SUPPLEMENTARY APPENDIX

This appendix has been provided by the authors to give readers additional information about their work.

Supplement to:

Genetic diversity of *Herpetospermum caudigerum* (Ser.) Baill using AFLP and chloroplast microsatellites

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Biotechnol. Biotechnol. Equip. 2019, **33**

Supplemental data

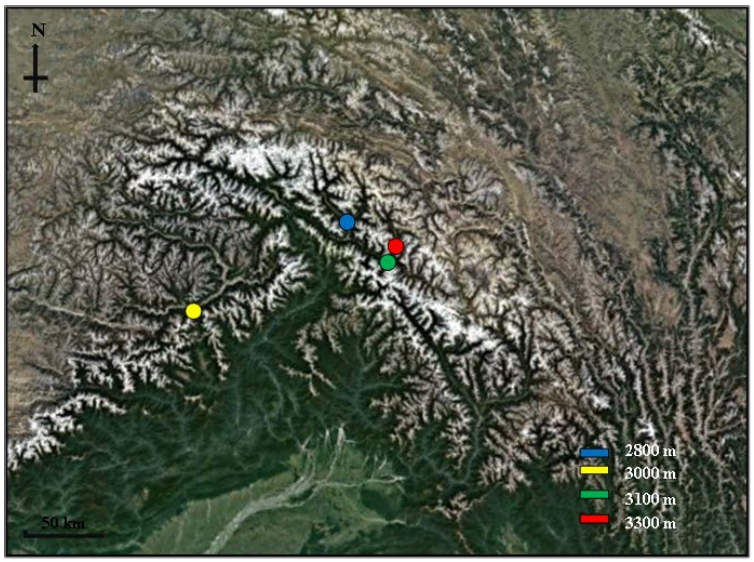

Figure S1 Four sampling sites of *H. caudigerum* Baill from Tibet.

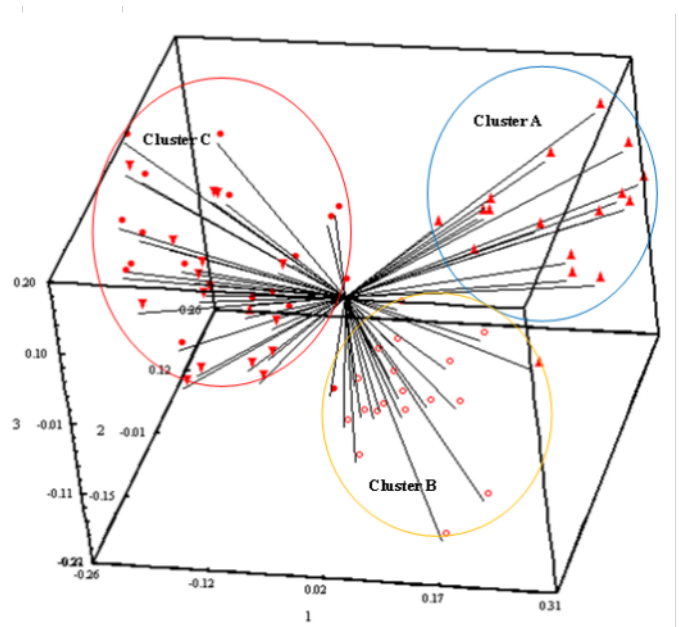

Figure S2 Principal coordinates analysis based on AFLP data.
Samples from 2800 m (up-pointing triangles); samples from 3000 m (down-pointing triangles); samples from 3100 m (filled circles); samples from 3300 m (open circles).

Table S1 AFLP primers used in four *H. caudigerum* Baill populations.

Code	Mse I (3-5′)	EcoR I (3′-5′)
1	M_{33}: 5'-GAT GAG TCC TGA GTA AGG-3'	E_{22}: 5'-GAC TGC GTA CCA ATT CCC -3'
2	M_{21}: 5'-GAT GAG TCC TGA GTA ACA-3'	E_{21}: 5'-GAC TGC GTA CCA ATT CCA -3'
3	M_{22}: 5'-GAT GAG TCC TGA GTA ACC-3'	E_{42}: 5'-GAC TGC GTA CCA ATT CTC -3'
4	M_{34}: 5'-GAT GAG TCC TGA GTA AGT-3'	E_{33}: 5'-GAC TGC GTA CCA ATT CGG -3'
5	M_{43}: 5'-GAT GAG TCC TGA GTA ATG-3	E_{41}: 5'-GAC TGC GTA CCA ATT CTA -3'
6	M_{43}: 5'-GAT GAG TCC TGA GTA ATG-3	E_{44}: 5'-GAC TGC GTA CCA ATT CTT -3'
7	M_{23}: 5'-GAT GAG TCC TGA GTA ACG-3'	E_{34}: 5'-GAC TGC GTA CCA ATT CGT -3'
8	M_{13}: 5'-GAT GAG TCC TGA GTA AAG-3'	E_{33}: 5'-GAC TGC GTA CCA ATT CGG -3'
9	M_{31}: 5'-GAT GAG TCC TGA GTA AGA-3'	E_{22}: 5'-GAC TGC GTA CCA ATT CCC -3'
10	M_{12}: 5'-GAT GAG TCC TGA GTA AAC-3'	E_{14}: 5'-GAC TGC GTA CCA ATT CAT -3'

Table S2 cpDNA SSR primers used in four *H. caudigerum* Biall populations.

Code	Region	Forward sequence(5′-3′)	Reverse sequence(3′-5′)
P01	*trn*T-*trn*L	CATTACAAATGCGATGCTCT	TCTACCGATTTCGCCATATC
P02	*trn*L-*trn*F	CGAAATCGGTAGACGCTACG	GGGGATAGAGGGACTTGAAC
P03	*trn*L-*trn*F	GGTTCAAGTCCCTCTATCCC	ATTTGAACTGGTGACACGAG
P04	*atp*B-*rbc*L	TAAACCCCGGACGAAAGTAGTGG	ACTTGCTTTAGTTTCGTTTGTGGTGA
P05	*trn*L-*trn*F	GGTTCAAGTCCCTCTATCCC	ATTTGAACTGGTGACACGAG
P06	*rpl*I6	GCTATGCTTAGTGTGTGACTCGTTG	CGTACCCATATTTTTCCACCACGAC
P07	cp-*trn*K	GGGTTGCCCGGGACTCGAAC	CAACGGTAGAGTACTCGGCTTTTA
P08	*trn*Q-*trn*G	TCGAACCTCCGAATAACAGG	CGCATTCGTTAGCTTGGAAG
P09	*trn*S-*psb*C	GGTTCGAATCCCTCTCTCTC	GGTCGTGACCAAGAAACCAC
P10	*psb*D-16S	CCACAAAAACGAAACGGTCT	ACTAACTAATCAGACGCGAGCC

Table S3 Variation sites in *trn*L-*trn*F-300 and *trn*L-*trn*F-396 religions among 4 populations.

Domain	Variation site	H1	H2	H3	H4	H5	H6	H7
P03-*trn*L-*trn*F-300	1	A	C	C	C	C	C	C
	2	G	A	A	A	A	A	A
	3	G	A	A	A	A	A	A
	4	T	G	G	G	G	G	G
	5	G	T	G	T	G	G	T
	6	T	G	G	G	G	G	G
	7	T	A	A	A	A	A	A
	8	T	A	A	A	A	A	A
	9	A	G	G	G	G	G	G
	10	T	A	A	A	A	A	A
	11	A	T	T	T	T	T	T
	12	A	T	T	T	T	T	T
	13	A	C	C	C	C	C	C
	14	T	G	G	G	G	G	G
	15	G	A	A	A	A	A	A
	16	A	A	A	T	T	T	T
	17	C	G	G	G	G	G	G
	18	T	G	G	G	G	G	G
	19	T	G	G	G	G	G	G
	20	G	A	A	A	A	A	A
P02-*trn*L-*trn*F-396	21	G	T	G	G	G	T	T
	22	C	A	A	A	A	A	A
	23	C	A	A	A	A	A	A
	24	C	A	A	A	A	A	A
	25	T	C	C	C	C	C	C
	26	A	T	T	T	T	T	T
	27	A	C	C	C	C	C	C
	28	A	C	C	C	C	C	C