

Identifying founding haplotypes reveals the history of the selfer, *Capsella rubella*.

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Background:

- Although many plants are outcrossing, the transition from selfing to outcrossing is one of the most common in flowering plants.
- Capsella rubella* (selfing) and *C. grandiflora* (outcrossing) are less than 100 kya diverged^{1,2,3}, providing a model of this transition.
- We identify the haplotypes that founded *C. rubella* to illuminate this transition.

Species	<i>C. rubella</i>	<i>C. grandiflora</i>
Mating Syst.	Predominantly selfing	Obligate outcrossing
Distribution	N. Africa, Mid. East, Europe, S. America	Greece, Italy, Albania
Syn. Diversity ⁴	0.4 %	1.8 %
π_N / π_S ⁴	0.173	0.144
Tajima's D _{syn} ⁴	0.42	-0.19

Questions:

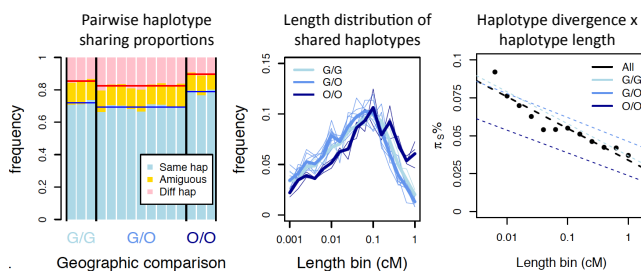
- When did *C. rubella* originate?
- How many chromosomes founded *C. rubella*?
- What is the effective population size of *C. rubella*?
- Is there evidence for recent growth in *C. rubella*?
- How has *C. rubella* spread across the world?

Data: RNA Seq aligned to *C. rubella* reference⁴.

- 6 *C. rubella* [from Greece (3) Algeria (1), Italy (1) & Argentina (1)].
- 5 *C. grandiflora* [From Greece].

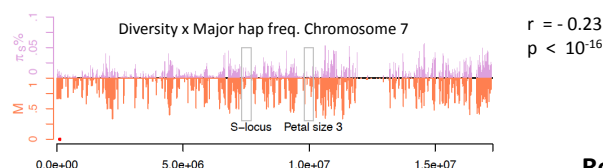
Patterns of haplotype sharing:

- Using *C. grandiflora* polymorphism, we place *C. rubella* samples on alternative founding haplotypes.
- Diversity between *C. rubella* samples, $\pi_{cr} = (1-p_0) \pi_{diff\ hap} + p_0 \pi_{same\ hap}$ where p_0 = prob. that two samples reside on the same founding haplotype.
- Assuming no divergence within haplotypes, and divergence between haplotypes = interspecific divergence, $p_0 \approx 0.8$.



- Two samples reside on the same haplotype for $\approx 80\%$ of their genome.
- Out of Greece [O] samples reside on the same hap. more often and for longer than comparisons within Greece [G] or across geog. Comparisons.
- From haplotype length x divergence, we estimate a 6% outcrossing rate.

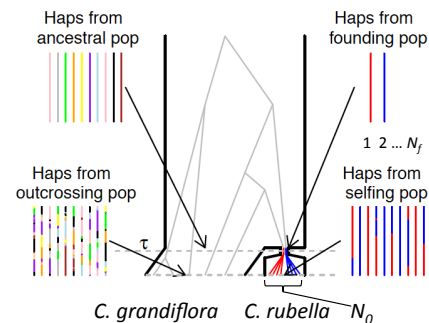
Genome-wide, π_S decreases with major hap. freq.



Summary: comparing within vs. between haplotypes

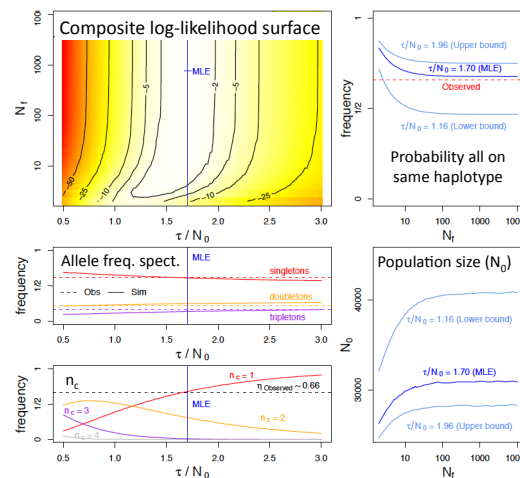
Haplotype	Same	Different
Syn. Diversity	0.05 %	2.22 %
π_N / π_S	.438	.139
AFS [Greece]	Slight excess of singletons	Excess of common alleles
AFS [Out-of-Greece]	Larger excess of singletons	Excess of common alleles

Conceptual model:



Inference:

- Samples –**
Observed (Four exchangeable samples: 3 Greek, 1 Italian).
Simulated (Four samples under the model above).
- Observations –**
Probability all reside on the same haplotype.
Obs. in sims: # founding chromosomes (the variable, N_f) and # lineages surviving to bottleneck (n_c).
Allele freq. spectrum when all on the same haplotype.
Obs. in sims: Distribution of coalescence times.



Conclusions:

Question	Answer
# founding chroms (N_f)	Potentially many (range 3 : ∞ , MLE = 750)
# effective chroms (N_0)	25,000 : 48,000 (MLE = 31,000)
Founding time (τ)	48 : 52 kya (MLE = 51 kya)
What is the demographic history of <i>C. rubella</i> ?	No recent growth in Greece Evidence for 'Out-of-Greece' event Structure and/or recent growth Out-of-Greece

References

- 1) Foxe et al. 2009. PNAS 106: 5241 – 5245.
- 2) Guo et al. 2009. PNAS 106: 5246 – 5251.
- 3) St. Onge, et al, 2011. Molecular Ecology 20: 3306–20.
- 4) *Capsella* Genome Consortium. The *Capsella rubella* genome provides insights into the causes and consequences of mating system evolution. *In prep*