MOHAMED AHMED FURNEAUX NOOR

Trinity College of Arts & Sciences
Duke University Durham, NC 27708
Phone: (919) 684-4863 Email: noor@duke.edu
https://sites.google.com/view/noor-lab

POSITION TITLE: PROFESSOR OF BIOLOGY AND INTERIM DEAN OF COLLEGE OF ARTS & SCIENCES

EDUCATION/TRAINING:

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
College of William and Mary, Williamsburg, Virginia	B.S.	05/1992	Biology
University of Chicago, Chicago, Illinois	Ph.D.	08/1996	Ecology & Evolution
Cornell University, Ithaca, New York	Postdoc	08/1998	Genetics & Development

A. Personal Statement

I have run a productive, continuously federally funded laboratory for over 22 years, and I have held numerous leadership roles in my university, including chair of my department, chair of the university's promotion and tenure committee, and dean of natural sciences. I have mentored a wide range of undergraduate students, graduate students, postdoctoral trainees, staff, and colleagues. I regularly present at workshops on mentoring, and I wrote a book with advice for new faculty hires on how to succeed in their new roles. I am passionate about promoting inclusive excellence, and I am eager to continue helping and learning how to help diverse early- and mid-career faculty excel at Duke University.

- Noor, M. A. F. 2012. You're Hired! Now What? A Guide for New Science Faculty. Sinauer Associates, Sunderland, Massachusetts. ISBN 978-0878939633, 96 pages.
- Noor, M. A. F., and C. S. S. Heil. 2012. Mentor vs. Monolith: Finding and being a good graduate advisor. American Scientist, 100: 450-453 doi:10.1511/2012.99.450

Ongoing projects that I would like to highlight include:

DEB-1754439 Noor (PI) 08/01/18-07/31/22
National Science Foundation
Collaborative Research: Reversing evolution to understand the genetic basis of species divergence
This study aims to revert an inversion distinguishing *Drosophila pseudoobscura* and *D. persimilis* and fine-map factors associated with reproductive isolation within the inverted region.
Role: PI, Collaborative PI is Carlos Machado, University of Maryland

DEB-2019789 Noor (PI) 01/01/21-12/31/23
National Science Foundation
Genetics and evolution of lethal alleles in Drosophila
This study aims to isolate hundreds lethal alleles from a natural population of *Drosophila melanogaster*, identify their genetic basis, and evaluate the evolutionary forces that allow especially the more frequent of these health-relevant alleles to persist.
Role: PI.

B. Positions, Scientific Appointments, and Honors

Positions and Employment

2022-2023 Interim Dean, Trinity College of Arts & Sciences, Duke University, Durham, NC
2019-2022 Dean of Natural Sciences, Trinity College of Arts & Sciences, Duke University, Durham, NC
2013-2017 Department Chair, Biology Department, Duke University, Durham, NC
2008- Professor, Biology Department, Duke University, Durham, NC
2005-2008 Associate Professor, Biology Department, Duke University, Durham, NC
2002-2005 Associate Professor, Department of Biological Sciences, Louisiana State University, Baton Rouge, LA
1998-2005 Assistant Professor, Department of Biological Sciences, Louisiana State University, Baton Rouge, LA

Other Experience/ Professional Activities (selected)

2016-2019 Editor-in-chief, *Evolution*
2016-2018 Treasurer, American Genetic Association
2014 President, Society for the Study of Evolution
2012-2014 Board of Directors, Genetics Society of America
2012 President, American Genetic Association
2011-2016 Associate editor, *Journal of Heredity*
2008-2010 Editorial Board, *Proceedings of the Royal Society of London Series B*
2006-2012 NIH, Genetic Variation and Evolution study section
chair of study section 2010-2012
2006-2007 Editor, *Evolution*
2005-2010 Editorial Board, *PLoS Biology*
2001-2005 Associate Editor, *Evolution*
2001-2003 Associate Editor, *Genetics*

Honors

2019 Stephen J. Gould Award, Society for the Study of Evolution
2014 Outstanding Postdoc Mentor Award, Office of Postdoc Services at Duke University
2013 Alumni Distinguished Undergraduate Teaching Award, Duke University
2011-2016 Earl D. McLean Professor of Biology, Duke University
2010 Dean's Award for Excellence in Mentoring, Duke University Graduate School
2008 Darwin-Wallace Medal, Linnean Society of London
2004-2005 Andrew Clinton Pereboom LSU Alumni Association Endowed Professorship
2004 Louisiana State University, College of Basic Sciences Research Award
2002 LSU Phi Kappa Phi Untenured Faculty Award in Natural and Physical Sciences
1998 American Society of Naturalists Young Investigator Prize
1996-1998 NSF/ Sloan postdoctoral fellowship in molecular evolution
(3 other university teaching awards not listed)

C. Contributions to Science

1. Chromosomal inversions as facilitators of speciation

Rates of speciation correlate with karyotypic change in many broad groups (including mammals), and researchers initially interpreted this correlation as resulting from underdominance of karyotypic heterozygosity. In the 1990s, several studies showed such underdominance was often absent, and interest waned in the role of inversions and other karyotypic changes in speciation despite the original correlations. My team's 2001 study presented an alternative model—karyotypic heterozygosity may foster the persistence of hybridizing species because of recombinational (rather than direct fitness) effects. We showed that virtually all differences between *Drosophila pseudoobscura* and *D. persimilis* map to inverted regions, and we showed more broadly that Drosophila species differing by inversions were more likely to be sympatric at low genetic divergence than Drosophila species not differing by inversions. Loren Rieseberg published a similar idea in a review that same year. Since that time, support for this model has grown dramatically in many plant and animal groups, and we

have continued to find support for this idea and develop it further: detecting patterns with targeted or whole-genome sequence divergence analogous to those observed with the mapping studies, showing the association of high divergence in both phenotype and genotype with inversions is stronger in sympatric populations than in allopatric populations of the same species, finding relatively recent exchange/ homogenization specifically in sympatric populations, showing that the interchromosomal effect from inversions may actually *increase* exchange outside inverted regions, and providing evidence of the "mixed geographical mode" theory of inversion origin and fixation. Finally, our most recent efforts have shown that inversions are not impermeable barriers to gene exchange, and we have found, characterized, and measured gene conversion rates in inverted regions vs. collinear regions of heterozygotes both within and between species. While most of our efforts have been in the model *Drosophila pseudoobscura/ D. persimilis* system, the implications extend (as evidenced by our works' broad citations) to all hybridizing species and to a broader understanding of what allows newly formed species to persist.

a. Noor, M. A. F., K. L. Grams, L. A. Bertucci, and J. Reiland. 2001. Chromosomal inversions and the reproductive isolation of species. *Proceedings of the National Academy of Sciences USA*, 98: 12084-12088. PMCID: PMC59771
b. McGaugh, S. E., and M. A. F. Noor. 2012. Genomic impacts of chromosomal inversions in parapatric Drosophila species. *Philosophical Transactions of the Royal Society of London Series B*, 367: 422-429. PMCID: PMC3233717
c. Korunes, K. L., and M. A. F. Noor. 2019. Pervasive gene conversion in chromosomal inversion heterozygotes. *Molecular Ecology*, 28: 1302-1315. PMCID: PMC6475484.
d. Korunes, K. L., C. M. Machado, and M. A. F. Noor. 2021. Inversions shape the divergence of *Drosophila pseudoobscura* and *Drosophila persimilis* on multiple timescales. Evolution 75: 1820-1834. PMCID: in progress. doi: 10.1111/evo.14278 .

2. Evidence of controversial evolutionary or genetic modes of speciation: reinforcement, a "one-allele" model, a direct role of meiotic drive within species in hybrid sterility, etc.

The field of speciation is infamous for its contentious debates about whether particular processes (e.g., "sympatric speciation") occur in nature. My team and I have devised creative tests for various controversial types of speciation over the years, and in many instances, found evidence of their operation. When finishing my PhD, I published a high-profile demonstration of speciation by reinforcement at a time when recent reviews and theoretical models by others had suggested it was largely implausible, and empirical studies in other systems subsequent to my work also found broad support for it in numerous taxa. My first PhD student found that one of the alleles causing reinforcement in *Drosophila pseudoobscura* operated as a "one-allele" enhancer of discrimination, demonstrating the first evidence for a theoretically predicted mechanism by which reinforcement may be feasible. Another of my PhD students found evidence that meiotic drive within species contributes to sterility in species hybrids (an idea dismissed in the 1990s but which was beginning to resurface with some recent work showing drive in hybrids), and I collaborated with a team showing evidence for gene transposition causing hybrid sterility. Yet another of my PhD students was able to explain the discrepancy between the theoretical prediction of dominant autosomal alleles causing F_1 hybrid sterility and the absence of any such alleles ever being mapped: epistasis modifies the dominance of such alleles (a finding highlighted in *Science*). All of these findings contribute to a broader understanding of genetic changes and evolutionary forces driving the origin of new species on our planet, and thus biodiversity more broadly.

a. Noor, M. A. 1995. Speciation driven by natural selection in *Drosophila*. *Nature*, 375: 674-675.
b. Ortíz-Barrientos, D., and M. A. F. Noor. 2005. Evidence for a one-allele assortative mating locus. *Science*, 310: 1467.
c. Chang, A. S., and M. A. F. Noor. 2010. Epistasis modifies the dominance of loci causing hybrid male sterility in the *Drosophila pseudoobscura* species group. *Evolution*, 64: 253-260. PMCID: PMC2827646. (Highlighted in *Science*)
d. McDermott, S. R., and M. A. F. Noor. 2012. Mapping of within-species segregation distortion in *Drosophila persimilis* and hybrid sterility between *D. persimilis* and *D. pseudoobscura*. *Journal of Evolutionary Biology*, 25: 2023-2032. PMCID: PMC3442956.

3. First identification of fine-scale variation in crossover rate in Drosophila; determined its pattern of evolution across related species and its effects on molecular variation

While crossover hotspots have been known in mammals and yeast for decades, the dogma in the literature was that Drosophila had a smooth recombination landscape—so much so that researchers would do third-order polynomial regressions to "smooth" out any apparent fine-scale crossover rate heterogeneity. My team published the first study demonstrating that fine-scale crossover rate variation does exist in Drosophila and that this fine-scale variation has molecular evolutionary implications (as evidenced by correlations with nucleotide diversity and codon bias). Our original study was conducted in *Drosophila pseudoobscura*, and the work was replicated thereafter by another team in *D. melanogaster*. We developed a means of separating the recombination-related effects of GC-biased gene conversion from selection on codon bias and found signatures of both processes. We also published the most comprehensive examination of variation in recombination rate within and between closely related species (using both historical LD-based approaches and single-generation crosses in both species), allowing the most definitive test to date of whether the relationship of recombination rate to diversity is driven by mutagenesis or selection. We found that although both local and global recombination rates diverged slightly between species, the overall correlation is clearly driven primarily by selection (definitely sweeps and likely some background selection—we are continuing to investigate the role of the latter). Further, most recently, through an unprecedentedly large-scale study examining variation within and between natural populations in recombination rate, we found strong evidence that divergence in recombination between populations of *D. pseudoobscura* had occurred and was driven by natural selection: one of the first direct demonstrations of the role of natural selection in driving change in this important genetic parameter. Overall, this body of research dramatically increases understanding of how local recombination rates influence genome evolution with implications extending well beyond Drosophila.

a. Kulathinal, R. J., S. M. Bennett, C. L. Fitzpatrick, and M. A. F. Noor. 2008. Fine-scale mapping of recombination rate in Drosophila refines its correlation to diversity and divergence. *Proceedings of the National Academy of Sciences USA*, 105: 10051-10056. PMCID: PMC2481358
b. McGaugh, S. E., C. S. S. Heil, B. Manzano-Winkler, T. L. Himmel, and M. A. F. Noor. 2012. Recombination modulates how selection affects linked sites in Drosophila. *PLoS Biology*, 10: e1001423. PMCID: PMC3496668.
c. Smukowski Heil, C. S., C. Ellison, M. Dubin, and M. A. F. Noor. 2015. Recombining without hotspots: A comprehensive evolutionary portrait of recombination in two closely related species of Drosophila. *Genome Biology and Evolution*, 7: 2829-2842. PMCID: PMC4684701.
d. Samuk, K. B. Manzano-Winkler, K. R. Ritz, and M. A. F. Noor. 2020. Natural selection shapes variation in genome-wide recombination rate in *Drosophila pseudoobscura*. *Current Biology*, 30: 1517-1528.

4. New approaches to genetics and evolution education

My team develops inquiry-based approaches for enhancing genetics and evolution education. This was concurrent with my creating the first and longest-running massive open online course (MOOC) on genetics and evolution, available in Coursera. My team has developed a suite of peer-reviewed activities for use at the high school and college levels for observing a selective sweep in progress (using Drosophila), studying signatures of natural selection in DNA sequences, and more. One of our activities is now marketed as a kit distributed by Carolina Biological Supply, making it easily available to schools around the country, and we have presented these efforts at both teacher workshops and national scientific conferences. I have also hired programmers to create mobile applications to assist students both through demonstrations and through creating a virtually infinite set of practice problems (e.g., pedigrees from which to determine mode of inheritance, genotype numbers to calculate gene order and recombination distance, Hardy-Weinberg problems). These resources are readily available in the Apple App Store and Google Play store to maximize dissemination and potential impact on student learning. Given the challenges faced in teaching genetics (quickly deemed "hard" by many students) and evolution (quickly deemed "controversial" by many students), we are proud to contribute works that will ease the jobs of educators and students alike, and the topics segue nicely with our research interests (e.g., recombination, selective sweeps).

a. Heil, C. S. S., M. J. Hunter, J. K. F. Noor, K. Miglia, B. Manzano-Winkler, S. R. McDermott, and M. A. F. Noor. 2012. Witnessing phenotypic and molecular evolution in the fruit fly. *Evolution: Education and Outreach*, 5: 629-634. PMCID: PMC3583343.
b. Heil, C. S. S., B. Manzano-Winkler, M. J. Hunter, J. K. F. Noor, and M. A. F. Noor. 2013. Witnessing evolution first-hand: A K-12 laboratory exercise in genetics and evolution using Drosophila. *American Biology Teacher*, 75: 116-119.

c. Noor, J. K. F., and M. A. F. Noor. 2013. Finding selection in all the right places: A college genetics laboratory inquiry-based learning exercise. Genetics Society of America Peer-Reviewed Education Portal (GSA-PREP). Retrieved from http://genetics-gsa.org/education/education_resource_Finding_Selection_MolEvolLab_2_7_13.shtml
d. Myers, R. B., B. Millman, and M. A. F. Noor. 2014. Genetics and Evolution: An iOS application to supplement introductory courses in transmission and evolutionary genetics. *G3*, 4: 779-781. PMCID: PMC4025476

Complete List of Published Work
http://www.ncbi.nlm.nih.gov/myncbi/browse/collection/49231097/?sort=date&direction=ascending