

Table 1. Locations and sample sizes of *Quercus crispula* (*Qc*) and *Q. crispula* var. *horikawae* (*Qch*) populations. Three populations (05Hx, 06Hx, and 07Hx) were identified as *Qch* in the field observation but were grouped to *Qc* in the genetic analysis (see Results 3.2).

Population		Taxon	Latitude	Longitude	Elevation	Sample size (number of individuals)		
Code	Location		(°N)	(°E)	(m)	Leaf size	cpDNA	ncEST-SSR
01C	1: Imabetsu, Aomori	<i>Qc</i>	41.189	140.507	20	0	0	22
02C	2: Hakkoda, Aomori	<i>Qc</i>	40.663	140.816	690	4	8	32
02H1	2: Hakkoda, Aomori	<i>Qch</i>	40.634	140.883	1030	8	7	31
02H2	2: Hakkoda, Aomori	<i>Qch</i>	40.650	140.864	1060	5	0	25
03C	3: Hachimori, Akita	<i>Qc</i>	40.365	140.027	140	0	0	24
04C	4: Moriyoshi, Akita	<i>Qc</i>	40.052	140.617	430	0	8	32
04H	4: Moriyoshi, Akita	<i>Qch</i>	39.977	140.526	1260	0	7	32
05Hx	5: Oga, Akita	<i>Qch</i>	39.903	139.756	620	4	7	31
06C	6: Chokai, Akita	<i>Qc</i>	39.144	139.967	490	4	8	32
06Hx	6: Chokai, Akita	<i>Qch</i>	39.132	139.976	740	4	8	32
06H	6: Chokai, Akita	<i>Qch</i>	39.118	139.992	1220	4	7	32
07C	7: Hanadate, Yamagata	<i>Qc</i>	38.789	140.594	580	4	7	32
07Hx	7: Hanadate, Yamagata	<i>Qch</i>	38.791	140.600	810	4	8	32
08C	8: Gassan, Yamagata	<i>Qc</i>	38.531	139.956	750	4	8	32
08H	8: Gassan, Yamagata	<i>Qch</i>	38.539	139.999	1390	4	8	29
09C	9: Tadami, Fukushima	<i>Qc</i>	37.251	139.380	570	0	8	31
09H	9: Tadami, Fukushima	<i>Qch</i>	37.235	139.366	760	0	8	32
10C	10: Tanigawa, Gunma	<i>Qc</i>	36.838	138.964	690	0	8	18
10H	10: Tanigawa, Gunma	<i>Qch</i>	36.818	138.945	1460	0	8	32
11C	11: Hakuba, Nagano	<i>Qc</i>	36.665	137.825	1170	0	0	26
11H	11: Hakuba, Nagano	<i>Qch</i>	36.660	137.811	1660	4	7	32
12C	12: Shirakawa, Gifu	<i>Qc</i>	36.273	136.891	620	0	0	24
13C	13: Kiso, Nagano	<i>Qc</i>	35.839	137.508	1320	0	0	24
14C	14: Shitara, Aichi	<i>Qc</i>	35.149	137.506	1010	0	0	24
Total						53	130	693

Table 2. Frequency of cpDNA haplotypes and genetic diversity of ncEST-SSR genotypes in *Quercus crispula* (*Qc*) and *Q. crispula* var. *horikawae* (*Qch*) populations. Population codes are shown in Table 1.

Population	cpDNA haplotype			ncEST-SSR genotype			
code	A	B	C		AR <sub>[32]</sub>	<i>H</i> <sub>E</sub>	<i>F</i> <sub>IS</sub>
01C	—	—	—		5.50	0.672	0.038
02C	8	0	0		5.38	0.647	-0.001
03C	—	—	—		5.73	0.649	0.014
04C	0	8	0		5.95	0.653	0.012
06C	0	8	0		6.23	0.676	0.062
07C	0	7	0		5.70	0.653	0.018
08C	8	0	0		6.00	0.660	0.066
09C	8	0	0		6.05	0.673	0.046
10C	8	0	0		5.49	0.650	0.024
11C	—	—	—		6.04	0.669	0.032
12C	—	—	—		6.01	0.677	0.038
13C	—	—	—		5.81	0.662	0.013
14C	—	—	—		6.02	0.676	0.006
<i>Qc</i> total	32	23	0	Mean	5.84	0.663	0.028
02H1	7	0	0		5.43	0.666	0.014
02H2	—	—	—		5.57	0.665	-0.014
04H	7	0	0		5.71	0.675	0.042
05Hx	7	0	0		5.20	0.620	0.026
06Hx	1	7	0		5.63	0.685	0.027
06H	0	7	0		5.89	0.695	0.054
07Hx	0	8	0		5.53	0.649	0.013
08H	8	0	0		5.04	0.646	-0.029
09H	8	0	0		5.98	0.652	0.015
10H	8	0	0		6.07	0.671	0.005
11H	1	0	6		5.77	0.692	0.008
<i>Qch</i> total	47	22	6	Mean	5.62	0.665	0.015

Figure 1

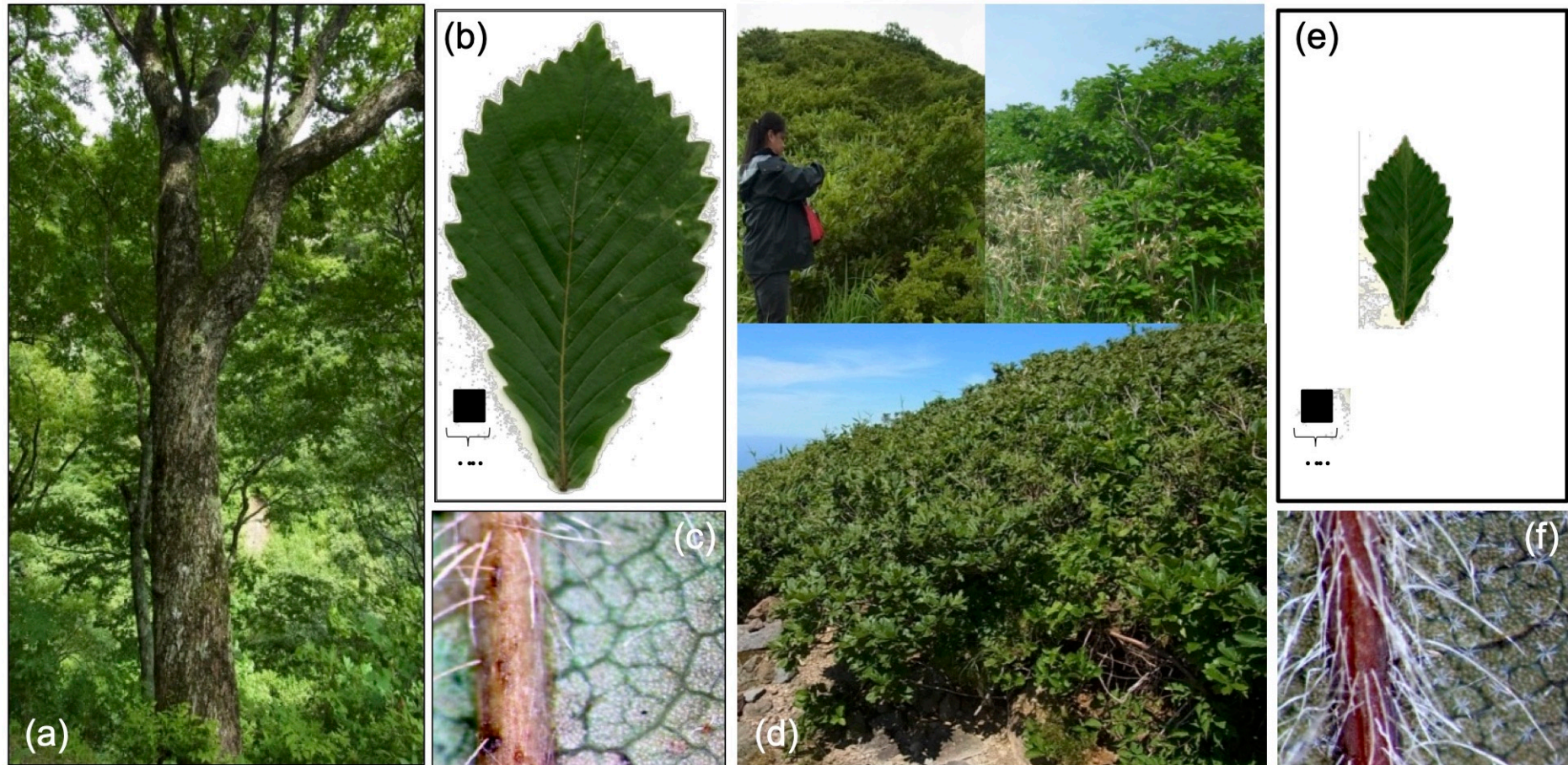


Figure 2

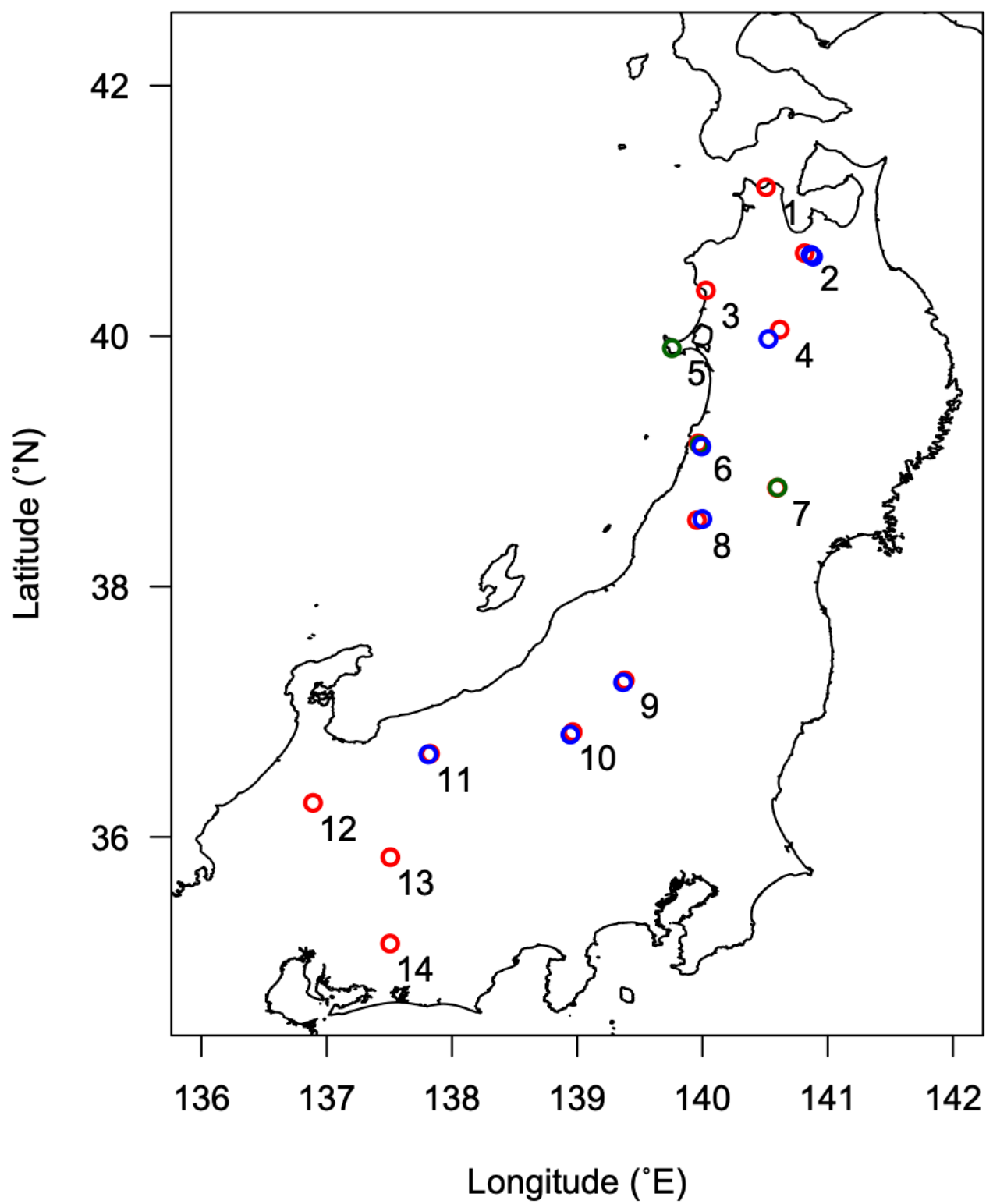


Figure 3

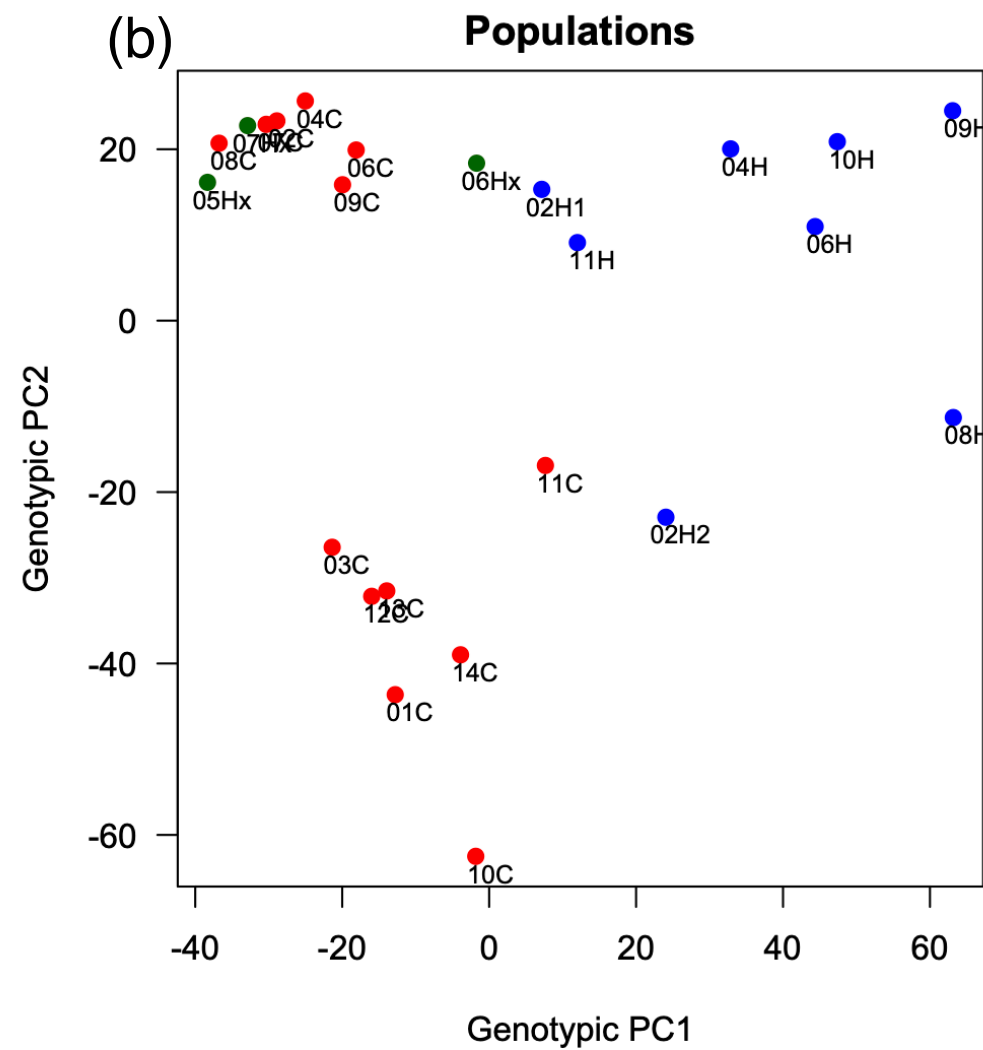
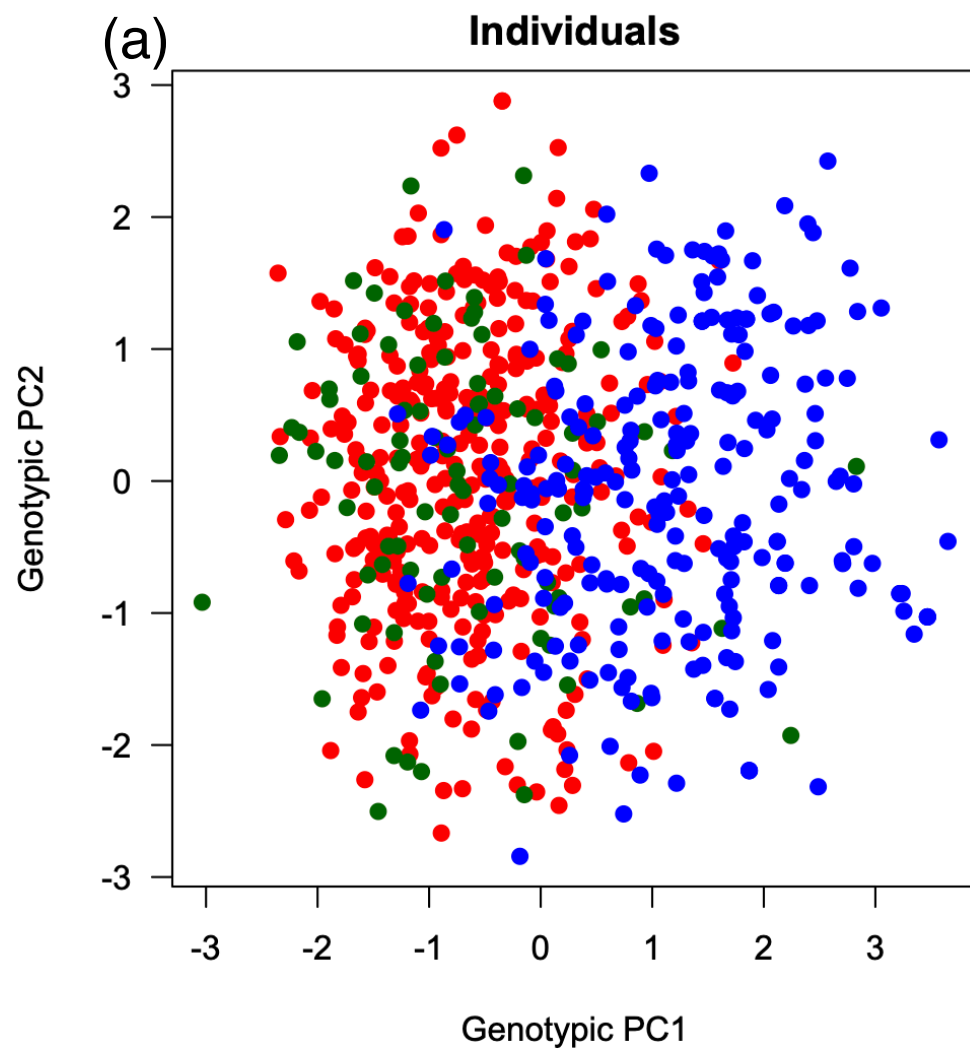


Figure 4

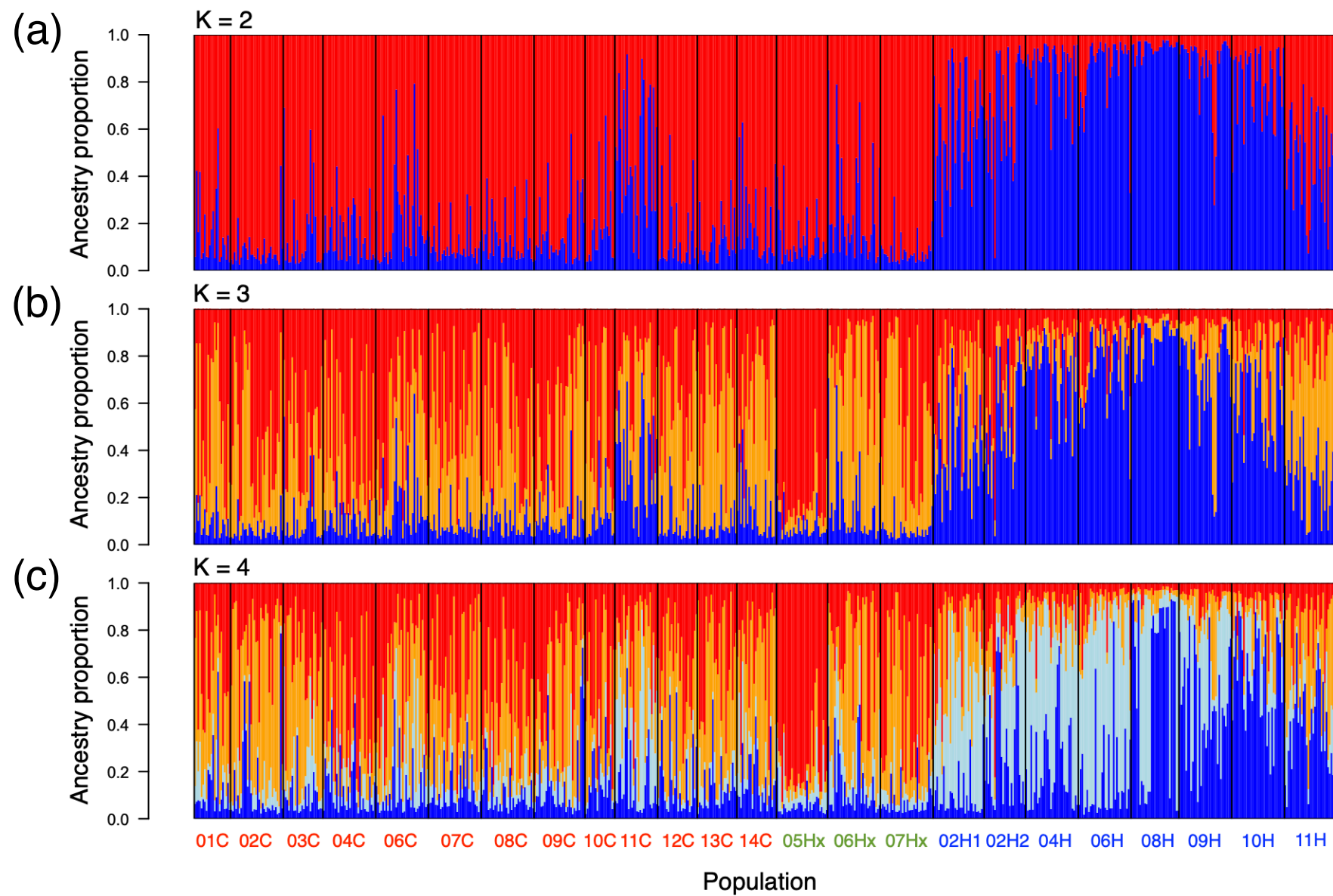


Figure 5

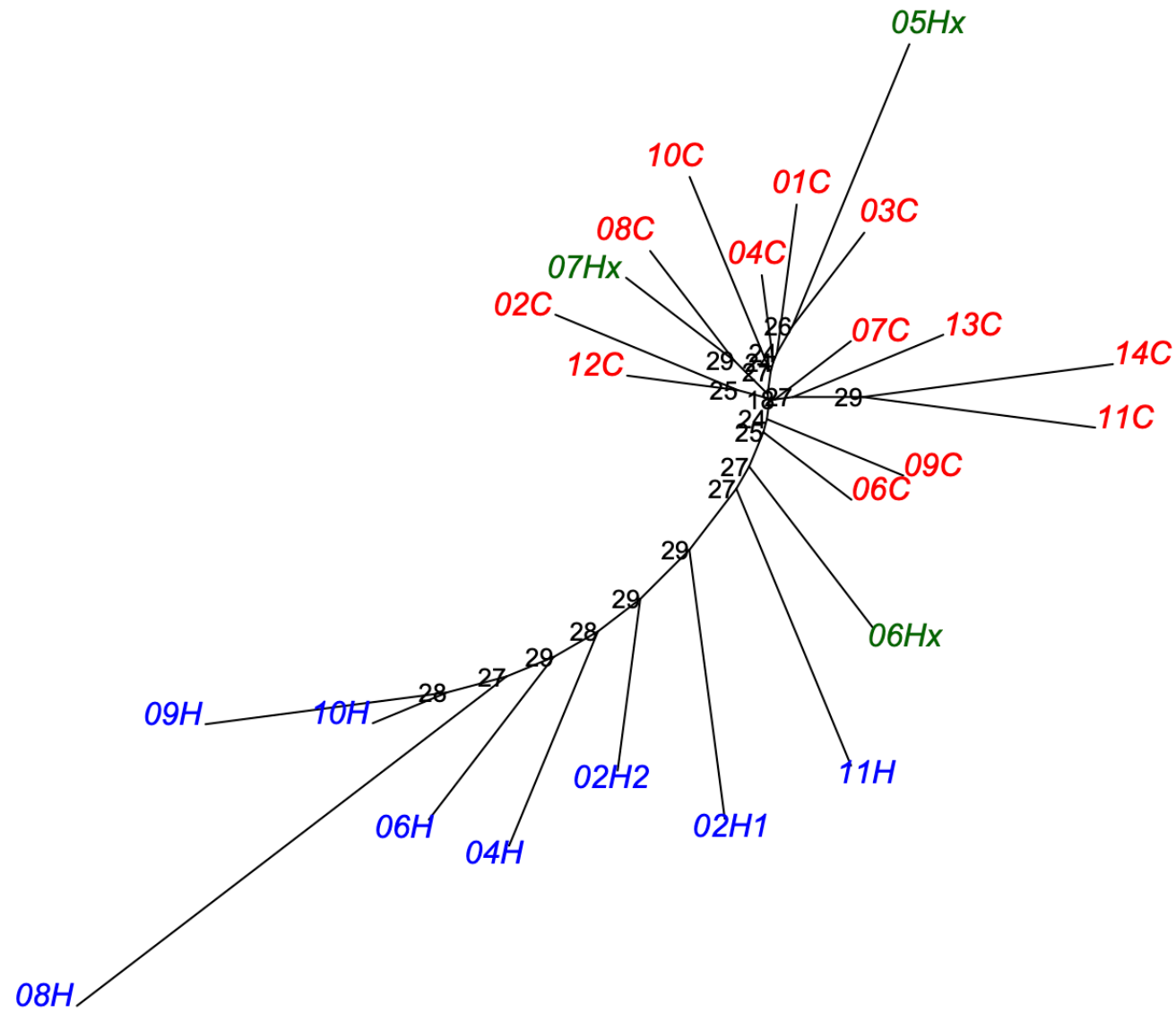




Figure 6

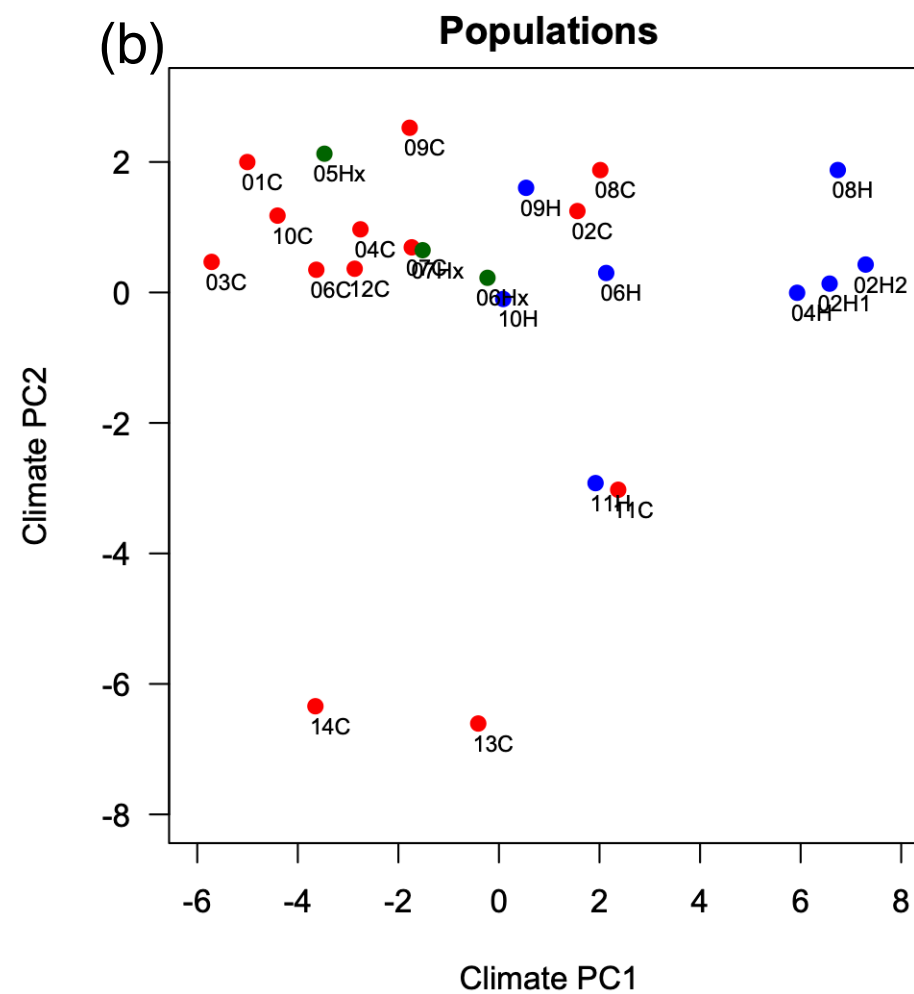
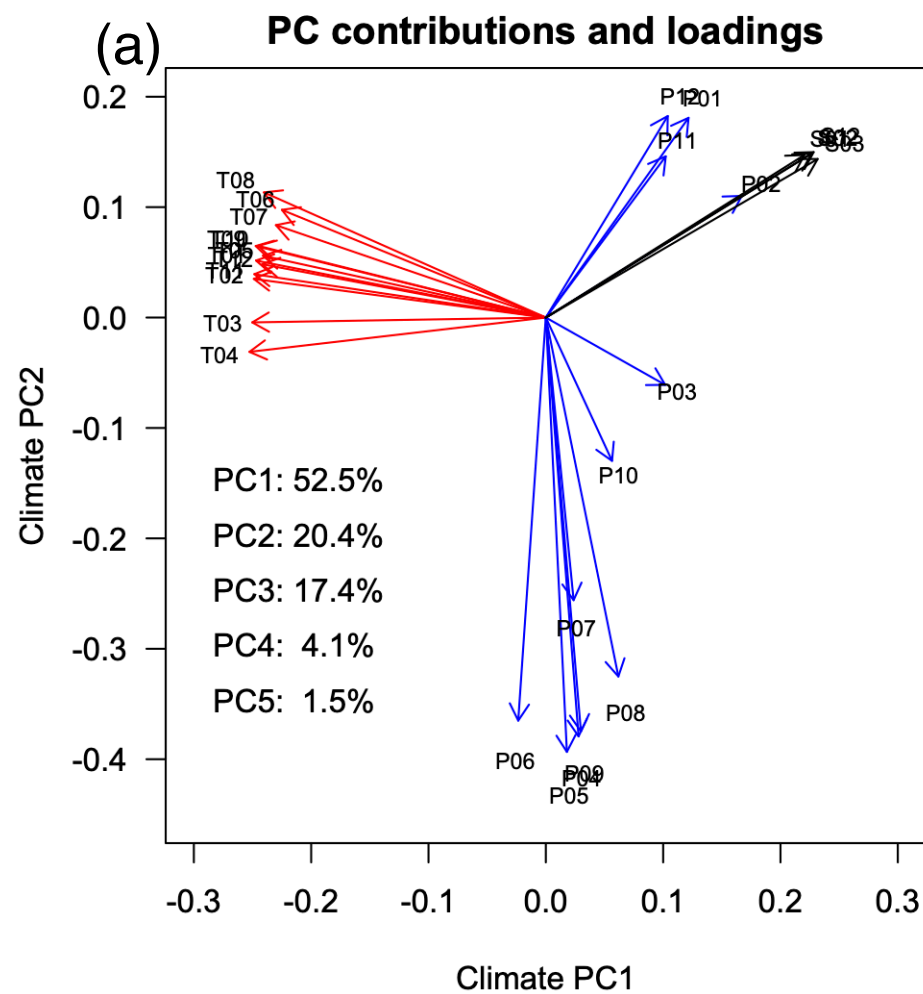




Figure 7

