

Arun Durvasula

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Education

PhD Human Genetics, University of California, Los Angeles (expected 2021)

Advisors: Kirk E. Lohmueller, Sriram Sankararaman

BS Biotechnology, University of California, Davis 2015

Experience and Employment

Research Assistant, Hancock Lab. MFLP/MPI-Plant Breeding
Research Intern, Ross-Ibarra Lab. University of California, Davis.

June 2015 - Sept 2016
June 2013 - June 2015

Grants and Awards

Stephen D. Cederbaum Travel Award, UCLA Genetics and Genomics (x2)	2018, 2019
Kenneth I. Shine Fellowship, UCLA	2018
Graduate Research Fellowship Program, National Science Foundation	2018
Vienna Biocenter Summer Internship Scholarship	2015
Undergraduate Travel Award, UC Davis Plant Sciences	2015

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: G3: Genes, Genomes, Genetics (4), Molecular Ecology Resources (2), PLoS Genetics (2), ISMB (1)

Presentations

1. Negative selection on complex traits limits genetic risk prediction accuracy between populations. PEQG, Virtual, (2020).
2. Recovering signals of ghost archaic introgression in African populations (conference talk), Human Evolution, Hinxton, United Kingdom (2019).
3. Demography drives differences in the distribution of gene expression (conference talk), SMBE, Yokohama, Japan (2018).
4. A statistical model for reference free inference of local divergent ancestry (invited seminar), Human Genetics Seminar Series, UCLA, Los Angeles, CA (2018).
5. Deep learning reveals local archaic ancestry (conference talk), RECOMB-Genetics, Los Angeles, CA (2017).
6. Population history of island *Arabidopsis thaliana* (conference talk), Vienna Biocenter Summer Symposium, Vienna, Austria (2015).

Publications

* - equal contribution

Preprints

1. PopSim Consortium. A community-maintained standard library of population genetic models (2019) *bioRxiv* (in review).
2. **Durvasula A**, Lohmueller K. Negative selection on complex traits limits genetic risk prediction accuracy between populations (2019). *bioRxiv* (in review).

Published

1. **Durvasula A**, Sankararaman S. Recovering signals of ghost archaic admixture in the genomes of present-day Africans (2020). *Science Advances* (in press).
2. **Durvasula A**, Sankararaman S. A statistical model for reference-free inference of local archaic ancestry (2019). *PLoS Genetics*.
3. Huber CD*, **Durvasula A***, Hancock AM, Lohmueller KE. Gene expression drives the evolution of dominance (2018). *Nature Communications*.
4. 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
5. 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 (2017). *Molecular Biology and Evolution*.
6. **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*
7. **Durvasula A***, Hoffman PJ*, Kent TV, Liu C, Kono TJY, Morrell PL, Ross-Ibarra J. (2016), angsd-wrapper: utilities for analysing next-generation sequencing data. *Mol Ecol Resour*.
Software available: <https://github.com/mojaveazure/angsd-wrapper>
8. 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*.

References

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email: sriram@cs.ucla.edu

Angela Hancock, Group Leader, Max Planck Institute for Plant Breeding Research Cologne, Germany

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