

Supplementary Materials

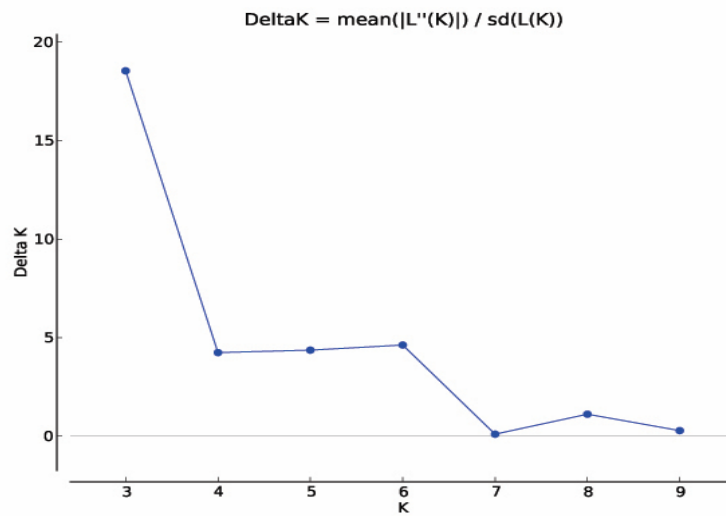


Figure S1. Relationship between the rational cluster K and estimated value ΔK .

Table S1. Values of F_{st} (below the diagonal) and N_m (above the diagonal) for pairwise comparison of *A. cremastogyne* populations estimated using 25 simple sequence repeat loci.

Population	AA	AC	B	F	I	J	K	N	Q	R	S	T	U	V
AA		7.815	9.75	20.583	10.62	9.75	9.009	9.365	11.114	10.62	10.62	10.62	9.365	12.25
AC	0.031		11.655	10.167	11.655	13.639	11.655	15.375	10.62	11.114	12.25	10.62	11.655	10.167
B	0.025	0.021		15.375	11.655	11.655	12.908	13.639	11.655	10.167	11.655	12.25	11.655	11.655
F	0.012	0.024	0.016		12.908	11.655	12.25	11.114	12.908	12.25	11.655	13.639	12.25	12.25
I	0.023	0.021	0.021	0.019		16.417	11.114	12.908	12.25	12.908	13.639	12.25	10.62	11.114
J	0.025	0.018	0.021	0.021	0.015		11.655	13.639	12.908	12.908	12.25	11.655	14.456	12.908
K	0.027	0.021	0.019	0.02	0.022	0.021		17.607	12.25	9.009	11.655	8.371	12.25	9.365
N	0.026	0.016	0.018	0.022	0.019	0.018	0.014		15.375	10.167	15.375	9.365	20.583	12.25
Q	0.022	0.023	0.021	0.019	0.02	0.019	0.02	0.016		8.679	12.908	9.75	14.456	10.167
R	0.023	0.022	0.024	0.02	0.019	0.019	0.027	0.024	0.028		8.371	10.62	12.908	6.507
S	0.023	0.02	0.021	0.021	0.018	0.02	0.021	0.016	0.019	0.029		8.371	13.639	11.655
T	0.023	0.023	0.02	0.018	0.02	0.021	0.029	0.026	0.025	0.023	0.029		9.365	8.083
U	0.026	0.021	0.021	0.02	0.023	0.017	0.02	0.012	0.017	0.019	0.018	0.026		9.365
V	0.02	0.024	0.021	0.02	0.022	0.019	0.026	0.02	0.024	0.037	0.021	0.03	0.026	

Table S2. Molecular variance analysis within and among *A. cremastogyne* populations estimated using 25 simple sequence repeat (SSR) loci.

Source of variation	Degree of freedom	Sum of squares	Mean square	Variance component	Percentage of variation (%)
Among populations	13	489.842	37.680	0.843	3.0
Within populations	161	4,385.044	27.236	27.236	97.0
Total	174	4,874.886		28.079	100