Supporting materials:

Table S1. Genetic diversities identified using SSRs in 288 green foxtail accessions.

Marker	GenotypeNo	AlleleNo	GeneDiversity	Heterozygosity	PIC
b159	77.0000	36.0000	0.9546	0.2025	0.9528
b165	38.0000	33.0000	0.9480	0.0263	0.9456
b180	55.0000	42.0000	0.9561	0.0964	0.9545
b186	49.0000	43.0000	0.9632	0.0294	0.9620
b236	74.0000	54.0000	0.9728	0.3452	0.9721
b237	34.0000	23.0000	0.8935	0.0650	0.8862
b241	53.0000	41.0000	0.9648	0.0474	0.9636
b266	40.0000	16.0000	0.7946	0.1773	0.7661
MPGD13	18.0000	12.0000	0.8027	0.0403	0.7780
MPGA32	40.0000	20.0000	0.8721	0.1279	0.8600
p4	47.0000	44.0000	0.8565	0.0451	0.8457
p29	58.0000	45.0000	0.9555	0.0800	0.9538
p45	23.0000	21.0000	0.7945	0.0159	0.7755
p80	47.0000	38.0000	0.9561	0.0804	0.9543
si227	51.0000	40.0000	0.9495	0.0620	0.9472
b174	77.0000	45.0000	0.9664	0.1629	0.9653
p20	44.0000	38.0000	0.9228	0.0302	0.9189
p3	46.0000	42.0000	0.9619	0.0141	0.9605
b218	59.0000	46.0000	0.9441	0.0504	0.9415
b182	40.0000	35.0000	0.9555	0.0224	0.9537
B1	19.0000	13.0000	0.7641	0.0493	0.7291
b101	51.0000	49.0000	0.9635	0.0145	0.9623
b102	44.0000	42.0000	0.9648	0.0234	0.9636
b109	42.0000	22.0000	0.9320	0.1042	0.9279
b117	21.0000	16.0000	0.8130	0.0235	0.7943
b123	36.0000	25.0000	0.9167	0.0389	0.9112
b126	39.0000	36.0000	0.9545	0.0111	0.9526
b145	39.0000	31.0000	0.9552	0.0317	0.9534
b153	141.0000	53.0000	0.9173	0.6469	0.9124
b163	40.0000	27.0000	0.9380	0.0617	0.9345
b169	35.0000	31.0000	0.9505	0.0163	0.9483
b171	52.0000	31.0000	0.9558	0.0970	0.9540
b181	41.0000	33.0000	0.9427	0.0316	0.9399
b185	53.0000	30.0000	0.8734	0.1993	0.8629
b187	40.0000	35.0000	0.9119	0.0185	0.9080
b189	48.0000	38.0000	0.9651	0.0498	0.9639

b200	27.0000	22.0000	0.9130	0.0211	0.9069
b217	43.0000	40.0000	0.9486	0.0112	0.9463
b224	46.0000	42.0000	0.9607	0.0195	0.9592
b242	41.0000	37.0000	0.9506	0.0149	0.9484
b246	57.0000	54.0000	0.9750	0.0175	0.9744
b247	52.0000	40.0000	0.9516	0.0522	0.9495
b249	57.0000	47.0000	0.9620	0.0469	0.9607
b250	64.0000	54.0000	0.9345	0.0735	0.9314
b258	107.0000	58.0000	0.9485	0.2694	0.9462
b269	34.0000	31.0000	0.9142	0.0115	0.9092
MPGA31	21.0000	17.0000	0.8054	0.0182	0.7831
MPGA50	32.0000	28.0000	0.9291	0.0287	0.9248
MPGD44	22.0000	19.0000	0.8741	0.0120	0.8624
p10	33.0000	28.0000	0.8729	0.0215	0.8628
p14	70.0000	44.0000	0.9326	0.1131	0.9293
p17x	83.0000	40.0000	0.9178	0.2057	0.9127
p2	44.0000	34.0000	0.9505	0.0430	0.9482
p32	39.0000	24.0000	0.8110	0.0623	0.7952
p33	24.0000	11.0000	0.7021	0.0570	0.6678
p41	92.0000	40.0000	0.9327	0.3271	0.9289
p42	20.0000	13.0000	0.7949	0.0308	0.7687
p44	40.0000	29.0000	0.7180	0.0542	0.6981
p59	41.0000	36.0000	0.9529	0.0295	0.9509
p78	34.0000	31.0000	0.8640	0.0134	0.8567
p8	26.0000	22.0000	0.8711	0.0215	0.8589
p88	48.0000	37.0000	0.9349	0.0912	0.9315
p89	83.0000	46.0000	0.9618	0.2103	0.9605
p98	41.0000	26.0000	0.8726	0.0737	0.8608
Si017	25.0000	23.0000	0.8090	0.0217	0.7881
Si119	29.0000	25.0000	0.8588	0.0148	0.8479
Si132	42.0000	35.0000	0.9439	0.0270	0.9411
x298	39.0000	27.0000	0.9274	0.0645	0.9230
x4	33.0000	26.0000	0.8688	0.0439	0.8577

Table S2. Comparations of genetic diversity between wild green foxtail and cultivated foxtail millet

Sample	Allele No	Genotype No	Gene Diversity	Heterozygosity	PIC
Wild					
Average	33.5072	46.3768	0.9082	0.0763	0.9010
Range	12~54	21~141	0.7021~0.9750	0.0111~0.6469	0.6687~0.9744
Std.	11.2689	21.1459	0.0649	0.1012	0.0729
Landrace					
Average	21.4348	25.0290	0.8598	0.0177	0.8447
Range	6~41	6~46	0.6310~0.9514	0~0.0444	0.5937~0.9528
Std.	9.1273	10.2081	0.0898	0.0156	0.1038

Table S3. List of annotated genes co-localized with SSR loci detected as genomic regions under selection

SSR Loci (Fst value)	Blast bit	Putative gene	Functional annotation
B1 (0.2044)	Chr9 (56,195,798~56,196,056)	Si037298m	ubiquitin-conjugating enzyme E2-21 kDa 1
P33 (0.2186)	Chr1 (33,331,843~33,332,002)	Si017865m	DREB-like protein
X4 (0.2325)	Chr9 (98,538~98,850)	Si033907m	PDR-like ABC transporter
P10 (0.1422)	Chr6 (7,486,774~7,486,973)	Si015085m	transmembrane transport
Si132 (0.1169)	Chr9 (45339944~45340318)	Si038719m	E3 ubiquitin-protein ligase RFWD3

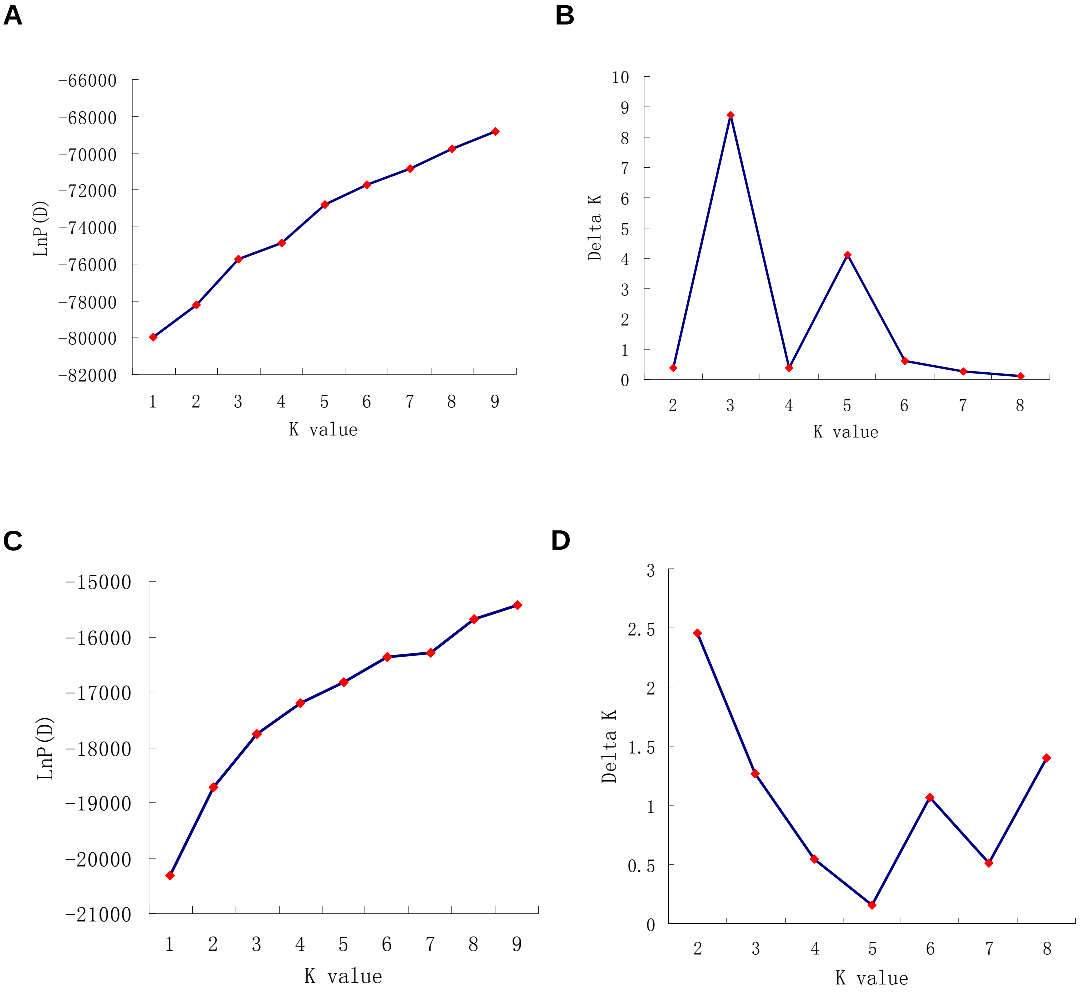

Figure S1. Determinations of value of K for substructuring. **(A)** and **(B)**: Optimal K identified by LnP(D) and delta K of PopA; **(C)** and **(D)**: Optimal K identified by LnP(D) and delta K of PopB.

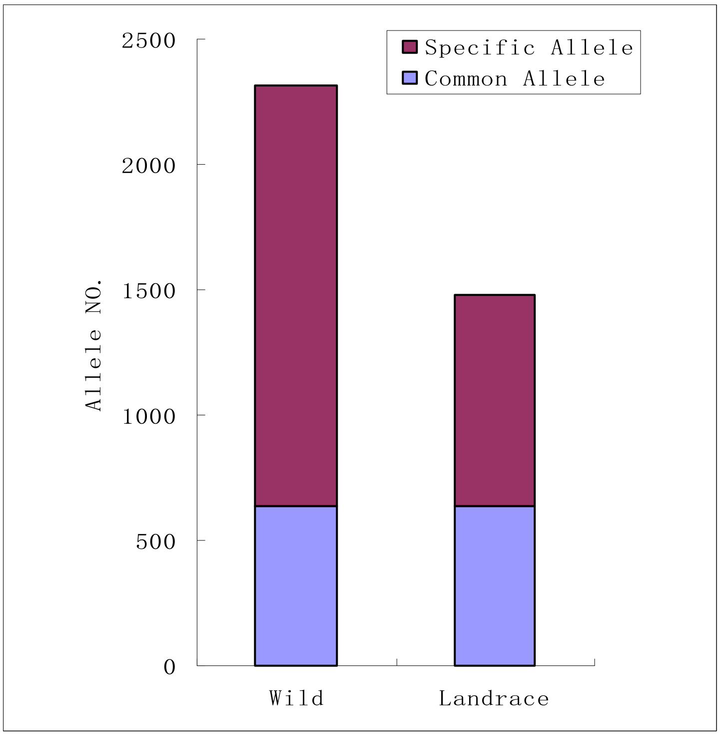

Figure S2. Sharing and specific alleles of wild green foxtail and domesticated foxtail millet detected using SSRs.

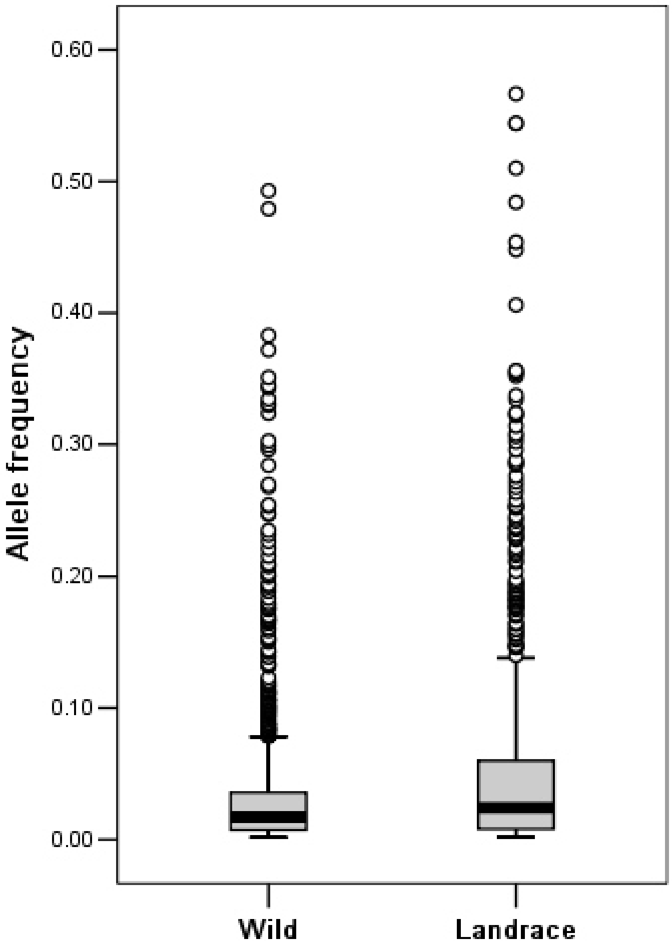

Figure S3. Allele frequencies of SSR loci in wild green foxtail and cultivated foxtail millet landraces.

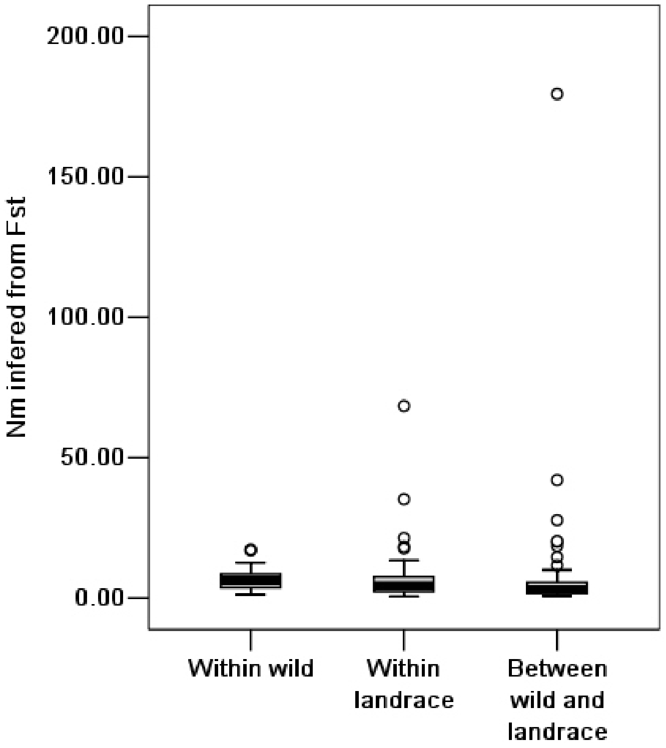

Figure S4. Gene flow estimated by Nm inferred from classical *F* test within and between green foxtail and foxtail millet.

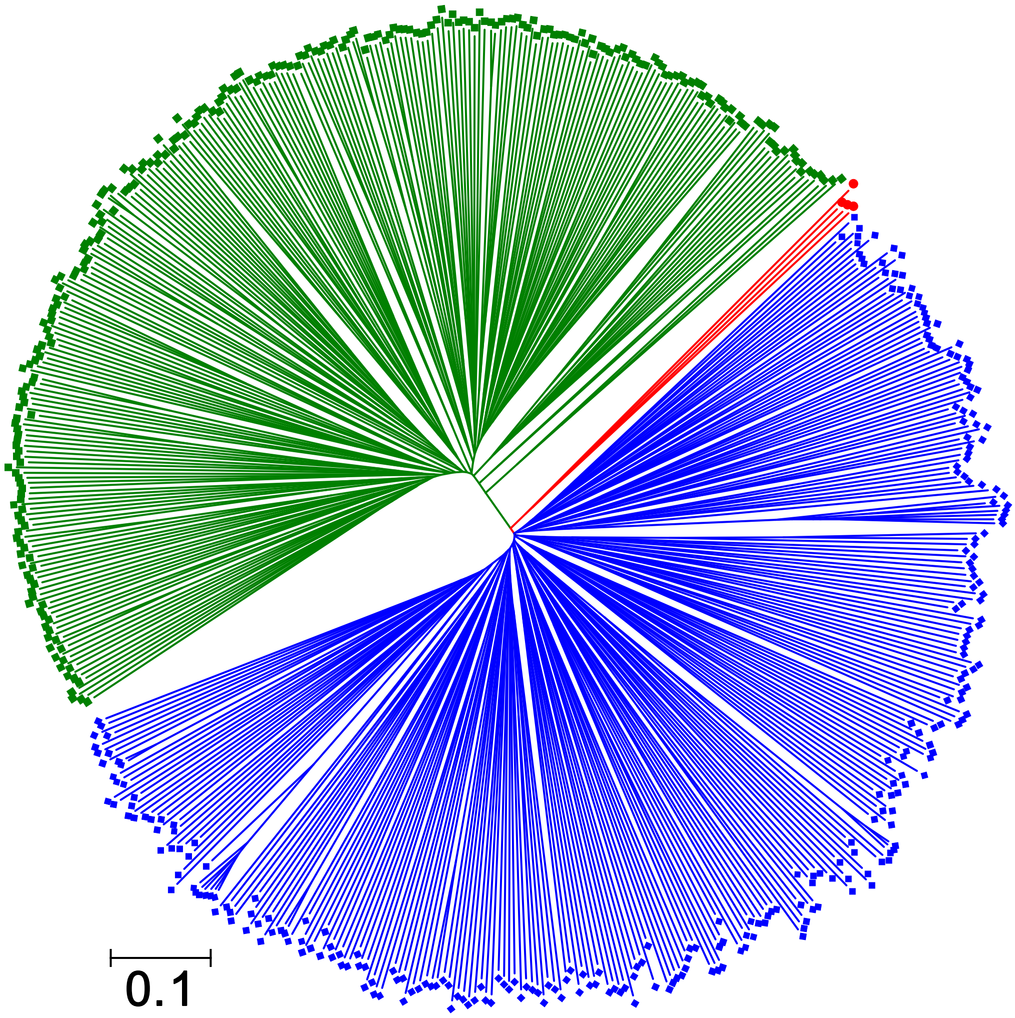

Figure S5. Unrooted neighbor-joining tree of Chinese *S.viridis* (Blue) and *S.italica* (Green), four accessions of *S.viridis* (Red) from north China (Chaoyang, Wuan, Changli and Dingxi) were genetically closer with domesticated *S.italica*.