**Supplementary Materials**

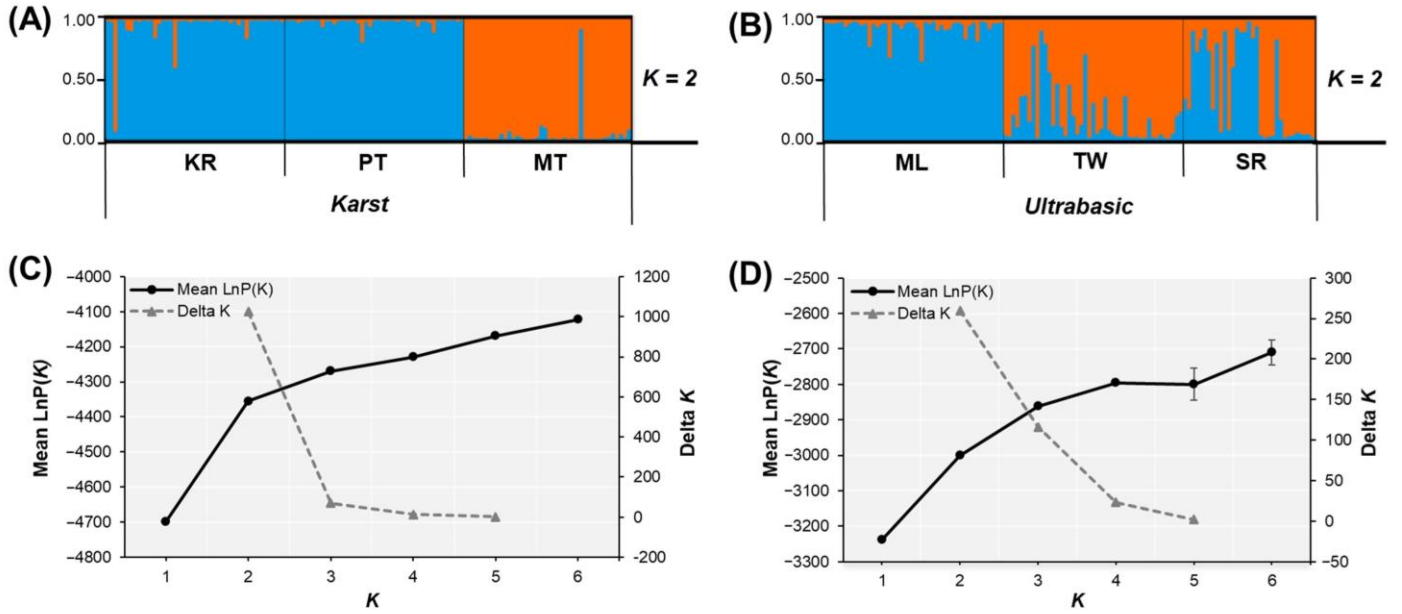



**Figure S1.** Separate STRUCTURE analyses for *H. celebica* for karst and ultrabasic populations: STRUCTURE bar plots at $K = 2$ (**A–B**) and corresponding mean LnP($K$) and Delta $K$ values (**C–D**).

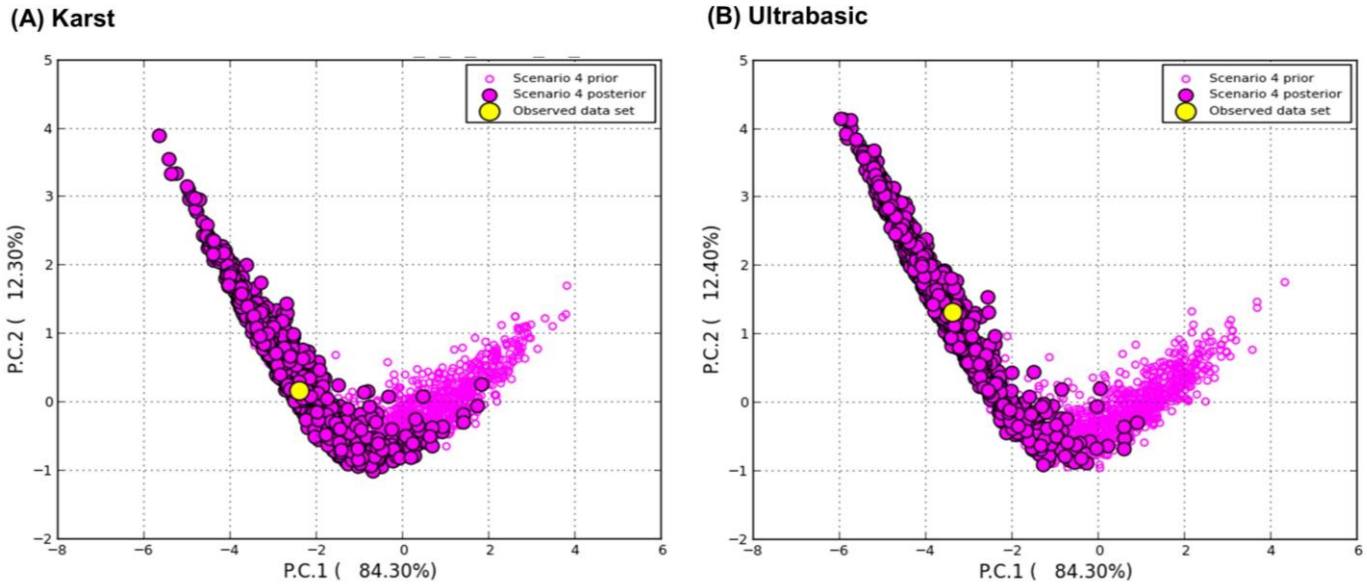



**Figure S2.** Model checking by principal component analysis (PCA) of summary statistics under Scenario 4 inferred using DIYABC. (**A**) Karst populations; (**B**) ultrabasic populations.

**Table S1.** List of 18 polymorphic SSR markers for *H. celebica*

| No | Locus | Repeat motif | Forward primer (5'–3') | Reverse primer (5'–3') |
|---|---|---|---|---|
| 1 | HC03 | (AAT)16 | AAACCAGTCACATACCGAAGT | CCCCGTTGTTTTCTTTCCTCT |
| 2 | HC05 | (AAT)19 | ATTCCCCTGGACAACATTTCT | GATATTCGTAGGGCCAGGCT |
| 3 | HC07 | (AC)16 | GCCAAGCACCACTAGTTGAC | TCGTCTCTCTGGTTATGGGC |
| 4 | HC09 | (AG)27 | TGCATACACTTCCCCGATCA | AGTACTGGACGCAGCTTCTT |
| 5 | HC17 | (ATT)22 | CCTTTTGTGGTGGGGAGTAA | ACTCACCATGCCAAACTAATGA |
| 6 | HC21 | (TA)19 | TTACCCGGCCCCAATAATCA | TCACGCCGAAAGACAATTGA |
| 7 | HC24 | (TC)20 | GGCGTTGTCACTAACCATGG | CCGTGTTGGGTGTTTCTGTC |
| 8 | HC27 | (TG)18 | GTGCATGTCTCGTGAAGGTG | TGGCCCAAAATCTGACAAGC |
| 9 | HC33 | (CTT)12 | GCCTGTCTCTGATCCTCCTC | ACCTGCCTTACTTGAGTGCT |
| 10 | HC36 | (AAG)12 | TCCAATACGCAAACACTCTAGA | TTCTTCCCACTTCACACGTT |
| 11 | HC37 | (AG)15 | GACTAAAACGAGCGCAGTGT | ACCAATTGCCATCGGTTCAG |
| 12 | HC39 | (AG)16 | ACTGCTGAGCGAGGATTTGT | AACCACGTTTTGCCTTCCTC |
| 13 | HC41 | (AG)12 | AGGAGAAGCAGGAGAAGCAG | TCCCCATTTCTCTGCCTTCA |
| 14 | HC42 | (AG)11 | AGGGTGAGCAGAGATTTGGA | AGTAGGGACACAGTACTGCA |
| 15 | HC43 | (AT)17 | GACCTTTCCTCCAAGTTGCC | GCACACAAACGAAGCTGCTT |
| 16 | HC49 | (AT)19 | TGTGATTGTGAGGAGTCTTGTG | CAACATGCTCCCATTTGGCT |
| 17 | HC50 | (AT)26 | ACCCTTAACCTGTGTCCTAAGA | CCCCTTTACCCGTACCCATT |
| 18 | HC52 | (AT)25 | GTGGGTGGGTCATGAGGTTA | GGAGGTAGGACTGGCACTTT |

**Table S2.** Wilcoxon signed-rank tests for heterozygosity excess and M-ratio deficiency under SMM and TPM mutation models

| Habitat | Population | Heterozygosity excess | | M-ratio deficiency | |
|---|---|---|---|---|---|
| | | SMM | TPM | SMM | TPM |
| Karst | KR | -0.356 | 0.267 | -2.934*** | -2.845*** |
| | PT | -1.689 | -1.245 | -2.845*** | -2.667** |
| | MT | -0.711 | -0.534 | -2.934*** | -2.578** |
| | Pooled | -2.756 | -1.778 | -2.934*** | -2.578** |
| Ultrabasic | ML | -1.580 | -1.070 | -2.701*** | -1.580 |
| | TW | -1.784 | -1.580 | -2.497** | -2.192** |
| | SR | -2.701 | -2.293 | -2.701** | -2.497** |
| | Pooled | -2.599 | -2.192 | -2.395** | -1.070 |

Z values are shown. Significance levels: * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$, based on permutation-derived $p$-values (1,000,000 permutations)

**Table S3.** Genetic differentiation ($F_{ST}$, lower diagonal) and gene flow ($N_m$, upper diagonal) among populations of *H. celebica*

| Populations | KR | PT | MT | ML | TW | SR |
|---|---|---|---|---|---|---|
| KR | 0 | 6.544 | 2.359 | 0.396 | 0.411 | 0.343 |
| PT | 0.037*** | 0 | 1.762 | 0.370 | 0.371 | 0.308 |
| MT | 0.096*** | 0.125*** | 0 | 0.403 | 0.401 | 0.336 |
| ML | 0.392*** | 0.407*** | 0.386*** | 0 | 2.607 | 2.126 |
| TW | 0.383*** | 0.406*** | 0.387*** | 0.090*** | 0 | 3.253 |
| SR | 0.426*** | 0.451*** | 0.429*** | 0.108*** | 0.073*** | 0 |

Significance of pairwise $F_{ST}$ values was tested using 10.000 permutations. Significant level: ***$p < 0.001$.

**Table S4.** Posterior probabilities of demographic scenarios in karst and ultrabasic populations

| Scenario | Demographic model | Posterior probability [95% confidence intervals] | |
|---|---|---|---|
| | | Karst | Ultrabasic |
| S1 | Constant | 0.0033 [0.0000–0.0083] | 0.0005 [0.0000–0.1223] |
| S2 | Expansion | 0.2633 [0.2492–0.2775] | 0.2346 [0.1504–0.3188] |
| S3 | Contraction | 0.0017 [0.0000–0.0067] | 0.0004 [0.0000–0.1447] |
| **S4** | **Bottleneck** | **0.7265 [0.7123–0.7406]** | **0.7643 [0.7382–0.7903]** |
| S5 | Bulge | 0.0052 [0.0002–0.0102] | 0.0003 [0.0000–0.1222] |

Posterior probabilities estimated using logistic regression (DIYABC v2.1.0).

**Table S5.** Posterior estimates of demographic parameters under the best-supported scenario (Scenario 4 – Bottleneck)

| Parameter | Posterior estimates [95% confidence intervals] | |
|---|---|---|
| | Karst | Ultrabasic |
| $N_1$ (current $N_e$) | $4.26\times10^4$ [$2.17\times10^4$–$4.97\times10^4$] | $4.39\times10^4$ [$2.36\times10^4$–$4.98\times10^4$] |
| $N_c$ ($N_e$ at bottleneck) | $6.38\times10^2$ [$3.79\times10^1$–$3.63\times10^3$] | $5.71\times10^2$ [$8.43\times10^1$–$2.72\times10^3$] |
| $N_d$ (pre-bottleneck $N_e$) | $2.48\times10^4$ [$2.32\times10^3$–$4.86\times10^4$] | $2.44\times10^4$ [$2.36\times10^3$–$4.86\times10^4$] |
| $t_1$ (bottleneck time; kya) | 118 [5–1200] | 32 [1–568] |
| $t_2$ (pre-bottleneck; kya) | 1734 [340–2940] | 1488 [217–2916] |

**Table S6.** Demographic parameter estimates inferred using MIGRAINE for karst and ultrabasic populations. Point estimates and 95% confidence intervals are shown.

| Habitat | $P_{GSM}$ | $\theta$ | $\theta_{anc}$ | $N_{ratio}$ | $Dg \times \mu$ | $T_{years}$ (kya) |
|---|---|---|---|---|---|---|
| Karst | 0.603 [0.531–0.604] | 4.156 [3.145–4.606] | 2.113 [2.098–3.538] | 1.967 [ 0.965–1.967] | 0.441 [0.327–0.599] | 26.460 [19.620–35.940] |
| Ultrabasic | 0.603 [0.523–0.603] | 3.021 [2.166–3.023] | 1.572 [1.553–2.204] | 1.922 [0.543–4.634] | 0.326 [0.227–0.375] | 19.560 [13.620–22.500] |

Parameters: proportion of multistep mutation under the GSM model ($P_{GSM}$), scaled current effective population size ($\theta$), scaled ancestral effective population size ($\theta_{anc}$), effective population size ratio ($N_{ratio}$), scaled demographic transition time ($Dg \times \mu$), and absolute demographic transition times ($T_{years}$, kya). A generation time of 60 years was assumed.