

Table 3. The list of *P*-value for *t*-test of the comparisons of the diversity indices between introduced region and native or source region.

<i>Species</i>	<i>Diversity indices</i>	<i>Calculations</i>	<i>Regions</i>	<i>n</i>	<i>t</i>	<i>P-value</i>
<i>B. attramentaria</i>	Haplotype diversity	Average of populations	Introduced vs Native	18	1.55	0.14
			Introduced vs Source	7	3.11	0.03
		Regional scale	Introduced vs Native	180	11.3	<0.0001
			Introduced vs Source	70	3.69	0.0008
	Haplotype richness	Average of populations	Introduced vs Native	18	1.43	0.17
			Introduced vs Source	7	2.25	0.07
		Regional scale	Introduced vs Native	60	1.79	0.079
			Introduced vs Source	60	4.75	<0.0001
HL6	Haplotype diversity	Average of populations	Introduced vs Native	14	9.31	<0.0001
			Introduced vs Source	7	5.84	0.0021
		Regional scale	Introduced vs Native	428	15.4	<0.0001
			Introduced vs Source	333	11.5	<0.0001
	Haplotype richness	Average of populations	Introduced vs Native	13	13.8	<0.0001
			Introduced vs Source	7	13.3	<0.0001
		Regional scale	Introduced vs Native	30	4.74	0.0003
			Introduced vs Source	30	4.00	0.0012
HL1	Haplotype diversity	Average of populations	Introduced vs Native	14	0.96	0.36
			Introduced vs Source	7	0.73	0.5
		Regional scale	Introduced vs Native	230	0.04	0.97
			Introduced vs Source	182	0.14	0.89
	Haplotype richness	Average of populations	Introduced vs Native	11	0.03	0.98
			Introduced vs Source	7	0.68	0.53
		Regional scale	Introduced vs Native	30	0.35	0.73
			Introduced vs Source	30	0.37	0.72