

Fig. S1. Mean depth distribution across sites of the raw data before filtering

Table S1. Nucleotide diversity (π) and Watterson's θ W calculated per pool using individual mpileup files and the
Variance-sliding.pl function in PoPoolation v1.2.2, with the following parameters: -min-count 2 -min-coverage
20 -max coverage 200 -window-size 1000 -step-size 1000 -min-covered-fraction 0.2.

Populations North - South	π	Watterson's θW
MON	0.013	0.016
BIC	0.014	0.018
JAL	0.016	0.019
СОЈ	0.017	0.018
NAP	0.013	0.013
ISV	0.015	0.015
YEL	0.009	0.010
ANN	0.016	0.019
POD	0.016	0.018
PAV	0.016	0.018
DAP	0.017	0.019
POL	0.014	0.017
ITS	0.017	0.020

Fig. S2. Relationship between the average amount of missing data (%) per population pair and their corresponding F_{ST} value. We allow a 25% of missing data per population (--missing-indv 0.75), meaning that it filters genotypes called below 75% across all populations. The Pearson correlation coefficient (r = 0.10) indicates a very week positive linear relationship. The coefficient of determination R²=0.01 suggests that only 1% of the variance in FST can be explained by the average amount of missing data, with a p-value of 0.38 indicating that this correlation is not statistically significant.



Fig. S3. Series of Principal Component Analysis (PCA) showing the first two axes of the genetic differentiation among the Kellet's whelk populations in the expanded and historical distribution range considering different amount of missing data. The proportion of missing data allowed, from the most restrictive option (no missed data) to a more lose one (50% of missing data), was explored by using the filter –max-missing implemented in VCFtools. Regardless the amount of missing data allowed, all PCAs show the same pattern in which MON and ITS are the most distant populations, BIC and POL are very similar and populations from the Santa Barbara Channel cluster together.





25% of missing data allowed, number of SNPs 46737





15% of missing data allowed, number of SNPs 42214

No missing data allowed, number of SNPs 30717

