

Genetic population divergence: markers and traits

Response from Latta and McKay

In our review [1] we summarized data of mean Q_{ST} and F_{ST} for 29 species and questioned the assertion that F_{ST} and Q_{ST} are strongly correlated [2,3]. Note that correlation of log-transformed values [1] is less than that for the untransformed values [3], which violate the assumption of normality. We argued that divergence in markers (F_{ST}) is a poor predictor of divergence in locally adaptive traits (Q_{ST}), and gave theoretical reasons why such a relationship should not be expected.

Crnokrak and Merila [4] suggest that our choice of studies accounts for the lack of strong correlation. Each review [1–3] includes studies using broad-sense estimates of Q_{ST} ; and/or assumptions about heritability within populations, thus departing somewhat from the strict assumptions of theory relating Q_{ST} and F_{ST} . As studies of F_{ST} and Q_{ST} accumulate, more studies will better meet these assumptions. Although sampling F_{ST} and Q_{ST} from separate populations is not ideal, studies are limited and if the correlation among species means has any generality, their inclusion should not introduce any systematic bias. All the studies that we

included enabled a formal calculation of Q_{ST} to be made. However, on review, we found an error in our calculation of $V_{g(w)}$ for some studies. We have updated our data set with corrected values (<http://www.dal.ca/~rglatta/QST/McKayLatta.html> gives an annotated summary of our calculations trait by trait and study by study) and recalculated our correlation ($r = 0.369$, $P = 0.049$ logarithmic) again finding an r^2 of <0.14 .

Moreover, much of the observed relationship derives from the observation that Q_{ST} is typically greater than F_{ST} [1–3]. Although this enables us to infer the action of local selection, it also induces a spurious correlation. If pairs of random numbers are constrained such that $0 < x < y < 1$, without any other relationship, the median correlation (1000 sets of 25) is $r = 0.67$. Thus, regardless of statistical significance, knowing marker F_{ST} enables little to be inferred about average Q_{ST} , save to suggest the lower limit representing the neutral case from which diversifying selection acts to increase Q_{ST} . Even less inference is possible about individual traits and certainly very little about the exact geographical patterns of adaptive population divergence within a species. We reiterate that, in simulations, diversifying selection on polygenic traits does not produce a response at neutral markers [5] such that markers cannot be expected to reflect adaptive differences. The stronger the local adaptation, the more Q_{ST} differs

from F_{ST} and the weaker the association. However, marker F_{ST} could predict the distribution of alleles at quantitative trait loci underlying adaptive traits, as these are expected to behave differently from the traits that they influence [5]. In this light, we can only welcome further theoretical development [6] on the evolutionary forces shaping F_{ST} and Q_{ST} .

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