

File S4

Implementation of the method of Martin et al. (2008)

We analyzed the simulated data sets with Martin et al.'s method (MARTIN *et al.* 2008b). This method involves two separate tests: Comparing the estimates of the intra-population G matrix and the covariance matrix of population means for proportionality, and secondly, testing the proportionality coefficient of these matrices against the F_{ST} of molecular markers. The first test should see selection that has a magnitude comparable to random drift, but a direction incompatible with \mathbf{G}^A . The second test should see selection that has a magnitude incompatible with random drift, whether balancing or disruptive. Both tests are based on the assumption that

$$E[\mathbf{D}] = \frac{2F_{ST}}{1 - F_{ST}} E[\mathbf{G}_X]$$

under neutrality. We performed these tests following the procedure described by the authors (CHAPUIS *et al.* 2008; MARTIN *et al.* 2008b). Thus, we estimated the G matrices using R's MANOVA with three covariance components: inter-population, inter-family and inter-individual. The inter-population covariance matrix was used as an estimate of $E[\mathbf{D}]$, whereas the inter-population covariance matrix was multiplied by two to yield an estimate of $E[\mathbf{G}_X]$, which is appropriate for full-sib study design (LYNCH and WALSH 1998). Because the phenotypic data was known to be multivariate normal, it was not Cox transformed, but we followed the recommendation of standardization (CHAPUIS *et al.* 2008).

After this, the proportionality of $E[\mathbf{D}]$ and $E[\mathbf{G}_X]$ was tested, and a 95 % confidence interval was derived for the proportionality coefficient using code provided by MARTIN *et al.* (2008a). The Bartlett p value of the proportionality test was recorded. To perform the second test of MARTIN *et al.* (2008b), a 95 % confidence interval was estimated for the F_{ST} using bootstrap over loci and the Weir-Cockerham estimator (WEIR and COCKERHAM 1984) implemented in Fstat (GOUDET 1995). The confidence interval of F_{ST} was transformed into the confidence interval of $\frac{2F_{ST}}{1-F_{ST}}$. This was compared with the confidence interval of the proportionality coefficient obtained from the phenotypic data. If these intervals did not overlap, this was taken as a signal of selection.

References

- CHAPUIS, E., G. MARTIN and J. GOUDET, 2008 Effects of Selection and Drift on G Matrix Evolution in a Heterogeneous Environment: A Multivariate Q(st)-F-st Test With the Freshwater Snail *Galba truncatula*. *Genetics* **180**: 2151-2161.
- GOUDET, J., 1995 FSTAT (Version 1.2): A computer program to calculate F-statistics. *Journal of Heredity* **86**: 485-486.

- LYNCH, M., and B. WALSH, 1998 *Genetics and analysis of quantitative traits*. Sinauer Associates Incorporated, New York.
- MARTIN, G., E. CHAPUIS and J. GOUDET, 2008a <http://www.isem.cnrs.fr/spip.php?article934>, pp. Institut des sciences de l'evolution montpellier, Montpellier.
- MARTIN, G., E. CHAPUIS and J. GOUDET, 2008b Multivariate Q(st)-F-st Comparisons: A Neutrality Test for the Evolution of the G Matrix in Structured Populations. *Genetics* **180**: 2135-2149.
- WEIR, B. S., and C. C. COCKERHAM, 1984 Estimating F-Statistics for the Analysis of Population-Structure. *Evolution* **38**: 1358-1370.