Supplementary Information

Increased risk of genetic swamping in the progenitor of the domesticated apple (*Malus sieversii*) from the diversity hotspot, Tien Shan, Kazakhstan

Table 1. Summary of pairwise contemporary and historical gene flow among the four redefined groups of the three *Malus* taxa. m (migration rate) is the number of immigrants per generation. H stands for historical while C refers to contemporary. mean HNm refers to the historical effective migration rate (Nem) that is the migration rate given the effective population size. Cm/Hm ratio was also presented as a measure of difference between the historical and contemporary gene flow. See Table 1 for the population acronyms.

	mean HNm	**mean Hm**	**lower Hm**	**upper Hm**	**mean Cm**	**95% CI of Cm**	**Cm/Hm**
m_TalKok->Ala	1.795163	0.000726	0.000503	0.000925	0.021800	0.018000	30.03
m_TalEW->Ala	1.029359	0.000416	0.000161	0.000644	0.024800	0.022300	59.58
m_Dom->Ala	0.910013	0.000368	0.000141	0.000563	0.030400	0.027800	82.61
m_Ala->TalKol	1.898579	0.001408	0.001116	0.001661	0.035300	0.018700	25.07
m_TalEW->TalKok	0.356213	0.000264	0.000000	0.000490	0.079700	0.039400	301.73
m_Dom->TalKok	0.723443	0.000536	0.000272	0.000790	0.061000	0.037300	113.71
m _Ala->TalEW	0.540516	0.001184	0.000702	0.001638	0.010800	0.010300	9.12
m _TalKol->TalEW	4.520675	0.013293	0.009904	0.015166	0.022000	0.014400	1.65
m _Dom->TalEW	0.632382	0.001385	0.000843	0.001919	0.031200	0.028400	22.52
m _Ala->Dom	0.928644	0.001466	0.000715	0.001669	0.084000	0.025500	57.29
m _TalKok->Dom	0.566246	0.000894	0.000477	0.001272	0.044400	0.019800	49.66
m _TalEW->Dom	1.283492	0.002027	0.001033	0.002821	0.097900	0.034500	48.31

Table S2. Detailed information on 17 microsatellite loci utilized in the study

No.	SSR primer	Fluorescently dye	Sequence	Allele range	Motif	Reference
1	MdBHLH3	FAM	CAACTCCCCTTATTCTTCTTCTCTC CACCTGACCTTCTCTCTACCTCTAC	-	AG	Faramarzi et al., [31]
2	NZmsPal8	HEX	GGCACAAGCACAAGGAAACA GTTTGAGCCAGTCCATTTTTCCCTAT	-	AG	
3	NzmsPal13	FAM	TCGATGAACAAGGCCCAAAG GTTTAGGGGGACGGAAGGAACAAG	-	AG	
4	NzmsPal36	HEX	CCTCAACAAATATAAGACTCTCTC GTTTCTCCACTCTGTCCGTACATT	-	AG	
5	P188-CH03d07	FAM	CAAATCAATGCAAAACTGTCA GGCTTCTGGCCATGATTTTA	186-226	AG	Dong, Y. et al., [32]
6	P290-Hi03a10	HEX	GGACCTGCTTCCCCTTATTC GTTTCAGGGAACTTGTTTGATGG	206-290	AG	
7	P300-Hi08h12	FAM	GAAGGAAATCATCATCAAGACG GTTTCAAGACCATGGAACAACTTGG	151-203	GAA	
8	CH05g08	FAM	CCAAGACCAAGGCAACATTT CCCTTCACCTCATTCTCACC	161–179	AG	Silfverberg-Dilworth, Eve, et al., [33]
9	CH03e03	HEX	GCACATTCTGCCTTATCTTGG AAAACCCACAAATAGCGCC	106–216	AG	
10	Hi23g02	FAM	TTTTCCAGGATATACTACCCTTCC GTTTCTTCGAGGTCAGGGTTTG	230–257	CAA	
11	CH03a09	HEX	GCCAGGTGTGACTCCTTCTC	125–143	AG	

			CTGCAGCTGCTGAAACTGG		
12	CH05a05	FAM	TGTATCAGTGGTTTGCATGAAC GCAACTCCCAACTCTTCTTTCT	198–230	AG
13	CH01c06	HEX	TTCCCCATCATCGATCTCTC AAACTGAAGCCATGAGGGC	146–188	AG
14	CH01f03b	FAM	GAGAAGCAAATGCAAAACCC CTCCCCGGCTCCTATTCTAC	137-183	AG
15	CH03c02	HEX	TCACTATTTACGGGATCAAGCA GTGCAGAGTCTTTGACAAGGC	166-136	AG
16	CH04c07	FAM	GGCCTTCCATGTCTCAGAAG CCTCATGCCCTCCACTAACA	98-135	AG
17	CH02a03	HEX	AGAAGTTTTCACGGGTGCC TGGAGACATGCAGAATGGAG	144-170	AG

Table S3. Summary of PCR amplification conditions

Primer number	Reference	PCR condition
1,2,3,4	Faramarzi et al., [31]	94 °C 2 min 30 sec, 4 cycles: 94 °C 30 sec, 65 °C 1 min, 72 °C 1 min, 30 cycle: 94 °C 30 sec, 60 °C 1 min and 72 °C 1 min; 72 °C 5 min (dropping 1 °C per cycle)
5,6,7	Dong, Y. et al., [32]	94 °C 4 min, 4 cycles: 94 °C 50 sec, 65 °C 55 sec, 72 °C 1 min, 30 cycle: 94 °C 50 sec, 65 °C 55 sec and 72 °C 1 min; 72 °C 5 min (dropping 1 °C per cycle)
8,9,10,12	Silfverberg-Dilworth, Eve, et al., [33]	94 °C 5 min, 10 cycles: 94 °C 30 sec, 58–53 °C 45 sec (dropping 0.5 °C per cycle) and 72 °C 1 min, 25 cycles: 94 °C 30 sec, 53 °C 45 sec and 72 °C 1 min; 72 °C 15 sec
11,13,14,15,16,17		94 °C 5 min, 38 cycles: 94 °C 30 sec, 60 °C 30 sec and 72 °C 1 min, 72 °C 10 min

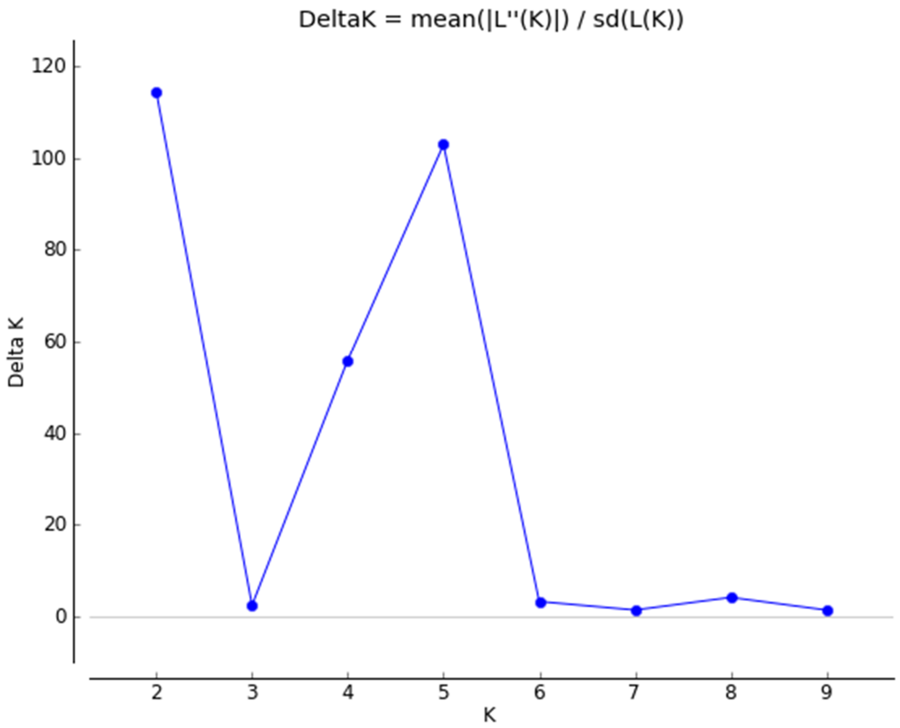

Figure S1. Delta K plot. Delta K values for each of K clusters from 2 to 9 were estimated by method of Evanno et al.,[43].

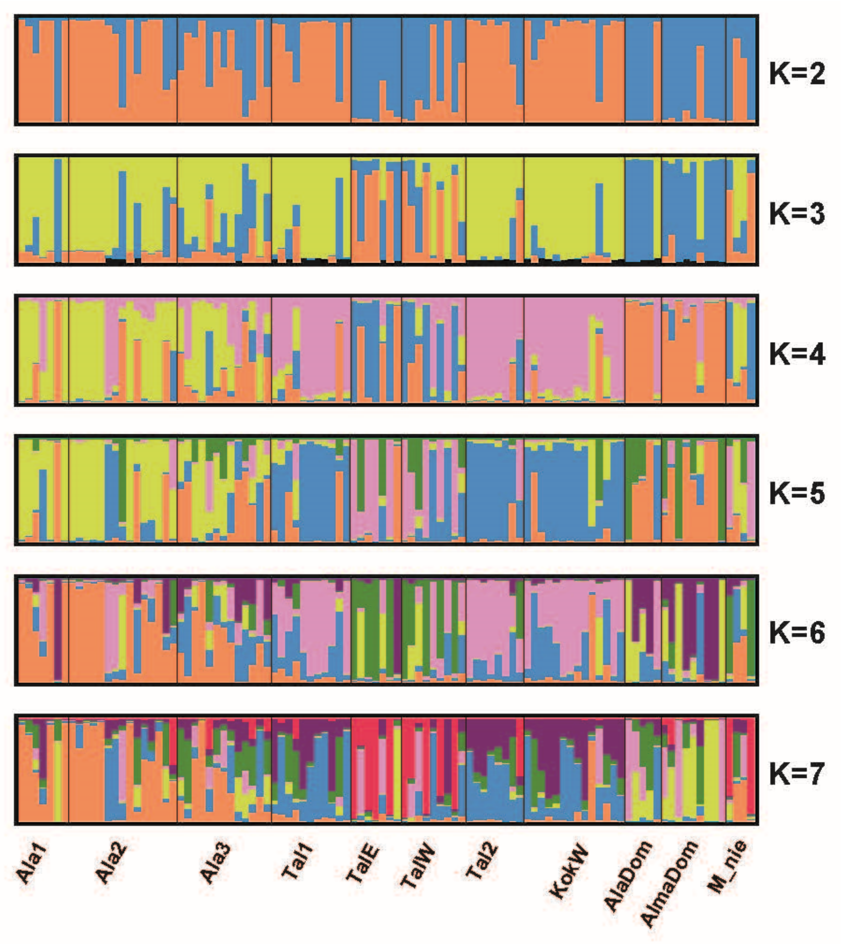

Figure S2. Bar plots of K = 2 to K = 7 from the Bayesian model-based group assignment on the 11 populations of the three *Malus* taxa with 13 nuclear SSRs. Populations are separated by solid vertical black lines. Colors represent assignments of loci into each of the 2–7 estimated groups. See Table 1 for population abbreviations.