**Supplementary methods**

Simulated scenarios evaluated considered (i) Scenario 1 with a population scenario from a reduced *N*e at time t3 to a higher *N*e at time t2, and then let the software decide whether *N*e remained constant or decreased as consequence of human activity at time t1 (with a range of time including recent extractions of *P. aspera* and human colonization; Fig. 2A), and (ii) Scenario 2 considering a reduction of *N*e from a time t3 to a time t2, when the software was free to decide whether *N*e remained the same of reduced as consequence of human activity at time t1 (Fig. 2B). Scenarios were evaluated in DIYABC using 3000000 simulations with mean genic diversity and Mean Garza-Williamson’s M and pre-evaluated with a Principal Component Analysis (PCA) to determine whether the observed data fitted in the prior distribution of parameters. Then both scenarios were evaluated to identify the most likely scenario using two methods, direct and logistic regression. Results were evaluated to detect bias in the simulations using model checking using the same parameter values than on the original simulations. Confidence on scenarios was also evaluated by model checking using a PCA with mean number of alleles and mean size variance, redefining summary statistics, using the statistics that were not used in the previous analysis. Finally, parameters were calculated and observed to detect anomalies in their distribution.

Table S1. Microsatellite markers for *Patellas aspera* developed and used in this study

|  |  |  |  |
| --- | --- | --- | --- |
| Locus | Primer sequences (5’-3’) | Amplicon size | Repeat motif |
|
| ASP2F | F: CGTACTTCAATTGGCGAAGC | 110-146 | (AAG)*n* |
| R: ACGATCTAGCAACCCCTGACT |
| ASP21F | F: GTGCATAAAATTTGGTTGCG | 168-188 | (AG)*n* |
| R: GAACCTGCAATAAGCAGATTTACA |
| ASP23F | F: TATGAACCGCCCCTTTAAGA | 165-216 | (TCA)*n* |
| R: AGCTGAGGGTGATGGTGATGT |
| ASP33F | F: GGTTCTACGTAAGACCGTCTGG | 235-275 | (AG)*n* |
| R: TCTTCAAATGAGGACTAAGCAGTT |
| ASP34F | F: AGATGTCCCATCTGAGGTGC | 245-275 | (GA)*n* |
| R: TACCCACCCGAACGACTATG |
| ASP15F | F: ACAGTCACGAACAGGGTATGTT | 156-222 | (TTC)*n* |
| R: ACCTCCCACAAGAAAGACTCCT |
| ASP24F | F: ATGTTCAAGCGATTGGAAGG | 160-214 | (GA)*n* |
| R: GCAGAACATTGTGACCCAAA |
| ASP36F | F: ACCCTTTTGTGTGATGAGGG | 288-344 | (GA)*n* |
| R: ATTGTTTGTAGTGGATGTTGAAGC |
| ASP38F | F: GAAGTTTATATCACTCAGGGCCTA | 302-352 | (AG)*n* |
| R: AGTCTAGAGTGCCGCGCTT |
| ASP17F | F: TAAATAAATGTACAACCATTGACACA | 148-168 | (AG)*n* |
| R: TACGGTTGTACGTGACAAGGA |
| ASP26F | F: ATTGGTGGACACCCACAATTA | 194-232 | (AG)9 |
| R: ATTGAGTCACCGGCGTAGTT |
| ASP27F | F: TTTTCTCAGGGTACTCCGGTT | 195-225 | (TC)10 |
| R: GGCATAATGGCAGGGTGAAT |

Table S2. Prior and mean posterior distribution of parameters for two demographic scenarios for *Patella aspera* individuals from the Archipelago of Madeira using DIYABC. Median posterior values (including q0.025 - q0.975) are included for the most likely scenario (Scenario 1).

|  |  |  |  |
| --- | --- | --- | --- |
|  | Scenario 1 | | Scenario 2 |
| Parameter | Prior | Median posterior  (q0.025 - q0.975) | Prior |
| Ne | 10 - 100000 | 2180 (450 - 7140) | 10 - 100000 |
| Net1 | 10 - 100000 | 6300 (1550 - 9800) | 10 - 100000 |
| Net2 | 10 - 100000 | 54000 (8570 – 98000) | 10 - 100000 |
| Net3 | 10 - 100000 | 1400 (45- 5150) | 10 - 100000 |
| t1 | 10 – 1000 | 538 (48 970) | 10 – 1000 |
| t2 | 10 – 15000 | 7200 (950 - 14500) | 10 – 15000 |
| t3 | 10 – 40000 | 25000 (7000 – 39000) | 10 – 40000 |

Table S3. Historical migration estimates calculated with MIGRATE-n among individuals of *Patella aspera* from 6 locations within Madeira Archipelago. Source populations are shown in the left.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Rocha do Navio | Porto Moniz | Paúl do Mar | Garajau | Desertas | Porto Santo |
| Rocha do Navio | - | 69.827 | 72.856 | 68.949 | 71.254 | 66.052 |
| Porto Moniz | 57.179 | - | 70.938 | 73.363 | 61.72 | 50.838 |
| Paúl do Mar | 48.247 | 70.08 | - | 67.012 | 82.451 | 71.879 |
| Garajau | 60.758 | 54.353 | 67.555 | - | 58.447 | 58.044 |
| Desertas | 67.343 | 70.635 | 70.562 | 52.676 | - | 65.786 |
| Porto Santo | 62.634 | 76.616 | 62.691 | 79.377 | 67.409 | - |

Table S4. Gene flow estimates calculated with BAYESASS among individuals of *Patella aspera* from 6 locations within Madeira Archipelago. Source and receiving populations are shown in the left and the top respectively.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Rocha do Navio | Porto Moniz | Paúl do Mar | Garajau | Desertas | Porto Santo |
| Rocha do Navio | 0.6819(0.0147) | 0.0172(0.0163) | 0.0139(0.0133) | 0.0162(0.0154) | 0.0166(0.0156) | 0.0138(0.0133) |
| Porto Moniz | 0.0153(0.0145) | 0.6838(0.0163) | 0.0137(0.0132) | 0.0160(0.0151) | 0.0166(0.0154) | 0.0137(0.0131) |
| Paúl do Mar | 0.2569(0.0291) | 0.2480(0.0321) | 0.9274(0.0277) | 0.2520(0.0308) | 0.2512(0.0291) | 0.2648(0.0269) |
| Garajau | 0.0153(0.0145) | 0.0169(0.0161) | 0.0138(0.0133) | 0.6828(0.0153) | 0.0175(0.0161) | 0.0136(0.0132) |
| Desertas | 0.0151(0.0144) | 0.0168(0.0161) | 0.0140(0.0134) | 0.0160(0.0152) | 0.6811(0.0139) | 0.0137(0.0130) |
| Porto Santo | 0.0155(0.0148) | 0.0174(0.0166) | 0.0172(0.0157) | 0.0171(0.0162) | 0.0170(0.0157) | 0.6805(0.0134) |

Table S5. Power analysis results using POWSIM to evaluate the power of 12 microsatellite markers of *P. aspera* to detect FST after a 10-50 generations from a drift event, assessed with Chi2 and Fischer probabilistic statistics.

|  |  |  |  |
| --- | --- | --- | --- |
| **Generation** | ***F*ST** | **Chi2** | **Fischer** |
| 10 | 0.003 | 0.567 | 0.533 |
| 20 | 0.005 | 0.967 | 0.967 |
| 30 | 0.007 | 1.000 | 1.000 |
| 40 | 0.010 | 1.000 | 1.000 |
| 50 | 0.012 | 1.000 | 1.000 |

Table S6. *FST*-based genetic distance among *Patella aspera* individuals from 6 populations located in the Madeira Archipelago. Values range from no genetic distance (*FST* = 0) to high genetic distance (*FST* = 1). Significant values with a p-value ≤ 0.05 are shown in bold.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Rocha do Navio | Porto Moniz | Paúl do Mar | Garajau | Desertas | Porto Santo |
| Rocha do Navio | 0,000 |  |  |  |  |  |
| Porto Moniz | 0.003 | 0,000 |  |  |  |  |
| Paúl do Mar | 0.006 | 0.009 | 0,000 |  |  |  |
| Garajau | 0.000 | 0,000 | 0,007 | 0,000 |  |  |
| Desertas | 0.004 | 0,006 | 0,005 | 0,001 | 0,000 |  |
| Porto Santo | 0.006 | 0,009 | **0,017** | **0,014** | 0,121 | 0,000 |

**SUPPLEMENTARY FIGURES**



Figure S1. Delta k (number of clusters) detected with STRUCTURE using STRUCTUR Harvester

|  |  |
| --- | --- |
|  |  |

Figure S2. Most likely scenario assessed with DIYABC for *Patella aspera* in the Archipleago of Madeira using the direct and logistic approach.

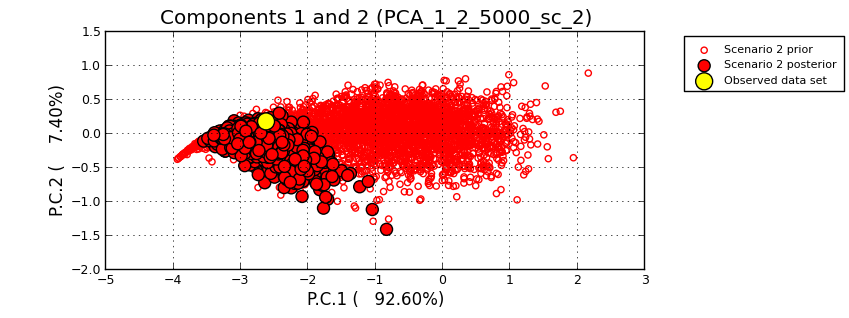


Figure S3. Model checking for the three scenarios (Scenarios 1-3) evaluated with DIYABC for *Patella aspera* in the Archipleago of Madeira.