**Table S2.** Values of genetic diversity (± standard error) across 11 loci of nine populations of *D. sturtevanti* from Atlantic Forest biome in Brazil. M – monomorphic; P – polymorphic; A – autosomic; S – sex chromosome linked (X or Y); *NT* = Total number of alleles of each locus; *PIC* = Polymorphism Information Content; *Na* – mean number of alleles; *Ne* – mean effective number of alleles; *HO* – mean observed heterozygosity; *HE* – mean expected heterozygosity; *F* – fixation index; *An* – null allele frequency estimate

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Locus | *NT* | *PIC* | *Na* | *Ne* | *HO* | *HE* | *F* | *An* |
| Dsturt\_B (M, A) | 2 | 0.060 | 1.78 ± 0.15 | 1.07 ± 0.02 | 0.07 ± 0.02 | 0.06 ± 0.02 | -0.05 ± 0.01 | 0.0002 |
| Dsturt\_D (M, A) | 3 | 0.032 | 1.44 ± 0.18 | 1.03 ± 0.01 | 0.03 ± 0.01 | 0.03 ± 0.01 | -0.04 ± 0.01 | 0.0006 |
| Dsturt\_E (P, A) | 11 | 0.833 | 6.44 ± 0.34 | 4.05 ± 0.37 | 0.50 ± 0.08 | 0.73 ± 0.03 | 0.31 ± 0.11 | 0.1479 |
| Dsturt\_G (P, A) | 12 | 0.854 | 6.33 ± 0.41 | 4.27 ± 0.35 | 0.49 ± 0.05 | 0.75 ± 0.02 | 0.35 ± 0.05 | 0.1478 |
| Dsturt\_I (P, S) | 10 | 0.843 | 4.89 ± 0.63 | 3.77 ± 0.46 | 0.00 ± 0.00 | 0.69 ± 0.05 | 1.00 ± 0.00 | 0.1825 |
| Dsturt\_J (P, A) | 11 | 0.815 | 5.33 ± 0.50 | 3.93 ± 0.34 | 0.31 ± 0.07 | 0.73 ± 0.03 | 0.60 ± 0.08 | 0.2454 |
| Dsturt\_K (P, A) | 8 | 0.820 | 5.67 ± 0.29 | 4.39 ± 0.31 | 0.48 ± 0.06 | 0.76 ± 0.03 | 0.39 ± 0.07 | 0.1627 |
| Dsturt\_L (P, A) | 13 | 0.858 | 7.00 ± 0.85 | 4.76 ± 0.50 | 0.37 ± 0.06 | 0.77 ± 0.03 | 0.51 ± 0.07 | 0.2245 |
| Dsturt\_M (P, A) | 9 | 0.818 | 6.11 ± 0.42 | 4.34 ± 0.37 | 0.44 ± 0.08 | 0.75 ± 0.02 | 0.42 ± 0.10 | 0.1887 |
| Dsturt\_N (P, A) | 16 | 0.907 | 7.67 ± 0.64 | 5.86 ± 0.53 | 0.15 ± 0.04 | 0.81 ± 0.02 | 0.82 ± 0.05 | 0.3682 |
| Dsturt\_O (P, A) | 14 | 0.859 | 7.00 ± 0.47 | 4.84 ± 0.46 | 0.68 ± 0.07 | 0.78 ± 0.02 | 0.12 ± 0.08 | 0.0774 |
| Mean ± S.E. | 9.91 ± 1.30 | 0.700 ± 0.098 | 5.42 ± 0.62 | 3.85 ± 0.45 | 0.43 ± 0.03 | 0.76 ± 0.01 | 0.44 ± 0.04 | 0.1587 ± 0.03 |