

Supplementary Material

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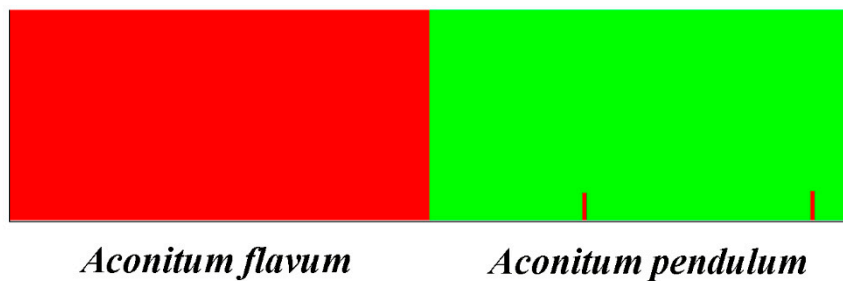


Figure S1. Results of BAPS analysis for two species of *Aconitum*.

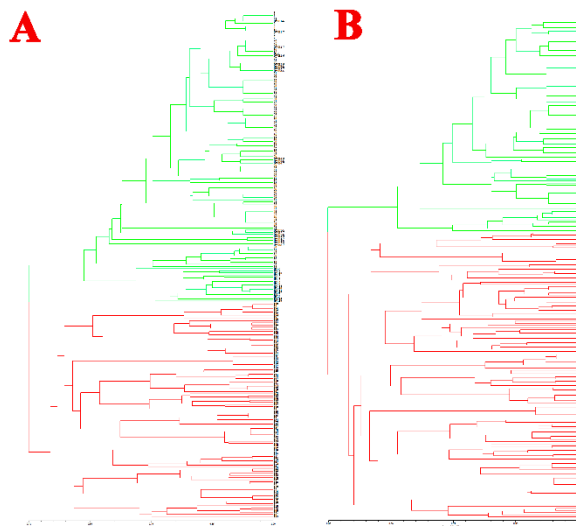


Figure S2. UPGMA clustering on verification of blind individuals (UBC808 and UBC853): (A) blind individuals from DWB and BM; (B) blind individuals from GQ and SL. Green represents *A. flavum* individuals; red represents *A. pendulum* individuals.

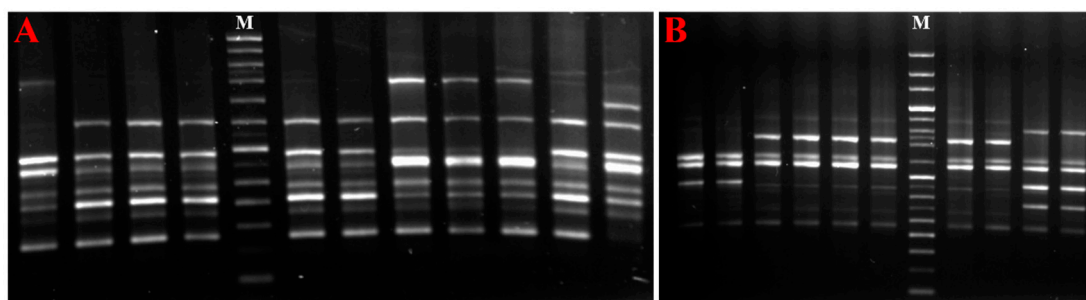


Figure S3. ISSR profiles of *A. flavum* and *A. pendulum* generated with primer UBC853: (A) DWB population; (B) QHL population; M = 100 bp + 200 bp TaKaRa DNA Ladder.

Table S1. Summary of banding profile and polymorphism revealed by 11 ISSR primers.

Primer ID	Primer sequence (5'-3')	TM (°C)	<i>A. flavum</i>				<i>A. pendulum</i>			
			TNB	NPB	PPB (%)	Size (bp)	TNB	NPB	PPB (%)	Size (bp)
UBC807	AGAGAG AGAGAG AGAGT	51.8	14	13	92.8 6	350- 1,200	17	14	82.3 5	300- 1,200
UBC808	AGAGAG AGAGAG AGAGC	59.6	17	16	94.1 2	300- 1,700	19	17	89.4 7	300- 1,700
UBC811	GAGAGA GAGAGA GAGAC	57.4	14	11	78.5 7	300- 1,300	18	15	83.3 3	300- 1,300
UBC812	GAGAGA GAGAGA GAGAA	52	16	14	87.5 0	400- 1,800	17	15	88.2 4	400- 1,800
UBC824	TCTCTCT CTCTCTC TCG	52	18	18	100. 00	400- 2,000	20	20	100. 00	400- 2,000
UBC825	ACACAC ACACAC ACACT	53	22	22	100. 00	400- 2,000	20	20	100. 00	400- 2,000
UBC826	ACACAC ACACAC ACACC	60	19	19	100. 00	300- 2,000	16	16	100. 00	300- 2,000
UBC846	CACACA CACACA CACART	52	19	19	100. 00	300- 1,800	20	20	100. 00	450- 1,800
UBC853	TCTCTCT CTCTCTC TCRT	50	13	12	92.3 1	550- 1,900	16	16	100. 00	550- 1,900
UBC887	DVDTCT CTCTCTC TCTC	52	20	20	100. 00	350- 2,000	21	21	100. 00	350- 2,000
UBC890	VHVG TG TGTGTGT GTGT	56	21	21	100. 00	350- 2,000	19	18	94.7 4	350- 2,000
Total	-	-	193	185	95.8 5	300- 2,000	203	192	94.5 8	300- 2,000
Means	-	-	17.55	16.82	95.8 5	-	18.45	17.45	94.5 8	-

D= (A, G, T); H= (A, C, T); R= (A, G); V= (A, C, G); Total Number of amplified Bands (TNB); Number of Polymorphic Bands (NPB), Percentage of Polymorphic Bands (PPB).

Table S2. Analysis of molecular variance (AMOVA) for ISSR variation surveyed in six populations of *A. flavum* (3) and *A. pendulum* (3)

Source of variation	<i>d.f.</i>	SSD	MSD	Variation components	Total variation (%)	<i>P</i> value ^a
<i>A. flavum</i>						
Between populations	2	596.373	298.187	9.59849	30.34	<i>P</i> < 0.001
Within populations	132	2,908.545	22.034	22.03443	69.66	<i>P</i> < 0.001
<i>A. pendulum</i>						
Between populations	2	865.13	432.565	15.17223	37.48	<i>P</i> < 0.001
Within populations	130	3,290.359	25.310	25.31045	62.52	<i>P</i> < 0.001

d.f.: Degrees of freedom, SSD: sum of squares, MSD: mean squared deviation;

^a: Significance tests after 1,000 permutations.

Table S3. Genetic differentiation among species calculated using different Bayesian approaches.

Model	populations differentiation (θ_B)					inbreeding coefficient (<i>f</i>)					DIC
	Mean	SD	2.50%	50%	97.50%	Mean	SD	2.50%	50%	97.50%	
Full model	0.265	0.032	0.201	0.266	0.324	0.554	0.272	0.050	0.567	0.976	2,517.43
<i>f</i> = 0 model	0.207	0.019	0.173	0.206	0.248	-	-	-	-	-	2,549.28
θ_B = 0 model	-	-	-	-	-	0.981	0.018	0.932	0.987	0.999	10,255.70
<i>f</i> free model	0.288	0.027	0.237	0.288	0.341	0.493	0.291	0.023	0.488	0.977	3,651.48

Hickory 1.1 Software uses the inbred coefficient (*f*), *f* = Full Model, 0 (assuming no inbreeding), free model and θ_B = 0 model (assuming no population structure). The model calculates genetic differentiation and the genetic structure parameters of *A. flavum* and *A. pendulum*. Model selection was based on the Deviation Information Criterion (DIC). Models with smaller DICs are preferred.