Mapping the genetic basis of heterosis using a panel of Near-Isogenic Lines

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Most new mutations are on average partially deleterious and partially recessive. In natural populations, finite population size, spatial structure, and a history of bottlenecks can all increase the probability of fixation of partially recessive deleterious alleles. Crosses between different populations are expected to generate individuals that are heterozygous for partially recessive deleterious alleles that have been fixed within populations. This could result in heterosis, defined here as the increase in fitness of the F1 relative to the mean of the parental lines. Heterosis is common in natural populations of plants and animals, yet only in few cases its genetic basis has been identified. We study the genetic basis of heterosis in two locally adapted populations of A. thaliana from Italy and Sweden using a panel of Near-Isogenic Lines (NILs) with introgression segments tilling across the genome in both genetic backgrounds. To determine the potential contributions of introgression segment size and/or specific genomic regions to overall heterosis, we generated F1 crosses between the ecotypes and backcrossed each NIL to its background genotype to generate a panel of heterozygous NILs. We grew these lines in two environments and quantified time to first flowering and fecundity (fruit production). We will discuss results for the heterozygous NILs, which we used to partition the overall heterosis into the effects of individual genomic regions. This study system is to our knowledge the first to leverage a panel of NILs to map the genetic basis of heterosis in natural populations and presents a unique opportunity to study the balance between mutation, selection, and drift in nature.