

Julien F. Ayroles, Ph.D.

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Research Scope: My group studies the biological basis for individual variation. We seek to understand how genes interact with each other and their environment to shape variation between individuals. The genetic architecture of complex traits is proving to be far more dynamic and context-dependent than previously thought. This has major implication for our ability to understand how populations evolve, how we study the genetic basis for complex traits and our ability to predict phenotype from genotype. We address this problem by developing experimental and analytical approaches aimed at improving our understanding of the genotype - phenotype map.

APPOINTMENTS

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|--------------|---|
| 2015-present | Assistant professor
Princeton University, Princeton, NJ
Department of Ecology and Evolutionary Biology and Lewis-Sigler Institute for Integrative Genomics |
| 2011-2015 | Harvard Junior Fellow
Cambridge, MA
Harvard Society of Fellows, Harvard University |
| 2003-2005 | Research and Field Assistant
Champaign, IL (Under Dr. Ken Paige)
University of Illinois, Department of Zoology |

EDUCATION

- | | |
|------|---|
| 2011 | Ph.D. in Genetics
North Carolina State University, Raleigh, Department of Genetics
Title: <i>A Systems Genetics Approach to the Dissection of Complex Traits in Drosophila melanogaster.</i> |
| 2005 | Master of Sciences in Natural Resources and Environmental Sciences
University of Illinois, Urbana-Champaign, Department of Animal Behavior |
| 2002 | Maîtrise (equivalent B.S.) in Organismal and Population Biology with honors
Paul Sabatier Université, Toulouse, France (Exchange program TASSEP) |
| 2001 | General degree in Biological Sciences (DEUG) with honors
Paul Sabatier Université, Toulouse, France |

PUBLICATIONS

- 2021 Henry, L.P. and Ayroles, J.F., 2021. **Meta-analysis suggests the microbiome responds to Evolve and Resequencing experiments in *Drosophila melanogaster***. *BMC microbiology*, 21(1):1-14
- 2021 Choi JY, Dai X, Peng JZ, Rughani P, Hickey S, Harrington E, Juul S, **Ayroles JF**, Purugganan M, Stacy E. (2020) Selection on ancient variations drives the adaptive radiation of *Metrosideros* across the Hawaiian archipelago. **PNAS** 118(37)
- 2021 Lea, A.J., Waigwa, C., Muhoya, B., Lotukoi, F., Peng, J., Henry, L., Abhyankar, V., Kamau, J., Martins, D., Gurven, M. and Ayroles, J.F., 2021. **Social gradients in health vary between rural and urban Turkana**. *medRxiv* (2021.07.23.21260771).
- 2021 Werkhoven Z, Bravin A, Skutt-Kakaria K, Reimers P, Pallares LF, **Ayroles JF**, De Bivort BL. (2020) The structure of behavioral variation within a genotype. **eLife** 10, p.e64988.
- 2021 Pallares LF, Lea AJ, Han C, Filippova EV, Andolfatto P, Ayroles JF. (2020) Diet unmasks genetic variants that regulate lifespan in outbred *Drosophila*. bioRxiv. **(under revision to Nature Genetics)**
- 2021 Henry L, Fernandez M, Ayroles JF. (2020) GxGxE interactions and adaptive potential of the microbiome in *Drosophila melanogaster*. bioRxiv. **(under review Current Biology)**
- 2021 Bruijning M, Henry LP, Forsberg SK, Metcalf CJ, **Ayroles JF**. (2020) When the microbiome defines the host phenotype: selection on vertical transmission in varying environments. **(in press, Nature Eco Evo)**
- 2020 Akhund-Zade J, Yoon D, Bangerter A, Polizos N, Campbell M, Soloshenko A, Zhang T, Wice E, Albright A, Narayanan A, Schmidt P, Saltz J, **Ayroles JF**, Klein M, Bergland B, de Bivort B. (2020) Wild flies hedge their thermal preference bets in response to seasonal fluctuations. bioRxiv. **(under revision Evolution)**
- 2020 Rau CD, Gonzales NM, Bloom JS, Park D, **Ayroles JF**, Palmer AA, Lusi AJ, Zaitlen N. (2020) Modeling Epistasis in Mice and Yeast Using the Proportion of Two or More Distinct Genetic Backgrounds: Evidence for Polygenic Epistasis. *Plos Genetics* 16(10), e1009165.
- 2020 Lea AJ., Martins D., Kamau, J., Gurven, M., **Ayroles, JF**. (2020). Urbanization and market integration have strong, nonlinear effects on cardiometabolic health in the Turkana. *Science advances*, 6(43), eabb1430
- 2020 Pallares LF, Picard S, **Ayroles JF** (2020) TM3'seq: a tagmentation-mediated 3'sequencing approach for improving scalability of RNAseq experiments. *G3: Genes, Genomes, Genetics* 10(1), 143-150
- 2019 Bruijning M, Metcalf J, Jongejans E and **Ayroles JF**. (2019). Exploring the fitness consequences of intra-genotypic variation. *Trends in Ecology and Evolution* 35(1): 22-33.

- 2019 Henry LP., Bruijning M., Forsberg KGS., **Ayroles JF**. (2020). Can The Microbiome Influence Host Evolutionary Trajectories? BioRxiv 700237 (**under revision Nature Communications**)
- 2019 Lea AJ, Subramaniam M, A Ko, T Lehtimäki, E Raitoharju, MikaKähönen, I Seppälä, N Mononen, O Raitakari, M Ala-Korpela, P Pajukanta, N Zaitlen, **Ayroles JF**. (2019). Genetic and environmental perturbations lead to regulatory decoherence. eLife 8, e40538
- 2019 Musharoff S, Park DS, A Dahl, JM Galanter, X Liu, S Huntsman, C Eng, Burchard EG, **Ayroles JF ***, Zaitlen N* (2019) Existence and implications of population variance structure. bioRxiv, 439661 (**in revision to AJHG**). (*equal contribution)
- 2018 Schrider DR, **Ayroles JF**, Matute DR, AD Kern AD. (2018). Supervised machine learning reveals introgressed loci in the genomes of *Drosophila simulans* and *D. sechellia*. PLoS genetics 14 (4), e1007341
- 2018 Dumitrascu B, Darnell G, **Ayroles JF**, Engelhardt BE. (2018). Statistical tests for detecting variance effects in quantitative trait studies. Bioinformatics 35(2): 200-210.
- 2015 Zwarts L, Broeck LV, Cappuyns E, **Ayroles JF**, Magwire MM, Vulsteke V, Clements J, Mackay TF, Callaerts P. (2015) The genetic basis of natural variation in mushroom body size in *Drosophila melanogaster*. Nature communications11(6).
- 2015 **Ayroles JF**, Buchanan SM, O'Leary C, Skutt-Kakaria K, Grenier JK, Clark AG, Hartl DL, de Bivort BL. (2015). Behavioral idiosyncrasy reveals genetic control of phenotypic variability. Proceedings of the National Academy of Sciences 112(21): 6706-11
- 2014 Matute DR*, **Ayroles JF***. (2014) Hybridization occurs between *Drosophila simulans* and *D. sechellia* in the Seychelles archipelago. Journal of evolutionary biology. 27(6):1057-68
- 2013 Corbett-Detig RB, Zhou J, Clark AG, Hartl DL, **Ayroles JF** . (2013). Genetic Incompatibilities Within Species are Widespread. Nature 504, 135–137. Faculty of 1000, Biology
- 2012 Huang W, Richards S, Carbone MA, Zhu D, Anholt RRH, **Ayroles JF**, et al. (2012) Epistasis Dominates The Genetic Architecture Of *Drosophila* Quantitative Traits. PNAS 109:15553-15559
- 2012 Massouras A, Waszak SM, Albarca M, Hens K, Holcombe K, **Ayroles JF**, Dermitzakis ET, Eric A Stone EA, Jensen J D, Mackay T.F.C, Deplancke B. (2012) Genomic Variation And Its Impact On Gene Expression In *Drosophila Melanogaster*. PLoS Genetics 8 (11): e1003055
- 2012 Mackay TFC*, Richards S*, Barbadilla A *, Stone EA*, **Ayroles JF***, Zhu D, Sònia Casillas. et. al. (2012) The *Drosophila* Genetics Reference Panel:A Community Resource for Analysis of Population Genomics and Quantitative Traits. Nature 482(7384):173-8. Faculty of 1000, Biology
- 2011 Ober U, **Ayroles JF**, Stone EA, Richards S, Zhu D, Gibbs RA, Stricker C, Gianola D, Schlather M, Mackay TFC, Simianer H. (2011) Using Whole Genome Sequence

- Data to Predict Quantitative Trait Phenotypes in *Drosophila melanogaster*. *PLoS Genetics* 8(5): e1002685. Faculty of 1000, Biology
- 2011 Rowe K, Singhal S, MacManes M, **Ayroles JF**, Morelli TL, Rubidge E, Bi K, Moritz C (2012). Museum Genomics: Low Cost And High Accuracy Genetic Data From Historical Specimens. *Molecular Ecology Resources* 11(6): 1082–1092
- 2011 **Ayroles JF**, Laflamme B, Wolfner MA, Mackay TFC. (2011) Sifting Through The Data: Identifying Top Candidates For Novel Seminal Protein Genes From *Drosophila* Whole Genome Expression Data. *Genetics Research* 93(6): 387-395
- 2010 Jumbo-Lucioni P*, **Ayroles JF***, Chambers MM, Jordan KW, Leips J, Mackay TF, De Luca M. (2010) Systems Genetics Analysis Of Body Weight And Energy Metabolism Traits In *Drosophila Melanogaster*. *BMC Genomics* 11(11): 297. (* Contributed equally)
- 2009 Edwards, A, **Ayroles JF**, Stone EA, Mackay TFC. (2009) A Transcriptional Network Associated With Natural Variation In *Drosophila* Aggressive Behavior. *Genome Biology* 10(7): R76.
- 2009 Mackay TFC, Stone EA, Ayroles JF. (2009) Quantitative Genetics: Prospects And Challenges. *Nature Review Genetics* 10(8): 565-577
- 2009 Morozova TV*, **Ayroles JF***, Jordan KW, Duncan LH, Carbone MA, Lyman RF, Stone EA, Govindaraju DR, Ellison RC, Mackay TF, Anholt RR. (2009) Alcohol Sensitivity In *Drosophila*: Translational Potential Of Systems Genetics. *Genetics* 183(2): 733-745 (* Contributed equally)
- 2009 Harbison ST, Carbone MA, **Ayroles JF**, Stone EA, Lyman RF, Mackay TFC (2009) Co-Regulated Transcriptional Networks Contribute to Natural Genetic Variation in *Drosophila* Sleep. *Nature Genetics* 41(3): 371-375
- 2009 **Ayroles JF**, Carbone MA, Stone EA, Jordan KW, Lyman RF, Magwire MM, Rollman SM, Duncan LH, Lawrence F, Anholt RH, Mackay TFC. (2009) Systems genetics of complex traits in *Drosophila melanogaster*. *Nature Genetics* 41(3): 299-307. Faculty of 1000, Biology
- 2009 Kocher SD, **Ayroles JF**, Stone EA, Grozinger CM. (2009) Genomics Of Pheromone Response: Cooperation And Conflict In Honey Bees. *Plos ONE* 5(2): e9116
- 2009 Stone EA, **Ayroles JF**. (2009) Modulated Modularity Clustering As An Exploratory Tool For Functional Genomic Inference. *PLoS Genetics* 5(5): e1000479
- 2009 **Ayroles JF**, Hughes KA, Reedy MM, Rodriguez-Zas SL, Drnevich JM, Rowe KC, Cáceres CE, Paige KN. (2009) Genome-Wide Assessment Of Inbreeding Depression In *Drosophila Melanogaster*. *Conservation Biology* 23(4): 920-930
- 2009 Carbone MA, **Ayroles JF**, Yamamoto A, Morozova TV, West SA, Magwire MM, Mackay TF, Anholt RR. (2009) Overexpression Of Myocilin In The *Drosophila* Eye Activates The Unfolded Protein Response: Implications For Glaucoma. *PLoS ONE* 4(1): e4216

- 2006 **Ayroles JF**, Gibson G. (2006) Analysis Of Variance Of Microarray Data. *Methods Enzymol* 411: -33
- 2006 Hughes KA, **Ayroles JF**, Reedy MM, Drnevich JM, Rowe KC, Ruedi EA, Cáceres CE, Paige KN. (2006) Segregating Variation In The Transcriptome: Cis Regulation And Additivity Of Effects. *Genetics* 173(3): 1347-1355.
- 2005 Dejean A, Solano PJ, **Ayroles JF**, Corbara B, Orivel J. (2005) Insect Behaviour: Arboreal Ants Build Traps to Capture Prey. *Nature* (434):973

BOOK CHAPTER

- 2020 Metcalf CJE*, Ayroles JF*. (2020). Chapter: "Why does intra-genotypic variance persist?" In book titled "Unsolved Problems in Ecology". Princeton University Press. (*equal contribution)

GRANTS

- 2020 - 2022 **Chan Zuckerberg Initiative DAF**
How does a western lifestyle modify immune response the Turkana people
- 2019 - 2021 **Mpala Funds**
Evolutionary functional genomics of the Turkana: signatures of past selection an responses to modern urbanization
- 2019 - 2021 **Catalysis Initiative**
A new paradigm to dissect the genetic basis of addictive behavior
- 2018 - 2023 **NIH NIEHS - R01**
Improved methods for inference of genotype-specific response to environmental toxins
- 2017 - 2022 **NIH- NIGMS R35**
A path to personalized phenotypic prediction: unlocking the context-dependency of allelic effects
- 2018 **San Diego Zoo Exploration funds**
- 2017 **New Ideas in the Natural Sciences**, Princeton University
- 2015 Banff International Research Station
- 2015 Foundation les Treilles
- 2014 3CPG – Cornell University
- 2014 Broad Institute SPARC (collaboration with Norbert Perrimon)
- 2012 Milton Research Award – Harvard University

TEACHING

- 2020 EEB309 "Introduction to Evolutionary Biology"
- 2020 EEB521 "Tropical Ecology" (graduate Students)
- 2020 EEB388 "Genomics in the wild"
- 2019 EEB380 "Ecology & Conservation of Africa"
- 2017 EEB409 "Understanding the evolution of adaptive systems"

2016 - 2021 ISC326 "Past, present and future of the human genome"

HONORS & AWARDS

2017 NIH Maximizing Investigators Research Award for young investigator

Kavli Fellow,
National
Academy of
Science

Richard B.

2013 Faculty of the 1000 (Genomics & Genetics, Evolutionary/Comparative Genetics)

2011

Junior Fel

2011 Kenneth R. Keller Award for Excellence in Doctoral Dissertation Research

SELECTED TALKS

2020 Harvard/MIT Evolutionary Genomics seminar series: Leveraging Evolutionary Mismatches to Study Genotype by Environment Interactions

2020 Cornell: Leveraging Evolutionary Mismatches to Study Genotype by Environment Interactions

2019 EEFG Gordon Conference: A Novel, Massively Parallel Mapping Framework to Unlock Genotype-Dependent Environmental Response

2019 Vienna Veterinärmedizinische Universität: The genetics of disruption: studying the genetic basis of environmental sensitivity.

2018 Duke University: From individual variation to the genetic basis of environmental sensitivity

2018 UT Austin: From individual variation to the genetic basis of environmental sensitivity

2018 Uppsala University: The complex Genetics of Complex Traits

2017 U Pennsylvania: Heritability and Prediction in Human Genetics

2017 Workshop: Latin-American School on Evolution (Sao Paolo)

2017 UCLA: The genetics of disruption: studying the genetic basis for phenotypic covariance

2017 Foundation les Treilles (organizer)

2016 Banff International Research Station

2016 American Society for Human Genetics

2016 Broad Institute: Behavioral individuality reveals genetic control of phenotypic variability

