Deciphering the genetic architecture of polygenic adaptation in *Tribolium castaneum*

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• Rationale:

How to detect and measure signals of polygenic adaptation?
Characterizing the dynamics of polygenic adaptation in populations undergoing environmental change is of primary importance for biologists. However, detecting the causal variants of polygenic traits under selection is challenging, as weak but meaningful associations are often under the barrier of statistical detection, and are hidden by phenotypic plasticity, genetic redundancy or drift.

• Integrative -omics approach:

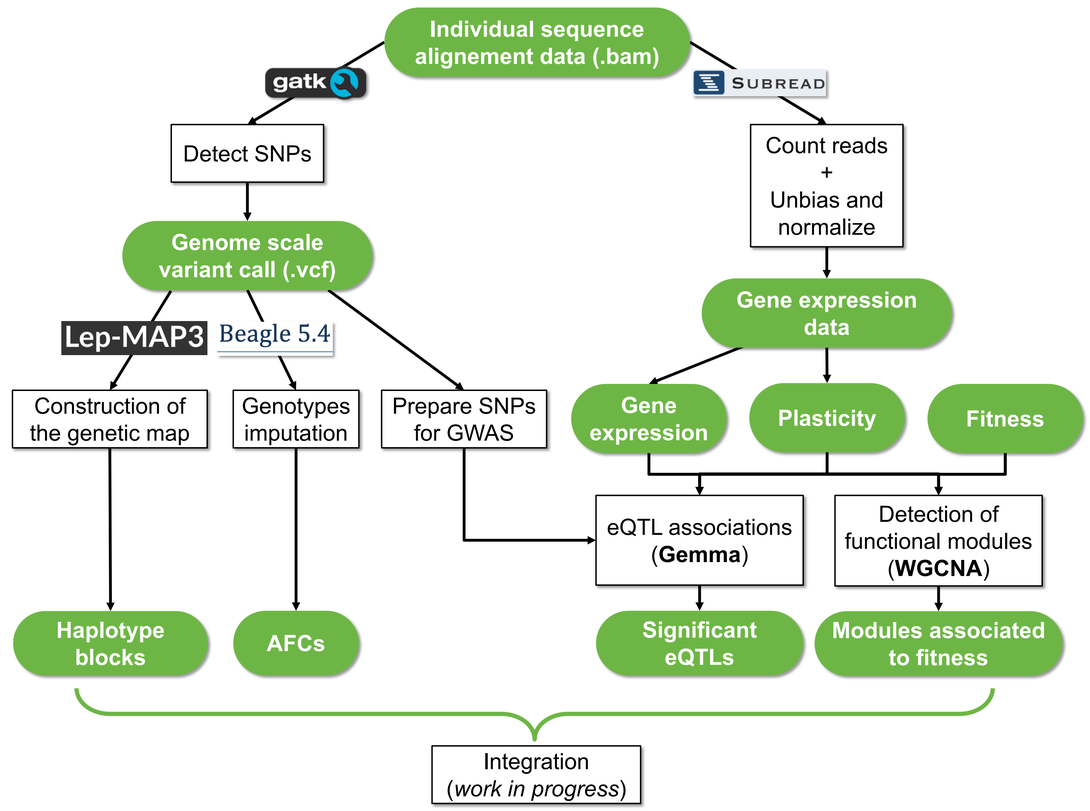
Here, we take advantage of **experimental evolution in the laboratory,** with populations of *Tribolium castaneum* adapting to stressful conditions (heat and drought). We apply an **integrative omics approach** at the levels of the genome, the transcriptome and the fitness to **decipher the genetic structure of polygenic adaptation**.

• Experimental evolution protocol:

One ancestral population is placed in two conditions: Control (**CT**) and Hot-Dry (**HD**). (4 replicate lines per condition). Populations evolved for **21 generations**. At generations 1 and 21, individual RNA-seq sampling and fitness measurements have been performed (614 samples, see E. L. Koch and F. Guillaume, 2020).

• (Preliminary) pipeline:

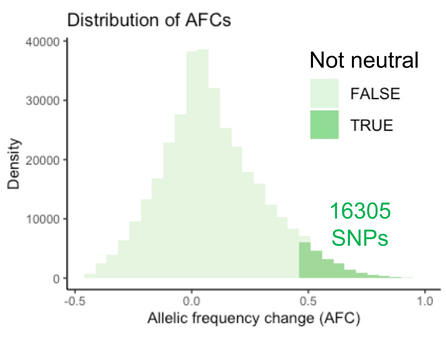
Individual RNA-seq samples are used to detect **single nucleotide polymorphisms (SNPs), allelic frequency changes (AFCs) and changes in gene expression and plasticity.**



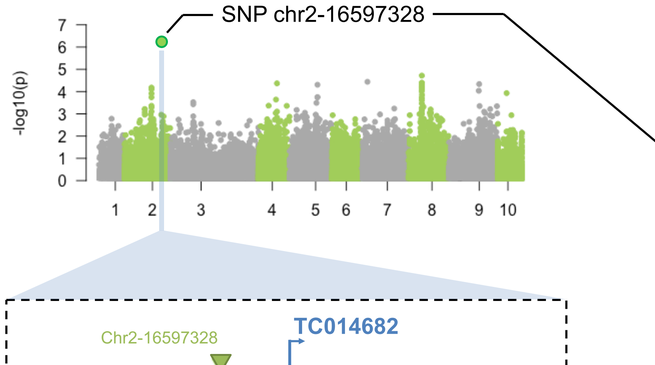
• Preliminary integrative approach:

• Between 3% and 6% of SNPs show a change in allele frequency (AFC) significantly higher than expected under neutrality.

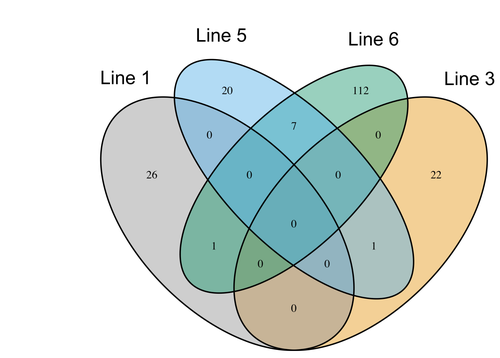
The distribution of AFCs under Control is assumed to be the result of drift, and is used as a control distribution for a bootstrap analysis (mean p-value < 0.05).

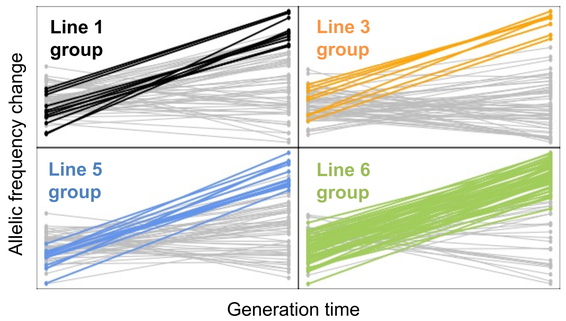


• One SNP *(Chr. 2, position 16597328)* is associated with the plastic response of gene TC014682 from module darkturquoise (FDR < 5%).
• This SNP belongs to a group of 189 SNPs under selection (< 1Mb of TC014682). None of the SNPs are located in TC013682.

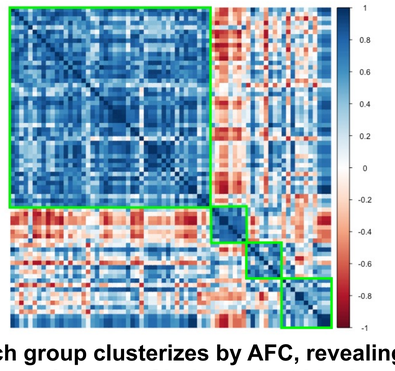


Chromosome 2, TC014682 1Mb region

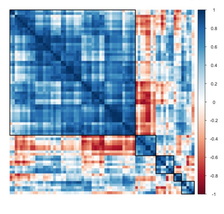




A redundant genetic structure emerges, where different groups of SNPs change in AFC in different lines, with almost no overlap.

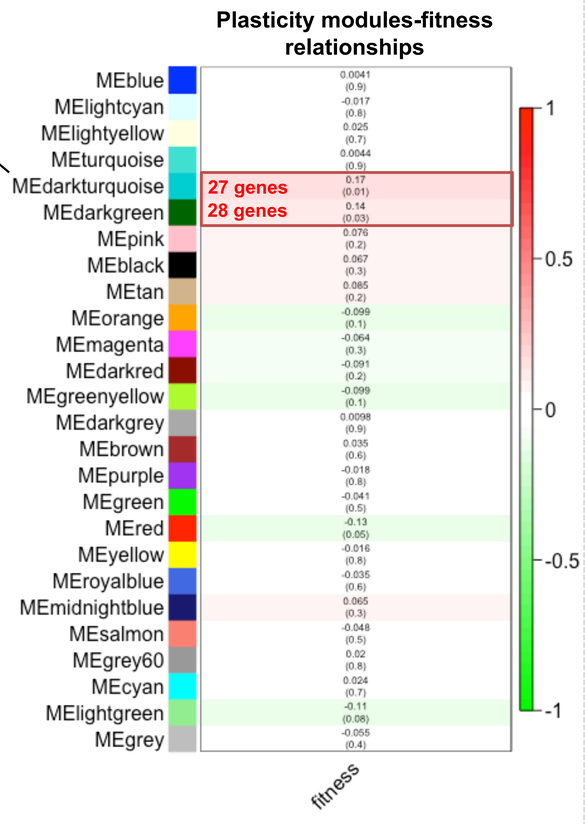


(AFC correlation matrix with hierarchical clustering)



Each group clusterizes by AFC, revealing the existence of independent blocks.

• No functional module of direct gene expression correlate with fitness in Hot-Dry in generation 1.
• Two functional modules of plastic response correlate with fitness (p-value < 0.05) in generation 1.



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