



Stick Insect Genomes Reveal Natural Selection's Role in Parallel Speciation **(Soria-Carrasco *et al.*)**

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About the paper:



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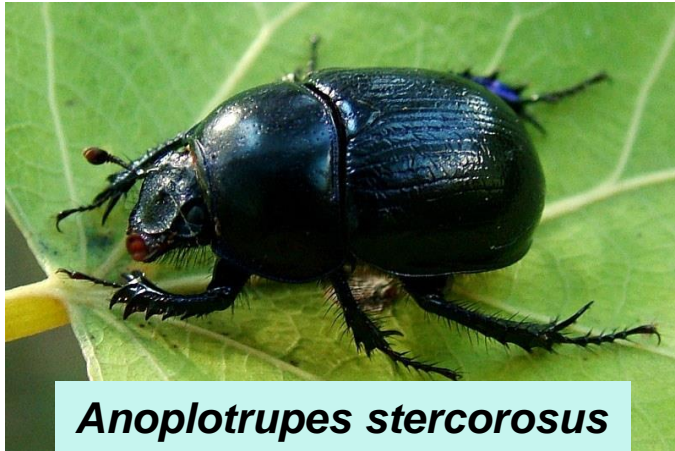
Web-link: <https://science.sciencemag.org/content/344/6185/738>

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 with white spots, perched on a green leaf of a Ceanothus spinosus plant. The insect's body is segmented and elongated, with long, thin legs. 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

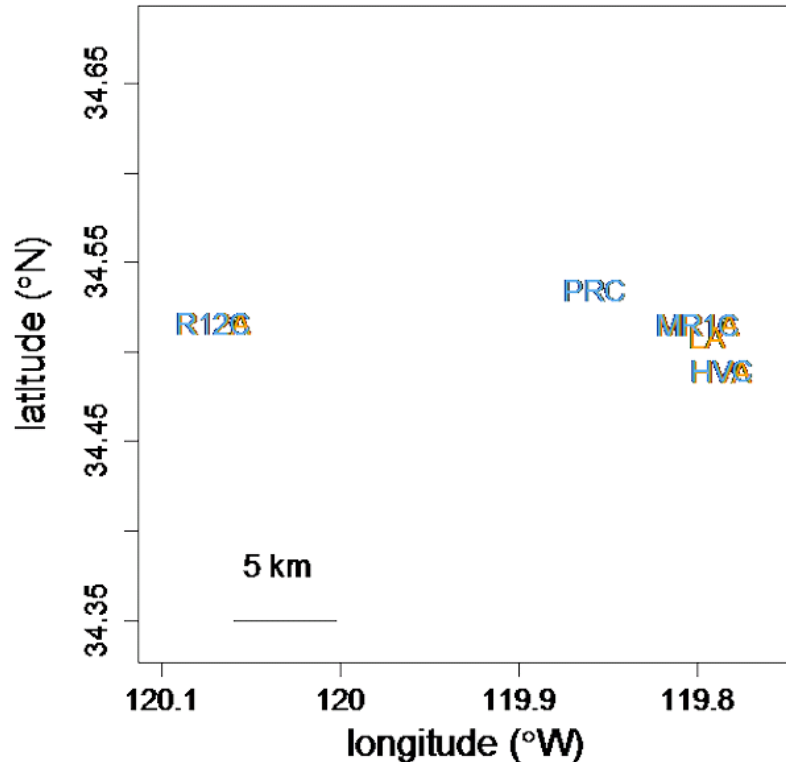
Questions, Methods and Results



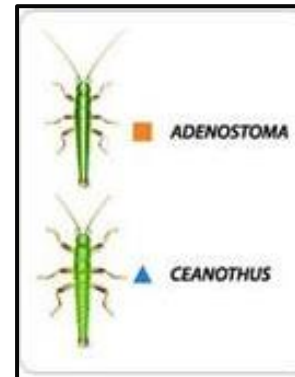
- **What are the effects of adaptation on genomic divergence?**
- **Can the underlying genetic changes driving the divergence of populations into new species be predicted or repeated?**

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

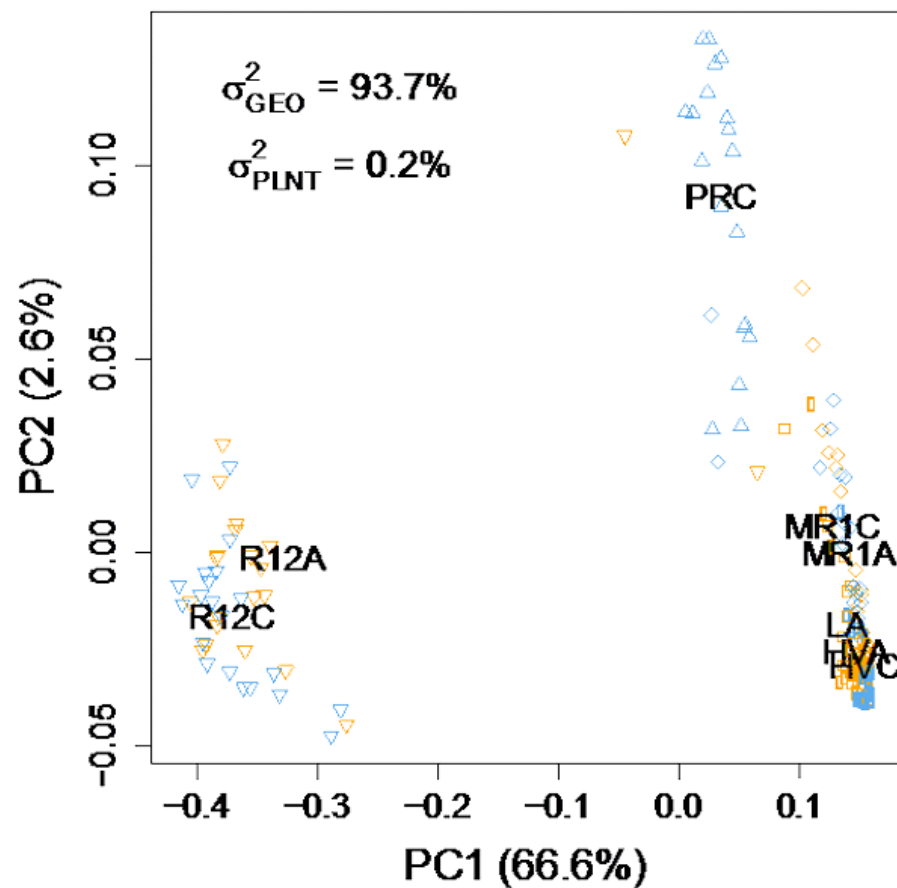
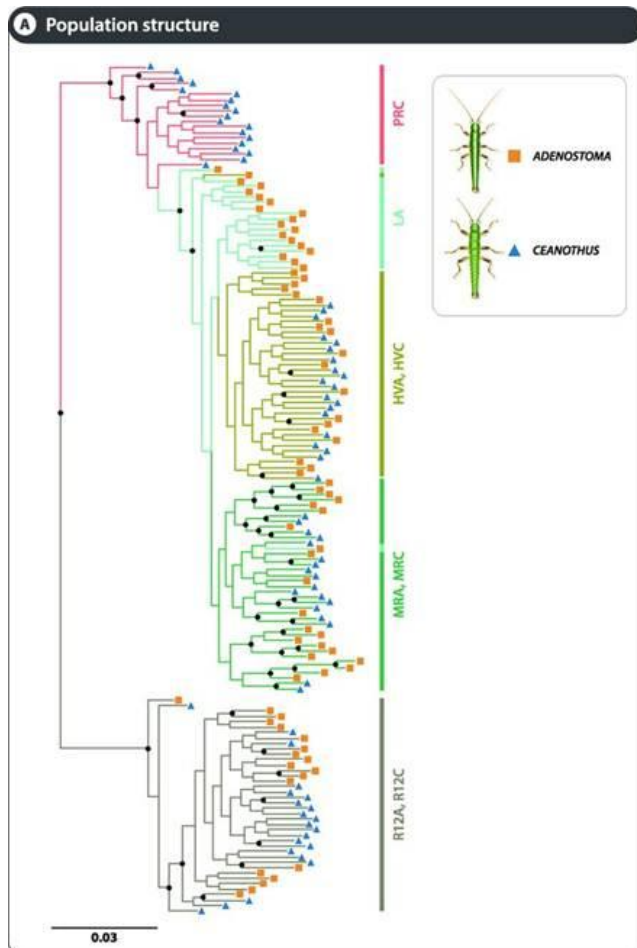


Sources (for this slide and next slide): [Science](#)

Questions, Methods and Results

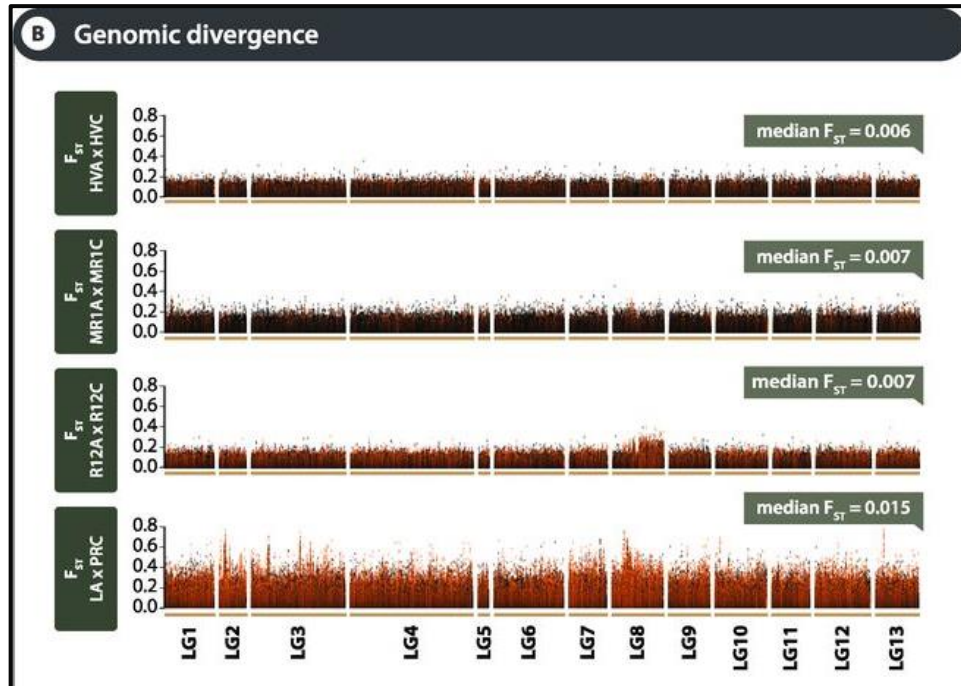


- Does genomic divergence vary geographically between different ecotype pairs?



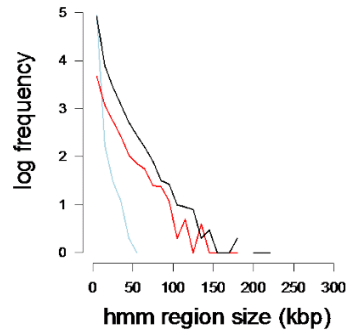
Questions, Methods and Results

Population Pair	HVA × HVC	MR1A × MR1C	R12A × R12C	LA × PRC
<i>Population characteristics</i>				
Geography	adjacent	adjacent	adjacent	separated
Gene flow ($N_e m$)	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

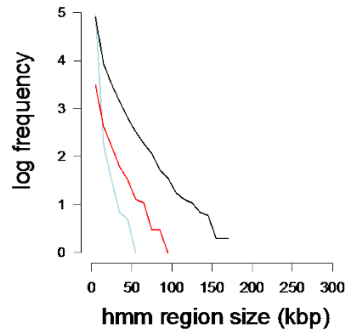


Questions, Methods and Results

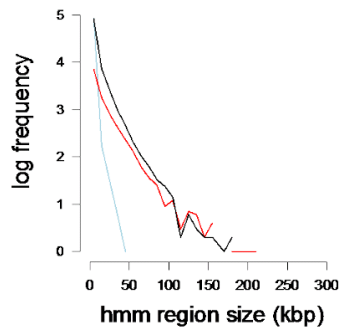
HVA x HVC



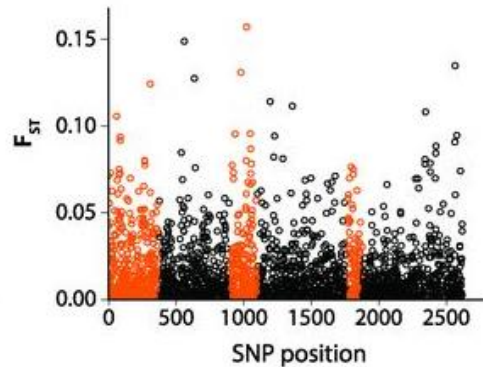
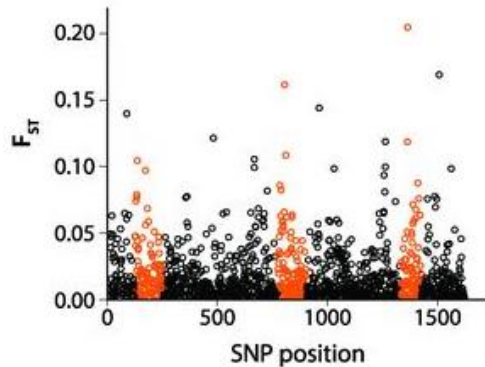
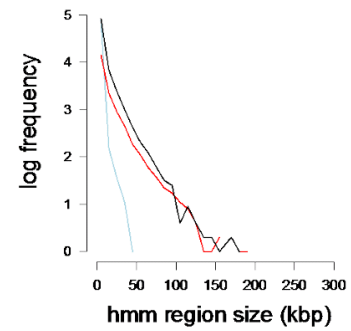
MR1A x MR1C



R12A x R12C



LA x PRC



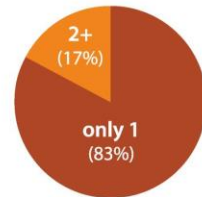
Distribution of the size of HMM regions (colours are: blue = low differentiation regions, black = moderate differentiation regions, red/orange = high differentiation regions). Absolute frequencies across the four categories are shown.

Questions, Methods and Results

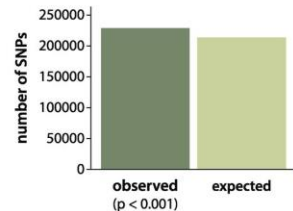
Test for parallelism of highly divergent SNPs. Quantiles refer to the empirical F_{ST} distribution.

	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

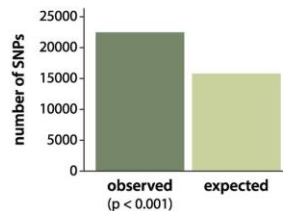
A Number of population pairs a SNP had high F_{ST} for



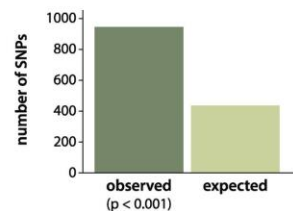
B High F_{ST} in 2 population pairs



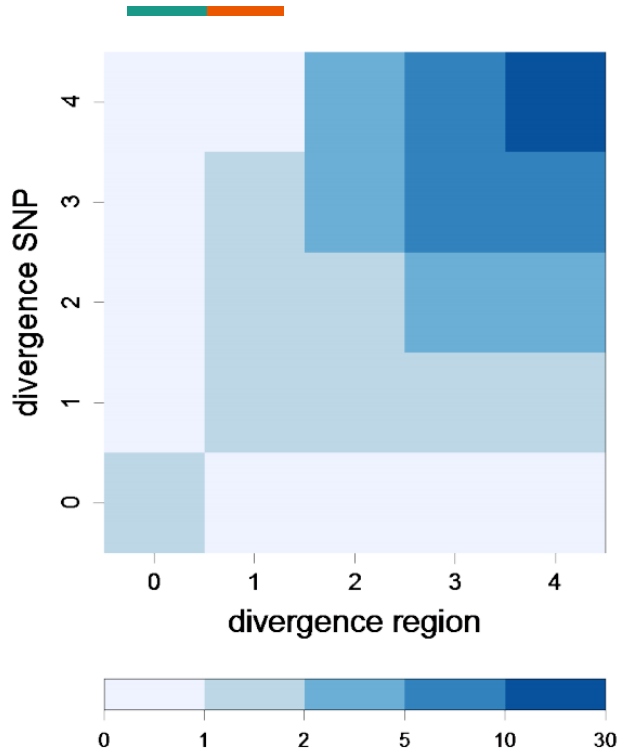
C High F_{ST} in 3 population pairs



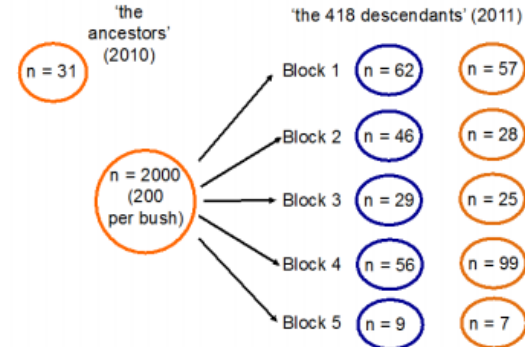
D High F_{ST} in 4 population pairs



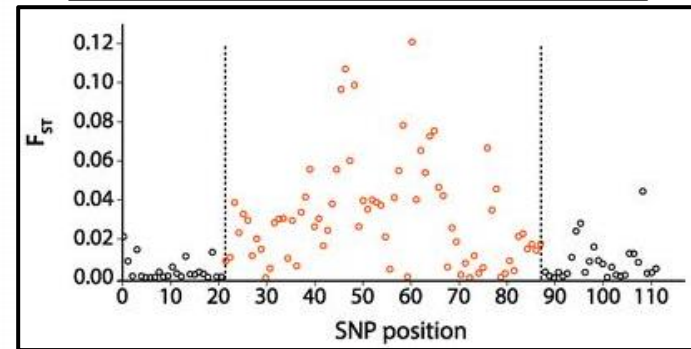
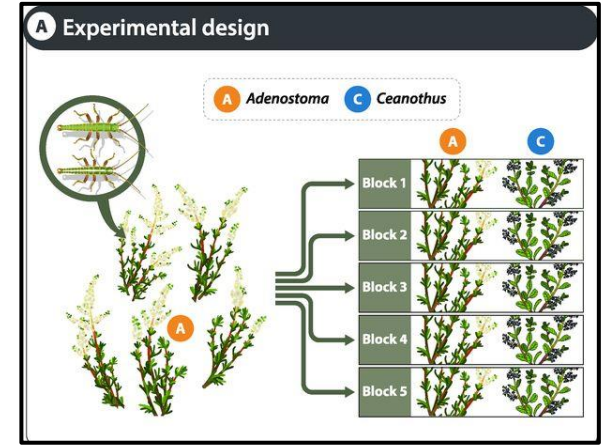
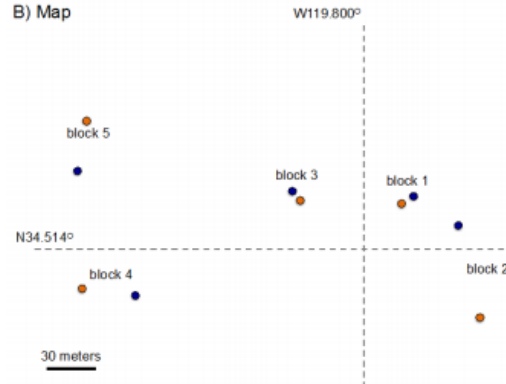
Questions, Methods and Results



A) Experimental design

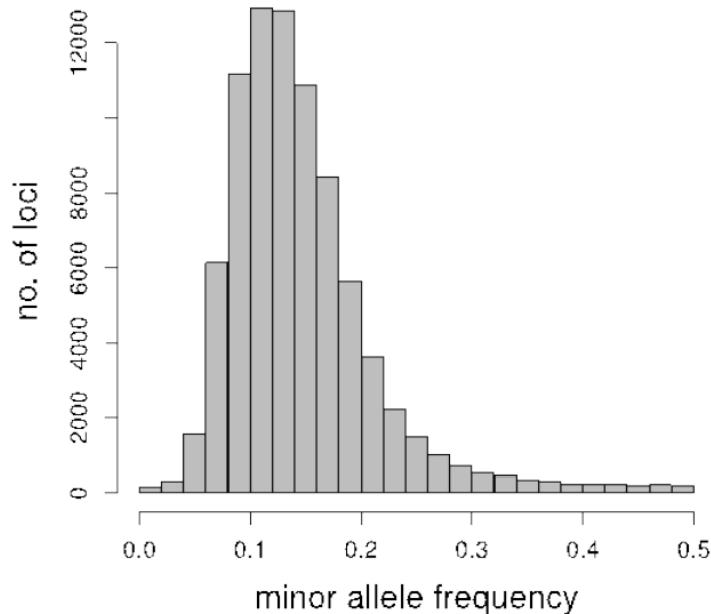


B) Map



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

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Any Questions/Suggestions?



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Thank-you!