PARKER MORGAN

## PERSONAL INFORMATION

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## EDUCATION

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

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*  
 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

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](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* msaa167. [10.1093/molbev/msaa167](https://doi.org/10.1093/molbev/msaa167)
- 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, Stevens 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 ZALENDE/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**: 267–288. [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: CC011/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)