Supporting Information:

Uncovering the genetic signature of quantitative trait evolution with replicated time series data

Susanne U. Franssen, Robert Kofler, Christian Schlötterer

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1 Supplementary Figures

1.1 Figure S1: Fitness functions used for the simulation of quantitative trait adaptation to a new fitness optimum

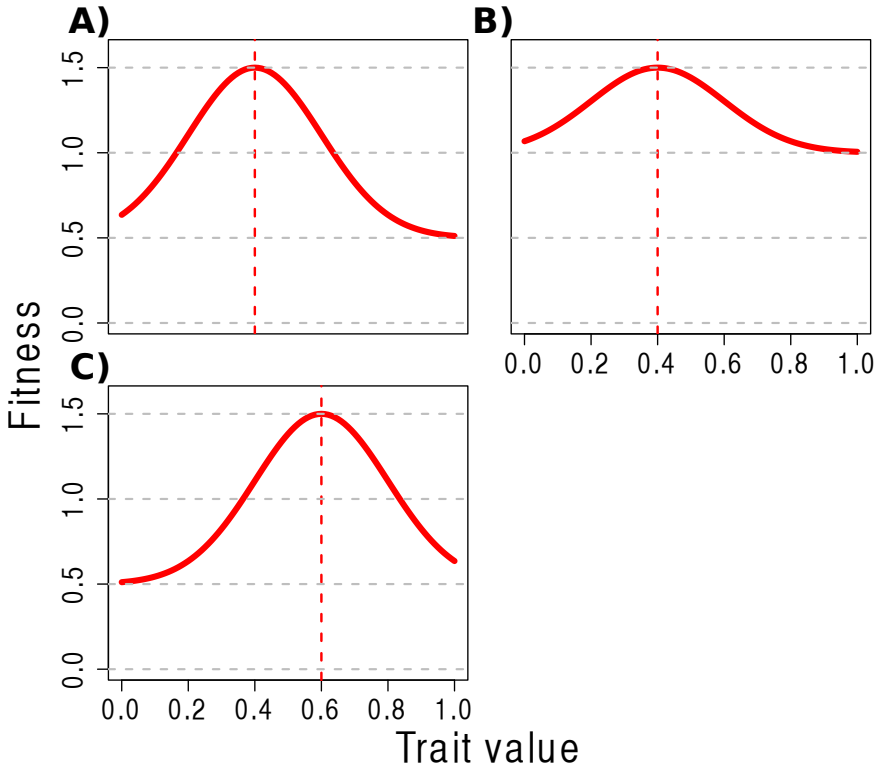

Figure 1: Fitness functions used for the simulation of quantitative trait adaptation to a new fitness optimum. A) Gaussian fitness function with default parameters: μ=0.4, standard deviation sd=0.2 and fitness range from 0.5 to 1.5 (Tab. 1). B) Gaussian fitness function with a reduced selection strength, i.e. a fitness range from 1 to 1.5 and C) Gaussian fitness with μ=0.6.

1.2 Figure S2: Polygenic adaptation to a new intermediate trait optimum on the phenotypic and genotypic level

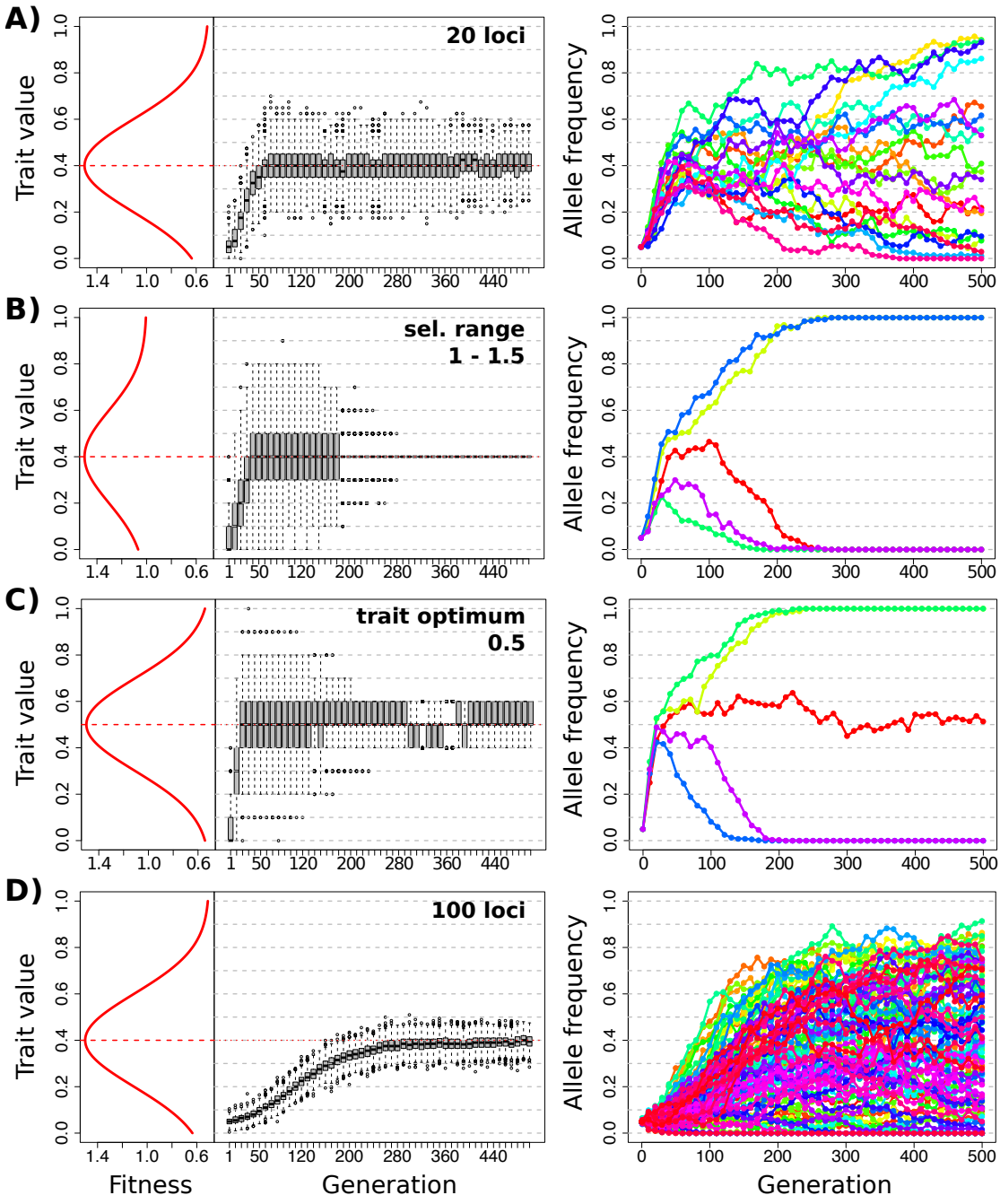

Figure 2: Polygenic adaptation to a new intermediate trait optimum on the phenotypic and genotypic level. Three characteristic phases of quantitative trait adaptation are reflected on both levels. Simulations were performed by modifying one of the default parameters (Fig. 1, Tab. 1), which is specified in the inset of the respective panel (A-C). Each panel shows the 3 characteristic phases in a single population adapting to a new trait optimum. The left panel shows the fitness function of each simulated trait along with trait values of the respective population (boxplots). In the right panel the respective trajectories of all selected alleles in the population are shown. The distinctiveness of the characteristic phases can be reduced when the number of contributing loci is substantially increased (D).

1.3 Figure S3: Change in phenotypic variance during adaptation to a new intermediate trait optimum

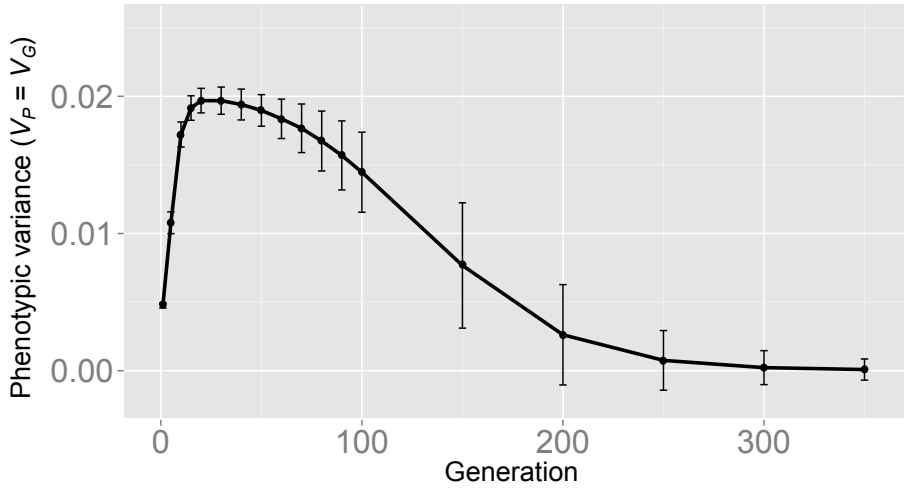

Figure 3: Change in phenotypic variance during adaptation to a new intermediate trait optimum. The phenotypic variance is depicted for the default parameter settings (Fig. 1, Tab. 1). Mean and standard deviation in V_P are shown across 500 replicate simulations. In the simulations the phenotypic variance equals the genetic variance (V_G) as environmental effects were not included in the model. Please note that the absolute value of $V_P = V_G$ is specific to our scaling of trait between 0 and 1 and therefore cannot be compared between simulations with different number of contributing loci. While the initial V_P here depends on the distribution of contributing alleles on founder genotypes, V_P increases rapidly in phase one, is maximal in phase 2 and ultimately decreases to zero at the end of phase 3.

1.4 Figure S4: Phase length of selection trajectories and phenotype response for various parameter settings

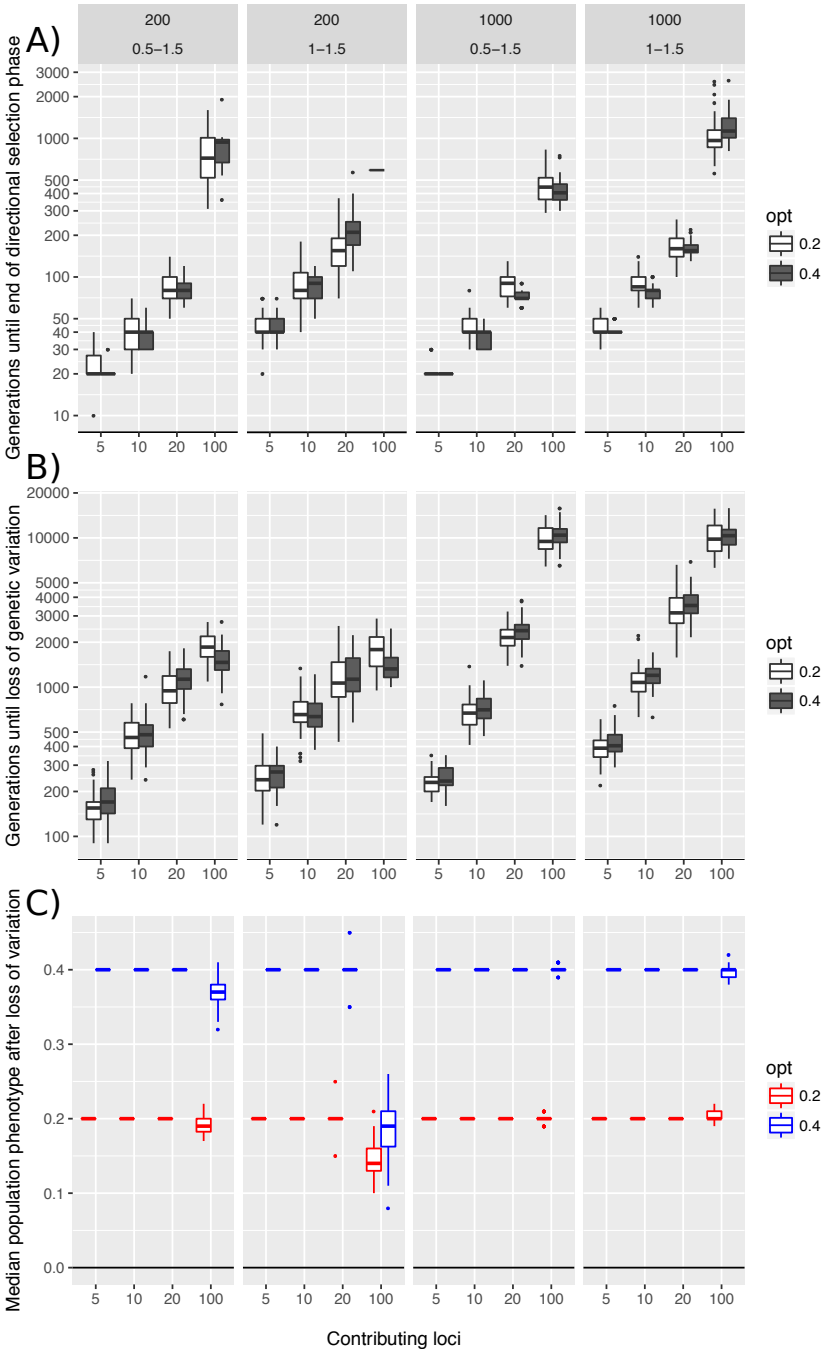

Figure 4: Phase length of selection trajectories and phenotype response for various parameter settings. Response values are shown with respect to $N_e \in \{200, 1000\}$, selection strength, i.e. range of phenotype fitness $\in \{0.5\text{-}1.5, 1\text{-}1.5\}$, optimal phenotype $\in \{0.2, 0.4\}$ and number of contributing loci $\in \{5, 10, 20, 100, 200\}$. Boxplots display values across 50 replicate simulations. A) End of the directional selection phase (phase1) defined by the first generation the population median phenotype reaches the optimum trait value. B) End of stabilizing selection (end of phase 3) defined by a loss of genetic variation (a standard deviation in the population phenotype equals zero). C) The median population phenotype at the time genetic variation has been lost. Phase length increases strongly with the number of contributing loci, larger N_e and to a lesser extent with reduced total selection strength. In the case of small N_e and a large number of contributing loci the phenotypic optimum is not reached by the population, mainly due to the loss of too many alleles necessary to reach the optimal phenotype.

1.5 Figure S5: Different allele frequencies of neutral and selected loci at the end of directional selection

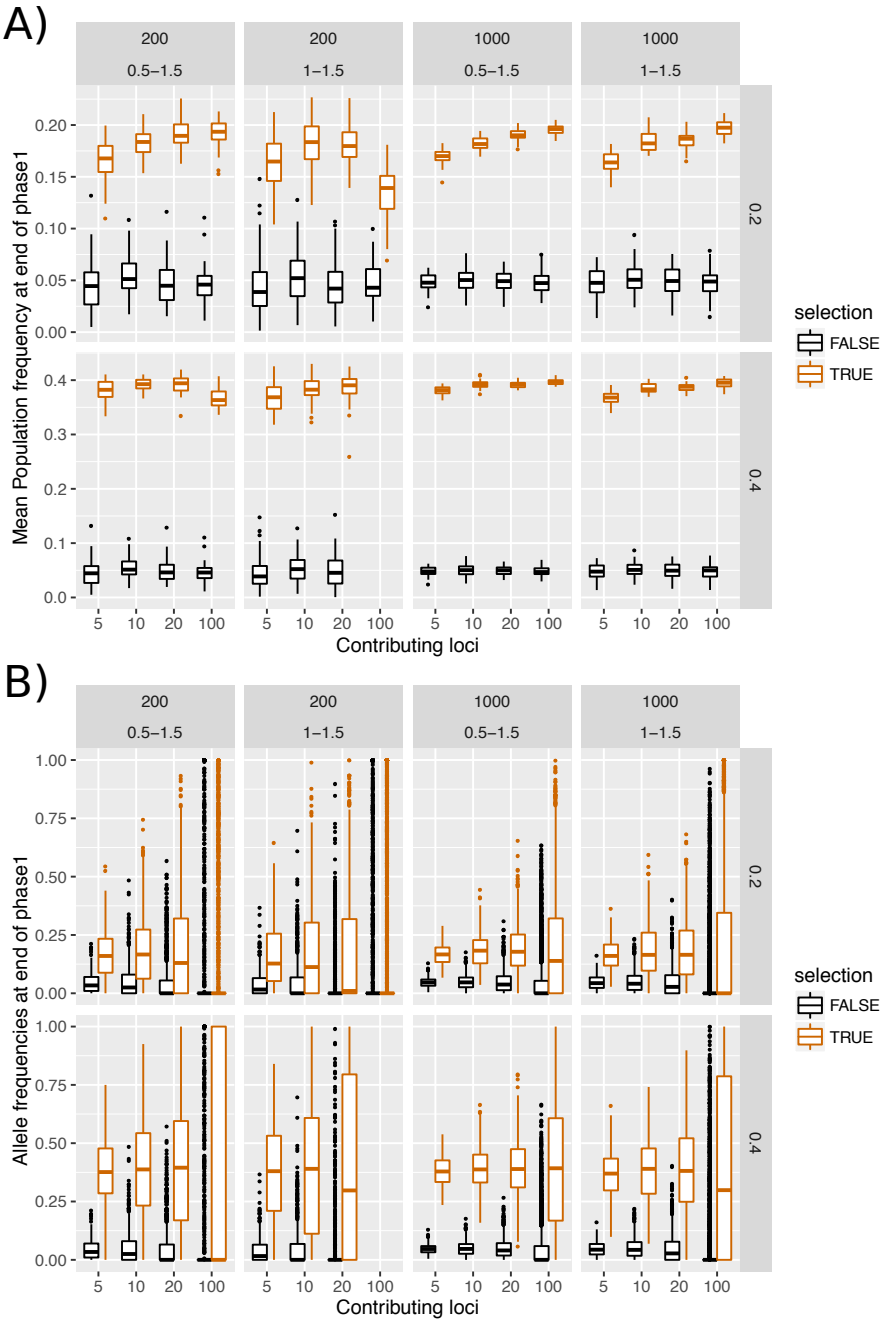

Figure 5: Different allele frequencies of neutral and selected loci at the end of directional selection (phase 1). Response values are shown for $N_e \in \{200, 1000\}$, selection strength, i.e. range of phenotype fitness $\in$ {0.5-1.5, 1-1.5}, optimal phenotype $\in \{0.2, 0.4\}$ and number of contributing loci $\in \{5, 10, 20, 100\}$. Each boxplot is based on 50 independent simulation scenarios. Columns with missing boxplot indicate that the median population phenotype never reached the optimum and therefore the end of the directional selection phase could not be determined (compare Fig. S4C). A) Mean population frequencies of all contributing loci vs. a matched number of neutrally-evolving loci of independent simulations at the end of the directional selection phase. B) Allele frequencies of all contributing loci vs. a matched number neutrally evolving loci from the same independent simulations as in A). If all contributing loci of the selected trait are known, mean population frequencies display a clear difference for means of neutrally-evolving alleles, in particular at the end of the directional selection phase (A). This difference is less pronounced if each locus is considered, rather than the average of all loci contributing to the trait (B). Differences between both scenarios become smaller with more contributing loci, smaller N_e (larger drift), closer optima and weaker selection.

1.6 Figure S6: Trajectories of quantitative trait loci after a change in the fitness optimum to an extreme phenotype

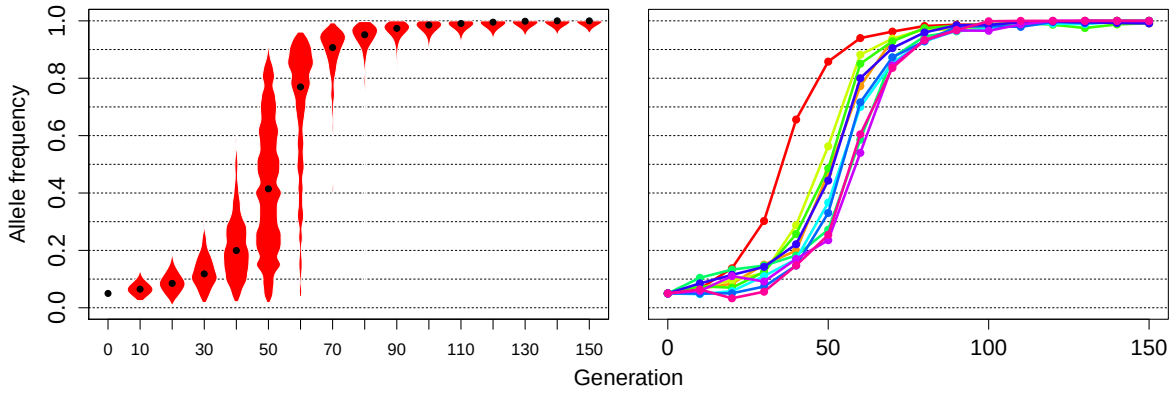

Figure 6: Trajectories of quantitative trait loci after a change in the fitness optimum to an extreme phenotype. Simulations were performed with the default parameters (Tab. 1) apart from an optimum trait value of 1 and a standard deviation of 0.3 in the Gaussian fitness function. The left plot shows the trajectories of one out of 5 equally contributing loci across 500 simulations summarized in violin plots, black dots indicate the median. The right plot shows examples for trajectories of the focal locus in 10 randomly chosen replicates. If the new optimum has an extreme trait value (here, a trait value of 1) all loci will eventually fix given a high enough starting frequency with respect to N_e.