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Supplementary data

Direct sequencing of RAPD products provides a set of SCAR markers for discrimination of sweet potato cultivars

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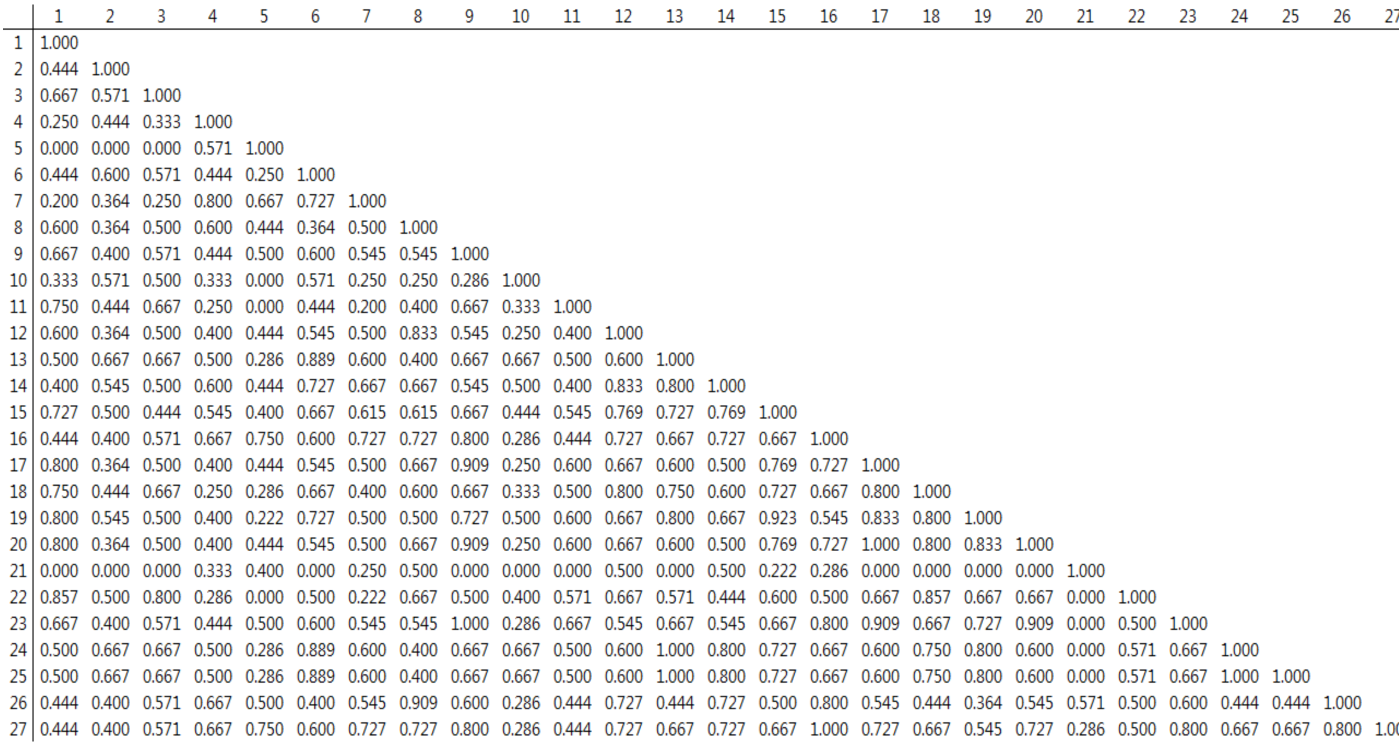
Supplementary Table 1. Analysis of DNA polymorphisms generated by 148 RAPD primers in 27 sweet potato cultivars

No	Primer	No. of fragment amplified	No. of polymorphic fragment	Poly-morphism (%)	No	Primer	No. of fragment amplified	No. of polymorphic fragment	Poly-morphism (%)
1	A01	4	0	0	25	D15	6	2	33
2	A02	7	3	43	26	D16	8	6	75
3	A03	7	1	14	27	D17	5	1	20
4	A04	8	2	25	28	D18	5	0	0
5	A05	9	7	78	29	D19	3	0	0
6	A06	3	2	67	30	D20	6	2	33
7	A08	4	0	0	31	E01	6	4	67
8	A09	4	1	25	32	E02	6	1	17
9	A10	10	7	70	33	E03	6	0	0
10	A11	8	5	63	34	E04	6	0	0
11	A12	4	0	0	35	E05	7	2	29
12	A13	6	6	100	36	E06	8	6	75
13	A14	6	3	50	37	E07	10	3	30
14	A15	6	2	33	38	E08	3	0	0
15	A16	9	5	56	39	E09	3	2	67
16	A17	5	3	60	40	E10	4	0	0
17	D07	4	1	25	41	E11	9	4	44
18	D08	5	0	0	42	E12	9	8	89
19	D09	5	1	20	43	E13	9	4	44
20	D10	6	4	67	44	E14	7	0	0
21	D11	4	0	0	45	E15	8	3	38
22	D12	3	0	0	46	E16	6	2	33
23	D13	3	2	67	47	E17	11	7	64
24	D14	4	0	0	48	E18	12	3	25
49	E19	17	10	59	73	G03	6	2	33
50	E20	10	6	60	74	G04	7	1	14
51	F01	9	4	44	75	G05	7	4	57
52	F02	3	0	0	76	G06	7	3	43
53	F03	7	3	43	77	G07	7	3	43
54	F04	6	2	33	78	G08	2	1	50
55	F05	9	2	22	79	G09	5	4	80
56	F06	9	3	33	80	G10	9	5	56
57	F07	3	2	67	81	G11	11	8	73
58	F08	3	0	0	82	G12	5	1	20
59	F09	6	3	50	83	G13	4	0	0
60	F10	7	1	14	84	G14	5	1	20
61	F11	5	3	60	85	G15	8	5	63
62	F12	6	2	33	86	G16	6	0	0
63	F13	8	7	88	87	G17	8	7	88
64	F14	8	5	63	88	G18	6	4	67
65	F15	3	0	0	89	G19	5	1	20
66	F16	8	4	50	90	G20	1	0	0
67	F17	6	4	67	91	H01	7	3	43
68	F18	4	2	50	92	H02	2	2	100
69	F19	6	4	67	93	H03	5	2	40
70	F20	8	7	88	94	H04	7	6	86
71	G01	10	5	50	95	H05	8	3	38
72	G02	6	3	50	96	H06	7	3	43
97	H07	7	5	71	124	AB06	6	2	33
98	H08	3	0	0	125	AB07	5	5	100
99	H09	1	0	0	126	AB08	9	7	78

100	H10	2	1	50
101	H11	2	1	50
102	H12	4	1	25
103	H13	2	0	0
104	H14	7	5	71
105	H15	5	2	40
106	H16	1	0	0
107	H17	4	1	25
108	H18	2	0	0
109	AA01	5	4	80
110	AA02	4	2	50
111	AA03	1	0	0
112	AA04	1	0	0
113	AA05	1	0	0
114	AA06	1	0	0
115	AA07	2	0	0
116	AA08	6	5	83
117	AA09	1	0	0
118	AA10	5	2	40
119	AB01	4	1	25
120	AB02	4	3	75
121	AB03	4	2	50
122	AB04	3	0	0
127	AB09	6	3	50
128	AB10	5	4	80
129	AC01	4	3	75
130	AC02	2	0	0
131	AC03	4	2	50
132	AC04	5	3	60
133	AC05	5	2	40
134	AC06	4	2	50
135	AC07	6	2	33
136	AC08	3	1	33
137	AC09	8	5	63
138	AC10	4	1	25
139	AE01	6	3	50
140	AE02	5	2	40
141	AE03	2	1	50
142	AE04	1	1	100
143	AE05	2	1	50
144	AE06	5	3	60
145	AE07	5	5	100
146	AE08	6	3	50
147	AE09	5	3	60
148	AE10	8	6	75
Total (148)		815	371	40

Supplementary Table 2. Genetic distances matrix among the 27 cultivars obtained from the 13 SCAR markers



	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27
1	1.000																										
2	0.444	1.000																									
3	0.667	0.571	1.000																								
4	0.250	0.444	0.333	1.000																							
5	0.000	0.000	0.000	0.571	1.000																						
6	0.444	0.600	0.571	0.444	0.250	1.000																					
7	0.200	0.364	0.250	0.800	0.667	0.727	1.000																				
8	0.600	0.364	0.500	0.600	0.444	0.364	0.500	1.000																			
9	0.667	0.400	0.571	0.444	0.500	0.600	0.545	0.545	1.000																		
10	0.333	0.571	0.500	0.333	0.000	0.571	0.250	0.250	0.286	1.000																	
11	0.750	0.444	0.667	0.250	0.000	0.444	0.200	0.400	0.667	0.333	1.000																
12	0.600	0.364	0.500	0.400	0.444	0.545	0.500	0.833	0.545	0.250	0.400	1.000															
13	0.500	0.667	0.667	0.500	0.286	0.889	0.600	0.400	0.667	0.667	0.500	0.600	1.000														
14	0.400	0.545	0.500	0.600	0.444	0.727	0.667	0.667	0.545	0.500	0.400	0.833	0.800	1.000													
15	0.727	0.500	0.444	0.545	0.400	0.667	0.615	0.615	0.667	0.444	0.545	0.769	0.727	0.769	1.000												
16	0.444	0.400	0.571	0.667	0.750	0.600	0.727	0.727	0.800	0.286	0.444	0.727	0.667	0.727	0.667	1.000											
17	0.800	0.364	0.500	0.400	0.444	0.545	0.500	0.667	0.909	0.250	0.600	0.667	0.600	0.500	0.769	0.727	1.000										
18	0.750	0.444	0.667	0.250	0.286	0.667	0.400	0.600	0.667	0.333	0.500	0.800	0.750	0.600	0.727	0.667	0.800	1.000									
19	0.800	0.545	0.500	0.400	0.222	0.727	0.500	0.500	0.727	0.500	0.600	0.667	0.800	0.667	0.923	0.545	0.833	0.800	1.000								
20	0.800	0.364	0.500	0.400	0.444	0.545	0.500	0.667	0.909	0.250	0.600	0.667	0.600	0.500	0.769	0.727	1.000	0.800	0.833	1.000							
21	0.000	0.000	0.000	0.333	0.400	0.000	0.250	0.500	0.000	0.000	0.000	0.500	0.000	0.500	0.222	0.286	0.000	0.000	0.000	0.000	1.000						
22	0.857	0.500	0.800	0.286	0.000	0.500	0.222	0.667	0.500	0.400	0.571	0.667	0.571	0.444	0.600	0.500	0.667	0.857	0.667	0.667	0.000	1.000					
23	0.667	0.400	0.571	0.444	0.500	0.600	0.545	0.545	1.000	0.286	0.667	0.545	0.667	0.545	0.667	0.800	0.909	0.667	0.727	0.909	0.000	0.500	1.000				
24	0.500	0.667	0.667	0.500	0.286	0.889	0.600	0.400	0.667	0.667	0.500	0.600	1.000	0.800	0.727	0.667	0.600	0.750	0.800	0.600	0.000	0.571	0.667	1.000			
25	0.500	0.667	0.667	0.500	0.286	0.889	0.600	0.400	0.667	0.667	0.500	0.600	1.000	0.800	0.727	0.667	0.600	0.750	0.800	0.600	0.000	0.571	0.667	1.000	1.000		
26	0.444	0.400	0.571	0.667	0.500	0.400	0.545	0.909	0.600	0.286	0.444	0.727	0.444	0.727	0.500	0.800	0.545	0.444	0.364	0.545	0.571	0.500	0.600	0.444	0.444	1.000	
27	0.444	0.400	0.571	0.667	0.750	0.600	0.727	0.727	0.800	0.286	0.444	0.727	0.667	0.727	0.667	1.000	0.727	0.667	0.545	0.727	0.286	0.500	0.800	0.667	0.667	0.800	1.0