Arun Durvasula

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Education

PhD Human Genetics, University of California, Los Angeles	2016-2021
BS Biotechnology, University of California, Davis	2011-2015

Experience

Graduate Research Fellow. Department of Human Genetics, UCLA.	2016-2021
Mentors: Dr. Kirk Lohmueller & Dr. Sriram Sankararaman	
Post-Bac Researcher. Max Planck Institute for Plant Breeding Research.	2015-2016
Mentor: Dr. Angela Hancock	
Undergraduate Researcher. University of California, Davis.	2013-2015
Mentor: Dr. Jeffrey Ross-Ibarra	

Grants and Awards

Graduate Research Fellowship Program, National Science Foundation	2018-2021
International Conference for Quantitative Genetics Early Career Researcher Scholarship	2020
Stephen D. Cederbaum Travel Award, UCLA Genetics and Genomics (x2)	2018, 2019
Kenneth I. Shine Fellowship, UCLA	2018
Vienna Biocenter Summer Internship Scholarship	2015
Undergraduate Travel Award, UC Davis Plant Sciences	2015

Publications

(* - equal contribution)

12. Molloy EK, **Durvasula A**, Sankararaman S. Advancing admixture graph estimation via maximum likelihood network orientation (2021). *Bioinformatics*. (Conference proceeding of ISMB, in press).

11. **Durvasula A**, Lohmueller K. Negative selection on complex traits limits phenotype prediction accuracy between populations (2021). *American Journal of Human Genetics*.

10. Boocock J, Sadhu MJ, **Durvasula A**, Bloom JS, Kruglyak L. Ancient balancing selection maintains incompatible versions of the galactose pathway in yeast (2021). *Science*.

    ▶ Highlighted in *Science*

9. PopSim Consortium. A community-maintained standard library of population genetic models (2020) *eLife*.

    ▶ Highlighted in *Nature Methods*

8. **Durvasula A**, Sankararaman S. Recovering signals of ghost archaic admixture in the genomes of present-day Africans (2020). *Science Advances*.

    ▶ F1000 recommended, highlighted in: New York Times, NPR, BBC

7. **Durvasula A**, Sankararaman S. A statistical model for reference-free inference of local archaic ancestry (2019). *PLoS Genetics*.

6. Huber CD*, **Durvasula A***, Hancock AM, Lohmueller KE. Gene expression drives the evolution of dominance (2018). *Nature Communications*.

5. Schumer M, Xu C, Powell D, **Durvasula A**, Skov L, Holland C, Sankararaman S, Andolfatto P, Rosenthal G, Przeworski M. Natural selection interacts with the local recombination rate to shape the evolution of hybrid genomes (2018). *Science*.

▶ F1000 recommended

4. Schweizer RM, **Durvasula A**, Smith J, Vohr SH, Stahler DR, Galaverni M, Thalmann O, Smith D, Randi E, Green RE, Lohmueller KE, Novembre J, Wayne RK. The evolutionary history of a selectively swept coat color and immunity locus in North American wolves (2018). *Molecular Biology and Evolution*.

3. **Durvasula A***, Fulgione A*, Gutaker RM, Alacakaptan SI, Flood PJ, Neto C, Alonso-Blanco C, Burbano HA, Pico FX, Tsuchimatsu T, Hancock AM. African genomes illuminate the early history and transition to selfing in *Arabidopsis thaliana* (2017). *Proceedings of the National Academy of Sciences*.

   ▶ F1000 recommended, highlighted in: *Science, Nature Plants*

2. **Durvasula A***, Hoffman PJ*, Kent TV, Liu C, Kono TJY, Morrell PL, Ross-Ibarra J. angsd-wrapper: utilities for analysing next-generation sequencing data (2016) *Mol Ecol Resour*.

1. Beissinger T, Wang L, Crosby K, **Durvasula A**, Hufford M, Ross-Ibarra J. Recent demography drives changes in linked selection across the maize genome (2016). *Nature Plants*.

Teaching and Service

Guest lecture: The neutral theory of evolution (UCLA), Spring 2019

Teaching assistant: Population Genetics (Undergraduate level course; UCLA), Spring 2018, 2019

Teaching assistant: Ecological Genomics (Graduate level course; UC Davis), Winter 2015

Mentoring: Scott Shi (undergraduate, UCLA); Mario Paciuc, Elliot Kang (Bruins in Genomics, UCLA)

Peer review: Molecular Ecology Resources; PLoS Genetics; G3: Genes, Genomes, Genetics; ISMB

Presentations

1. Linking human evolutionary history to phenotypic variation (invited seminar). University of Toronto (2021)

2. Linking human evolutionary history to phenotypic variation (invited seminar). Salk Institute (2021)

3. Negative selection on complex traits limits genetic risk prediction accuracy between populations (conference talk). PEQG, Virtual, (2020).

4. Recovering signals of ghost archaic introgression in African populations (conference talk), Human Evolution, Hinxton, United Kingdom (2019).

5. Demography drives differences in the distribution of gene expression (conference talk), SMBE, Yokohama, Japan (2018).

6. A statistical model for reference free inference of local divergent ancestry (invited seminar), Human Genetics Seminar Series, UCLA, Los Angeles, CA (2018).

7. Deep learning reveals local archaic ancestry (conference talk), RECOMB-Genetics, Los Angeles, CA (2017).

8. Population history of island *Arabidopsis thaliana* (conference talk), Vienna Biocenter Summer Symposium, Vienna, Austria (2015).

Software

ANGSD-wrapper: `https://github.com/ANGSD-wrapper/angsd-wrapper`
ArchIE: `https://github.com/sriramlab/ArchIE`
OrientAGraph: `https://github.com/ekmolloy/OrientAGraph`
stdpopsim: `https://github.com/popsim-consortium/stdpopsim`