Supplementary Information

Biogeography and evolution of seeder and resprouter forms of *Erica coccinea* (Ericaceae) in the fire-prone Cape *fynbos*

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Running title: Biogeography of seeder and resprouter *Erica coccinea*

Table S1. Priors and summary statistics for ‘two-groups’ and ‘three-groups’ ABC models.

Set	Parameter	Distribution	Minimum	Maximum
‘two-groups’	N1	Uniform	10	100000
	N2	Uniform	10	15000
	ta	Uniform	1	10000
	t1	Uniform	1	10000
	Nb	Uniform	10	10000
	Mutation rate	Log-uniform	1E-005	1E-003
‘three-groups’	N1	Uniform	10	100000
	N2	Uniform	10	15000
	N3	Uniform	10	15000
	ta	Uniform	1	10000
	t1	Uniform	1	10000
	t2	Uniform	1	10000
	Mutation rate	Log-uniform	1E-005	1E-003

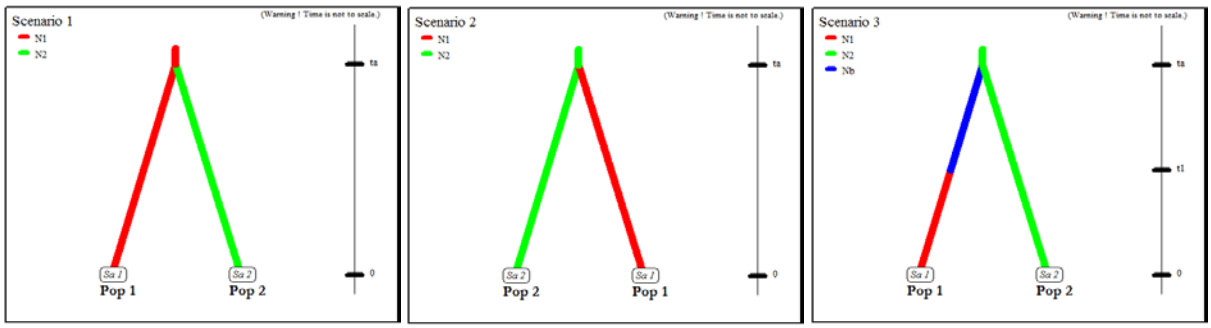
All ABC models were base in the following summary statistics:

- One sample statistics: mean number of alleles, mean genic diversity, mean size variance and mean Garza-Williamson’s M statistic.
- Two sample statistics: mean number of alleles, mean genic diversity, mean size variance, Fst, Classification Index, shared allele distance and $(d\mu)^2$ distance.

Table S2. Ribotype definition (see Fig. 2 in main text for ribotype distribution and Fig. 3 for a network connecting ribotypes).

	position in alignment (bp)																	
Ribotype	**81**	**113**	**132**	**187**	**241**	**253**	**280**	**283**	**284**	**298**	**481**	**501**	**550**	**559**	**636**	**648**	**682**	**719**
I	C	T	T	C	T	T	T	-	-	-	C	C	A	C	G	T	-	T
II	C	T	T	C	T	T	T	-	-	-	C	C	G	C	T	T	-	N
III	C	T	T	C	T	T	T	-	-	-	C	C	G	C	G	T	-	T
IV	C	T	T	C	T	T	T	-	-	-	C	C	G	T	G	T	-	T
V	C	A	T	C	T	T	T	-	-	-	C	C	G	T	G	T	-	T
VI	C	T	C	C	T	T	T	-	-	-	C	C	G	T	G	T	-	N
VII	C	T	C	C	T	T	T	G	T	T	C	C	G	T	G	T	-	T
VIII	C	T	C	C	T	C	T	G	T	T	C	C	G	T	G	T	-	T
IX	C	T	C	C	T	T	T	G	T	T	C	C	G	T	G	T	A	T
X	C	T	C	C	T	T	T	G	T	T	C	C	G	C	G	T	A	T
XI	C	T	C	A	T	T	T	G	T	T	C	C	G	T	G	T	-	N
XII	C	T	C	A	T	T	T	G	T	T	C	C	G	T	G	C	-	C
XIII	T	T	T	C	T	T	T	-	-	-	C	C	G	T	G	T	-	T
XIV	T	T	T	C	C	T	T	-	-	-	C	C	G	T	G	T	-	T
XV	C	T	C	C	T	T	T	-	-	-	C	G	G	T	G	T	-	N
XVI	C	T	C	C	T	T	T	-	-	T	C	G	G	T	G	T	-	T
XVII	C	T	C	C	T	T	T	-	-	-	C	C	G	T	G	T	-	T
XVIII	C	T	C	C	T	T	C	-	-	-	T	C	G	T	G	T	-	T

A:



B:

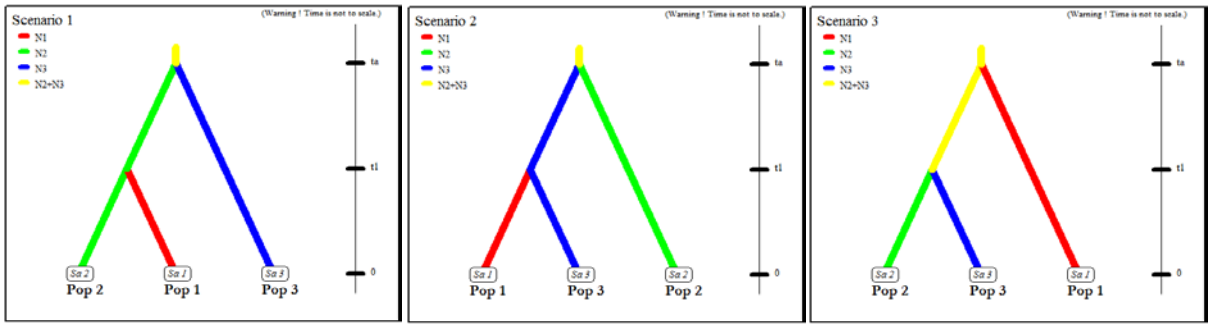


Figure S1 A: Basic ‘two-groups’ models compared using ABC. Pop 1 refers to seeders and Pop 2 to resprouters. Notice that in Scenario 1, seeders are the ancestral lineage while in Scenario 2 resprouters are ancestral. Scenario 3 includes a population size change in the seeders. Finally, ta refers to the splitting time between seeder and resprouter forms and t1 to the time of population size change in seeders. B: A similar set of ABC models but with resprouters divided in western (Pop 2) and eastern (Pop 3) groups (see main text). In Scenario 3, t1 refers to the splitting time between western and eastern resprouters.

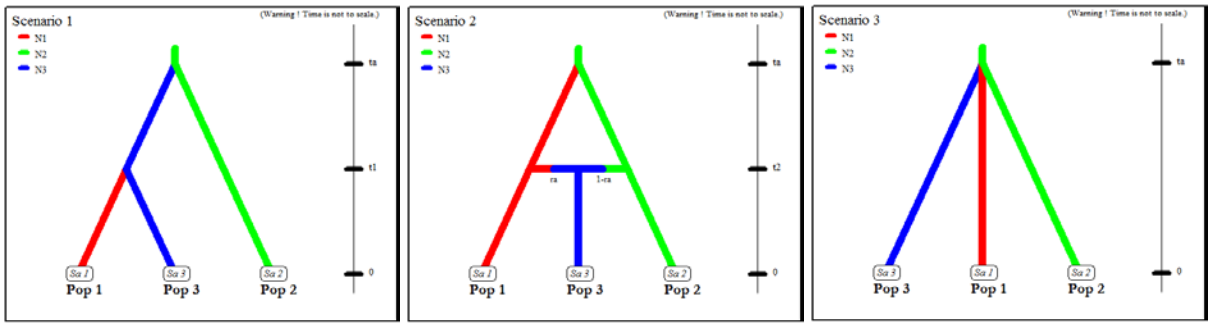


Figure S2 ‘Three-groups’ models compared using ABC. Pop 1 refers to seeder populations, Pop 2 to resprouter populations, and Pop 3 to mixed populations. Two separated sets of models were run (see main text), one for the mixed populations from the Cape Peninsula (S01 and R02) and the other for those from the Caledon region (S09, R05 and R07). Notice that t2 refers to the time of secondary contact between seeders and resprouters.

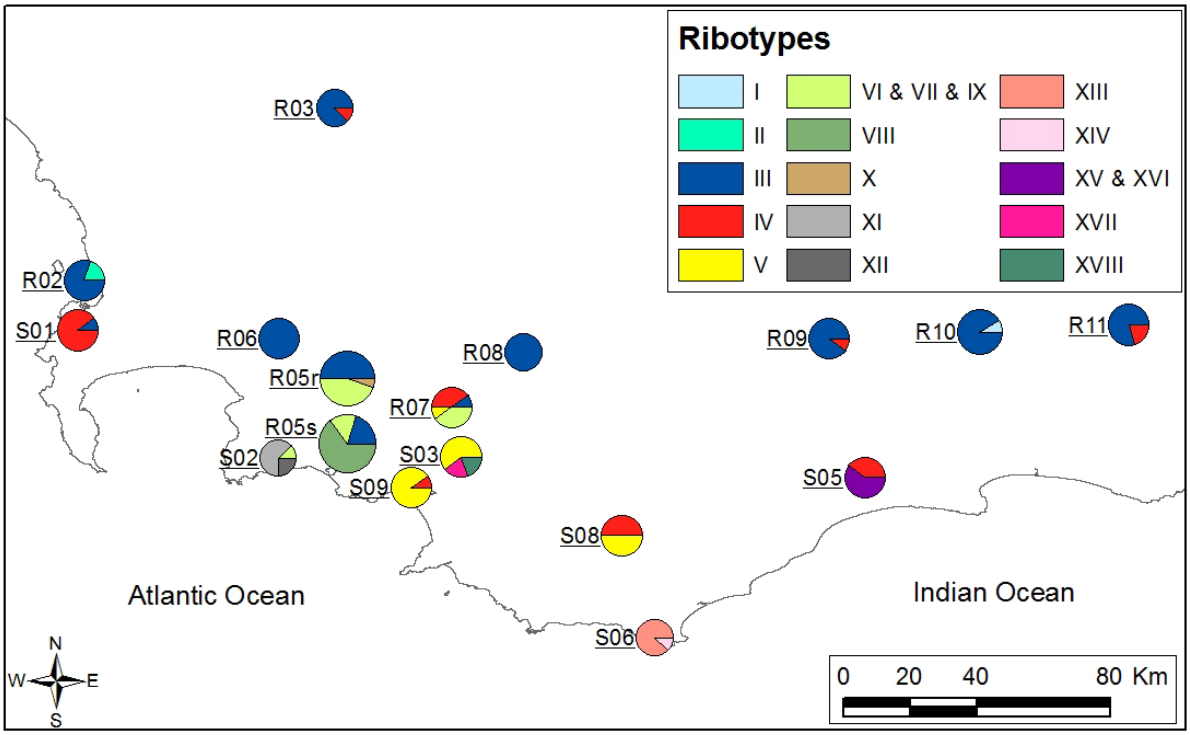


Figure S3 Geographic distribution of 15 ITS ribotypes found in *E. coccinea* once indels were removed. Pie charts are proportional to sample size. Notice that a prefix 'S' indicates a seeder population and a prefix 'R' a resprouter population, except for R05 where both seeders (R05s) and resprouters (R05r) were sampled.

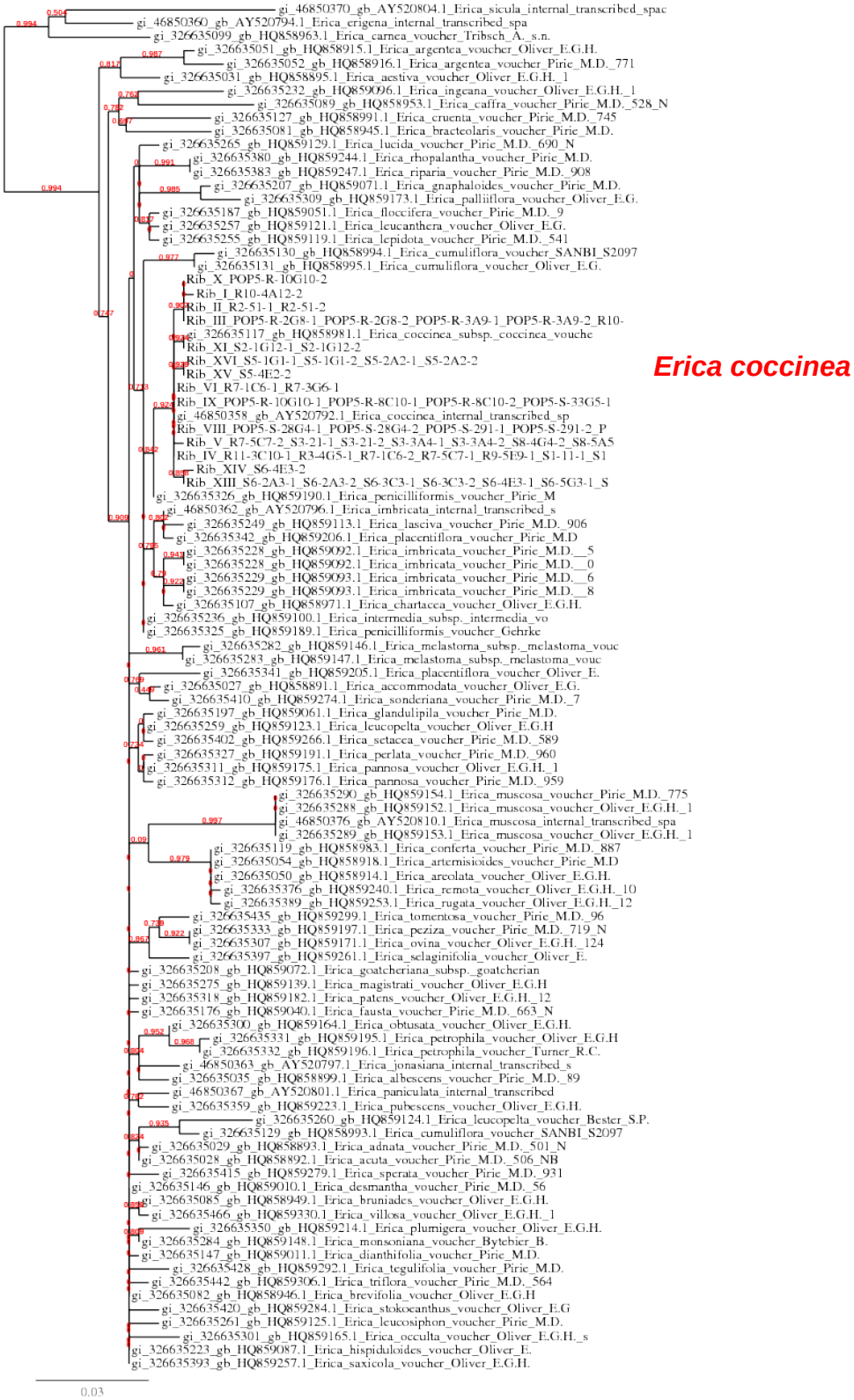


Fig. S4 Maximum likelihood phylogenetic tree obtained from PhyML. The branch length is proportional to the number of substitutions per site. Branch support is the probability of an approximate likelihood ratio test.

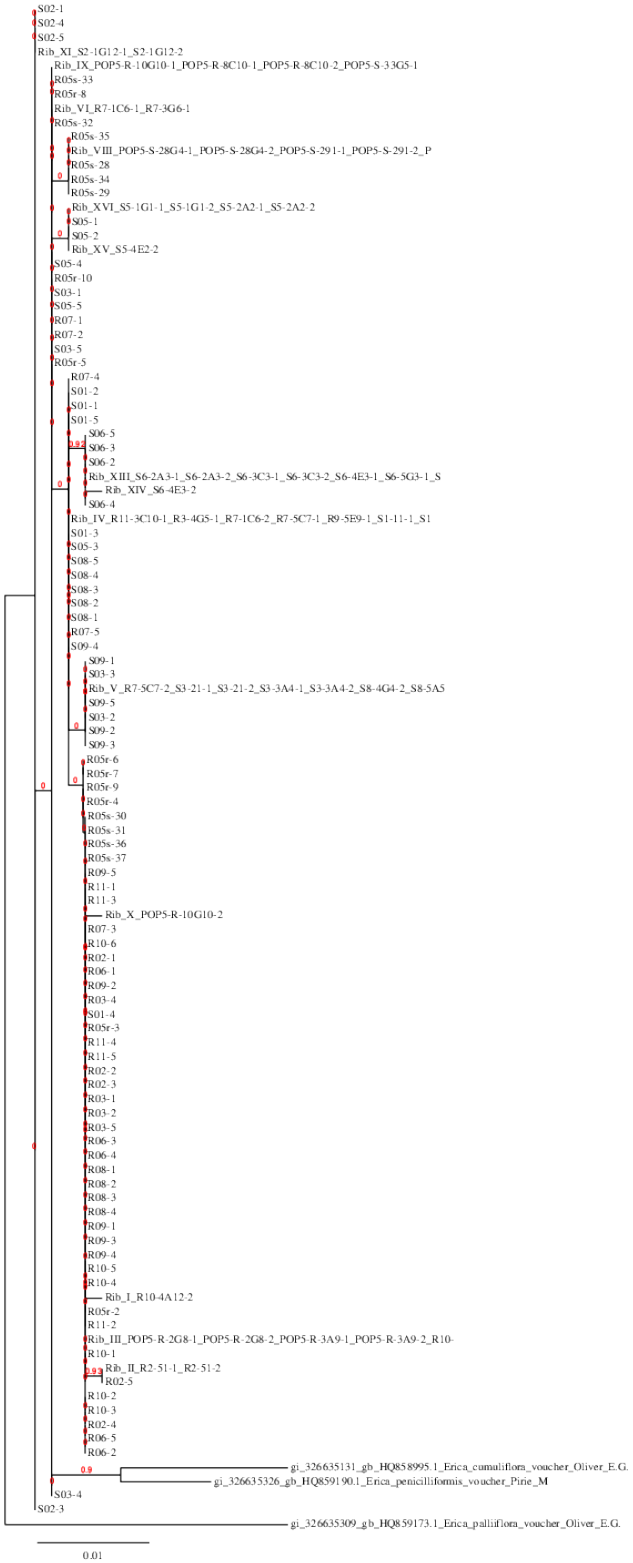


Fig. S5 Maximum likelihood phylogenetic tree based on both phased and unphased *E. coccinea* ITSs and close outgroups. The branch length is proportional to the number of substitutions per site. Branch support was obtained by bootstrapping.