**Table S1: Number of male and female individuals genotyped for each population (Åland, Gotland, Öland, Saaremaa, and Uppland)** in the main experiment (2009) and the pilot experiment (2007), and number of individuals included in each PCA1 (larval and pupal traits only), PCAM (male adult traits only) and PCAF (female adult traits only).

**Table S2: Pearson correlation matrices for the larval and pupal traits, the adult male traits and the adult females traits.** Values are Pearson correlative values (*R*) and asterisks denote significance at the 0.05 (\*), 0.01 (\*\*) and 0.001 (\*\*\*) levels.The Bonferroni alpha values were corrected for 27, 15 and 91 correlations, respectively.

**Table S3: Eigen values, cumulative proportion of variance value and component loadings for the four first principal components of the principal component analysis performed on the larval and pupal traits.** Highest values from each PCA appear in bold for easier visualization of the results.

**Table S4: Eigen values, cumulative proportion of variance value and component loadings for the three first principal components of the principal component analysis performed on the male adult traits.** Highest values from each PCA appear in bold for easier visualization of the results.

**Table S5: Eigen values, cumulative proportion of variance value and component loadings for the three first principal components of the principal component analysis performed on the female adult traits.** Highest values from each PCA appear in bold for easier visualization of the results.

**Table S6: Minimum allele frequency (MAF), and minor allele for the 49 SNPs genotyped**. Each *Pgi* locus was genotyped twice. SNPs tagged with “(f)” failed our quality criteria, while SNPs tagged with “(\*)” were genotyped for the 2007 pilot study. HWE: Hardy Weinberg Equilibrium; MAF: Minimum Allele Frequency; Gen: Genotyping; Homoz: Homozygote.Åland (ÅL), Gotland (GO), Öland (ÖL), Saaremaa (SA), and Uppland (UP).

**Table S7: Details of statistical analyses showing significant results, including statistical models used for each trait, as well as the explanatory variables included in the models.** Models of inheritance are given within brackets as Dominant, Recessive or Additive. Both main effects and interactions are reported. “NS” stands for non-significant.

**Table S8: The 15 SNPs showing significant environment effect on allele frequency, with the type of substitution and allele frequencies.** The minimum allele frequency for each SNP is shown in bold to ease visualization of the results. Allele frequencies differences between environments were calculated using directed permutation tests (1e+6 random permutations). The *p-*values give the posterior probability of the hypothesis that there is no difference between the environment types.