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**The potential impact of mining on population genetic variation in the Banded Ironstone Formation endemic *Tetratheca erubescens* (Elaeocarpaceae)**

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**Supplementary Materials**

**Table S1.** Summary of chi-square tests for departure from Hardy-Weinberg equilibrium for each locus and site. ns = not significant; \* =  $P < 0.05$ ;

\*\* =  $P < 0.005$ ; \*\*\* =  $P < 0.001$ .

LOCUS	SITE													
	A	B	C	D	E	F	G	H	I	J	K	L	M	N
<b>Te30</b>	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns
<b>Te15</b>	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	**	ns	***	ns
<b>Te25</b>	***	ns	ns	*	***	ns	ns	**	**	***	*	ns	***	ns
<b>TpC130</b>	ns	ns	ns	ns	*	ns	ns	ns	ns	ns	ns	ns	ns	ns
<b>Te10</b>	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	***	ns	**
<b>Te21</b>	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns
<b>TpB4</b>	ns	ns	***	ns	***	ns	ns	***	***	*	*	ns	***	*
<b>Te23</b>	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	**	ns
<b>TpB11</b>	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns
<b>Te29</b>	ns	ns	*	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns
<b>TpC131</b>	***	*	*	ns	ns	ns	ns	ns	ns	ns	***	ns	ns	ns

**Table S2.** Summary statistics for 11 microsatellite loci in *Tetradthea erubescens* for all 435 samples. N = number of samples; Na = No. of different alleles; Ne = No. of effective alleles; I = Shannon's information index; Ho = observed heterozygosity; He = expected heterozygosity; uHe = unbiased expected heterozygosity; F = fixation index

Locus	N	Na	Ne	I	Ho	He	uHe	F
<b>Te30</b>	435	4.000	1.680	0.799	0.414	0.405	0.405	-0.022
<b>Te15</b>	434	7.000	2.713	1.350	0.576	0.631	0.632	0.088
<b>Te25</b>	433	7.000	2.599	1.163	0.591	0.615	0.616	0.039
<b>TpC130</b>	435	7.000	1.457	0.663	0.347	0.314	0.314	-0.107
<b>Te10</b>	435	4.000	2.769	1.125	0.508	0.639	0.640	0.205
<b>Te21</b>	435	2.000	1.019	0.052	0.014	0.018	0.018	0.243
<b>TpB4</b>	435	5.000	1.864	0.734	0.262	0.464	0.464	0.435
<b>Te23</b>	432	10.000	3.693	1.594	0.632	0.729	0.730	0.133
<b>TpB11</b>	432	6.000	2.925	1.266	0.551	0.658	0.659	0.163
<b>Te29</b>	435	3.000	1.893	0.817	0.400	0.472	0.472	0.152
<b>TpC131</b>	435	4.000	1.754	0.698	0.294	0.430	0.430	0.316

**Mean and SE over Loci for each Pop**

	N	Na	Ne	I	Ho	He	uHe	F
<b>Mean</b>	434.182	5.364	2.215	0.933	0.417	0.489	0.489	0.149
<b>SE</b>	0.377	0.691	0.236	0.127	0.055	0.061	0.061	0.046

**Table S3.** Summary of genetic differentiation statistics by locus, and in total.  $F_{is}$  = inbreeding coefficient within individuals;  $F_{st}$  = inbreeding coefficient within sites, relative to total genetic differentiation among sites;  $G_{is}$  = inbreeding coefficient within individuals, adjusted for bias;  $G_{st}$  = analog of  $F_{st}$ , adjusted for bias;  $G'_{stN}$  = Nei's standardized  $G_{st}$ ;  $G'_{stH}$  = Hedricks standardized  $G_{st}$ ;  $G''_{st}$  = Hedricks standardized  $G_{st}$ , further corrected for bias when the number of sites is small.  $D_{est}$  = Jost's estimate of differentiation.

	<b>Te30</b>	<b>Te15</b>	<b>Te25</b>	<b>TpC130</b>	<b>Te10</b>	<b>Te21</b>	<b>TpB4</b>	<b>Te23</b>	<b>TpB11</b>	<b>Te29</b>	<b>TpC131</b>	<b>Total</b>
<b>Fis</b>	-0.094	0.017	-0.028	-0.194	0.109	0.170	0.344	0.067	0.008	0.008	0.228	0.051
<b>Fst</b>	0.065	0.069	0.059	0.075	0.108	0.090	0.132	0.070	0.153	0.142	0.104	0.098
<b>Gis</b>	-0.078	0.034	-0.011	-0.178	0.125	0.186	0.358	0.084	0.025	0.024	0.244	0.068
<b>Gst</b>	0.052	0.054	0.045	0.063	0.093	0.073	0.114	0.054	0.139	0.129	0.087	0.083
<b>G'stN</b>	0.056	0.058	0.048	0.068	0.099	0.078	0.121	0.058	0.148	0.137	0.093	0.089
<b>G'stH</b>	0.086	0.140	0.114	0.091	0.230	0.074	0.200	0.186	0.335	0.227	0.147	0.155
<b>G''st</b>	0.090	0.143	0.117	0.095	0.235	0.080	0.207	0.189	0.342	0.234	0.152	0.161
<b>Dest</b>	0.036	0.090	0.073	0.030	0.151	0.001	0.098	0.139	0.228	0.112	0.065	0.079

**Table S4.** Summary of the hierarchical Analysis of Molecular Variance (AMOVA) for all sites and two regions (region 1. sites A, B, C, D, E, F G and N; region 2. Sites H, I, J, K, L, and M).

<b>Source</b>	<b>df</b>	<b>SS</b>	<b>MS</b>	<b>Est. Var.</b>	<b>%</b>
<b>Among Regions</b>	1	71.920	71.920	0.187	3%
<b>Among Sites</b>	12	382.733	31.894	0.856	13%
<b>Within Sites</b>	421	2242.163	5.326	5.326	84%
<b>Total</b>	434	2696.816		6.369	100%

**Table S5.** Summary statistics for 11 microsatellite loci in *Tetradthea erubescens*, for all sites except C, D, F and N.  $N$  = number of samples;  $N_a$  = No. of different alleles;  $N_e$  = No. of effective alleles;  $I$  = Shannon's information index;  $H_o$  = observed heterozygosity;  $H_e$  = expected heterozygosity;  $uH_e$  = unbiased expected heterozygosity;  $F$  = fixation index.

Locus	N	Na	Ne	I	Ho	He	uHe	F
<b>Te30</b>	316	4.000	1.777	0.850	0.449	0.437	0.438	-0.028
<b>Te15</b>	315	7.000	3.002	1.415	0.578	0.667	0.668	0.134
<b>Te25</b>	316	7.000	2.657	1.191	0.563	0.624	0.625	0.097
<b>TpC130</b>	316	6.000	1.513	0.704	0.383	0.339	0.340	-0.129
<b>Te10</b>	316	4.000	2.890	1.166	0.557	0.654	0.655	0.148
<b>Te21</b>	316	2.000	1.026	0.068	0.019	0.025	0.025	0.240
<b>TpB4</b>	316	5.000	1.837	0.719	0.247	0.456	0.456	0.458
<b>Te23</b>	315	10.000	3.744	1.608	0.651	0.733	0.734	0.112
<b>TpB11</b>	315	6.000	3.009	1.317	0.578	0.668	0.669	0.135
<b>Te29</b>	316	3.000	1.761	0.735	0.364	0.432	0.433	0.158
<b>TpC131</b>	316	4.000	1.855	0.732	0.294	0.461	0.462	0.362

**Mean and SE over Loci for each Pop**

	N	Na	Ne	I	Ho	He	uHe	F
<b>Mean</b>	315.727	5.273	2.279	0.955	0.426	0.500	0.500	0.153
<b>SE</b>	0.141	0.675	0.248	0.131	0.057	0.061	0.061	0.049

**Table S6.** Summary statistics for 11 microsatellite loci in *Tetradthea erubescens*, with samples from all sites, but sample sizes adjusted evenly across sites so that total N is equivalent to 316 (Table 7).  $N$  = number of samples;  $N_a$  = No. of different alleles;  $N_e$  = No. of effective alleles;  $I$  = Shannon's information index;  $H_o$  = observed heterozygosity;  $H_e$  = expected heterozygosity;  $uH_e$  = unbiased expected heterozygosity;  $F$  = fixation index.

Locus	N	Na	Ne	I	Ho	He	uHe	F
<b>Te30</b>	316	4.000	1.704	0.812	0.421	0.413	0.414	-0.019
<b>Te15</b>	315	7.000	2.637	1.325	0.568	0.621	0.622	0.085
<b>Te25</b>	314	7.000	2.526	1.145	0.561	0.604	0.605	0.072
<b>TpC130</b>	316	7.000	1.401	0.619	0.313	0.286	0.287	-0.094
<b>Te10</b>	316	4.000	2.780	1.124	0.491	0.640	0.641	0.234
<b>Te21</b>	316	2.000	1.016	0.046	0.016	0.016	0.016	-0.008
<b>TpB4</b>	316	5.000	1.780	0.697	0.244	0.438	0.439	0.444
<b>Te23</b>	315	10.000	3.804	1.614	0.641	0.737	0.738	0.130
<b>TpB11</b>	313	6.000	2.899	1.260	0.550	0.655	0.656	0.161
<b>Te29</b>	316	3.000	1.916	0.822	0.408	0.478	0.479	0.146
<b>TpC131</b>	316	4.000	1.759	0.710	0.282	0.431	0.432	0.347

**Overall mean and SE**

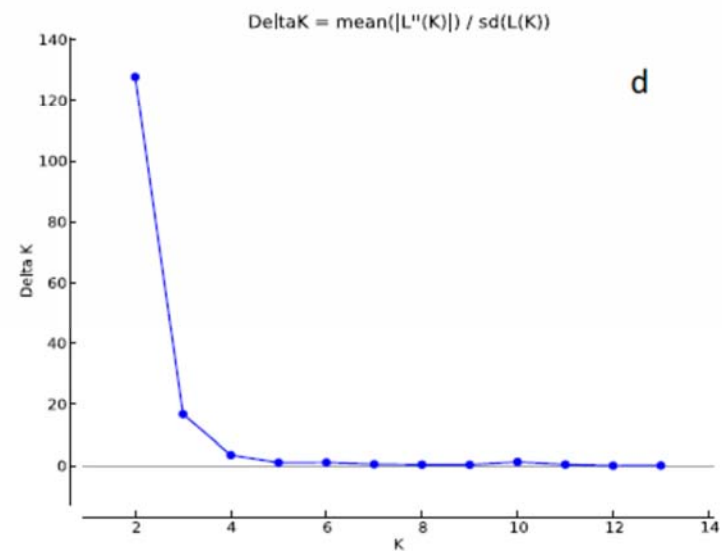
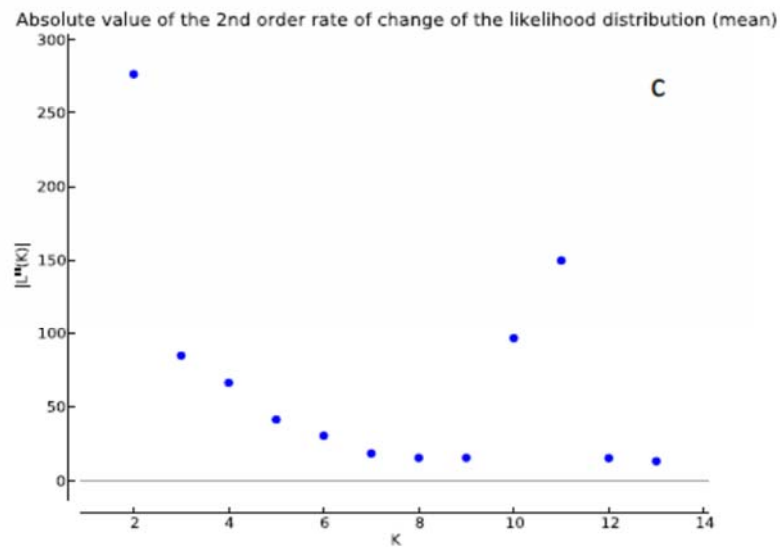
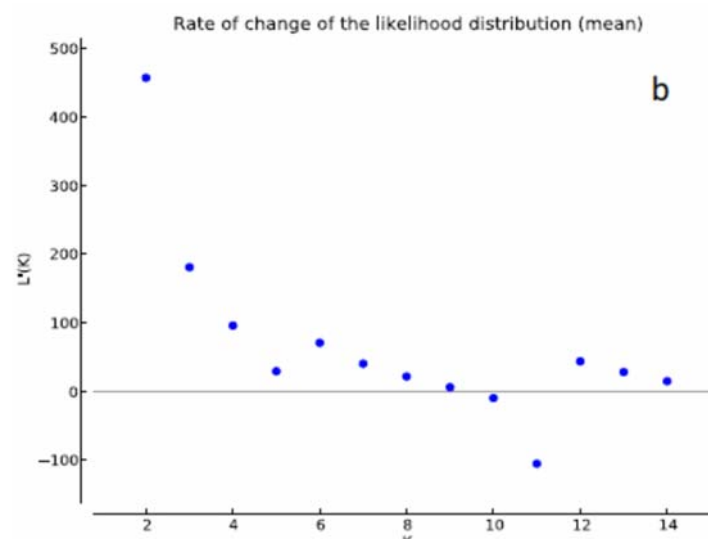
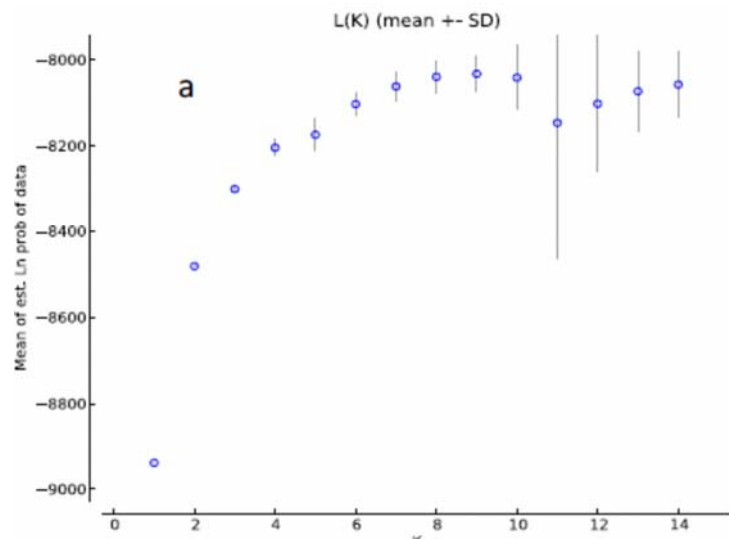
	N	Na	Ne	I	Ho	He	uHe	F
<b>Mean</b>	315.364	5.364	2.202	0.925	0.409	0.484	0.484	0.136
<b>SE</b>	0.310	0.691	0.242	0.129	0.055	0.062	0.062	0.048

**Table S7.** Summary of genetic differentiation statistics by locus for the dataset from all sites except C, D, F and N.  $F_{is}$  = inbreeding coefficient within individuals;  $F_{st}$  = inbreeding coefficient within sites, relative to total genetic differentiation among sites;  $G_{is}$  = inbreeding coefficient within individuals, adjusted for bias;  $G_{st}$  = analog of  $F_{st}$ , adjusted for bias;  $G'_{stN}$  = Nei's standardized  $G_{st}$ ;  $G'_{stH}$  = Hedricks standardized  $G_{st}$ ;  $G''_{st}$  = Hedricks standardized  $G_{st}$ , further corrected for bias when the number of sites is small.  $D_{est}$  = Jost's estimate of differentiation.

	<b>Te30</b>	<b>Te15</b>	<b>Te25</b>	<b>TpC130</b>	<b>Te10</b>	<b>Te21</b>	<b>TpB4</b>	<b>Te23</b>	<b>TpB11</b>	<b>Te29</b>	<b>TpC131</b>	<b>Tot</b>
<b>Fis</b>	-0.100	0.071	0.043	-0.223	0.058	0.170	0.385	0.054	0.037	-0.013	0.285	0.065
<b>Fst</b>	0.068	0.066	0.057	0.076	0.097	0.087	0.122	0.063	0.102	0.166	0.103	0.089
<b>Gis</b>	-0.084	0.087	0.059	-0.208	0.074	0.185	0.399	0.070	0.053	0.003	0.300	0.081
<b>Gst</b>	0.056	0.051	0.042	0.065	0.083	0.071	0.104	0.048	0.088	0.154	0.086	0.075
<b>G'stN</b>	0.062	0.056	0.047	0.072	0.091	0.078	0.114	0.053	0.097	0.168	0.094	0.082
<b>G'stH</b>	0.099	0.148	0.112	0.099	0.221	0.072	0.185	0.173	0.242	0.252	0.155	0.146
<b>G''st</b>	0.104	0.153	0.116	0.106	0.228	0.080	0.194	0.177	0.250	0.265	0.163	0.153
<b>Dest</b>	0.045	0.103	0.073	0.036	0.151	0.002	0.090	0.131	0.169	0.116	0.076	0.077



**Fig. S1.** Summary Evanno et al (2005) plots from STRUCTURE and STRUCTURE HARVESTER analysis for detecting the number of  $K$  groups that best fit the data. Graphs include: a. the mean and SD of the estimated Ln probability of the data for each  $K$  from 10 replicates; b. the rate of change of the likelihood distribution (from a.); c. the absolute value of the 2<sup>nd</sup> order rate of change of the likelihood distribution (from b.); and d. delta ( $K$ ), which is the mean value of the second order rate of change of the likelihood distribution (from c.) / the SD of the Ln probability of the data for each  $K$  (from a.).



**Fig. S2.** Logarithmic association between number of plants and number of alleles at 11 microsatellite loci for *Tetradthea erubescens*.

