

Dominance hierarchy and the genetic load linked to self-incompatibility alleles in Brassicaceae



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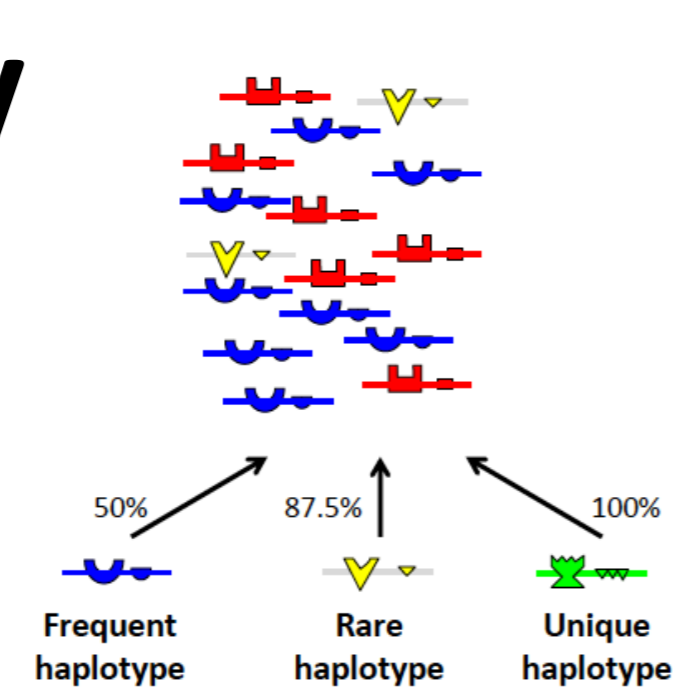
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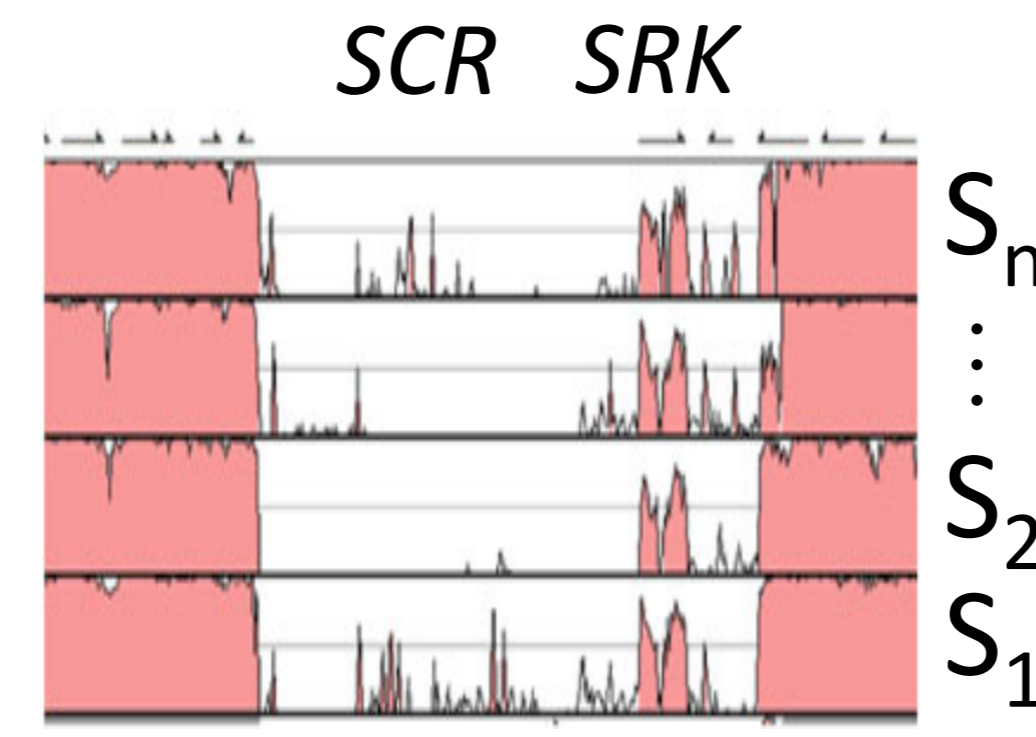


1. Self-incompatibility

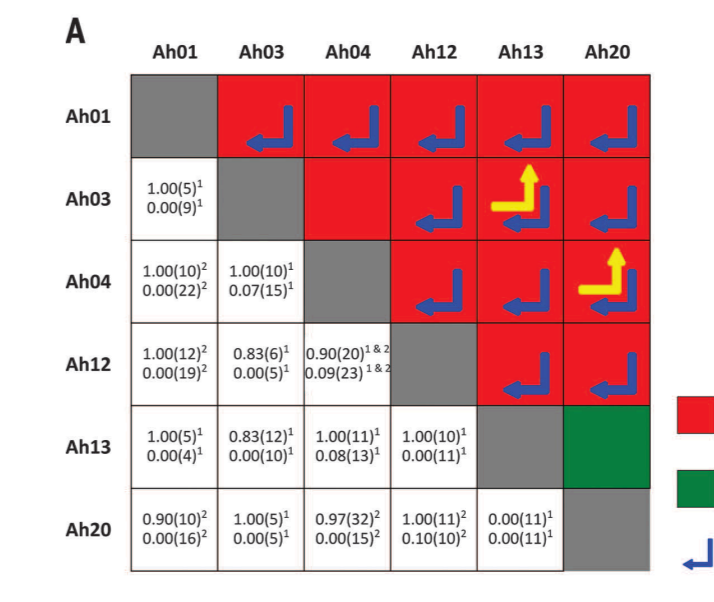
A large number of recognition specificities stably segregate over long evolutionary times because of **long-term balancing selection**.



Genomic sequencing of the S-locus region of several allelic lines shows a very simple structure, with a **30-110kb non-recombining region containing no gene** except those directly involved in self-recognition and modifiers of their expression.



The allelic lines form a **linear dominance hierarchy**



2. Long-term balancing selection and the sheltered genetic load

Linkage to a strongly balanced polymorphism

+

Enforced heterozygosity

=

Reduced efficacy of purifying selection for **genes linked to the S-locus region**

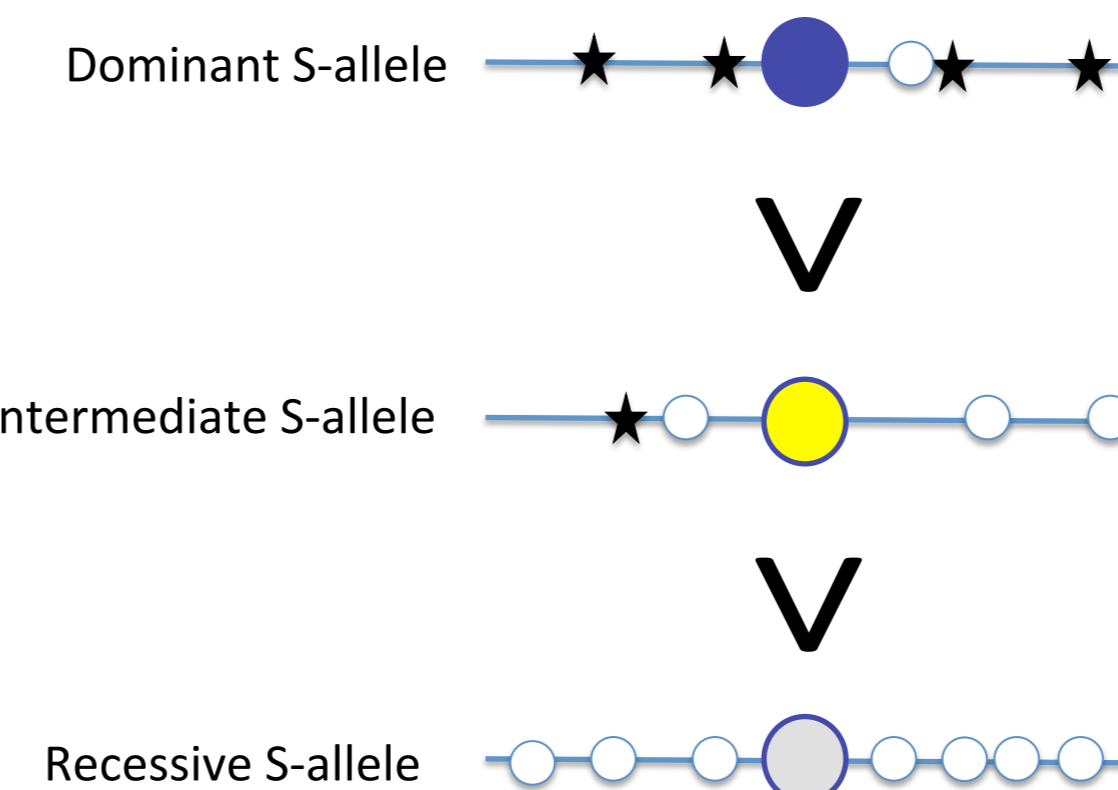
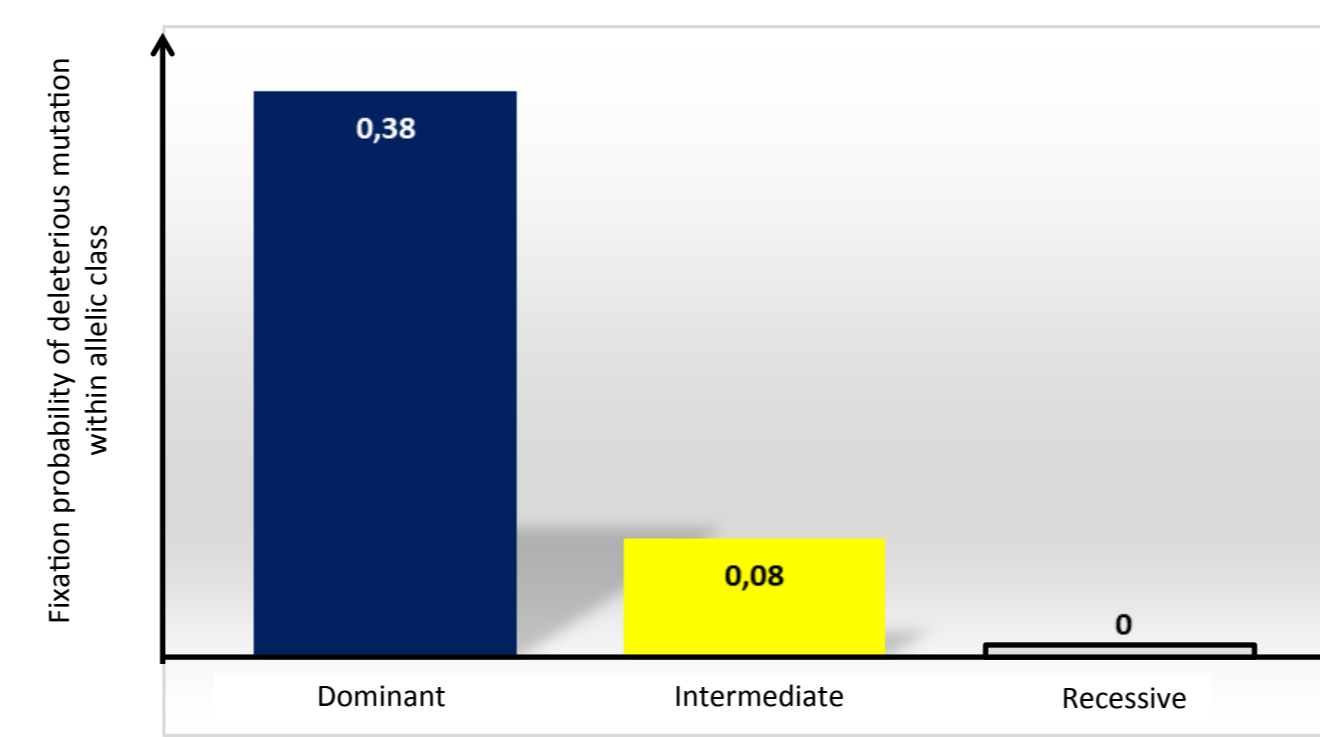
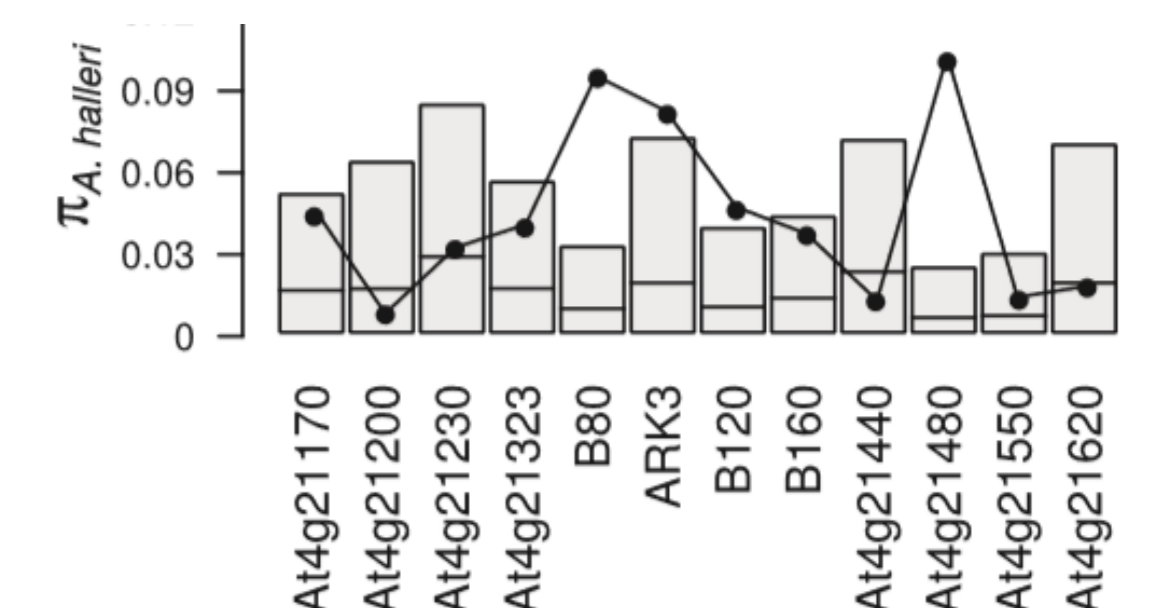


Figure 3. The fixation probability of deleterious mutations is higher when fully linked to dominant than to recessive allelic classes. Modified from Laurens et al. (2009)

➤ Plants homozygous for a dominant S-allele (S15) grow slower and smaller than heterozygotes for this allele, while no phenotypic difference was detected between homozygous and heterozygous for a recessive S-allele (S01) (Laurens et al. 2009)

✓ **The sheltered load is detectable at the phenotypic level, but where are the mutations causing it ?**

➤ Yet, the S-locus region itself contains no gene apart from *SCR* and *SRK*, and the region with increased polymorphism is very narrow (Roux et al. 2013)



Theoretical predictions and phenotypic evidence suggest a strong accumulation of deleterious mutations linked to dominant S-alleles.
Can we detect them at the genomic level ?

3. Do dominant S-alleles accumulate a larger number of deleterious mutations ?

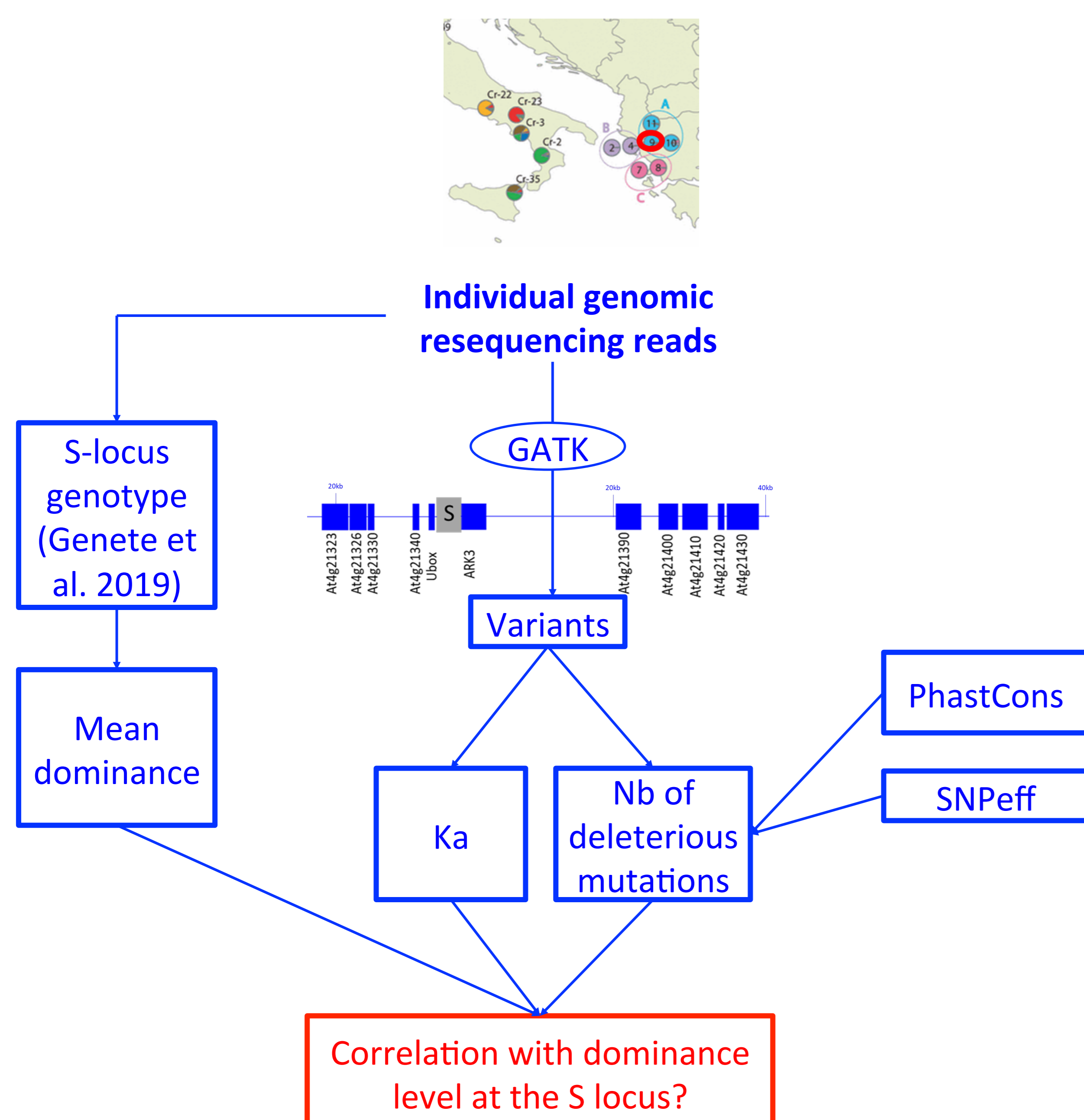


Figure 6. Our general approach to test the hypothesis of a correlation between the mean number of deleterious mutations and dominance of the S-alleles carried by individuals

Figure 7. In six *Arabidopsis halleri* populations from Japan (n=47 individuals, data from Kubota et al. 2014).

A. halleri

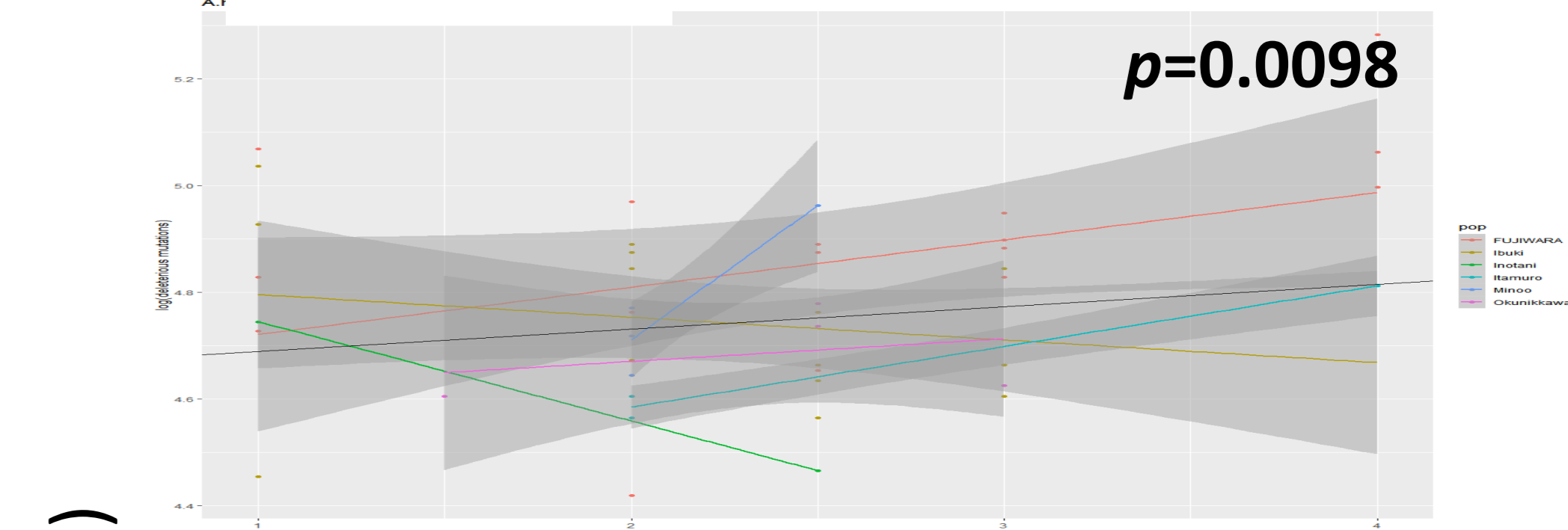


Figure 8. In five *Arabidopsis lyrata* populations from Europe and USA (n=25 individuals, data from Mattila et al. 2017)

A. lyrata

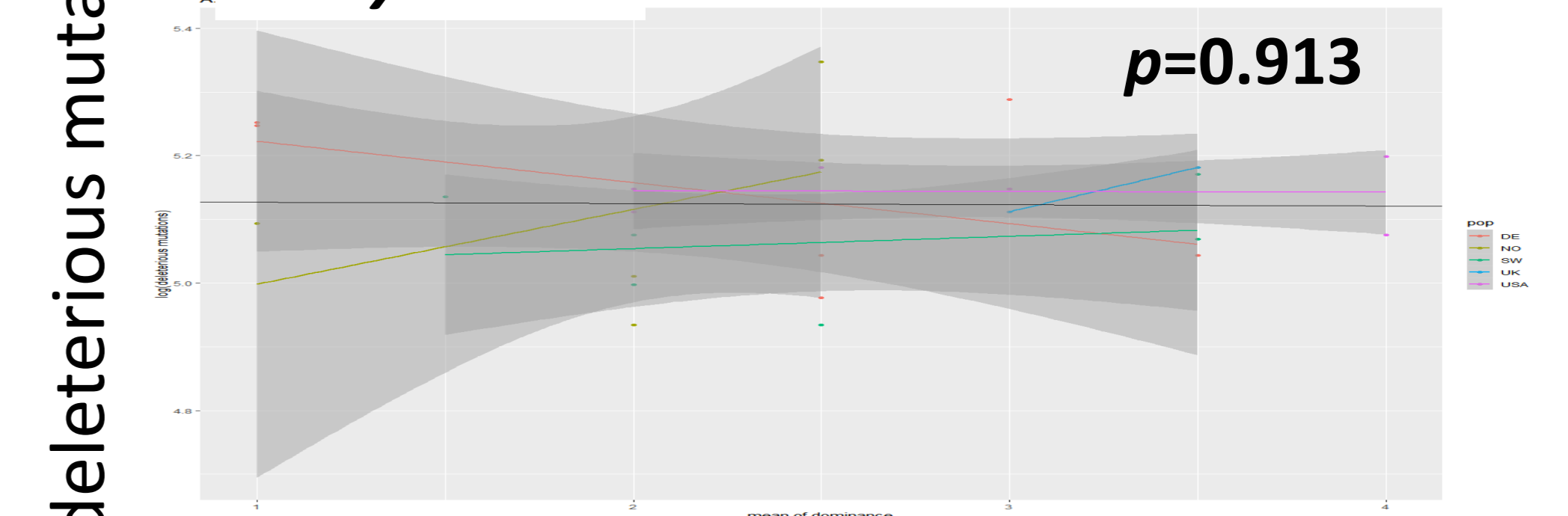
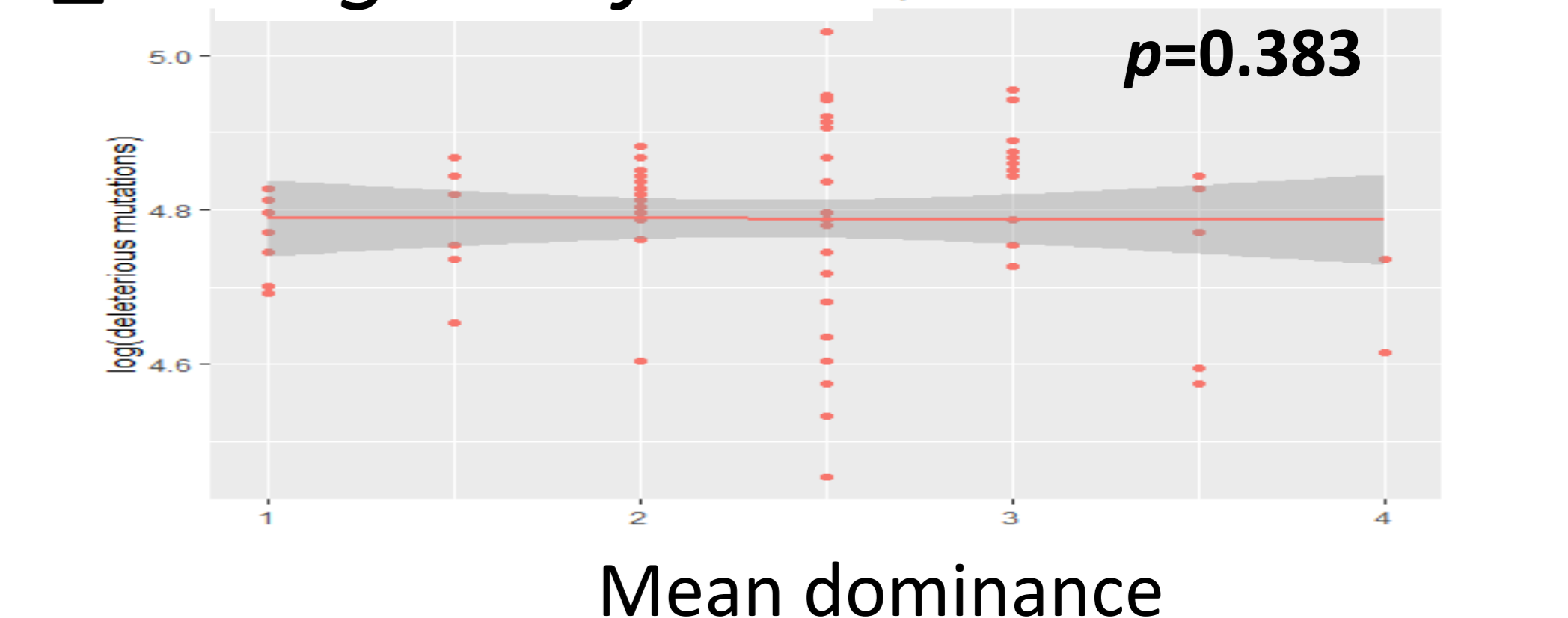


Figure 9. In one *Capsella grandiflora* population from Greece (n=84 individuals, data from Josephs et al. 2017).

C. grandiflora



4. Conclusions

✓ As predicted by theory, we find a correlation between dominance and the # deleterious mutations in *A. halleri*, but not *A. lyrata* or *C. grandiflora*

5. Perspectives

- Phased data based on parent-offspring trios
- Linked genes vs. complete genomic distribution
- Can results in the different species be explained by differences in population structure and population history ?