**Supplementary tables**

**Table S1.** Details of the seven *B. edulis* microsatellite loci developed in this study. See table S2 for polymorphism characteristics in each of the studied populations.

|  |  |  |
| --- | --- | --- |
| **Locus** | **Primer sequences (5'‒3')** | **Number of alleles** |
| AC8 | CGCTGTAGACGTGTCATTCG CTCTCACCTCCCCATACGTG | 2 |
| AAC92 | GCGTCACCTCTTTCAAAGCA CTCGTTCTCTCTCCCTGTCC | 5 |
| AAC71 | GTTTTGCCTTTCCCCTTGGT GGAGAGTGGAGAGTGTGGAC | 6 |
| ACC81 | GACCACCACCACAAACAGAC TTGTTTCAGTGGCATGGGTG | 7 |
| AT102 | TGGCAGTAGAGGTTGAACGT TCGAGGCAGGCTAAATTCCA | 7 |
| AC101 | GTGAGTGGCTGTGTGAATGG ACGCACCCTATTGATCGAGT | 8 |
| AC111 | GCCATCACATCTTTCTTTGTCC CCCATCACAAGACCAGCATG | 11 |

**Table S2.** Observed heterozygosity (*H*o), expected heterozygosity (*H*e), uncorrected exact test results based on 10,000 Monte Carlo permutations (*p*-exact) and Bonferroni corrected *p*-values. *P*-values that remained significant after correction for multiple tests are highlighted in bold and underlined.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Locus** | **Population 1** | | | | **Population 2** | | | | | **Population 3** | | | |
| ***H*o** | ***H*e** | ***p*-exact** | ***p*-value** | ***H*o** | ***H*e** | ***p*-exact** | ***p*-value** | | ***H*o** | ***H*e** | ***p*-exact** | ***p*-value** |
| AAC92 | 0.167 | 0.621 | 0.031 | 1.000 | 0.308 | 0.625 | 0.003 | 1.000 | | 0.333 | 0.600 | 0.196 | 1.000 |
| AAC71 | 0.800 | 0.600 | 1.000 | 1.000 | 0.308 | 0.643 | 0.002 | 1.000 | | 0.667 | 0.800 | 0.468 | 1.000 |
| AC8 | 0.800 | 0.644 | 1.000 | 1.000 | 0.857 | 0.519 | 0.027 | 1.000 | | 0.333 | 0.333 | 1.000 | 1.000 |
| AT102 | 0.800 | 0.756 | 0.497 | 1.000 | 0.750 | 0.562 | 0.417 | |  | monomorphic | | | |
| AC111 | 0.667 | 0.878 | 0.0002 | 1.000 | 0.428 | 0.474 | 0.542 | 1.000 | | 0.667 | 0.800 | 0.467 | 1.000 |
| AC101 | 1.000 | 0.844 | 0.795 | 1.000 | 0.071 | 0.140 | 0.037 | 1.000 | | 1.000 | 0.733 | 1.000 | 1.000 |
| ACC81 | 0.667 | 0.712 | 0.137 | 1.000 | monomorphic | | | | | monomorphic | | | |
| **Locus** | **Population 4** | | | | **Population 5** | | | | | **Population 6** | | | |
| ***H*o** | ***H*e** | ***p*-exact** | ***p*-value** | ***H*o** | ***H*e** | ***p*-exact** | ***p*-value** | | ***H*o** | ***H*e** | ***p*-exact** | ***p*-value** |
| AAC92 | 0.500 | 0.429 | 1.000 | 1.000 | monomorphic | | | | | 1.000 | 1.000 | 1.000 | 1.000 |
| AAC71 | 0.250 | 0.536 | 0.429 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | | 1.000 | 1.000 | 1.000 |  |
| AC8 | 0.250 | 0.250 | 1.000 | 1.000 | monomorphic | | | | | monomorphic | | | |
| AT102 | 0.500 | 0.821 | 0.314 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | | monomorphic | | | |
| AC111 | 0.500 | 0.857 | 0.120 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | | monomorphic | | | |
| AC101 | 1.000 | 0.750 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | | 1.000 | 1.000 | 1.000 | 1.000 |
| ACC81 | monomorphic | | | | monomorphic | | | | | monomorphic | | | |
| **Locus** | **Population 7** | | | | **Population 8** | | | | | **Population 9** | | | |
| ***H*o** | ***H*e** | ***p*-exact** | ***p*-value** | ***H*o** | ***H*e** | ***p*-exact** | ***p*-value** | | ***H*o** | ***H*e** | ***p*-exact** | ***p*-value** |
| AAC92 | 0.000 | 0.429 | 0.142 | 1.000 | 0.800 | 0.733 | 1.000 | 1.000 | | 0.500 | 0.429 | 1 | 1.000 |
| AAC71 | 0.500 | 0.429 | 1.000 | 1.000 | 1.000 | 0.556 | 0.127 | 1.000 | | 0.750 | 0.857 | 0.655 | 1.000 |
| AC8 | 0.250 | 0.250 | 1.000 | 1.000 | 0.200 | 0.200 | 1.000 | 1.000 | | 1 | 0.6 | 0.399 | 1.000 |
| AT102 | 0.250 | 0.250 | 1.000 | 1.000 | 0.400 | 0.356 | 1.000 | 1.000 | | monomorphic | | | |
| AC111 | 0.750 | 0.892 | 0.122 | 1.000 | 1.000 | 0.800 | 1.000 | 1.000 | | 0.667 | 0.533 | 1.000 | 1.000 |
| AC101 | 0.500 | 0.429 | 1.000 | 1.000 | 0.333 | 0.333 | 1.000 | 1.000 | | 1.000 | 0.571 | 0.314 | 1.000 |
| ACC81 | 0.250 | 0.250 | 1.000 | 1.000 | monomorphic | | | | | monomorphic | | | |
| **Locus** | **Population 10** | | | | **Population 11** | | | | | **Population 12** | | | |
| ***H*o** | ***H*e** | ***p*-exact** | ***p*-value** | ***H*o** | ***H*e** | ***p*-exact** | ***p*-value** | | ***H*o** | ***H*e** | ***p*-exact** | ***p*-value** |
| AAC92 | 0.250 | 0.750 | 0.141 | 1.000 | 0.333 | 1.000 | 0.201 | 1.000 | | 0.667 | 0.600 | 1.000 | 1.000 |
| AAC71 | monomorphic | | | | 1.000 | 0.800 | 1.000 | 1.000 | | 1.000 | 0.800 | 1.000 | 1.000 |
| AC8 | 0.750 | 0.536 | 1.000 | 1.000 | 0.667 | 1.000 | 1.000 | 1.000 | | 0.667 | 0.533 | 1.000 | 1.000 |
| AT102 | monomorphic | | | | monomorphic | | | | | 0.667 | 0.800 | 0.601 | 1.000 |
| AC111 | 0.00 | 0.571 | 0.085 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | | 0.667 | 0.600 | 1.000 | 1.000 |
| AC101 | monomorphic | | | | monomorphic | | | | | 1.000 | 0.933 | 1.000 | 1.000 |
| ACC81 | monomorphic | | | | monomorphic | | | | | 0.333 | 0.333 | 1.000 | 1.000 |

(table continues on the next page)

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Locus** | **Population 13** | | | | **Population 14** | | | |  | | | |
| ***H*o** | ***H*e** | ***p*-exact** | ***p*-value** | ***H*o** | ***H*e** | ***p*-exact** | ***p*-value** |  |  |  |  |
| AAC92 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 |  |  |  |  |
| AAC71 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 |  |  |  |  |
| AC8 | 1.000 | 1.000 | 1.000 | 1.000 | monomorphic | | | |  |  |  |  |
| AT102 | monomorphic | | | | monomorphic | | | |  |  |  |  |
| AC111 | 1.000 | 1.000 | 1.000 | 1.000 | monomorphic | | | |  |  |  |  |
| AC101 | 1.000 | 1.000 | 1.000 | 1.000 | monomorphic | | | |  |  |  |  |
| ACC81 | 1.000 | 1.000 | 1.000 | 1.000 | monomorphic | | | |  |  |  |  |

**Table S3.** Genetic distances among *B. edulis* populations. The upper part of the table shows pairwise *F*st values. FDR corrected *p*-values are provided in the lower part of the table with significant values (< 0.05) highlighted in bold.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 |
| 1 | \* | 0.2367 | 0.1241 | 0.0518 | 0.1621 | 0.1294 | 0.2202 | 0.0767 | 0.1703 | 0.2028 | 0.1076 | 0.1775 | -0.1281 | 0.2339 |
| 2 | **0.0091** | \* | 0.2299 | 0.2822 | 0.1839 | 0.3374 | 0.1315 | 0.1501 | 0.1297 | 0.0558 | 0.1479 | 0.2706 | 0.1766 | 0.2989 |
| 3 | 0.4116 | 0.0846 | \* | 0.2109 | 0.1675 | 0.1675 | 0.1850 | 0.0370 | 0.0493 | 0.1852 | 0.0500 | -0.0230 | -0.0194 | 0.2627 |
| 4 | 0.5799 | **0.0137** | 0.2140 | \* | 0.2517 | 0.0750 | 0.1916 | 0.0962 | 0.3521 | 0.3085 | 0.2295 | 0.2490 | -0.0127 | 0.2965 |
| 5 | 0.9999 | 0.9999 | 0.9999 | 0.9999 | \* | 0.0000 | 0.1579 | 0.1831 | 0.3152 | 0.2276 | 0.2124 | 0.1300 | 0.1111 | 0.3333 |
| 6 | 0.9999 | 0.9999 | 0.9999 | 0.9999 | 0.9999 | \* | 0.2381 | 0.2027 | 0.4127 | 0.3373 | 0.2124 | 0.0440 | 0.1111 | 0.4286 |
| 7 | 0.1532 | 0.1532 | 0.3394 | 0.2854 | 0.7665 | 0.7788 | \* | 0.0930 | 0.3162 | 0.1933 | 0.2741 | 0.2096 | 0.1825 | -0.0213 |
| 8 | 0.3007 | 0.0846 | 0.5766 | 0.2562 | 0.4116 | 0.4116 | 0.2854 | \* | 0.1393 | 0.1614 | 0.1169 | 0.1261 | -0.0497 | 0.2027 |
| 9 | 0.1532 | 0.1532 | 0.3821 | 0.1532 | 0.4327 | 0.4327 | 0.1532 | 0.1532 | \* | 0.0554 | -0.1345 | 0.0633 | 0.0615 | 0.4859 |
| 10 | 0.1743 | 0.4327 | 0.4116 | 0.1532 | 0.9999 | 0.4327 | 0.3821 | 0.2140 | 0.6122 | \* | 0.0514 | 0.2218 | 0.0857 | 0.2866 |
| 11 | 0.3821 | 0.1532 | 0.8527 | 0.1532 | 0.8527 | 0.8527 | 0.1532 | 0.3342 | 0.9999 | 0.8389 | \* | 0.0630 | -0.0909 | 0.3290 |
| 12 | 0.1532 | **0.0422** | 0.9999 | 0.1532 | 0.5201 | 0.8527 | 0.2140 | 0.1532 | 0.2854 | 0.2140 | 0.4327 | \* | 0.0625 | 0.2898 |
| 13 | 0.9999 | 0.9999 | 0.9999 | 0.9999 | 0.9999 | 0.9999 | 0.9999 | 0.9999 | 0.9999 | 0.9999 | 0.9999 | 0.9999 | \* | 0.2000 |
| 14 | 0.9999 | 0.9999 | 0.9999 | 0.9999 | 0.9999 | 0.9999 | 0.9999 | 0.9999 | 0.9999 | 0.9999 | 0.9999 | 0.9999 | 0.9999 | \* |

**Table S4:** Results of generalized linear models relating five different genetic diversity statistics to mean tree age. (A) model of the number of *B. edulis* genets (weighted by the number of sporocarps), in which a Poisson distribution was used to account for non-linearity in the data. (B-E) models of Shannon’s H, the Simpson’s index, mean pairwise relatedness and mean sMLH respectively. These models were fitted with a Gaussian distribution.

|  |  |  |  |
| --- | --- | --- | --- |
| **(A)** | **Genets / sporocarps** | | |
| *Predictors* | *Incidence Rate Ratios* | *CI* | *p* |
| (Intercept) | 0.94 | 0.50–1.76 | 0.846 |
| Mean tree age | 0.99 | 0.97–1.00 | **0.009** |
| Observations | 14 | | |
| R2 Nagelkerke | 0.525 | | |

|  |  |  |  |
| --- | --- | --- | --- |
| **(B)** | **Mean tree age** | | |
| *Predictors* | *Estimates* | *CI* | *p* |
| (Intercept) | 114.76 | 78.22–151.30 | **<0.001** |
| Shannon’s H | -39.94 | -67.77–-12.10 | **0.016** |
| Observations | 14 | | |
| R2 Nagelkerke | 1.000 | | |

|  |  |  |  |
| --- | --- | --- | --- |
| **(C)** | **Mean tree age** | | |
| *Predictors* | *Estimates* | *CI* | *p* |
| (Intercept) | 122.59 | 84.62–160.56 | **<0.001** |
| Simpson’s index | -93.09 | -152.14–-34.05 | **0.009** |
| Observations | 14 | | |
| R2 Nagelkerke | 1.000 | | |

|  |  |  |  |
| --- | --- | --- | --- |
| **(D)** | **Mean tree age** | | |
| *Predictors* | *Estimates* | *CI* | *p* |
| (Intercept) | 107.29 | 71.96–142.61 | **<0.001** |
| *r* | -359.82 | -641.04–-78.60 | **0.028** |
| Observations | 14 | | |
| R2 Nagelkerke | 1.000 | | |

|  |  |  |  |
| --- | --- | --- | --- |
| **(E)** | **Mean tree age** | | |
| *Predictors* | *Estimates* | *CI* | *p* |
| (Intercept) | 13.01 | -60.91–86.92 | 0.736 |
| sMLH | 55.56 | -9.73–120.84 | 0.121 |
| Observations | 14 | | |
| R2 Nagelkerke | 1.000 | | |

**Table S5:** Results of a generalized linear model of the number of *B. edulis* genets (weighted by the number of sporocarps) including the main tree species present within each site as a three-level factor. A Poisson distribution was used to account for non-linearity in the data.

|  |  |  |  |
| --- | --- | --- | --- |
| **(A)** | **Genets / sporocarps** | | |
| *Predictors* | *Incidence Rate Ratios* | *CI* | *p* |
| (Intercept) | 1.41 | 0.66–2.80 | 0.344 |
| Mean tree age | 0.98 | 0.96–0.99 | **0.001** |
| Main tree species birch | 1.07 | 0.32–2.69 | 0.898 |
| Main tree species oak | 12.78 | 1.05–128.58 | **0.034** |
| Observations | 14 | | |
| R2 Nagelkerke | 0.676 | | |