**Table S1.** *iadema setosum*. Summary statistics describing nucleotide-sequence variability by sample (from DNAsp and Arlequin outputs)

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sample | Statistic |  |  |  |  |  |  |  |  |  |
|  | *N* | *H* | *S* | *Si* | *Ss* | *P* | *Eta* | π ± SD | *K* ± SD | *Hd* ± SD |
| Sa1 | 11 | 7 | 5 | 8 | 16 | 8 | 16 | 0.004 ± 0.002 | 4.97 ± 2.62 | 0.891 ± 0.074 |
| Sa2 | 22 | 8 | 5 | 13 | 21 | 8 | 21 | 0.004 ± 0.002 | 4.68 ± 2.38 | 0.823 ± 0.050 |
| Bat | 75 | 28 | 18 | 21 | 45 | 24 | 45 | 0.004 ± 0.002 | 4.98 ± 2.45 | 0.939 ± 0.011 |
| Pa1 | 36 | 24 | 19 | 26 | 43 | 17 | 43 | 0.005 ± 0.003 | 5.51 ± 2.71 | 0.963 ± 0.017 |
| Pa2 | 31 | 18 | 11 | 12 | 30 | 18 | 30 | 0.004 ± 0.002 | 5.22 ± 2.59 | 0.955 ± 0.018 |
| Pa3 | 42 | 24 | 18 | 19 | 38 | 19 | 39 | 0.004 ± 0.002 | 4.85 ± 2.41 | 0.937 ± 0.024 |
| Mal | 16 | 12 | 9 | 15 | 25 | 10 | 25 | 0.005 ± 0.003 | 5.74 ± 2.90 | 0.958 ± 0.036 |
| Bal | 47 | 30 | 26 | 29 | 47 | 18 | 47 | 0.004 ± 0.002 | 4.89 ± 2.43 | 0.950 ± 0.019 |
| Lo1 | 38 | 25 | 21 | 28 | 40 | 12 | 40 | 0.004 ± 0.002 | 4.58 ± 2.29 | 0.959 ± 0.018 |
| Lo2 | 21 | 16 | 12 | 17 | 26 | 9 | 26 | 0.004 ± 0.002 | 4.37 ± 2.25 | 0.971 ± 0.023 |
| Lan | 80 | 52 | 44 | 47 | 72 | 25 | 72 | 0.004 ± 0.002 | 4.76 ± 2.35 | 0.967 ± 0.011 |
| Si1 | 31 | 26 | 22 | 35 | 50 | 15 | 50 | 0.005 ± 0.003 | 6.06 ± 2.96 | 0.987 ± 0.012 |
| Si2 | 30 | 19 | 14 | 20 | 34 | 14 | 34 | 0.004 ± 0.002 | 4.42 ± 2.24 | 0.926 ± 0.038 |
| Si3 | 23 | 18 | 14 | 19 | 29 | 10 | 29 | 0.004 ± 0.002 | 4.58 ± 2.33 | 0.976 ± 0.020 |
| Ke1 | 57 | 42 | 34 | 43 | 74 | 31 | 74 | 0.005 ± 0.003 | 5.87 ± 2.84 | 0.983 ± 0.008 |
| Ke2 | 61 | 44 | 39 | 37 | 60 | 23 | 60 | 0.005 ± 0.003 | 5.84 ± 2.83 | 0.972 ± 0.012 |
| Luw | 66 | 45 | 37 | 40 | 65 | 25 | 66 | 0.004 ± 0.002 | 4.66 ± 2.31 | 0.974 ± 0.010 |
| Ban | 8 | 8 | 8 | 10 | 19 | 9 | 19 | 0.006 ± 0.003 | 6.51 ± 3.44 | 1.000 ± 0.063 |
| Amb | 21 | 16 | 12 | 23 | 38 | 15 | 38 | 0.005 ± 0.003 | 5.89 ± 2.93 | 0.971 ± 0.023 |
| Jay | 2 | 2 | 2 | 3 | 3 | 0 | 3 | 0.003 ± 0.003 | 3.01 ± 2.46 | 1.000 ± 0.500 |
| Total sample | 718 | 259 | 191 | 86 | 219 | 133 | 227 | 0.005 ± 0.002 | 5.23 ± 2.80 | 0.971 ± 0.003 |

*Eta*, total number of mutations; *H*, number of haplotypes; *Hd*, haplotype diversity; *K*, average number of nucleotide differences; *N*, sample size; *P*, number of parsimony-informative sites; *π*, nucleotide diversity per site; *S*, number of singletons (*i.e.*, haplotypes sampled only once in a given sample); *Si*, number of nucleotide sites with a single substitution; *Ss*, number of variable sites.