**ERRATUM**

In a recent publication (Benestan et al., Molecular Ecology. 24: 3299–3315), we documented by means of a RADseq study, a fine scale population structure and evaluated the power of this data set for performing population assignment in the American lobster. First, our results revealed the existence of a hierarchical genetic structure separating lobsters from the northern and southern part of the range (FCT= 0.0011). Then, at a finer scale, we found population subdivision (11 genetically distinct populations), also with modest FST values, averaging 0.00185. Later, our results showed that at the regional scale we could reach a assignment success of 94.2% whereas at the population level, success was lower but still relatively high with 80.8%. We also assessed the potential for population assignment of our data set using the method of Anderson (2010), which consists in choosing a panel of markers based on FST ranking using a *training* data set and then performing assignment test using this panel of markers on a completely separate *hold-out* dataset. This showed that the highest success was achieved when performed with the top 3000 markers and then decreased with a higher number of SNPs.

Unfortunately, while the Anderson’s method was applied properly at the regional level, whereby very high assignment success was achieved without a high-grading bias, the method was not applied correctly at the population level. That is, the ranking of markers was made by mistake using all individuals followed by assignment test on the *hold-out* data set. When correcting for this mistake, our assignment success at the population level reduced dramatically to reach on average of 39.4% of individuals correctly re-assigned to the population where they were sampled. At first sight, these re-analyses therefore suggest that the higher assignment success obtained earlier was overly optimistic because it may have been caused by the high-grading bias, although we did intent to eliminate such bias in our analysis.

Alternatively however, and given the relatively small number of samples for each location (n=36 on average), dividing the samples into a *training* and a *hold-out* sets (on average n=18 each) may have resulted in biased FST values when ranking the markers due to sampling errors associated with too low sample size. Thus, we aimed at clarifying whether the differences in assignment success obtained previously and when properly applying the Anderson’s method was caused either (i) by a real problem of high-grading bias due to using the same individuals in ranking then in testing or (ii) potentially due to a down-grading effect associated with a reduced sample size causing biases in FST estimation when ranking the markers for subsequent population assignment.

Herein we explored this problem in different ways, first by using data from the two regional clusters for which sample size is large (n= 306 and 280 for the north and the south respectively). We thus applied the Anderson’s method properly (as was done in Benestan *et al.* 2015) and compare the assignment success with that obtained when we voluntarily provoked a full high-grading effect by using the same individuals for ranking and for testing (known as the classic *leave and out* method). While the assignment success obtained was indeed higher when creating the high-grading scenario, the difference between both results was modest, that is the mean success increased from 94.5% on average to 97.0%. From this, we conclude that the high-grading effect exist but is minimal in this system and would not be sufficient to alter our conclusions.

In contrary, the success of regional assignment revealed a much stronger down-grading effect associated with a reduction of sample size used for ranking markers based on FST measures (Figure 1). Assignment success was reduced by about 10% when using only 20 individuals (approximately the same number we used for the assignment at the population level) relative to the maximal values being achieved when using more than 150 individuals. This was true either when applying the Anderson’s method properly (Figure 2) or when provoking a high-grading scenario.

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Figure 1. Proportion of assignment success in relation to the number of individuals used for ranking SNPs (*training* set) considering the North (points in red) and the South (point in blue) reference populations, using the 3000 top-ranked SNPs as was done in Benestan et al. (2015)

Clearly then, regional assignment success was still high after correcting for high-grading bias (94.5% instead of 97%). Then, regional assignment success corrected for high-grading bias and using the same number of samples that we have in our sampling location (which was about 36 individuals) should not be really different (say more or less 10%) from the one observed using more individuals. To test this hypothesis, we selected randomly 36 samples from each region, ranked SNPs based on half of these samples (*training* set), kept the 3000 top-ranked SNPs for performing the assignment test and then calculated the assignment success on the *hold-out* set. In this case, assignment success was about 60%, which is close to the 50% of success in the case of random assignment test with only two groups (the two regions). Here again, we observed that the down-grading effect caused by reduced sample size was much more pronounced than the high-grading effect estimated above.

We further illustrate this by comparing the 50-50 scenario we had used at the population level for applying the Anderson’s method with the one retaining 30 individuals (*versus* 18 on average) for ranking and using the remaining individuals for testing. Our results show that while assignment success remains modest in both, it is higher for the 30 individuals with average values increasing from 31.7% (92 individuals correctly assigned on 290 as *hold-out* set) to 39.4% of assignment success (30 individuals correctly assigned on 76 individuals as *hold-out* set) when considering about 18 to 30 individuals respectively. However, a important point to consider is also that the estimation of success rate will also depend on the number of individuals available for testing assignment as sampling error will be at pay there as well. Thus we observed a strong and highly significant correlation between the number of individuals/population available for testing and assignment success when applying the 50-50 scenario (P-value < 0.001, R2=0.99).

These additional analyses demonstrate that high assignment success can be achieved in situation of weak absolute genetic differentiation (e.g. FST = 0.00185), as long as the sample size is relatively high. Results also indicate that high-grading bias may not always be important as shown by the modest difference obtained between the Anderson’s method and a full high-grading scenario. In contrast, our results also illustrate that applying Anderson’ method (splitting samples into *training* and *holdout* datasets) will be problematic in most standard studies using sample size similar to ours (sample sizes in standard GBS or RADseq studies are often comparable to these used in our study, that is say 30-40 sampling location), at least in studies or organisms with weak population differentiation (FST < 0.01), because it may systematically result in a down-grading effect that will artefactually reduce the apparent assignment success.. Thus, any further studies aiming at quantifying assignment success and correcting for high-grading bias should be designed to analyse large sample size (at least n =50) per location.