**Table S1.** Freshwater mollusks that were historically and presently detected in Corsica.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Species name** | **Habitat** |  | **Identified in sites** | **Average headcount per site** |
| *Galba truncatula* | Lotic, Lentic |  | 2, 5, 11, 16 | **0.06** (± 0.38) from 0 to 3 |
| *Bulinus truncatus* | Lotic, Lentic |  | 1, 2, 3, 11 | **2.28** (± 13.95) from 0 to >100 |
| *Bithynia tentaculata* | Lotic, Lentic |  | 13 | **0.02** (± 0.28) from 0 to 3 |
| *Ancylus fluviatilis* | Lotic |  | All except 16 | **26.68** (± 40.53) from 0 to >100 |
| *Potamopyrgus antipodarum* | Lotic, Lentic |  | All except 4 and 12 | **48.03** (± 46.38) from 0 to >100 |
| *Physa acuta* | Lentic, Lotic |  | 3, 6, 7, 8, 9, 15, 16, 21, 23 | **17.38** (± 34.29) from 0 to >100 |
| *Pisidium casertanum* | Lotic, ditches, ponds |  | 8, 11, 15, 21, 22, 23 | **1.45** (± 7.10) from 0 to 50 |
| *Gyraulus laevis* | Lentic, lotic |  | 20, 23 | **0.06** (± 0.34) from 0 to 3 |
| *Gyraulus* sp. | Lentic, lotic |  | 6, 7, 12, 14, 15, 17, 20, 23 | **2.99** (± 8.66) from 0 to 50 |
| *Radix balthica* | Lentic, Lotic |  | 1, 2 | **0.11** (± 1.21) from 0 to 13 |
| *Theodoxus fluviatilis* | Lotic |  | 23 | **0.87** (± 5.26) from 0 to 50 |
| *Stagnicola palustris* | Ponds |  | \_ |  |
| *Planorbis planorbis* | Ponds, lentic |  | \_ |  |
| *Moitessieria corsica* | Groundwater |  | \_ |  |
| *Sphaerium lacustre* | Lentic |  | \_ |  |
| *Unio mancus* | Lotic |  | \_ |  |
| *Acroloxus lacustris* | Lentic |  | \_ |  |
| *Hippeutis complanatus* | Ponds, ditches |  | \_ |  |

These data are recovered from the work of Mouthon, 1982 and confirmed with the INPN 2020 database. Lentic = still water, Lotic = flowing water. The displayed median headcount for each species reported by the malacological survey consider the six measure units conducted on each sites as separate values.

**b**

**a**

**Figure S2.** Number of sequences generated per species in equimolar controls, **a**. results for pooled DNA (N = 12) and **b.** resultsfor pooled PCR products (N = 16). The first three columns are associated to the three technical replicate realized for each pool category, the fourth column give the expected composition of the sample in number of distinct DNA ordered per genus.