



Stick Insect Genomes Reveal Natural Selection's Role in Parallel Speciation

(Soria-Carrasco *et al.*)

Om Vaknalli (18376)

2nd Year BS-MS Natural Sciences, IISER-Bhopal

17th June 2019, IISER-Bhopal

About the paper:



Authors: Víctor Soria-Carrasco, Zachariah Gompert, Aaron A. Comeault, Timothy E. Farkas, Thomas L. Parchman, J. Spencer Johnston, C. Alex Buerkle, Jeffrey L. Feder, Jens Bast, Tanja Schwander, Scott P. Egan, Bernard J. Crespi, Patrik Nosil.

Publication Details: Science (IF: 37. 205), 16 May 2014: Vol. 344, Issue 6185, pp. 738-742

274 Citations

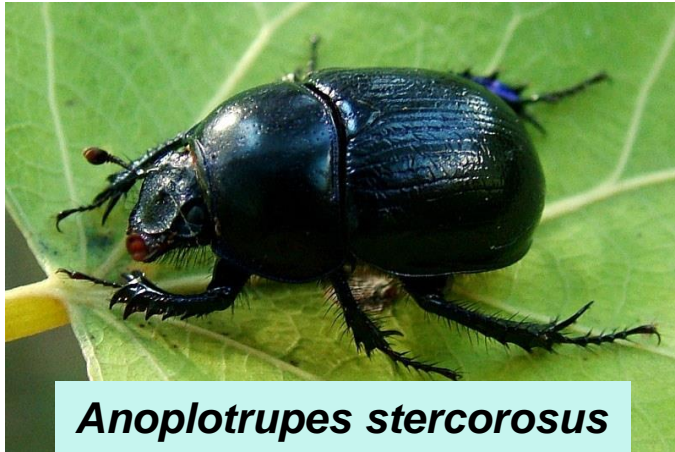
Web-link: <https://science.sciencemag.org/content/344/6185/738>

Introduction:

- Parallel Evolution
- Parallel Speciation



Geotrupes spiniger



Anoplotrupes stercorosus



Sphaeridium lunatum

Sources: BioLib.cz (top),
arthropodafotos.de (Extreme left),
Insektarium (left)

Introduction: The Main Question



- **What is the genomic basis of parallel speciation?**

Introduction: The Model Organism

A close-up photograph of a Timema cristinae, a green stick insect, perched on a green, spiny plant stem. The insect has a segmented body with small white spots and long, thin antennae. The background is dark, making the green insect and plant stand out.

Timema cristinae (Cristina's Stick Insect) on *Ceanothus spinosus*

Introduction: The Model Organism



© Alice T. Cristinae on *Adenostoma fasciculatum*



Ceanothus spinosus



Adenostoma fasciculatum flowers



Adenostoma fasciculatum

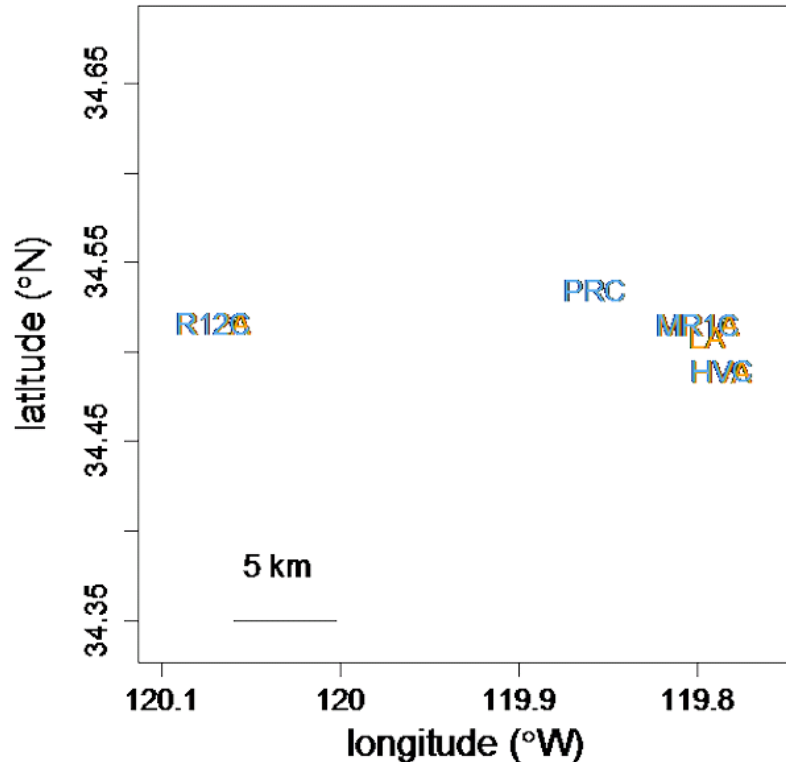
Questions, Methods and Results



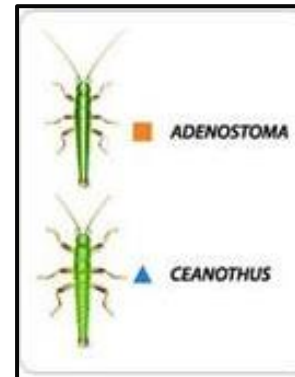
- **What are the effects of adaptation on genomic divergence?**
- **Can the underlying genetic changes driving the divergence of populations into new species be predicted or repeated?**

Sources for Previous Slide: [picssr](#) (top left), [nathistoc](#) (top right), [Calscape](#) (bottom left), [Calscape](#) (bottom right)

Questions, Methods and Results



| Population Pair | HVA × HVC | MR1A × MR1C | R12A × R12C | LA × PRC |
|---|-----------|-------------|-------------|-----------|
| <i>Population characteristics</i> | | | | |
| Geography | adjacent | adjacent | adjacent | separated |
| Gene flow ($N_e m$) | 28 | 37 | 93 | 11 |
| No. individuals sequenced (per individual population) | 20, 20 | 20, 20 | 21, 21 | 19, 19 |

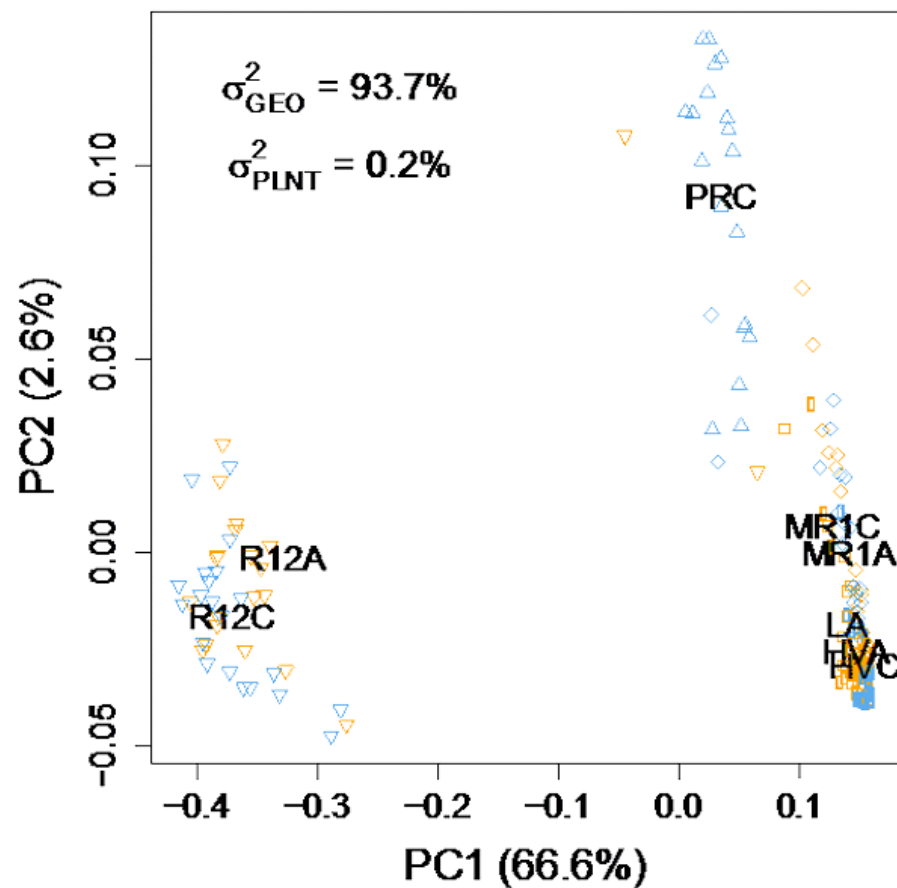
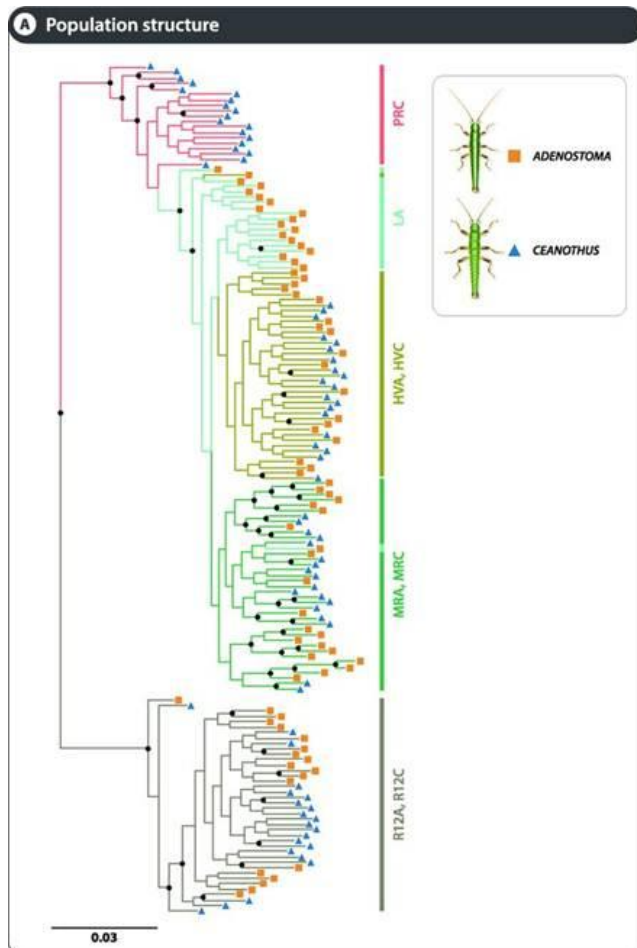


Sources (for this slide and next slide): [Science](#)

Questions, Methods and Results

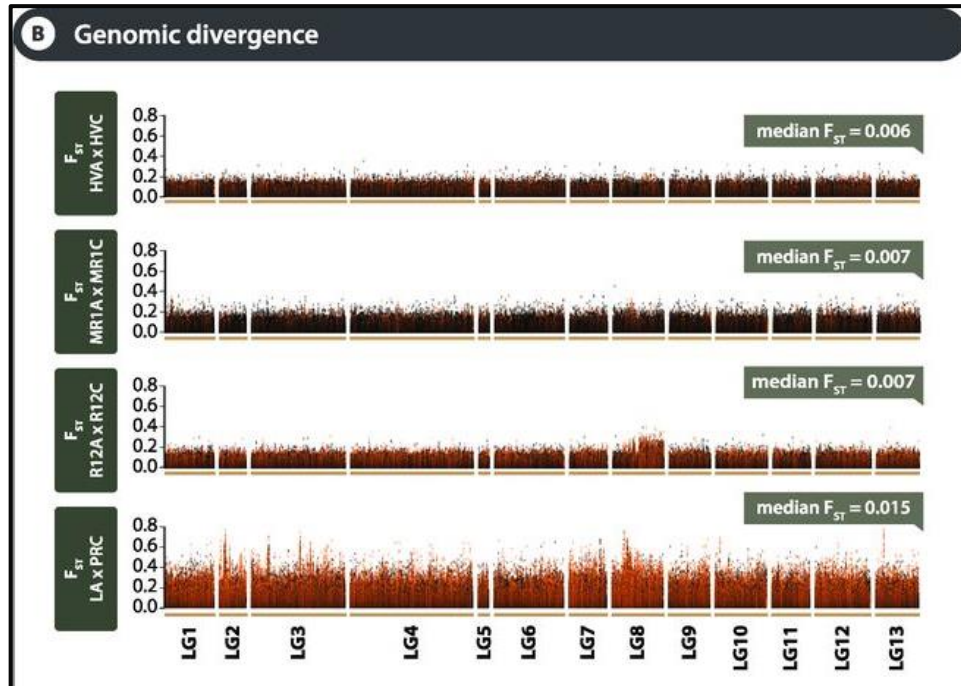


- Does genomic divergence vary geographically between different ecotype pairs?



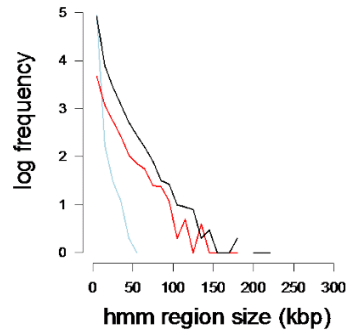
Questions, Methods and Results

| Population Pair | HVA × HVC | MR1A × MR1C | R12A × R12C | LA × PRC |
|---|-------------|-------------|-------------|--------------|
| <i>Population characteristics</i> | | | | |
| Geography | adjacent | adjacent | adjacent | separated |
| Gene flow (N_m) | 28 | 37 | 93 | 11 |
| No. individuals sequenced (per individual population) | 20, 20 | 20, 20 | 21, 21 | 19, 19 |
| <i>Genome characteristics from all SNPs</i> | | | | |
| Mean MAF | 17% | 20% | 19% | 20% |
| Mean F_{ST} | 0.013 | 0.015 | 0.015 | 0.031 |
| Median F_{ST} | 0.006 | 0.007 | 0.007 | 0.015 |
| Range of F_{ST} | 0.000–0.358 | 0.000–0.461 | 0.000–0.398 | 0.000–0.8000 |
| 90th quantile | 0.035 | 0.041 | 0.041 | 0.083 |
| 95th quantile | 0.050 | 0.058 | 0.056 | 0.116 |

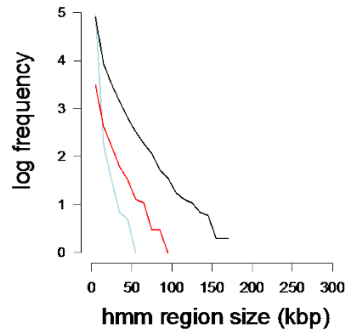


Questions, Methods and Results

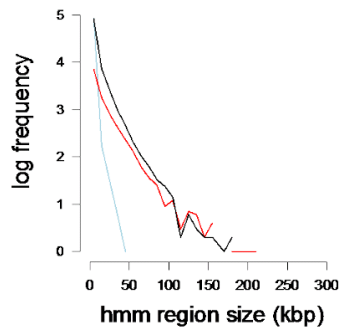
HVA x HVC



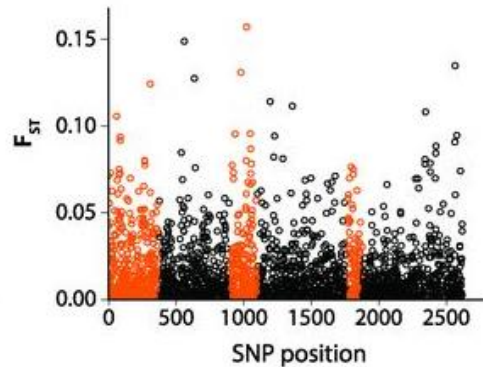
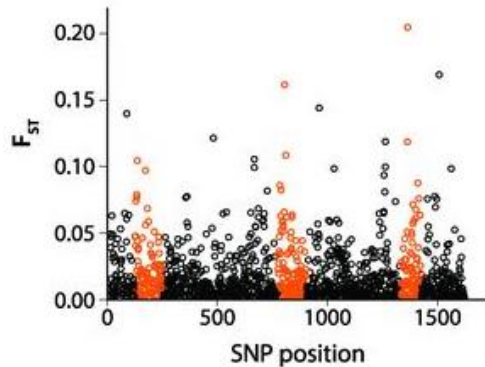
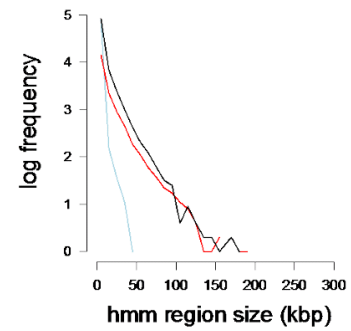
MR1A x MR1C



R12A x R12C



LA x PRC



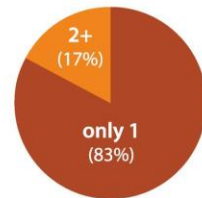
Distribution of the size of HMM regions (colours are: blue = low differentiation regions, black = moderate differentiation regions, red/orange = high differentiation regions). Absolute frequencies across the four categories are shown.

Questions, Methods and Results

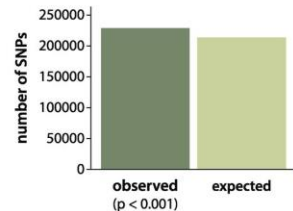
Test for parallelism of highly divergent SNPs. Quantiles refer to the empirical F_{ST} distribution.

| | Observed number of SNPs | Expected number of SNPs | p-value | Enrichment (observed / expected) |
|--|-------------------------|-------------------------|---------|----------------------------------|
| >90 th quantile in 2 population pairs | 228,347 | 213,423 | <0.001 | 1.07 |
| >90 th quantile in 3 population pairs | 22,366 | 15,809 | <0.001 | 1.41 |
| >90 th quantile in 4 population pairs | 945 | 439 | <0.001 | 2.15 |
| >90 th quantile in 2 or more population pairs | 251,658 | 229,671 | <0.001 | 1.10 |
| >99 th quantile in 2 population pairs | 4757 | 2582 | <0.001 | 1.84 |
| >99 th quantile in 3 population pairs | 94 | 17 | <0.001 | 5.53 |
| >99 th quantile in 4 population pairs | 0 | 0 | n/a | n/a |
| >99 th quantile in 2 or more population pairs | 4851 | 2600 | <0.001 | 1.87 |

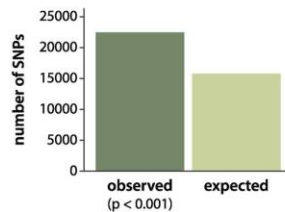
A Number of population pairs a SNP had high F_{ST} for



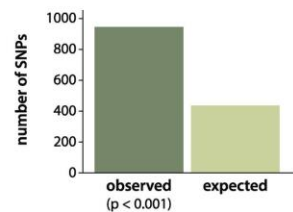
B High F_{ST} in 2 population pairs



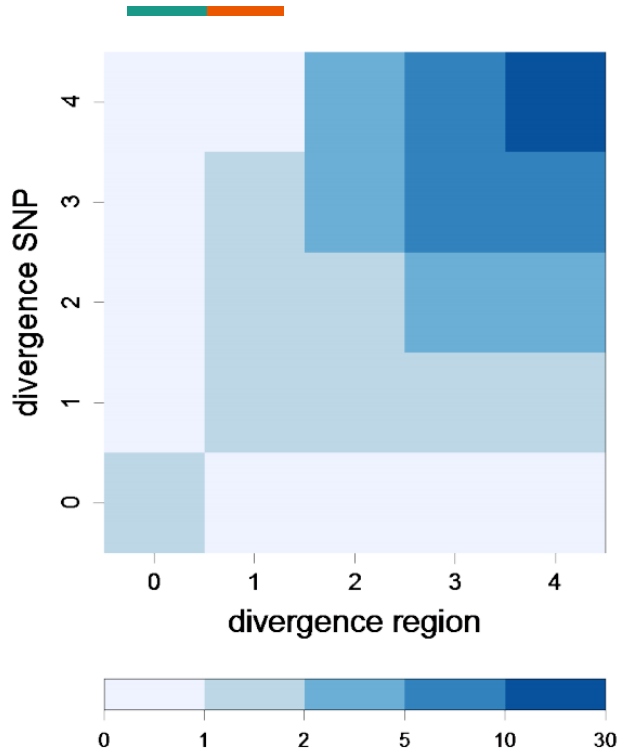
C High F_{ST} in 3 population pairs



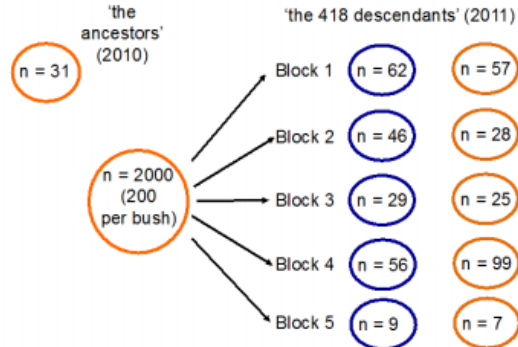
D High F_{ST} in 4 population pairs



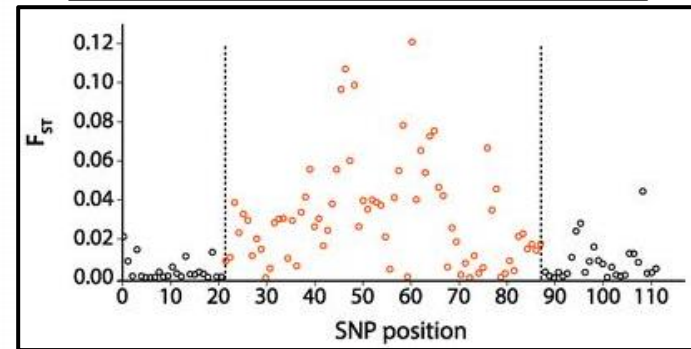
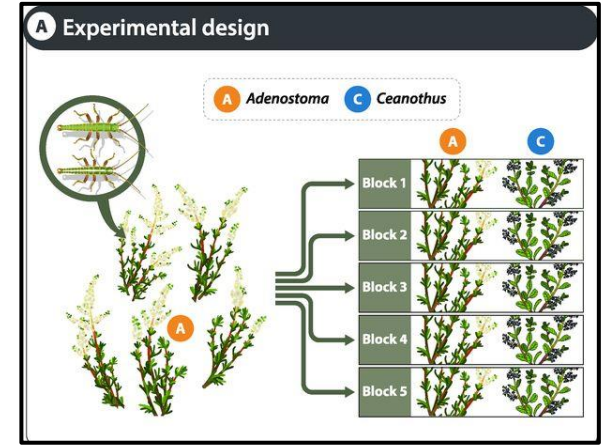
Questions, Methods and Results



A) Experimental design

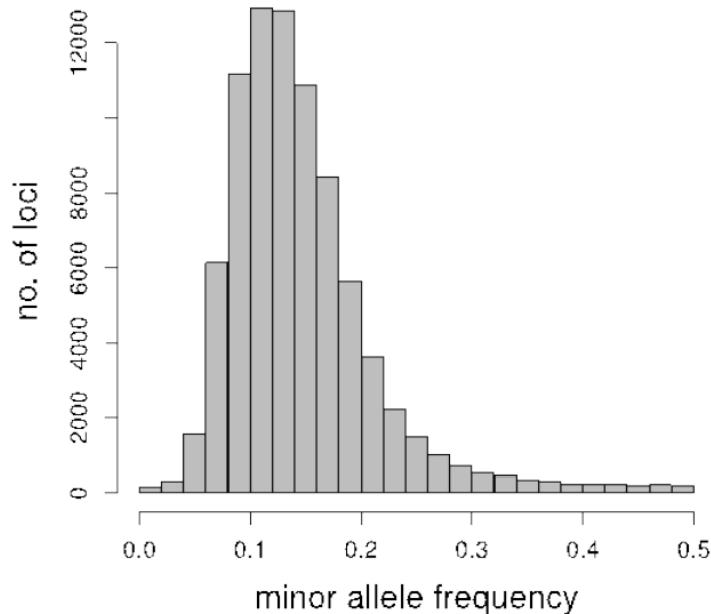


B) Map



Questions, Methods and Results

B) maf distribution LA



- What other factors affect the parallel genetic divergence?

Questions, Methods and Results



- What are the functions of genomic regions exhibiting parallel divergence?

Conclusion



- Early parallel speciation ➡ Non-parallel genetic divergence
- Some regions show parallel divergence
 - More coding genes than expected
- Divergent selection ➡ Repeated genomic divergence
- “Though repeated evolutionary scenarios would likely result in idiosyncratic outcomes, there may be a repeatable component driven by selection that can be detected, even at the genome level and during the complex process of speciation”, quoted from Soria-Carrasco *et al.*, 2014

References



- 1. D. L. Stern, Nat. Rev. Genet. 14, 751–764 (2013).
- 2. R. D. H. Barrett, H. E. Hoekstra, Nat. Rev. Genet. 12, 767–780 (2011).
- 3. M. K. Burke, Proc. R. Soc. London Ser. B 279, 5029–5038 (2012).
- 4. D. M. Weinreich, N. F. Delaney, M. A. Depristo, D. L. Hartl, Science 312, 111–114 (2006).
- 5. J. R. Meyer et al., Science 335, 428–432 (2012).
- 6. J. B. Losos, Lizards in an Evolutionary Tree: Ecology and Adaptive Radiation of Anoles (Univ. California Press, Berkeley, CA, 2009).
- 7. F. C. Jones et al., Nature 484, 55–61 (2012).
- 8. G. L. Conte, M. E. Arnegard, C. L. Peichel, D. Schluter, Proc. R. Soc. London Ser. B 279, 5039–5047 (2012).
- 9. Heliconius Genome Consortium, Nature 487, 94–98 (2012).
- 10. D. Schluter, L. M. Nagel, Am. Nat. 146, 292–301 (1995).
- 11. J. L. Feder, S. P. Egan, P. Nosil, Trends Genet. 28, 342–350 (2012).
- 12. H. Ellegren et al., Nature 491, 756–760 (2012).
- 13. S. H. Martin et al., Genome Res. 23, 1817–1828 (2013).
- 14. H. Ellegren, Trends Ecol. Evol. 29, 51–63 (2014).
- 15. P. Nosil, Am. Nat. 169, 151–162 (2007).

References



- 16. P. Nosil et al., Proc. R. Soc. London Ser. B 279, 5058–5065 (2012).
- 17. P. Nosil, B. J. Crespi, C. P. Sandoval, Nature 417, 440–443 (2002).
- 18. Z. Gompert et al., Ecol. Lett. 17, 369–379 (2014).
- 19. H. D. Rundle et al., Science 287 , 306-8. (2000)
- 20. P. Holter, The American Naturalist (2004)
- 20. Evolution by Mark Ridley, 3rd Edition

Any Questions/Suggestions?



Acknowledgements

- I would like to thank Prof. Nagarjun Vijay for giving me this opportunity to present.
- Special thanks to Mr. Aswin Soman for guiding me through the nitty-gritties of presentation.
- Lastly, I thank everyone here for taking the time out from your schedules to attend this presentation.



Thank-you!