

**MATING SYSTEM DYNAMICS OF *OCOTEA TENERA***

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[REDACTED]

**MATERIALS AND METHODS**

[REDACTED]

**Tissue collection and electrophoresis**—Fruits were collected from

[REDACTED]

**Data analysis**—Multilocus ( $\chi^2$ ) and single locus ( $\chi^2$ ) tests

[REDACTED]

**TABLE 1.** Multilocus and single locus outcrossing rates ( $t_m$ )

Year	Sample Size	$t_m$	SE
15	45	1.123	(0.12)
15	45	1.950 <sup>a</sup>	(0.29)
15	46	0.157 <sup>a</sup>	(0.13)
15	46	2.335	(0.13)
15	74	1.151	(0.12)
15	74	0.832	
15	56	0.588 <sup>a</sup>	
15	74	0.965	
18	172	0.965	(0.09)
18		0.953	(0.10)
18		0.640 <sup>a</sup>	(0.07)
18		0.846 <sup>a</sup>	(0.04)

<sup>a</sup> Outcrossing rate significantly different from 1.00 based on comparison of 95% confidence intervals.

standard errors of  $t_m$  values were calculated via Tukey's jackknife (Sokal and Rohlf, 1981). This method provides a parametric procedure for

[REDACTED]

**RESULTS**

Most individuals were scored for all three loci. Only individuals scored for at least two loci were included in

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TABLE 2. Multilocus and single-locus outcrossing rate estimates for trees heterozygous ( $t_{het}$ ) or homozygous ( $t_{hom}$ ) at the *Gdh* locus.  $N_f$  and  $N_s$  are sample sizes of families and seeds, respectively.

TABLE 3. Multilocus and single-locus outcrossing rate estimates for trees of normal and *g* ( $t_{het}$ ) or *g* ( $t_{hom}$ ) maternal trees.  $N_f$  and  $N_s$  are sample sizes of families and seeds, respectively.  $N_f$  indicate the sample size of

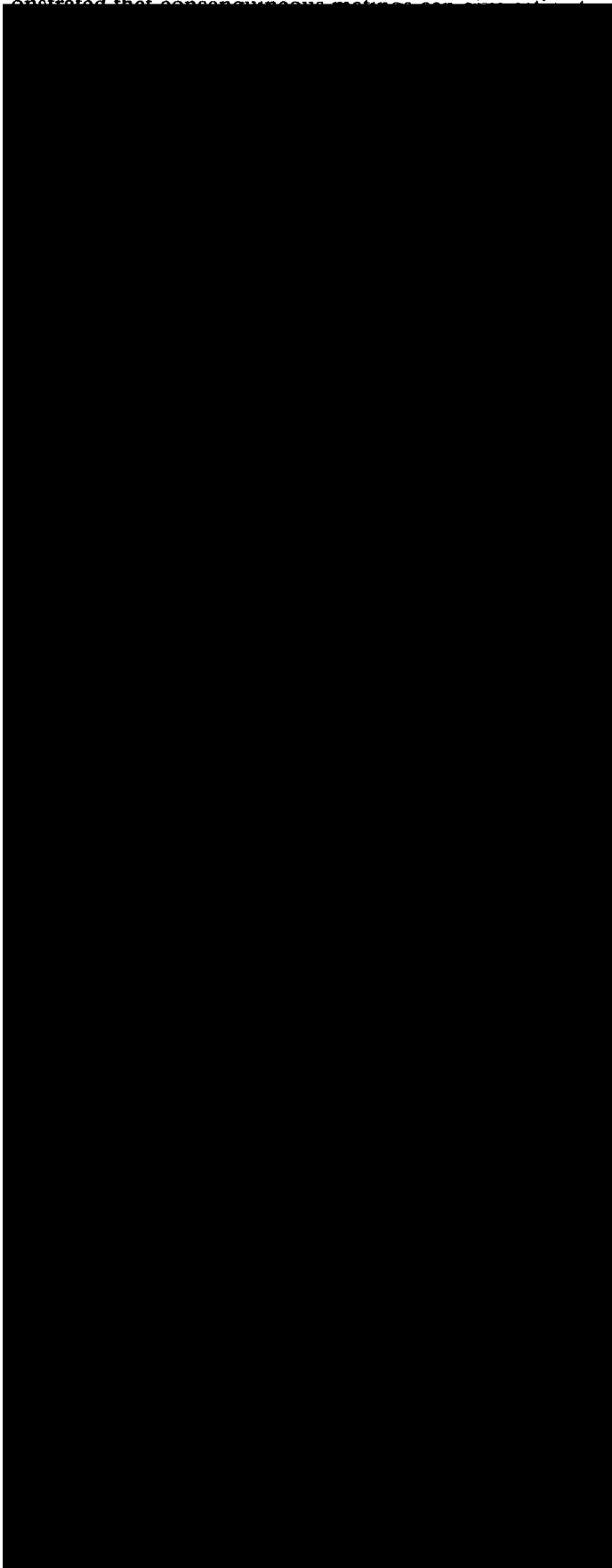
0.909	(0.26)	8	27	1.999	NA	7	18
1.642	NA	8	27	1.074	NA	7	18
0.083	NA	8	28	0.144	NA	7	18
0.918	(0.11)	8	28	1.022	(0.23)	7	18
1.075	(0.14)	9	52	1.081		5	21
0.690	(0.16)	9	52	0.792		5	21
0.482		9	42	0.250		5	13
0.905		9	52	1.137 <sup>a</sup>		5	21
0.974	(0.10)	14	167	1.012	NA	4	6
		14	202	0.501	(0.97)	4	11
		14	182	0.122	NA	4	7
		14	202	0.541 <sup>ab</sup>	(0.06)	4	11

<sup>a</sup> Outcrossing rate significantly different from 1.00,  $P < 0.05$ .  
<sup>b</sup> Outcrossing rates significantly differ between families,  $P < 0.05$ .

loci have been found in other species and suggested to



onstrated that consanguineous mating can significantly



efficiency of nutrient allocation in gender system evolution of *O. tenera* and related species.

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