**Supplementary table 1.**

List of *G. oceanicus* COI haplotypes from Krebes et al. (2011) which are available in BOLD. Number of identical sequences added to this study were determined based on haplotype frequencies.

|  |  |  |
| --- | --- | --- |
| **BOLD Sequence** | **Haplotype in Krebes et al. (2011)** | **Number of sequences added to this study** |
| **GBCMA3463-12** | **O1** | **21** |
| **GBCMA3464-12** | **O3** | **1** |
| **GBCMA3466-12** | **O4** | **1** |
| **GBCMA3467-12** | **O5** | **4** |
| **GBCMA3468-12** | **O6** | **1** |
| **GBCMA3462-12** | **O7** | **84** |
| **GBCMA3469-12** | **O8** | **1** |
| **GBCMA3465-12** | **O9** | **26** |
| **GBCMA3470-12** | **O10** | **19** |
| **GBCMA3471-12** | **O11** | **34** |
| **GBCMA3472-12** | **O12** | **1** |
| **GBCMA3473-12** | **O13** | **1** |
| **GBCMA3474-12** | **O14** | **3** |
| **GBCMA3475-12** | **O16** | **1** |
| **GBCMA3478-12** | **O18** | **1** |
| **GBCMA3479-12** | **O19** | **6** |
| **GBCMA3480-12** | **O20** | **3** |
| **GBCMA3481-12** | **O21** | **2** |
| **GBCMA3482-12** | **O22** | **12** |
| **GBCMA3476-12** | **O23** | **1** |
| **GBCMA3477-12** | **O24** | **2** |
| **GBCMA3461-12** | **O25** | **5** |

**Supplementary table 2**. Results of demographic and spatial mismatch distribution analyses along with Tajima’s D and Fu’s F neutrality tests for each demographic group. (HI=Harpending's Raggedness index, pHI=significance of HI, SSD=Sum of Squared Deviation, pSSD=significance of SSD, TD=Tajima’s D, pTD=significance of TD, FF=Fu’s F, pFF=significance of FF).

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Index** | | ***Gammarus oceanicus*** | | | ***Littorina saxatilis*** | | | ***Semibalanus balanoides*** | |
| **GaA** | **GaB** | **GaC** | **LiA** | **LiB** | **LiC** | **SeA** | **SeB** |
| **Mismatch distribution  under sudden expansion** | **HI** | **0.019** | **0.026** | **0.235** | **0.437** | **0.0527** | **0.187** | **0.0242** | **0.0122** |
| **pHI** | **0.33** | **0.45** | **0.66** | **0.62** | **0.56** | **0.42** | **0.44** | **0.68** |
| **SSD** | **0.001** | **0.004** | **0.007** | **0.001** | **0.0232** | **0.003** | **0.0129** | **0.001** |
| **pSSD** | **0.26** | **0.27** | **0.38** | **0.4** | **0.53** | **0.22** | **0.3** | **0.75** |
| **Mismatch distribution  under spatial expansion** | **HI** | **0.019** | **0.026** | **0.235** | **0.437** | **0.0527** | **0.187** | **0.0242** | **0.0122** |
| **pHI** | **0.66** | **0.73** | **0.38** | **0.62** | **0.48** | **0.36** | **0.8** | **0.9** |
| **SSD** | **0.001** | **0.003** | **0.001** | **0.001** | **0.0252** | **0.003** | **0.0181** | **0.001** |
| **pSSD** | **0.65** | **0.69** | **0.0** | **0.11** | **0.29** | **0.05** | **0.29** | **0.96** |
| **Tajima’s D** | **TD** | **-1.801** | **-1.24** | **-2.285** | **-2.294** | **-0.695** | **-1.477** | **-2.017** | **-2.356** |
| **pTD** | **0.008** | **0.07** | **0.0** | **0.0** | **0.273** | **0.055** | **0.002** | **0.0** |
| **Fu’s F** | **FF** | **-25.8** | **-14.23** | **44.905** | **-5.752** | **-1.3819** | **-3.06** | **-25.57** | **-25.37** |
| **pFF** | **0.0** | **0.001** | **0.0** | **0.0** | **0.319** | **0.002** | **0.0** | **0.001** |