

Table 2. Information about the 21 SSR loci used in this study, including names, bin location, repetition size, number of alleles, genetic diversity value (*He*) and *P-value* of the genetic differentiation test (Raymond and Rousset, 2004) for the four heterotic groups in the 25 Orange Flint lines set.

Marker	Bins	Repetition	No. of Alleles	He	<i>P-value</i> ¹
phi001	1.03	AG	5.00	0.77	0.0002
Bnlg400	1.09	-	7.00	0.83	0.0582
umc1065	2.05	(AC4)17	7.00	0.72	0.0260
bnlg1169	2.08	(AG)14	5.00	0.75	0.3483
Bnlg602	3.04	-	7.00	0.74	0.5331
Bnlg197	3.07	-	5.00	0.75	0.7520
phi026	4.05	CT	6.00	0.78	0.0009
phi093	4.08	CTAG	3.00	0.60	0.0310
phi113	5.03	GTCT	5.00	0.69	0.0494
Bnlg609	5.06	-	10.00	0.86	0.0949
nc013	6.05	AG	4.00	0.67	0.0040
phi089	6.08	ATGC	2.00	0.48	0.8848
phi057	7.01	GCC	5.00	0.69	0.0218
phi116	7.06	TGAC-GAC	2.00	0.48	0.0125
phi119	8.02	AG	4.00	0.72	0.4014
phi015	8.08	TTTG	3.00	0.64	0.1585
phi068	9.01	AT	3.00	0.59	0.0132
Bnlg127	9.03	-	14.00	0.90	0.0004
phi041	10.00	AGCC	4.00	0.67	0.2024
bnl1451	10.02	(AG)34	3.00	0.36	0.0253
bnlg1839	10.07	(AG)24	4.00	0.51	0.0210
Media	-	-	5.14	0.68	-

¹Genetic differentiation test were performed on the complete set of 26 lines and as described in Raymond and Rousset (2004). Significant *P-values* (5%) are indicated in bold. - Missing data.