



Supplement

The following supplementary materials are available for this article: Lin, K.-H., Chang, Y.-W., Lai, Y.-C., Hwang, S.-Y. 2023 Potential of sweet potato (*Ipomoea batatas* (L.) Lam.) breeding populations evaluated based on expressed sequence tags-simple sequence repeats. *Taiwania* 68(3): 303-313. doi: [10.6165/tai.2023.68.303](https://doi.org/10.6165/tai.2023.68.303)

Table S1. Summary of sweet potato accessions used in this study.

Accession	Breeding population	Geographic region	Main agronomic trait	Plant materials
TN57	Hybrid	Taiwan	yellow flesh	leaf
TN73	Hybrid	Taiwan	purple flesh	leaf
Lizixiang	Hybrid	China	yellow flesh	leaf
Norin21	Hybrid	Japan	suitable for table use	tissue culture
TN27	Hybrid	Taiwan	yellow flesh	leaf
TN31	Hybrid	Taiwan	white flesh	leaf
Kokei	Hybrid	Japan	suitable for table use	tissue culture
Okinawa_Mosaic_Purple	Hybrid	Japan	red flesh	tissue culture
Mei_Kao_Huang_Pi	Hybrid	USA	suitable for table use	tissue culture
Simon_1	Hybrid	Brazil	white flesh	leaf
PI286629	Hybrid	China	suitable for table use	tissue culture
PI286631	Hybrid	NewZealand	suitable for table use	tissue culture
PI344138	Hybrid	NewCaledonia	suitable for table use	tissue culture
TN26	Hybrid	Taiwan	yellow flesh	leaf
OK822	Hybrid	USA	suitable for table use	tissue culture
OK825	Hybrid	USA	suitable for table use	tissue culture
OK829	Hybrid	USA	suitable for table use	tissue culture
OK832	Hybrid	USA	suitable for table use	tissue culture
OK897	Hybrid	USA	suitable for table use	tissue culture
TN60	Hybrid	Taiwan	yellow flesh	tissue culture
Norin13	Hybrid	Japan	suitable for table use	tissue culture
Norin25	Hybrid	Japan	suitable for table use	tissue culture
TN24	Hybrid	Taiwan	yellow flesh	leaf
TN25	Hybrid	Taiwan	yellow flesh	leaf
TN34	Hybrid	Taiwan	suitable for feed use	leaf
TN36	Hybrid	Taiwan	suitable for feed use	leaf
TN37	Hybrid	Taiwan	suitable for feed use	leaf
TN40	Hybrid	Taiwan	suitable for feed use	leaf
TN49	Hybrid	Taiwan	suitable for feed use	leaf
TN50	Hybrid	Taiwan	suitable for feed use	leaf
L3151	Hybrid	USA	suitable for table use	tissue culture
458_PNG	Hybrid	PNG	suitable for table use	tissue culture
79_PNG	Hybrid	PNG	suitable for table use	tissue culture
PI315343	Hybrid	Philippines	suitable for table use	tissue culture
TI00062	Hybrid	Thailand	suitable for table use	tissue culture
TI00056	Hybrid	Thailand	suitable for table use	tissue culture
TI00090	Hybrid	Thailand	suitable for table use	tissue culture
TI00097	Hybrid	Thailand	suitable for table use	tissue culture
TN10	Hybrid	Taiwan	white flesh	tissue culture
TN17	Hybrid	Taiwan	yellow flesh	tissue culture
Tainan17	Hybrid	Taiwan	yellow flesh	tissue culture
Nan_Kua_Yu	Landrace	Taiwan	suitable for table use	tissue culture
Purple_Leaf_Variety	Landrace	Taiwan	suitable for table use	leaf
Yellow_Leaf_Variety	Landrace	Taiwan	suitable for table use	leaf
Rainbow_Leaf_Variety	Landrace	Taiwan	decoration	leaf
TNNew31	Landrace	Taiwan	white flesh	leaf
Japanese_Variety	Landrace	Japan	suitable for table use	tissue culture
Kintoki	Landrace	Japan	suitable for table use	tissue culture
Changhua	Landrace	Taiwan	suitable for tableuse	leaf



White_Skin_With_Purple_Flesh	Landrace	Japan	purple flesh	leaf
Chingshey_Purple	Landrace	Taiwan	suitable for table use	leaf
TN64	Polycross	Taiwan	orange flesh	leaf
TN66	Polycross	Taiwan	red flesh	leaf
TN71	Polycross	Taiwan	white flesh	leaf
Kyushu101	Polycross	Japan	suitable for table use	tissue culture
Taoyuan1	Polycross	Taiwan	suitable for table use	tissue culture
TN69	Polycross	Taiwan	red flesh	leaf
Ayamurasaki_Purple	Polycross	Japan	suitable for table use	tissue culture
TN72	Polycross	Taiwan	suitable for table use	leaf
Nanyo	Polycross	Japan	suitable for table use	tissue culture
Fatena	Polycross	PNG	suitable for table use	tissue culture
TN63	Polycross	Taiwan	yellow flesh	leaf
Dwarf	Polycross	Philippines	suitable for table use	tissue culture
White_Centennial	Polycross	USA	suitable for table use	tissue culture
longamai	Polycross	Tonga	suitable for table use	tissue culture
Palawan_No.2	Polycross	Philippines	suitable for table use	tissue culture
Air_Rooting	Polycross	Philippines	suitable for table use	tissue culture
Ipangha_Mestiza	Polycross	Philippines	suitable for table use	tissue culture
UPCAACC169	Polycross	Philippines	suitable for table use	tissue culture
Kinang_Kong	Polycross	Philippines	suitable for table use	tissue culture
Kyukei53	Polycross	Japan	suitable for table use	tissue culture
Chiayi	Polycross	Taiwan	suitable for table use	tissue culture
Hung_An_Ching_Hsin_Wei	Polycross	Taiwan	suitable for table use	tissue culture
Pai_Wei_Pai_Mix	Polycross	Taiwan	suitable for table use	tissue culture
Kapangan	Polycross	Indonesia	suitable for table use	tissue culture
Indonesia3/6	Polycross	Indonesia	suitable for table use	tissue culture
Dorio	Polycross	SolomonIs	suitable for table use	tissue culture
OrchidIsland10	Polycross	Taiwan	suitable for table use	tissue culture
Sasuk	Polycross	PNG	suitable for table use	tissue culture
Mipi_Kenggon	Polycross	PNG	suitable for table use	tissue culture
Jimbenamp	Polycross	PNG	suitable for table use	tissue culture
Junamp	Polycross	PNG	suitable for table use	tissue culture
Komea	Polycross	PNG	suitable for table use	tissue culture
Kawa53	Polycross	PNG	suitable for table use	tissue culture
Mangalda	Polycross	Philippines	suitable for table use	tissue culture
White_Skin_Variety	Polycross	Taiwan	suitable for starch use	tissue culture
Traisang_Puto	Polycross	Taiwan	suitable for table use	tissue culture
Man_Rak	Polycross	Thailand	suitable for table use	tissue culture
Corazon_De_Huarango	Polycross	USA	suitable for table use	tissue culture
Trifida1	Wild	Venezuela	resistance to diseases and insects	tissue culture
Trifida2	Wild	Venezuela	resistance to diseases and insects	tissue culture
Trifida3	Wild	Colombia	resistance to diseases and insects	tissue culture
Trifida4	Wild	Guatemala	resistance to diseases and insects	tissue culture
Trifida5	Wild	Guatemala	resistance to diseases and insects	tissue culture
Trifida6	Wild	Nicaragua	resistance to diseases and insects	tissue culture

**Table S2.** Primer sequences, GenBank accession number, repeat motifs, annealing temperature, and size range for the 31 EST-SSRs.

Name	GenBank accession number	Repeat motif	Forward primer	Reverse primer	Annealing temperature (°C) (size range, bp)
1010	CB330762	(CTG) ₄	GCGGTTTCCATGGCTATGCC	AGCAGCCTGAGCCACATCTGG	57 (214-235)
1110	CJ755313	(TC) ₃	GTGTCCAGGCAGGTGAATCAGC	CCCGTTCCCCATTGAAGC	57 (1850243)
1210	EE877901	(CT) ₃	AAGGGATGGAATGTGCAAAGCAG	AGAGGTGTTGCCACCGGGTG	57 (135-239)
1310	CJ756099	(CT) ₅	CTCCTTTGGGATTGGCAGTTGG	GATTTGATCCCGCAAATCCAGG	57 (185-199)
1510	CB329940	(CT) ₃	CCCGGACCGTGTTAAGTACTTGG	AGCTCCAAGCATCGCCCATC	59 (166-184)
1610	CJ758508	(CT) ₃	TGTTGATCCAACCAGGGCCAG	TCATCGTCAAGACACTCGGATCTTATC	57 (133-145)
1810	CJ753668	(CCG) ₃	ACCAAGGAGGTTGAGCTCTCGG	GCACAGGTGATGCTCTTGGTGAG	57 (143-158)
2100	AU224157	(TC) ₅	GTTCTTGATCACACCCCGGAGG	AGGCTGCACAGATGTGAATTGCAC	59 (145-163)
2210	CJ770048	(TTC) ₆	GGTGATACGCCGAGTTTTTGCTC	AGTCACGCCCTTCAAGAAACGC	57 (124-142)
2310	DV035480	(CA) ₃	AGAGCCCAGATGGTGACATCTTG	TGGCTCTCAGTGTGGAACCTTTC	57 (229-251)
2410	CJ770117	(GA) ₃	AAGAAGGGTGGGTGGTTTGCAG	GGGTGTTGCTGGGTTGGGG	57 (131-143)
2610	DV034589	(GC) ₃	GGAGAGCCGCTCTGATCACTT	GCAGGATTAGCGGAGCCGTC	57 (105-141)
2710	CJ772506	(CCA) ₃	TGGGATGTTTCGAATGGTGAC	CATGGCTCGGGCTTCCAAAG	57 (131-140)
2810	CJ758520	(ATG) ₅	GCGGCTGCCTTTGTGAACG	TTCAGTCCCTAAAGGGAGCAGGAG	57 (204-219)
2910	CJ753920	(CTCCAC) ₃	CACCTACAAGCGCAGAAGATTTCC	CTCCTCGACTAATGGACCCATGC	57 (343-385)
3010	CJ757610	(TC) ₃	CAAAGTCCTTGACTTTGAAGGCC	TGGCTTCATTGTGATCCTGGTCC	57 (316-422)
3100	AU224776	(GCG) ₅	GATACTGTCATTGGCGGAGGCC	CATCCCCCAAGCACGCG	57 (157-169)
3110	CJ759937	(CT) ₃	TGTTACCAGACACAACAGGCCTCC	CTGCATATGGGTCTGGAGGAACG	57 (198-208)
3210	BM878740	(GA) ₃	TGGGTGCGAGTTTCATTTCTTGG	AGCTTGTTCACCTCGAAGC	57 (181-201)
3510*	BU692646	(ATGGAA) ₃	TGTGCTGGATAGCGAATTACAGC	TGCATAGGGGAAAGGTATAGGTTG	57 (191-233)
3610*	BU692471	(CAA) ₅	ACACTCACTCTGCTTCTCCTGCTG	TGACGTTTGCATTGGCGATG	57 (189-207)
3710	BU692248	(TG) ₄	CAAGAAACGCACCTCCGGTATGG	TTCCGGTAGGAACAGGCGAGC	57 (112-118)
3910*	BU691143	(AGA) ₅	AGAGAGATTTCCGGCGATGC	CAATATTGACCACGACGAACAC	57 (154-197)
4010*	BU690977	(CTGCAA) ₃	GTAGTCACATCTCTCAAC	TCCTCAAGAACAACCTGCC	57 (176-194)
4110*	BU690969	(CAC) ₆	CGCAGATGGTGAACATGCCTATG	TTCTCACTTCCCAGAGCAACACC	59 (103-139)
4210*	BU690750	(CACCAT) ₃	ACTATGCAGATGGTGAAGATGC	TTACATGCCAGAGCAACACCCAC	57 (117-153)
4410*	BU690375	(CGC) ₅	CCAAGCACTTATTCTTCCGAG	ATGTAGGCAGTTCTGTTGGGGAGC	57 (87-108)
4510*	BU690134	(GCA) ₆	GAGGAACTTTTACGACACAGGAGG	TTGATGACGAGCACACTTGCTG	59 (117-129)
4610*	CB330729	(GAAGCC) ₃	TGCTCTTTCTTTGCCCTCAAC	TCCCAGCTTACGCGTGTCAATG	57 (152-176)
5100	AU223805	(GT) ₃	CGTGCATGGGGAAACTGGG	CGTTATCCTGCGTCATATTCACGG	57 (161-175)
9100	CB330817	(AAG) ₃	TGTCGGAGAAGGTGGCAGACAG	GCGACACTCCTCGCTCTCAGG	57 (183-255)

* Primers were from Hu, J., Nakatani, M., Mizuno, K., & Fujimura, T. (2004). Development and characterization of microsatellite markers in sweetpotato. *Breeding Science*, 54, 177–188.

Marker names with bold letters indicate that those EST-SSRs were removed from the investigation because of the presence of null alleles.

**Table S3.** Estimated null allele frequencies of the 31 EST-SSR loci.

Locus	Hybrid	Landrace	Polycross	Wild
3710	0.8458	0.7905	0.8491	0.9129
2710	0.7685	0.7314	0.7599	0.9129
9100	0.0009	0	0	0
4410	0.0654	0	0.1175	0
2210	0	0	0	0
3210	0	0	0	0
4110	0	0	0	0
3910	0	0.2257	0	0
3510	0	0	0	0.223
2610	0	0.1723	0.0124	0.1942
3100	0.0434	0.0636	0	-
3610	0.3533	0.2025	0.2243	0
4510	0.5186	0.3911	0.4545	0.4296
1210	0	0	0	-
1110	0	0	0	0
4210	0	0	0	0
2100	0.4659	0.4746	0.6053	0.8249
3110	0.9006	0.9487	0.9468	-
1610	0	0	0	0
5100	0.4791	0.5477	0.4554	0.7359
2810	0.6442	0.6667	0.5305	0.4259
2410	0.0174	0.0732	0	0.1111
1510	0	0	0	0
1010	0	0	0.0406	0.6342
2310	0	0	0	0
4610	0	0	0	0
4010	0	0	0.1257	0
3010	0	0	0	0
1810	0.006	0	0.0043	0
1310	0	-	0.0674	-
2910	0	0	0	0

Bold letters indicate loci with high null allele frequencies across sample stratification.

**Table S4.** Top BlastX hits for the 31 EST-SSR loci.

Name	GenBank accession number	Annotation	Score/E-value	Plant
1010	CB330762	Chloroplast photosystem II subunit X	87/1e-15	<i>Vigna radiata</i>
1110	CJ755313	DNA binding protein	92/5e-17	<i>Ricinus communis</i>
1210	EE877901	WRKY transcription factor	238/6e-61	<i>Populustomentosax P. bolleana</i>
1310	CJ756099	7S RNA binding protein	160/1e-37	<i>Arabidopsis thaliana</i>
1510	CB329940	Chlorophyll a-b binding protein 16	498/6e-139	<i>Nicotiana tabacum</i>
1610	CJ758508	DNA-binding protein	219/4e-55	<i>Catharanthus roseus</i>
1810	CJ753668	Protein SYM1	180/2e-43	<i>Ricinus communis</i>
2100	AU224157	CBL-interacting protein kinase 13	122/2e-26	<i>Vitis vinifera</i>
2210	CJ770048	GATA domain class transcription factor	107/3e-21	<i>Malus xdomestica</i>
2310	DV035480	Carboxyl-terminal peptidase	149/1e-34	<i>Zea mays</i>
2410	CJ770117	NAC domain-containing protein	159/6e-37	<i>Ricinus communis</i>
2610	DV034589	DNA binding protein	92/1e-16	<i>Zea mays</i>
2710	CJ772506	Conserved hypothetical protein	157/2e-36	<i>Ricinus communis</i>
2810	CJ758520	HAP2	152/6e-35	<i>Arabidopsis thaliana</i>
2910	CJ753920	Zinc finger (C3HC4-type RING finger) family protein	108/9e-22	<i>Arabidopsis thaliana</i>
3010	CJ757610	CDP-diacylglycerol synthetase	332/3e-89	<i>Solanum tuberosum</i>
3100	AU224776	Predicted protein	74/9e-12	<i>Populustrichocarpa</i>
3110	CJ759937	Triacylglycerol lipase	134/1e-29	<i>Ricinus communis</i>
3210	BM878740	DNA-binding protein	222/4e-56	<i>Daucus carota</i>
3510*	BU692646	Zinc ion binding protein	167/4e-40	<i>Zea mays</i>
3610*	BU692471	Hypothetical protein LOC100246506	80/1e-13	<i>Vitis vinifera</i>
3710	BU692248	AtGDU6 (<i>Arabidopsis thaliana</i> GLUTAMINE DUMPER 6)	54/8e-06	<i>Arabidopsis thaliana</i>
3910*	BU691143	Rhomboid family protein AtRBL2	156/8e-37	<i>Arabidopsis thaliana</i>
4010*	BU690977	AP2 domain-containing protein	85/3e-19	<i>Arabidopsis lyrata subsp. Lyrata</i>
4110*	BU690969	N-acetyltransferase	301/3e-80	<i>Arachishypogaea</i>
4210*	BU690750	acetyltransferase complex ard1 subunit	173/1e-41	<i>Ricinus communis</i>
4410*	BU690375	SHOOT2 protein	69/3e-10	<i>Glycine max</i>
4510*	BU690134	R2r3-myb transcription factor	110/5e-23	<i>Ricinus communis</i>
4610*	CB330729	Proline-rich protein	131/1e-28	<i>Capsicum annuum</i>
5100	AU223805	Protease inhibitor/seed storage/lipid transfer protein family protein	73/1e-11	<i>Arabidopsis lyrata subsp. Lyrata</i>
9100	CB330817	Chloroplast protein 12	175/4e-42	<i>Fagus crenata</i>

*Primers were from Hu, J., Nakatani, M., Mizuno, K., & Fujimura, T. (2004). Development and characterization of microsatellite markers in sweetpotato. *Breeding Science*, 54, 177–188.

Marker names with bold letters indicate that those primers were removed from the investigation because of the presence of null alleles.



Fig. S1. Number of hybrid, landrace, polycross, and wild sweet potato accessions collected in different geographic regions in this study.

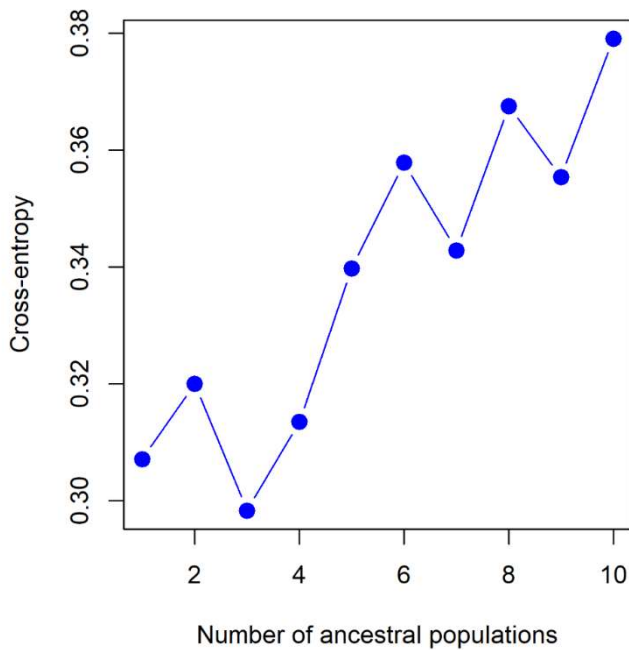


Fig. S2. Minimum cross-entropy for evaluation of clustering scenarios analyzed using LEA.

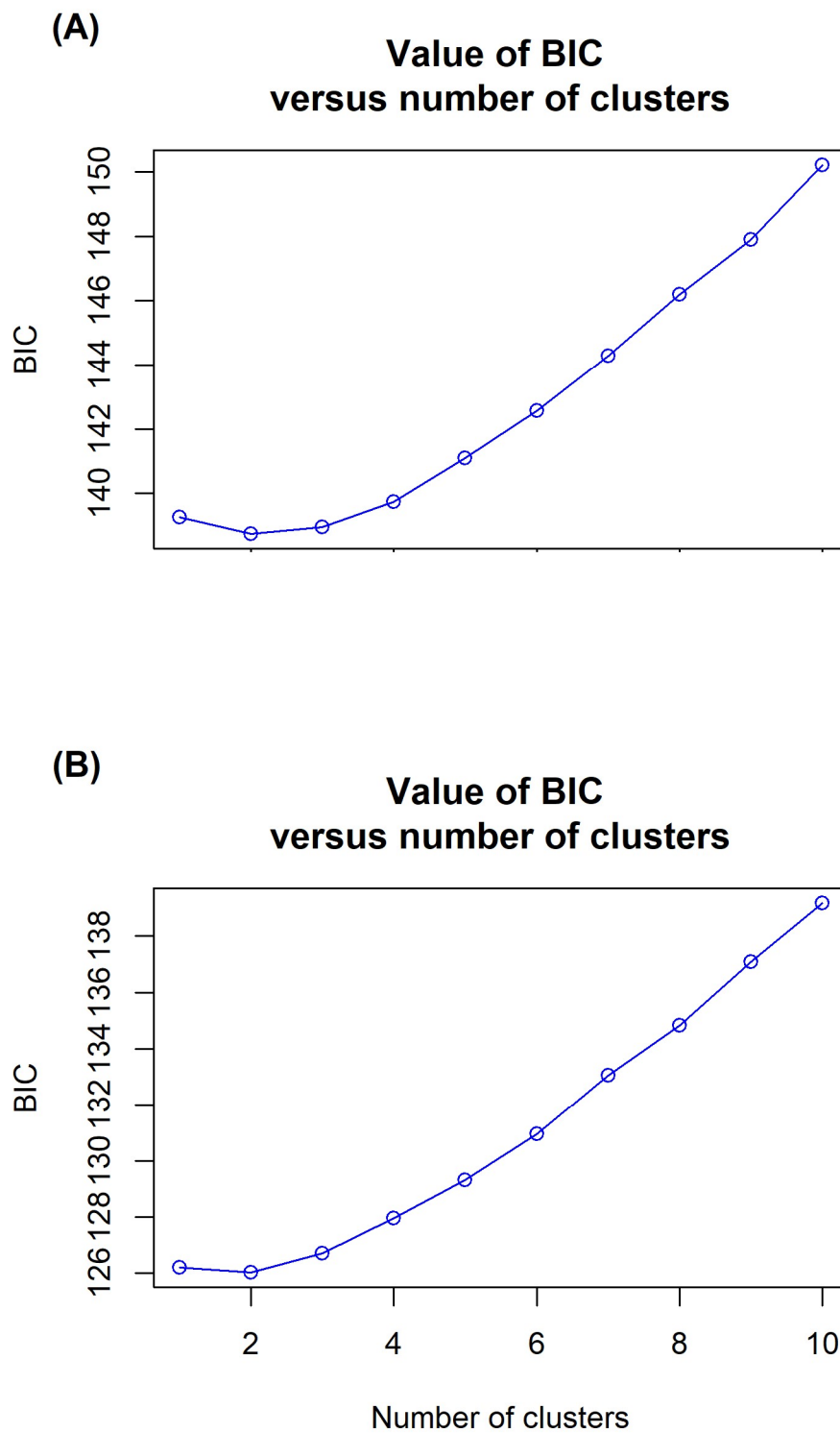


Fig. S3. Bayesian information criterion with wild sweet potato included **(A)** and without wild sweet potato **(B)** for evaluation of clustering scenarios using DAPC.

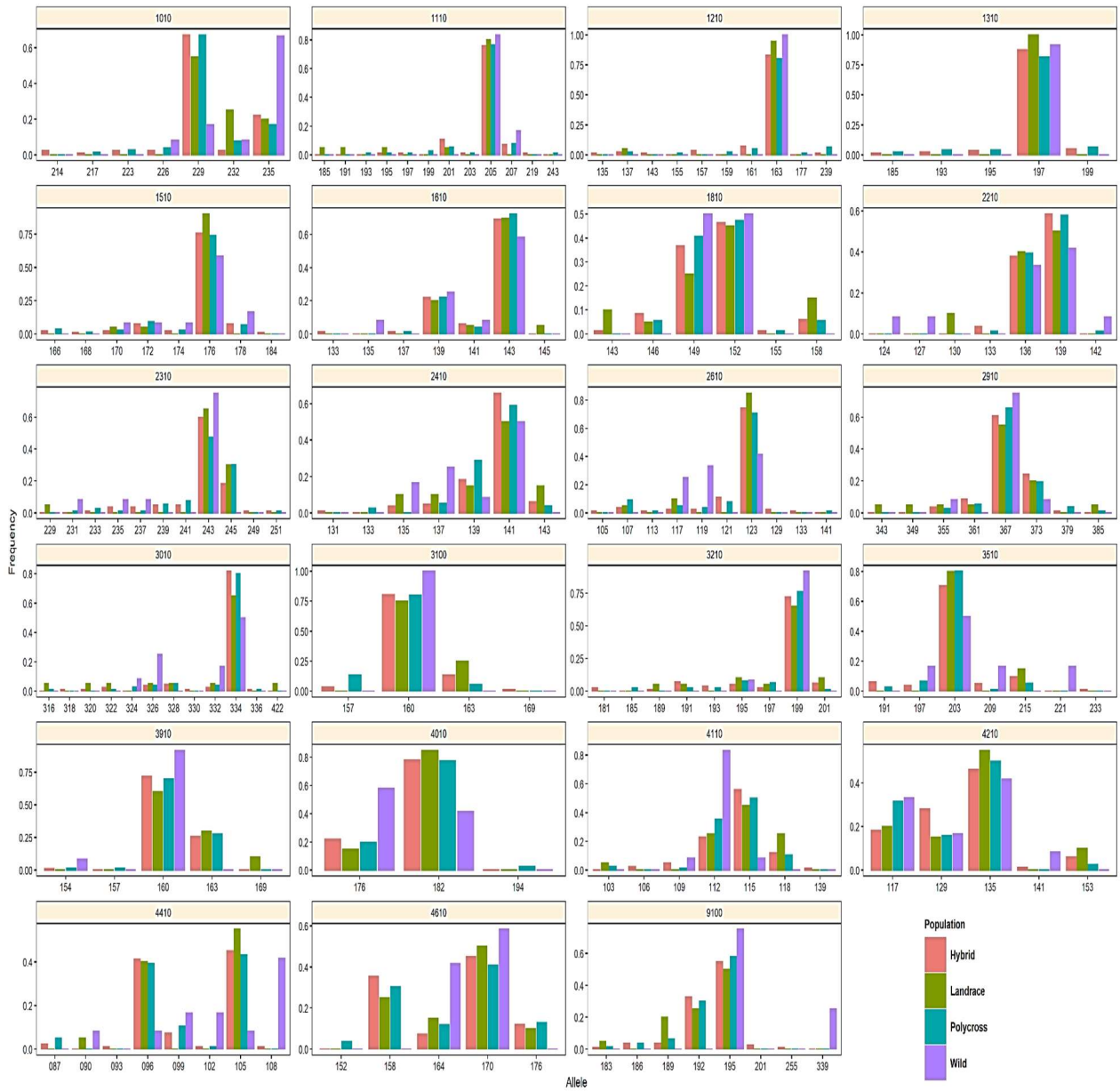


Fig.S4. Allele frequencies of the 23 EST-SSR loci in sweet potato breeding populations and wild sweet potato (*Ipomoea trifida*).