

TABLE 2 Estimates of genetic diversity and total inbreeding for each dataset that used microsatellite as marker. Species: *A. germinans* (Ag), *A. schaueriana* (As), *L. racemosa* (Lr), and *R. mangle* (Rm); Allelic richness (Ar); Expected heterozygosity (H_E); Observed heterozygosity (H_o); Inbreeding coefficient (F_{IS}); and the reference for each dataset. Results are shown as mean calculated across loci of all populations of each dataset \pm standard deviation.

Species	Ar	H_E	H_o	F_{IS}	References
Ag	2.543 \pm 0.302	0.456 \pm 0.071	0.672 \pm 0.154	-0.422 \pm 0.154	Hodel et al., 2016
Ag	2.260 \pm 0.390	0.325 \pm 0.111	0.276 \pm 0.127	0.181 \pm 0.187	Kennedy et al., 2020
Ag	2.624 \pm 0.751	0.438 \pm 0.171	0.432 \pm 0.306	0.218 \pm 0.244	Mori et al., 2015
Ag	2.551 \pm 0.658	0.239 \pm 0.108	0.224 \pm 0.302	0.132 \pm 0.158	O-Zavala et al., 2019
As	2.416 \pm 0.563	0.236 \pm 0.086	0.171 \pm 0.063	0.248 \pm 0.104	Mori et al., 2015
Lr	1.551 \pm 0.398	0.204 \pm 0.160	0.106 \pm 0.059	0.475 \pm 0.165	S-Lima et al., 2021
Rm	2.416 \pm 0.299	0.428 \pm 0.067	0.314 \pm 0.070	0.221 \pm 0.137	de la Cruz et al., 2018
Rm	1.798 \pm 0.724	0.196 \pm 0.156	0.190 \pm 0.105	-0.015 \pm 0.324	Francisco et al., 2018
Rm	2.452 \pm 0.247	0.425 \pm 0.062	0.489 \pm 0.105	-0.089 \pm 0.127	Hodel et al., 2016
Rm	2.350 \pm 0.257	0.419 \pm 0.071	0.493 \pm 0.112	-0.089 \pm 0.123	Hodel et al., 2017
Rm	2.532 \pm 0.500	0.350 \pm 0.122	0.310 \pm 0.106	0.093 \pm 0.125	Kennedy et al., 2016
Rm	2.407 \pm 0.395	0.317 \pm 0.096	0.265 \pm 0.129	0.211 \pm 0.222	Kennedy et al., 2017
Rm	1.729 \pm 0.237	0.370 \pm 0.113	0.366 \pm 0.129	0.026 \pm 0.221	Takayama et al., 2013

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