

**Supporting Information for Online Publication for:**

**Effects of landscape, resource use, and body size on genetic structure in bee populations**

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**Table of Contents:**

<b>Table S1</b>	Page 2
<b>Table S2</b>	Page 3
<b>Table S3</b>	Page 4
<b>Table S4</b>	Page 7
<b>Table S5</b>	Page 9
<b>Figure S1</b>	Page 11

# MOLECULAR ECOLOGY

Species	Body size	Orchids	Orchid species	Nesting
<i>Eug. sapphirina</i>	9	6	<i>Houlletia odoratissima</i> , <i>Mormodes</i> , <i>Notylia barkeri</i> , <i>Sievekingia fimbriata</i> , <i>Stanhopea ecornuta</i> , <i>Trichocentrum capistratum</i>	Wood cavity
<i>Eug. dodsoni</i>	10	14	<i>Catasetum bicolor</i> , <i>Coeliopsis hyacinthosma</i> , <i>Cycnoches guttulatum</i> , <i>Dressleria</i> , <i>Gongora horichiana</i> , <i>G. maculata</i> , <i>G. quinquenervis</i> , <i>Kefersteinia lacteal</i> , <i>Kegeliella</i> , <i>Mormodes igneum</i> , <i>Notylia linearis</i> , <i>Notylia sp.</i> , <i>Peristeria</i> , <i>Sievekingia suavis</i>	Hard, nut shaped, on twig or branch
<i>Eug. mixta</i>	11	18	<i>Catasetum bicolor</i> , <i>C. thompsonii</i> , <i>Coryanthes speciosa</i> , <i>C. trifoliata</i> , <i>Cycnoches</i> , <i>Dichaea panamensis</i> , <i>Gongora quinquenervis</i> , <i>Kefersteinia costaricensis</i> , <i>Kegeliella</i> , <i>Mormodes atropurpureum</i> , <i>M. cartonii</i> , <i>M. igneum</i> , <i>M. colossus</i> , <i>M. maculatum</i> , <i>M. powellii</i> , <i>Notylia</i> , <i>Peristeria pendula</i> , <i>Sievekingia fimbriata</i>	Hollow stem or branch
<i>Eug. maculilabris</i>	12	9	<i>Coryanthes</i> , <i>Cycnoches</i> , <i>Dichaea</i> , <i>Kefersteinia</i> , <i>Lacaena spectabilis</i> , <i>Lycaste</i> , <i>Mormodes</i> , <i>Notylia</i> , <i>Peristeria</i>	Nest unknown
<i>Eug. championi</i>	13	10	<i>Cycnoches</i> , <i>Dichaea</i> , <i>Dressleria dilecta</i> , <i>D. eburnean</i> , <i>D. kerryae</i> , <i>Mormodes atropurpureum</i> , <i>Notylia</i> , <i>Peristeria</i> , <i>Sobralia</i> , <i>Stanhopea cirrhata</i>	Dome under a leaf or in epiphyte
<i>Eug. flammea</i>	14	8	<i>Catasetum maculatum</i> , <i>Cycnoches egertonianum</i> , <i>Gongora</i> , <i>Peristeria leucoxantha</i> , <i>Sievekingia fimbriata</i> , <i>Stanhopea cirrhata</i> , <i>S. oculate</i> , <i>S. panamensis</i>	Ground cavity
<i>Eug. imperialis</i>	15	20	<i>Catasetum macrocarpum</i> , <i>C. saccatum</i> , <i>Coryanthes trifoliata</i> , <i>Cycnoches egertonianum</i> , <i>Dichaea</i> , <i>Gongora maculate</i> , <i>G. quinquenervis</i> , <i>Kefersteinia</i> , <i>Kegeliella kupperi</i> , <i>Mormodes</i> , <i>Notylia buchtienii</i> , <i>Peristeria</i> , <i>Polycycnis muscifera</i> , <i>Sobralia</i> , <i>Stanhopea candida</i> , <i>S. cirrhata</i> , <i>S. ecornuta</i> , <i>S. costaricensis</i> , <i>Trichocentrum maculatum</i> , <i>Trichopilia maculata</i>	Ground or rock cavity

**Table S1.** For each species, the body size, number and names of the orchid morphospecies visited, and the nesting habitat, as reported in Roubik & Hanson (2004).

Species	N	Mean depth of coverage	Retained reads	Assembled loci (pre-filtering)	Polymorphic loci (pre-filtering)	SNPs (pre-filtering)	Filtering	Assembled loci (post-filtering)	Polymorphic loci (post-filtering)
<i>E. sapphirina</i>	107	47.27x	296,581,295	153,924	14,229	193,697	$p=4,$ $r=0.75$	10,485	7,025
<i>E. dodsoni</i>	65	11.26x	32,220,986	51,257	948	9,434	$p=3,$ $r=0.75$	292	124
<i>E. mixta</i>	51	19.55x	99,403,380	92,712	8,927	82,742	$p=3,$ $r=0.75$	13,138	4,296
<i>E. maculilabris</i>	37	14.72x	64,371,382	85,557	7,532	26,620	$p=1,$ $r=0.75$	19,355	4,448
<i>E. championi</i>	121	10.3x	92,578,500	66,226	5,326	88,882	$p=4,$ $r=0.75$	2,238	1,298
<i>E. flammea</i>	25	18.35x	36,453,361	52,669	4,525	28,132	$p=2,$ $r=0.75$	13,423	3,141
<i>E. imperialis</i>	88	10.3x	81,510,644	76,344	7,496	86,086	$p=4,$ $r=0.75$	1,546	626

**Table S2.** Summary of Stacks output generated using the *process\_radtags* and *denovo\_map.pl* pipelines. Stacks was run for each orchid bee species separately. For each species, the sample size (N), the mean depth of coverage, number of reads retained after cleaning the raw genomic data using *process\_radtags*, and the output from *denovo\_map.pl*, including the number of assembled loci, polymorphic loci, and SNPs prior to filtering, the chosen parameter values, and the number of assembled loci and polymorphic loci post filtering. Polymorphic loci were filtered using the populations program and loci were processed if they were present in at least two fewer than the number of sampled sites ( $p$ ) and at least in 75% of individuals ( $r$ ). Species are listed from smallest to largest body size. Post filtering, there was one SNP per polymorphic locus. The *populations* program, which is embedded in the *denovo\_map.pl* pipeline, used the parameter values  $m=3$ ,  $M=1$ ,  $n=2$ , where  $m$  is the minimum stack depth parameter that controls the number of raw reads required to form an initial stack,  $M$  is the distance allowed between stacks, which represents the number of nucleotides that may be different between two stacks in order to merge them, and  $n$  is the distance allowed among catalog loci.

# MOLECULAR ECOLOGY

Species	Size (mm)	Orchids	Site 1	Site 2	For (E)	For (BS)	Km (E)	Km (BS)	GD
<i>Eug. sapphirina</i>	9	6	Agua Buena	Agua Buena	1	1	0	0	0.083
<i>Eug. sapphirina</i>	9	6	Agua Buena	Las Alturas	69.53	72.57	80.7	81.9	0.076
<i>Eug. sapphirina</i>	9	6	Agua Buena	Saladero	23.06	92.42	21	33.9	0.075
<i>Eug. sapphirina</i>	9	6	Bromelias	Agua Buena	94	94	15.4	15.4	0.054
<i>Eug. sapphirina</i>	9	6	Bromelias	Bromelias	1	1	0	0	0.049
<i>Eug. sapphirina</i>	9	6	Bromelias	Las Alturas	74.75	74.75	95.5	95.5	0.051
<i>Eug. sapphirina</i>	9	6	Bromelias	Las Cruces	71.83	89.23	77.5	78.1	0.054
<i>Eug. sapphirina</i>	9	6	Bromelias	Saladero	53.96	92.89	36.1	47.6	0.050
<i>Eug. sapphirina</i>	9	6	La Gamba	Agua Buena	53.6	94.95	34.9	39.5	0.027
<i>Eug. sapphirina</i>	9	6	La Gamba	Bromelias	66.65	94.54	50.4	53.2	0.026
<i>Eug. sapphirina</i>	9	6	La Gamba	La Gamba	1	1	0	0	0.023
<i>Eug. sapphirina</i>	9	6	La Gamba	Las Alturas	69.5	69.5	48.5	48.5	0.027
<i>Eug. sapphirina</i>	9	6	La Gamba	Las Cruces	81.66	81.66	27.7	27.7	0.028
<i>Eug. sapphirina</i>	9	6	La Gamba	Saladero	99.81	99.81	13.8	13.8	0.026
<i>Eug. sapphirina</i>	9	6	Las Alturas	Las Alturas	1	1	0	0	0.072
<i>Eug. sapphirina</i>	9	6	Las Alturas	Saladero	76.01	76.01	61	61	0.070
<i>Eug. sapphirina</i>	9	6	Las Cruces	Agua Buena	62.05	88.2	62	64.4	0.083
<i>Eug. sapphirina</i>	9	6	Las Cruces	Las Alturas	62.09	62.09	22.5	22.5	0.077
<i>Eug. sapphirina</i>	9	6	Las Cruces	Las Cruces	1	1	0	0	0.084
<i>Eug. sapphirina</i>	9	6	Las Cruces	Saladero	90.31	90.31	41.7	41.7	0.076
<i>Eug. sapphirina</i>	9	6	Saladero	La Gamba	99.81	99.81	13.8	13.8	0.024
<i>Eug. sapphirina</i>	9	6	Saladero	Saladero	1	1	0	0	0.069
<i>Eug. dodsoni</i>	10	14	Agua Buena	Agua Buena	1	1	0	0	0.069
<i>Eug. dodsoni</i>	10	14	Agua Buena	Saladero	23.06	92.42	21	33.9	0.048
<i>Eug. dodsoni</i>	10	14	Bromelias	Agua Buena	94	94	15.4	15.4	0.045
<i>Eug. dodsoni</i>	10	14	Bromelias	Bromelias	1	1	0	0	0.062
<i>Eug. dodsoni</i>	10	14	Bromelias	Las Cruces	71.83	89.23	77.5	78.1	0.064
<i>Eug. dodsoni</i>	10	14	La Gamba	Agua Buena	53.6	94.95	34.9	39.5	0.032
<i>Eug. dodsoni</i>	10	14	La Gamba	Bromelias	66.65	94.54	50.4	53.2	0.035
<i>Eug. dodsoni</i>	10	14	La Gamba	La Gamba	1	1	0	0	0.045
<i>Eug. dodsoni</i>	10	14	La Gamba	Las Cruces	81.66	81.66	27.7	27.7	0.044
<i>Eug. dodsoni</i>	10	14	Las Cruces	Agua Buena	62.05	88.2	62	64.4	0.061
<i>Eug. dodsoni</i>	10	14	Las Cruces	Las Cruces	1	1	0	0	0.097
<i>Eug. dodsoni</i>	10	14	Saladero	Agua Buena	23.06	92.42	21	33.9	0.045
<i>Eug. dodsoni</i>	10	14	Saladero	Bromelias	53.96	92.89	36.1	47.6	0.045
<i>Eug. dodsoni</i>	10	14	Saladero	La Gamba	99.81	99.81	13.8	13.8	0.039

# MOLECULAR ECOLOGY

<i>Eug. dodsoni</i>	10	14	Saladero	Las Cruces	90.31	90.31	41.7	41.7	0.060
<i>Eug. dodsoni</i>	10	14	Saladero	Saladero	1	1	0	0	0.056
<i>Eug. championi</i>	13	11	Agua Buena	Agua Buena	1	1	0	0	0.074
<i>Eug. championi</i>	13	11	Agua Buena	Las Alturas	69.53	72.57	80.7	81.9	0.059
<i>Eug. championi</i>	13	11	Bromelias	Agua Buena	94	94	15.4	15.4	0.002
<i>Eug. championi</i>	13	11	Bromelias	Bromelias	1	1	0	0	0.002
<i>Eug. championi</i>	13	11	Bromelias	Las Cruces	71.83	89.23	77.5	78.1	0.002
<i>Eug. championi</i>	13	11	La Gamba	Agua Buena	53.6	94.95	34.9	39.5	0.036
<i>Eug. championi</i>	13	11	La Gamba	Bromelias	66.65	94.54	50.4	53.2	0.002
<i>Eug. championi</i>	13	11	La Gamba	La Gamba	1	1	0	0	0.032
<i>Eug. championi</i>	13	11	La Gamba	Las Cruces	81.66	81.66	27.7	27.7	0.031
<i>Eug. championi</i>	13	11	La Gamba	Saladero	99.81	99.81	13.8	13.8	0.034
<i>Eug. championi</i>	13	11	Las Alturas	Agua Buena	69.53	72.57	80.7	81.9	0.067
<i>Eug. championi</i>	13	11	Las Alturas	Bromelias	74.75	74.75	95.5	95.5	0.002
<i>Eug. championi</i>	13	11	Las Alturas	La Gamba	69.5	69.5	48.5	48.5	0.032
<i>Eug. championi</i>	13	11	Las Alturas	Las Alturas	1	1	0	0	0.060
<i>Eug. championi</i>	13	11	Las Alturas	Las Cruces	62.09	62.09	22.5	22.5	0.056
<i>Eug. championi</i>	13	11	Las Alturas	Saladero	76.01	76.01	61	61	0.059
<i>Eug. championi</i>	13	11	Las Cruces	Agua Buena	62.05	88.2	62	64.4	0.064
<i>Eug. championi</i>	13	11	Las Cruces	Las Cruces	1	1	0	0	0.055
<i>Eug. championi</i>	13	11	Saladero	Agua Buena	23.06	92.42	21	33.9	0.067
<i>Eug. championi</i>	13	11	Saladero	Bromelias	53.96	92.89	36.1	47.6	0.002
<i>Eug. championi</i>	13	11	Saladero	Las Cruces	90.31	90.31	41.7	41.7	0.056
<i>Eug. championi</i>	13	11	Saladero	Saladero	1	1	0	0	0.061
<i>Eug. flammea</i>	14	8	La Gamba	La Gamba	1	1	0	0	0.167
<i>Eug. flammea</i>	14	8	La Gamba	Las Alturas	69.5	69.5	48.5	48.5	0.175
<i>Eug. flammea</i>	14	8	Las Alturas	La Gamba	69.5	69.5	48.5	48.5	0.163
<i>Eug. flammea</i>	14	8	Las Alturas	Las Alturas	1	1	0	0	0.163
<i>Eug. flammea</i>	14	8	Las Alturas	Las Cruces	62.09	62.09	22.5	22.5	0.054
<i>Eug. flammea</i>	14	8	Las Cruces	La Gamba	81.66	81.66	27.7	27.7	0.055
<i>Eug. flammea</i>	14	8	Las Cruces	Las Cruces	1	1	0	0	0.045
<i>Eug. flammea</i>	14	8	Las Cruces	Saladero	90.31	90.31	41.7	41.7	0.013
<i>Eug. imperialis</i>	15	20	Agua Buena	Agua Buena	1	1	0	0	0.064
<i>Eug. imperialis</i>	15	20	Bromelias	Agua Buena	94	94	15.4	15.4	0.057
<i>Eug. imperialis</i>	15	20	Bromelias	Bromelias	1	1	0	0	0.054
<i>Eug. imperialis</i>	15	20	La Gamba	Agua Buena	53.6	94.95	34.9	39.5	0.025
<i>Eug. imperialis</i>	15	20	La Gamba	Bromelias	66.65	94.54	50.4	53.2	0.020

<i>Eug. imperialis</i>	15	20	La Gamba	La Gamba	1	1	0	0	0.020
<i>Eug. imperialis</i>	15	20	La Gamba	Saladero	99.81	99.81	13.8	13.8	0.016
<i>Eug. imperialis</i>	15	20	Saladero	Agua Buena	23.06	92.42	21	33.9	0.032
<i>Eug. imperialis</i>	15	20	Saladero	Bromelias	53.96	92.89	36.1	47.6	0.027
<i>Eug. imperialis</i>	15	20	Saladero	Saladero	1	1	0	0	0.028

**Table S3.** For each species, its body size, the number of orchid morphospecies visited, the site pairs between which genetic distances were calculated (Site 1 & Site 2), the percent of the distance between them that was forested when calculated using Euclidian paths (For. (E)), the percent of the distance between them that was forested when calculated using Broken-stick paths (For. (BS)), the Euclidian geographic distance between them (Km (E)), the Broken-stick geographic distance between them (Km (BS)), and the average genetic distance among individuals between those pairs (Hamming genetic distance).

# MOLECULAR ECOLOGY

Species	Model	AIC	AICc	$\Delta$ AICc	Model Summary
<i>Eug. sapphirina</i>	<b>Full (E)</b>	<b>-39633.7</b>	<b>-39633.69</b>	<b>0</b>	Km (E) = 0.000058 For (E) = -0.00017  $t = 7.82, P < 0.001$ $t = -49.5, P < 0.001$
	Km (E)	-37599.99	-37599.99	-2033.7	
	For (E)	-39574.77	-39574.77	-58.92	
	Intercept	-37355.1	-37355.09	-2278.6	
	Full (BS)	-39365.78	-39365.77	-267.92	
	Km (BS)	-37584.11	-37584.1	-2049.59	
	For (BS)	-39077.91	-39077.9	-555.79	
<i>Eug. dodsoni</i>	Full (E)	-11777.71	-11777.68	-27.88	Km (BS) = -0.000067 For (BS) = -0.00012  $t = -2.12, P = 0.036$ $t = -13.0, P < 0.001$
	Km (E)	-11639.4	-11639.38	-166.18	
	For (E)	-11761.27	-11761.25	-44.31	
	Intercept	-11436.86	-11436.84	-368.72	
	<b>Full (BS)</b>	<b>-11805.59</b>	<b>-11805.56</b>	<b>0</b>	
	Km (BS)	-11645.41	-11645.39	-160.17	
	For (BS)	-11803.22	-11803.2	-2.36	
<i>Eug. championi</i>	Full (E)	-47630.4	-47595.95	-47630.4	Km (BS) = -0.000064 For (BS) = -0.00013  $t = -11.1, P < 0.001$ $t = -31.3, P < 0.001$
	Km (E)	-46906.2	-46878.64	-46906.2	
	For (E)	-47417.6	-47390.04	-47417.6	
	Intercept	-45447.31	-45426.64	-45447.31	
	<b>Full (BS)</b>	<b>-48031.57</b>	<b>-47997.12</b>	<b>-48031.56</b>	
	Km (BS)	-47116.26	-47088.7	-47116.25	
	TreeBS	-47912.54	-47884.98	-47912.53	
<i>Eug. flammea</i>	<b>Full (E)</b>	<b>-1438.61</b>	<b>-1438.406</b>	<b>0</b>	Km (E) = 0.00057 For (E) = -0.00085  $t = 6.0, P < 0.001$ $t = -16.1, P < 0.001$
	Km (E)	-1256.073	-1255.937	-182.469	
	For (E)	-1406.346	-1406.21	-32.196	
	Intercept	-1223.928	-1223.847	-214.559	
	<b>Full (BS)</b>	<b>-1438.61</b>	<b>-1438.406</b>	<b>0</b>	
	Km (BS)	-1256.073	-1255.937	-182.469	
	TreeBS	-1406.346	-1406.21	-32.196	

# MOLECULAR ECOLOGY

<i>Eug. imperialis</i>	Full (E)	-26737.65	-26737.63	-338.3	Km (BS) = -0.00021 Km (BS) = -0.000049  $t = -26.3, P < 0.001$ $t = -12.0, P < 0.001$
	Km (E)	-26728.77	-26728.76	-347.17	
	For (E)	-25295.59	-25295.58	-1780.35	
	Intercept	-24822.72	-24822.71	-2253.22	
	<b>Full (BS)</b>	<b>-27075.95</b>	<b>-27075.93</b>	<b>0</b>	
	Km (BS)	-26936.14	-26936.13	-139.8	
	For (BS)	-26444.21	-26444.19	-631.74	

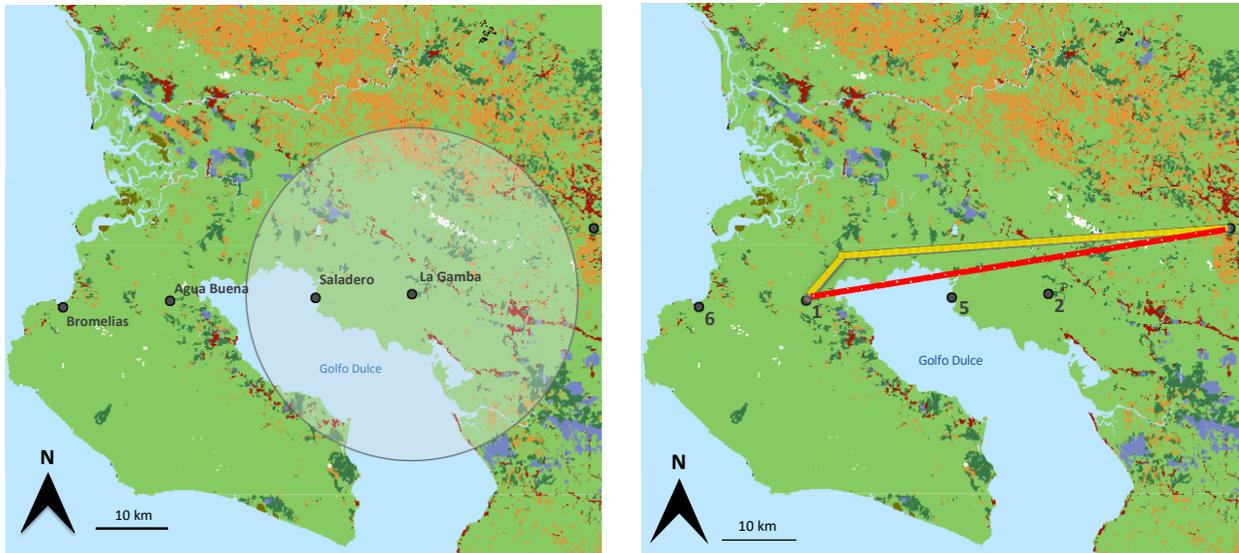
**Table S4.** Results from Maximum Likelihood of Population Effects (MLPE) models assessing the joint effects of the amount of land that was forested and geographic distance among site pairs on genetic distance among pairs of individuals. For each species, seven models were compared, a full model (Full (E)) that included as fixed effects the Euclidian geographic distance and amount of land that was forested along that path among site pairs, a model that included only Euclidian geographic distance (Geo (E)), a model that included only the amount of land that was forested (For (E)), a full model (Full (BS)) that included as fixed effects the Broken-stick geographic distance and amount of land that was forested along that path among site pairs, a model that included only Broken-stick geographic distance (Geo (BS)), a model that included only the amount of land that was forested (For (E)), and an intercept-only model (Intercept). Columns 3-6 show AIC and sample-size corrected AIC (AICc) values, the difference in AICc from the best model, and model results, including estimates for fixed effects and associated t and P-values.

# MOLECULAR ECOLOGY

Species	Model	AIC	AICc	$\Delta$ AICc	Model Summary
<i>Eug. sapphirina</i>	<b>Full (E)</b>	<b>-27921.08</b>	<b>-27921.07</b>	<b>0</b>	Km (E) = 0.00013 For (E) = -0.000065  $t = 11.9, P < 0.001$ $t = -9.82, P < 0.001$
	Km (E)	-27827.86	-27827.85	-93.22	
	For (E)	-27785.01	-27785	-136.07	
	Intercept	-27645.89	-27645.89	-275.18	
	Full (BS)	-27826.33	-27826.32	-94.75	
	Km (BS)	-27828.12	-27828.11	-92.96	
	TreeBS	-27644.9	-27644.89	-276.18	
<i>Eug. dodsoni</i>	<b>Full (E)</b>	<b>-8385.668</b>	<b>-8385.625</b>	<b>0</b>	Km (E) = 0.00016 For (E) = 0.00011  $t = 4.0, P < 0.001$ $t = 4.2, P < 0.001$
	Km (E)	-8370.469	-8370.441	-15.184	
	For (E)	-8371.935	-8371.907	-13.718	
	Intercept	-8357.691	-8357.674	-27.951	
	Full (BS)	-8383.545	-8383.502	-2.123	
	Km (BS)	-8361.176	-8361.147	-24.478	
	TreeBS	-8385.064	-8385.036	-0.589	
<i>Eug. championi</i>	<b>Full (E)</b>	<b>-40852.16</b>	<b>-40852.15</b>	<b>0</b>	Km (E) = 0.000068 For (E) = -0.00012  $t = 11.3, P < 0.001$ $t = -16.5, P < 0.001$
	Km (E)	-40589.04	-40589.04	-263.11	
	For (E)	-40728.96	-40728.95	-123.2	
	Intercept	-40529.75	-40529.74	-322.41	
	Full (BS)	-40617.49	-40617.48	-234.67	
	Km (BS)	-40593.78	-40593.77	-258.38	
	TreeBS	-40588.87	-40588.86	-263.29	
<i>Eug. flammea</i>	<b>Full (E)</b>	<b>-1266.913</b>	<b>-1266.63</b>	<b>0</b>	Km (E) = 0.0032 For (E) = 0.04  $t = 40.4, P < 0.001$ $t = -35.2, P < 0.001$  *No paths went over water for this species, so Full (E) and Full (BS) are identical
	Km (E)	-1000.5586	-1000.3709	-266.2591	
	For (E)	-950.5323	-950.3445	-316.2855	
	Intercept	-949.1541	-949.0419	-317.5881	
	<b>Full (BS)*</b>	<b>-1266.913</b>	<b>-1266.63</b>	<b>0</b>	
	Km (BS)	-1000.5586	-1000.3709	-266.2591	
	TreeBS	-950.5323	-950.3445	-316.2855	

<i>Eug. imperialis</i>	Full (E)	-20769.57	-20769.55	0	Km (E) = 0.000075 For (E) = 0.00024  $t = 4.4, P < 0.001$ $t = 28.1, P < 0.001$
	Km (E)	-20074.27	-20074.26	-695.29	
	For (E)	-20752.27	-20752.26	-17.29	
	Intercept	-19647.13	-19647.12	-1122.43	
	Full (BS)	-20754.82	-20754.79	-14.76	
	Km (BS)	-20291.12	-20291.1	-478.45	
	For (BS)	-20455.06	-20455.04	-314.51	

**Table S5.** Results from Maximum Likelihood of Population Effects (MLPE) models assessing the joint effects of the amount of land that was forested and geographic distance among site pairs on genetic distance among pairs of individuals, using a dataset that included only genetic distances estimated from individuals at different sites. For each species, seven models were compared, a full model (Full (E)) that included as fixed effects the Euclidian geographic distance and amount of land that was forested along that path among site pairs, a model that included only Euclidian geographic distance (Geo (E)), a model that included only the amount of land that was forested (For (E)), a full model (Full (BS)) that included as fixed effects the Broken-stick geographic distance and amount of land that was forested along that path among site pairs, a model that included only Broken-stick geographic distance (Geo (BS)), a model that included only the amount of land that was forested (For (E)), and an intercept-only model (Intercept). Columns 3-6 show AIC and sample-size corrected AIC (AICc) values, the difference in AICc from the best model, and model results, including estimates for fixed effects and associated t and P-values.



**Figure S1.** *Left panel:* The percent forest within a circle of radius 24 km was calculated using GIS. Light green = pastureland; dark green = forest; blue = water. *Right panel:* The percent forest between pairs of sites was calculated using both Euclidian (yellow) and Broken-stick (red) paths.