Inheritance of RAPD Markers in Melon (*Cucumis melo* L.)

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Introduction: Genetic markers have been employed in diversity analysis (2,3,4,7,8) and the construction of maps in melon (1,9). The use of random amplified polymorphic DNA (RAPD) has allowed for discrimination of elite (2,7) and unadapted germplasm (3,4,8). Because of their relative low cost and low technological attributes they have been valuable for diversity analysis (2,7). However, except for the mapping of several RAPD marker loci by Baudracco-Arnas and Pitrat (1996), the genetics RAPD markers in melon has not been widely characterized. This is likely due to the relatively low level of RAPD polymorphisms (~15-20%) in melon. The bands used for diversity analysis are repeatable (4,7), but their genetic attributes have not been characterized. This report details the genetics of RAPD markers assessed in F_2 progeny segregating in four melon populations.

Materials and Methods: Crosses were made between an experimental inbred line SA 200 ('Chargyne') x 'Top Mark', WI 998 x 'Top Mark', Charentais-1 x AR5, and 'Top Mark' x AR5. These crosses were made to produce segregating populations that would be useful in mapping disease resistance and sex expression in melon. SA 200 is a gynoecious Charentais market type received from Clause Seed Company (Bretigny-Sur-Orge Cedex, France), Charentais-1 is a gynoecious Charentais market type inbred line received from Petoseed Company (now associated with Seminis, Woodland Calif., USA), AR5 and "Top Mark' are disease resistant U.S. Western Shipper market types released by the USDA, ARS, and WI 998 is a gynoecious line released by the USDA, ARS. Each F_1 was self-pollinated to produce four F2 populations (i.e., SA 200 x 'Top Mark', WI 998 x 'Top Mark', Charentais-1 x AR5, and 'Top Mark' x AR5) segregation analyses.

DNA was extracted and subjected to PCR using RAPD primers from Operon (Alameda, Calif., USA) and University of British Columbia (UVBC; designated BC; Vancouver, BC, Canada) and electrophoresis was carried out according to Staub et al. (7). Initially, a survey of all parents was made using about 1,500 primers to identify polymorphism specific to the contrasting parents in a particular cross. Primer products were identified by their primer designation (e.g., B12 = Operon primer and BC541 = UVBC primer) (Table 1). When a primer produced more than one product that was useable for analysis, it was given a lower case letter designation from cathodal to anodal migration position (e.g., BC541a).

Data were obtained for dominant RAPD loci from F_2 families and analyzed by chi-square analysis for conformity to expected 3:1 (df = 1) Mendelian single-factor segregation ratios.

Results and Discussion: The primers examined yielded between 25 to 40% polymorphisms (band differences between parents) depending on the cross (data not presented). Potentially useful bands were characterized as having a mobility between 200 to 2,500 bp. Putative loci were then identified as those possessing bands that were reproducible and bright and used for segregation analysis (Table 1). Initially, examination of parents of SA 200 x 'Top Mark', WI 998 x 'Top Mark', Charentais-1 x AR5, and 'Top Mark' x AR5 produced 264, 241, 244, and 251 reproducible band differences between respective parents (putative loci) (data not presented). On average, this represents 17% recovery of potentially useable bands (loci) from the survey of 1,500 primers.

After this initial assessment, 41, 27, 90, and 38, bands (loci) segregated in a predictable manner in progeny from SA 200 x 'Top Mark', WI 998 x 'Top Mark', Charentais-1 x AR5, and 'Top Mark' x AR5 matings, respectively (Table 1). This represents, on average, 3.3% recovery of useable loci from the initial survey of 1,500 primers.

Given the fact that individuals are sometimes misclassified even when scoring loci that historically have proven to reproducible bright RAPD bands, we are attempting RAPD to SCAR conversion at some

Table 1. F_2 single factor segregation for RAPD primer products[z] in melon (*Cucumis melo* L.).

Cross	Primer	bp	No. F2	Obs	Exp	Chi. sq	*P* value>
SA 200	M7	675	76	57	57	NA	NA
x TM	U13	831	76	57	57	NA	NA
	AT7a	1275	76	57	57	NA	NA
	AV11	815	79	59	59.25	0.00	0.95
	D16	1850	77	58	57.75	0.00	0.95
	AB17	831	78	59	58.5	0.00	0.95
	AC7a	450	78	58	58.5	0.00	0.95
	AG15	975	78	58	58.5	0.00	0.95
	R11	1100	78	59	58.5	0.00	0.95
	U10	870	78	59	58.5	0.00	0.95
	AV11	1900	74	55	55.5	0.00	0.95
	Y13	610	74	56	55.5	0.00	0.95
	AV1	1375	70	53	52.5	0.00	0.95
	K4	564	50	37	37.5	0.01	0.70
	I4b	831	71	54	53.25	0.01	0.70
	E8	1300	76	58	57	0.02	0.70
	M7	650	76	56	57	0.02	0.70
	W3a	1000	75	55	56.25	0.03	0.70
	R19b	564	75	55	56.25	0.03	0.70
	C13	1275	73	56	54.75	0.03	0.70
	Y15	1050	71	52	53.25	0.03	0.70
	AM14a	1500	78	60	58.5	0.04	0.70
	Y13	575	74	54	55.5	0.04	0.70
	P6	1200	79	61	59.25	0.05	0.70
	AE3a	1250	75	58	56.25	0.05	0.70
	AL9	1650	75	58	56.25	0.05	0.70
	E8	675	76	59	57	0.07	0.70
	AH2b	500	76	55	57	0.07	0.70
	C20	700	76	55	57	0.07	0.70
	AB4b	1325	45	32	33.75	0.09	0.70
	AI11	600	78	56	58.5	0.11	0.70
	W10c	830	78	56	58.5	0.11	0.70
	AA14	1375	74	53	55.5	0.11	0.70
	AG2	1375	74	53	55.5	0.11	0.70
	B11	1400	80	63	60	0.15	0.10
	AK5b	1500	78	62	58.5	0.21	0.10
	G6	1890	78	55	58.5	0.21	0.10
	AF7	1370	70	49	52.5	0.23	0.10
	G8	1375	79	63	59.25	0.24	0.10
	L1	564	79	63	59.25	0.24	0.10
	AJ12	750	75	60	56.25	0.25	0.10
WI 998	A16	1600	92	69	69	NA	NA
x TM	AT2	800	84	63	63	NA	NA
	BC226	1400	92	69	69	NA	NA
	O2-1	1100	88	66	66	NA	NA
	AF7	947	91	68	68.25	0.00	0.95
	AL8-1	820	75	56	56.25	0.00	0.95
	E6-1	1100	86	64	64.5	0.00	0.95
	AH9-1	1050	78	58	58.5	0.00	0.95
	Z9	2050	78	59	58.5	0.00	0.95
	AB4-2	1300	93	69	69.75	0.01	0.70
WI 998	AK5	800	93	69	69.75	0.01	0.70
x TM	M7-2	750	87	66	65.25	0.01	0.70
	AO8	1600	84	64	63	0.02	0.70
	A11-1	960	76	56	57	0.02	0.70
	AI8-1	800	89	68	66.75	0.02	0.70
	AT7-1	860	87	64	65.25	0.02	0.70
	AD12	1100	86	66	64.5	0.03	0.70
	AB16-1	1375	78	57	58.5	0.04	0.70
	AJ20	800	92	71	69	0.06	0.70
	J7	1600	92	67	69	0.06	0.70
	AG13	975	88	68	66	0.06	0.70
	AI9	520	93	72	69.75	0.07	0.70
	J7	700	93	72	69.75	0.07	0.70
	AB16	1400	87	63	65.25	0.08	0.70
	AH3-2	1700	87	63	65.25	0.08	0.70
	AT7-1	950	85	66	63.75	0.08	0.70
	V1-1	564	82	59	61.5	0.10	0.70
Charent.	Z3a	700	92	69	69	NA	NA
x AR5	D16	2200	93	70	69.75	0.00	0.95
	F1	1100	93	70	69.75	0.00	0.95
	O19a	1200	93	70	69.75	0.00	0.95
	AB4b	1350	93	70	69.75	0.00	0.95
	AT2b	1000	93	70	69.75	0.00	0.95
	AU19	580	93	70	69.75	0.00	0.95
	BC299	700	93	70	69.75	0.00	0.95
	AU2a	1400	90	67	67.5	0.00	0.95
	BC628	830	90	68	67.5	0.00	0.95
	I4	970	93	69	69.75	0.01	0.95
	AB8	1350	93	69	69.75	0.01	0.95
	AT15b	1890	91	69	68.25	0.01	0.95
	H2	600	89	66	66.75	0.01	0.95
	C20	1000	93	71	69.75	0.02	0.70
	D9a	800	93	71	69.75	0.02	0.70
	E6	700	93	71	69.75	0.02	0.70
	U13	1000	93	71	69.75	0.02	0.70
	AA12	830	93	71	69.75	0.02	0.70
	R5a	1000	91	67	68.25	0.02	0.70
	AV4	2027	91	67	68.25	0.02	0.70
	AB17	1000	44	32	33	0.03	0.70
	R11	1300	90	69	67.5	0.03	0.70
	S4	1910	93	68	69.75	0.04	0.70
	W10	575	93	68	69.75	0.04	0.70
	AF12b	800	93	68	69.75	0.04	0.70
	AL9a	1890	93	68	69.75	0.04	0.70
	C10	900	92	71	69	0.06	0.70
	AU2b	700	92	67	69	0.06	0.70
	AB1	831	93	72	69.75	0.07	0.70
	AD12	1000	93	72	69.75	0.07	0.70
	AM1	950	93	72	69.75	0.07	0.70
	AP2	1375	93	72	69.75	0.07	0.70
	BC541a	2100	93	72	69.75	0.07	0.70

Cross	Primer	bp	No. F2	Obs	Exp	Chi. sq	*P* value>
Charent. x AR5	B11	950	93	67	69.75	0.11	0.70
	N11a	1375	93	67	69.75	0.11	0.70
	Y10	775	93	67	69.75	0.11	0.70
	AF7b	831	93	67	69.75	0.11	0.70
	AH20	500	93	67	69.75	0.11	0.70
	AJ17	700	93	67	69.75	0.11	0.70
	AK3	500	92	66	69	0.13	0.70
	L15	800	93	73	69.75	0.15	0.70
	Y15	1000	93	73	69.75	0.15	0.70
	AF20c	580	93	73	69.75	0.15	0.70
	AG4a	1400	93	73	69.75	0.15	0.70
	AT2a	1100	93	73	69.75	0.15	0.70
	BC388	1100	93	73	69.75	0.15	0.70
	J4	831	93	66	69.75	0.20	0.50
	AG10a	530	93	66	69.75	0.20	0.50
	AL8b	400	93	66	69.75	0.20	0.50
	L1	800	91	72	68.25	0.21	0.50
	Q10	1580	91	72	68.25	0.21	0.50
	AK5	800	78	62	58.5	0.21	0.50
	AV11	1000	89	63	66.75	0.21	0.50
	B14	1400	92	65	69	0.23	0.50
	F3	400	92	73	69	0.23	0.50
	AX16	1100	92	65	69	0.23	0.50
	D9b	750	93	74	69.75	0.26	0.50
	J7c	400	93	74	69.75	0.26	0.50
	BC654	1000	93	74	69.75	0.26	0.50
	U8	974	93	65	69.75	0.32	0.50
	AE2b	550	93	65	69.75	0.32	0.50
	AF20a	2300	93	65	69.75	0.32	0.50
	AJ12	800	93	65	69.75	0.32	0.50
	AT15a	2000	91	73	68.25	0.33	0.50
	L11	1110	92	64	69	0.36	0.50
	C13	1375	93	75	69.75	0.40	0.50
	K4	700	93	75	69.75	0.40	0.50
	N11b	1000	93	75	69.75	0.40	0.50
	U1	1904	93	75	69.75	0.40	0.50
	AT2c	780	93	75	69.75	0.40	0.50
	BC388	1000	93	75	69.75	0.40	0.50
	O19c	400	93	64	69.75	0.47	0.30
	AF7a	840	93	64	69.75	0.47	0.30
	AM19	1900	89	61	66.75	0.50	0.30
	AL9b	600	93	76	69.75	0.56	0.30
	AF20b	1375	93	77	69.75	0.75	0.30
	AG4b	700	93	77	69.75	0.75	0.30
	X17	700	67	44	50.25	0.78	0.30
	X19	1910	93	62	69.75	0.86	0.30
	A17b	900	87	73	65.25	0.92	0.30
	Z3b	600	92	61	69	0.93	0.30
	AI14	700	93	78	69.75	0.98	0.30
	AN1	800	93	78	69.75	0.98	0.30
	J7b	775	93	61	69.75	1.10	0.20
Charent. x AR5	AF7c	600	93	79	69.75	1.23	0.20
	T17a	1910	78	49	58.5	1.54	0.20
	AF12a	1000	93	59	69.75	1.66	0.10
	U7	1050	87	52	65.25	2.69	0.10
TM x AR5	K4 c	831	43	32	32.25	0.00	0.95
	E6	960	62	47	46.5	0.01	0.95
	Z11 b	300	42	31	31.5	0.01	0.95
	X16	575	38	29	28.5	0.01	0.95
	AM18	831	22	16	16.5	0.02	0.70
	AF7	831	45	33	33.75	0.02	0.70
	AG15	974	45	33	33.75	0.02	0.70
	F1	2027	43	33	32.25	0.02	0.70
	Z18	831	43	33	32.25	0.02	0.70
	BC388	1090	76	56	57	0.02	0.70
	AX19	300	98	72	73.5	0.03	0.70
	W7	831	40	29	30	0.03	0.70
	AX20	900	42	33	31.5	0.07	0.70
	BC526	825	39	31	29.25	0.10	0.70
	AJ20	1375	44	31	33	0.12	0.70
	AT3	1570	44	35	33	0.12	0.70
	AV11 b	831	40	28	30	0.13	0.70
	AF20	1400	22	15	16.5	0.13	0.70
	AP2	1100	43	30	32.5	0.15	0.70
	AV11 a	960	72	57	54	0.16	0.50
	K4 a	975	42	29	31.5	0.19	0.50
	AQ6	947	45	31	33.75	0.22	0.50
	H2	825	43	35	32.25	0.23	0.50
	AO18 a	1800	43	35	32.25	0.23	0.50
	BC299	700	40	33	30	0.30	0.50
	U5	564	45	37	33.75	0.31	0.50
	U10	835	45	37	33.75	0.31	0.50
	O6	625	42	28	31.5	0.39	0.50
	T1	947	69	57	51.15	0.53	0.30
	AX6 a	575	45	29	33.75	0.67	0.30
	W10	835	74	50	55.5	0.55	0.30
	Z11 a	1584	43	37	32.25	0.69	0.30
	AD12	1000	73	61	54.75	0.71	0.30
	E1	795	76	50	57	0.86	0.30
	L2	1000	42	37	31.5	0.96	0.30
	AB3	835	42	37	31.5	0.96	0.30
	Q10 a	1800	73	45	54.75	1.74	0.10
	Z8	831	44	41	33	1.94	0.10

[z] Products designated as primer and lower case letter (e.g., AC7a) (NA = not applicable).

of the loci (e.g., $M7_{675}$, $U13_{831}$, $AT7a_{1275}$, $A16_{1600}$, $AT2_{800}$, $BC226_{1400}$, $02\text{-}1_{1100}$, and $Z3a_{700}$). Although this type of conversion has proven difficult in cucumber (6), if success is achieved in melon we will make additional conversions. This will allow for the development of a standard array of SCARs markers, and permit their use in diversity analysis and genetic map construction along with previously published codominant markers (5). A standard marker array and the use of reference accessions from previous studies (e.g., 7) will provide powerful set of tools for diversity analysis.

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