**Table 4. Summary of outcomes from applying the framework recommended by Unmack et al. (2022) to assess which lineages of *H. klunzingeri* sensu lato are also candidate species.** Diagnostic molecular markers: SNPs = number of absolute fixed differences/number of fixed differences (5% tolerance); all values but one are highly statistically-significant (P < 0.001; \*P = 0.026): Alloz = number of fixed differences (10% tolerance): Cyt*b* = +++ unequivocally diagnosable, numerous fixed nucleotide differences; ++ = unequivocally diagnosable, some fixed nucleotide differences; + distinct primary clades but not unequivocally diagnostic. Terminology for comparative geographic distribution follows Figure S5; see also Unmack et al., 2022). Sampling intensity: the extent to which each lineage has been geographically sampled (all pairwise comparisons reflect intense genomic sampling).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Diagnostic molecular markers | | |  |  | Candidate |
| Pairwise comparison | SNP | Alloz | Cyt*b* | Comparative distribution | Sampling intensity | species? |
| KN vs KE+ | 93/186 | 4 | +++ | parapatry/widespread/no barrier | adequate vs strong | yes |
| KN vs KS | 224/455 | 12 | +++ | allopatry/moderate/genuine gap | adequate vs strong | yes |
| KN vs KW+ | 264/443 | 14 | +++ | allopatry/shallow | adequate vs strong | yes |
| KE+ vs KS | 39/313 | 10 | + | parapatry/partial | strong vs strong | yes |
| KE+ vs KW+ | 64/296 | 11 | +++ | allopatry/shallow | strong vs strong | yes |
| KS vs KW+ | 6\*/37 | 1 | ++ | allopatry/moderate/genuine gap | strong vs strong | probably |