

Testing a theory for the evolution of inversions

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INTRODUCTION

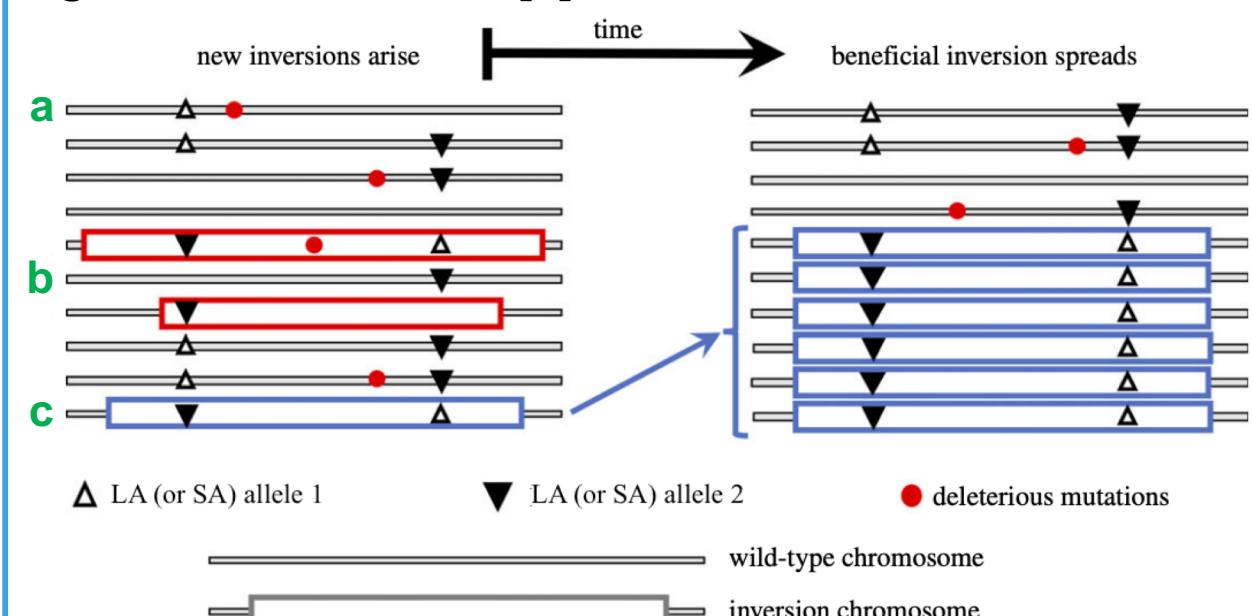
Inversions are structural genetic variants that suppress recombination.

An influential theory [1] predicts that inversions are favoured when they capture sets of locally adapted (LA) alleles (Fig. 1).

Put simply, in the absence of an inversion, a given LA allele sometimes resides with disadvantageous migrant alleles due to recombination (e.g. chromosomes **a** or **b** in Fig. 1).

However, an inversion-associated LA allele can avoid residing with disadvantageous migrants entirely (e.g. chromosome **c** in Fig. 1). Sets of LA alleles thus coupled are favoured—and the lucky inversion spreads in the population.

Figure 1. Modified from [2].



Now consider the case of sex-specific adaptation, in which males and females constitute two ‘local environments’ for evolution. Inversions arise, capture sets of sexually antagonistic (SA) alleles (e.g. a pair of female-beneficial alleles), and—as in Fig. 1—these lucky inversions spread [3].

Thus, if the theory is correct, **inversions should be enriched for SA alleles**.

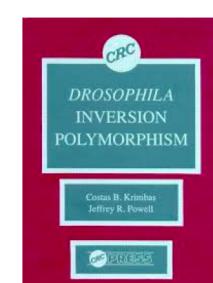
AIMS & METHODS

Are inversions enriched for SA variation?

Study organism

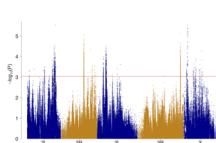


Inversion dataset



Breakpoints from common ($N=21$) and rare ($N=363$) polymorphic inversions [4,5]

SA dataset



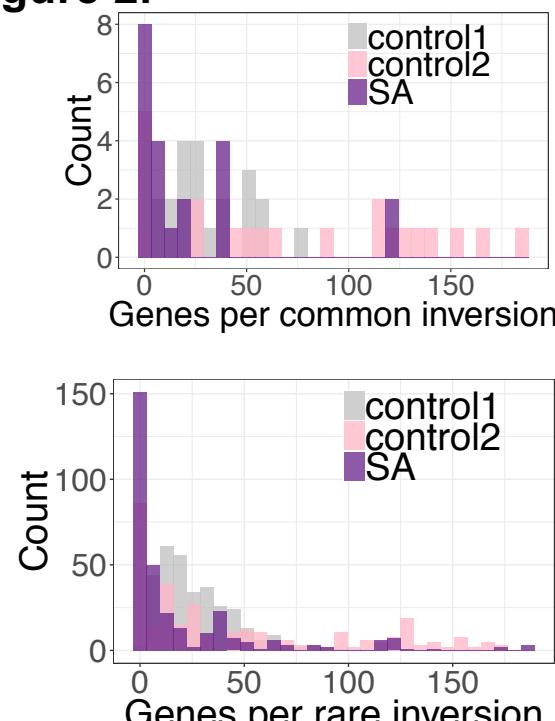
Genome-wide candidate SA polymorphisms ($N=2,372$) from a recent GWAS [6]

CONCLUSIONS

RESULTS (Preliminary—suggestions welcome!)

Test A. Are inversions enriched for SA genes?

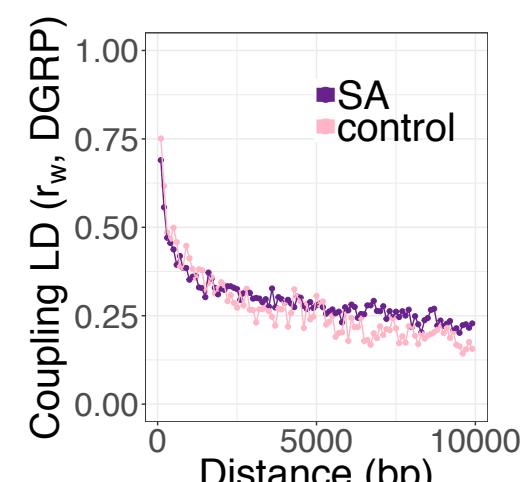
Figure 2.



Control1: Number of SA genes expected if distributed at random along the genome.
Control2: Number of genes associated with an orthogonal phenotype to SA.

Test B. Is there higher LD between SA alleles (relative to non-SA alleles) within common inversions that harbour SA alleles?

Figure 3.



Coupling LD: correlation coefficient between pairs of alleles with the same effect (e.g. pairs of female-beneficial alleles).

DGRP: wild US population of *D. melanogaster*.
Control: Top 2,372 SNPs from a GWAS of an orthogonal phenotype to SA.

References

- [1] Kirkpatrick & Barton 2006, *Genetics*; [2] Connallon et al. 2018, *Phil. Trans. B*; [3] Connallon et al., *in prep.*; [4] Lemeunier & Aulard 1992; [5] Chakraborty et al. 2018, *Nat. Gen.*; [6] Ruzicka et al. 2019, *PLOS Biol.*