

## Genetic Analysis of Isozyme Variants in Cucurbita pepo

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Considerable isozyme polymorphism has been identified in cultivars of Cucurbita pepo (1,2,3,4), and a correlation between the particular activity bands and fruit types was noted by Ignart and Weeden (1). We report here a genetic analysis of several enzyme systems previously found to be polymorphic. Two linkage groups were identified. Genetic linkage proved not to be the basis of at least one of the isozyme/morphological correlations reported by Ignart and Weeden.

Three crosses were made between C. pepo cultivars: Senator x Table Queen, Goldrush x Table King, and Blackjack x Early Prolific. Senator, Goldrush, and Blackjack were zucchini types displaying the isozyme phenotypes already described (1). The phenotypes for the acorn squash Table King and Table Queen, have also been described (1). The isozyme phenotypes of Early Prolific, a yellow straightneck type, were similar to those reported in (1) for cultivars of this type, except that PGM had the "A" phenotype. Isozyme analysis was performed as described previously (1,3). Additive expression of the parental banding patterns was observed in the  $F_1$  hybrids. Novel bands, representing new heterodimeric forms, also could be seen in the  $F_1$  isozyme phenotypes for GPI, AAT, and MDH enzyme systems. Identification of allelic forms was straightforward in systems such as SKDH, LAP, EST, and ALDO, in which one major band was seen in each parent. Genetic analysis of the other enzyme systems was relatively easy once the parental and  $F_1$  phenotypes were compared.

The loci identified and their segregation patterns for the appropriate  $F_2$  populations are presented in Table 1. In addition to the reported isozyme loci, the Senator x Table Queen  $F_2$  segregated for fruit shape (oblong vs. round) and habit (bush vs. vine), the Goldrush x Table King  $F_2$  for fruit shape (oblong vs. round) and fruit color (yellow vs. green), and the Blackjack x Early Prolific  $F_2$  for fruit color (yellow, light green and dark green) and leaf mottling (M). The data on the morphological characters in this last cross was of poor quality due to a severe infection of powdery mildew in the  $F_2$  population. Thus, this data is not presented.

In cross 1236 and 1237 (derived from different Goldrush x Table King  $F_1$  plants) nine isozyme loci segregated. In both populations the locus coding the "cytosolic GPI-2" isozymes (1), designated Gpi-c2, was linked to Aat-p2, the locus specifying the more slowly migrating chloroplast AAT isozymes (AAT-5 in Ignart and Weeden) (Table 2). The loci Skdh, Aldo-p, and Est also exhibited non-random assortment (Table 2). In both populations the apparent gene order was Skdh - Aldo-p - Est.

In the Senator x Table Queen  $F_2$  population six isozyme loci segregated (Table 1), and one linkage group was identified: Gpi-c2 - Aat-p2 (Table 2). There also was a correlation between Skdh and growth habit; however, the highly skewed ratio obtained for the habit character (Table 1) suggested that other factors besides genetic linkage may have contributed to this correlation. Eight isozyme loci segregated in the Blackjack x Early Prolific  $F_2$ , all displaying phenotypic ratios close to the expected 1:2:1

(Table 1). The loci Skdh and Aldo-p again showed linkage (Table 2). The results also indicated a linkage between the fruit color and the MDH-2 phenotype (data not presented); however, the powdery mildew infestation interfered with the scoring of fruit color, and this linkage requires further verification.

#### Literature Cited

1. Ignart, F. and N. F. Weeden. 1984. Allozyme variation in cultivars of Cucurbita pepo L. Euphytica 33:779.
2. Kirkpatrick, K. J., D. S. Decker and H. D. Wilson. 1985. Allozyme differentiation in the Cucurbita pepo complex: C. pepo var. medullosa vs. C. texana. Econ. Bot. 39:289.
3. Puchalski, J. T. and R. W. Robinson. 1978. Comparative electrophoretic analysis of isozymes in Cucurbita species. Cucurb. Genet. Coop. 1:39.
4. Wall, J. R. 1969. A partial survey of the genus Cucurbita for electrophoretic variants of esterase and leucine amino peptidase. Southwestern Naturalist 14:141.

Table 1. Number of individuals with designated phenotypes in F<sub>2</sub> populations.

Cross	Isozyme or Trait	N	Phenotype			$\chi^2$
			Fast or +	Heterozygous	Slow or -	
<u>Senator x Table Queen</u>						
	AAT-4	26	6	13	7	0.07
	AAT-5	35	9	17	9	0.03
	GPI-2	35	10	19	6	1.2
	LAP	16	3	7	6	1.4
	MDH	35	14	14	7	4.2
	SKDH	34	7	22	5	3.8
	Fruit Shape	27	18		9	1.0
	Habit	35	13		22	27**
<u>Goldrush x Table King</u>						
1236	AAT-4	45	11	27	7	2.5
	AAT-5	43	10	24	9	0.6
	ALDO	44	16	20	8	3.3
	EST	41	15	17	9	2.9
	GPI-2	45	12	26	7	2.2
	LAP	45	7	30	8	5.0
	MDH-3	44	14	22	8	1.6
	PGM-2	45	10	28	7	3.1
	SKDH	45	16	22	7	3.6
	Fruit Shape	38	26		12	0.9
	Fruit Color	39	34		5	3.1
1237	AAT-4	47	11	17	19	6.3*
	AAT-5	47	8	22	17	3.6
	ALDO	46	8	26	12	1.5
	EST	45	10	26	9	1.1
	GPI-2	47	8	27	12	1.7
	LAP	46	12	24	10	0.26
	MDH-3	47	13	19	15	1.9
	PGM-2	46	6	28	12	3.7
	SKDH	47	6	24	17	5.2
	Fruit Shape	42	33		9	0.28
<u>Blackjack x Early Prolific</u>						
	AAT-2	53	12	27	14	0.17
	AAT-4	54	9	34	11	3.8
	ALDO	54	15	26	13	0.22
	GPI-2	54	19	27	8	4.5
	LAP	46	16	23	7	3.5
	MDH-3	54	8	32	14	3.2
	MDH-4	54	18	22	14	2.4
	SKDH	54	15	25	14	0.33

\* Significant at  $p \geq 0.05$ .

\*\* Significant at  $p \geq 0.01$ .

Table 2. Joint segregation data for isozyme loci displaying significant deviations from random assortment.

Loci	No. plants with designated phenotype*											$\chi^2$	Recomb. Fract.
	N	F/F	F/H	F/S	H/F	H/H	H/S	S/F	S/H	S/S			
<u>Goldrush x Table King 1326</u>													
Gpi-c2 : Aat-p2	43	9	1	0	3	19	2	0	4	5	35.8	13 ± 4	
Skdh : Aldo-p	44	11	5	0	4	15	1	1	1	6	35.0	16 ± 4	
Skdh : Est	41	10	4	1	5	12	2	0	1	6	26.7	19 ± 5	
Aldo-p : Est	40	13	2	0	2	14	1	0	0	8	56.0	6 ± 3	
<u>Goldrush x Table King 1327</u>													
Gpi-c2 : Aat-p2	47	6	2	0	2	20	0	0	5	12	48.8	10 ± 3	
Skdh : Aldo-p	46	2	6	0	3	16	7	1	1	10	17.6	24 ± 5	
Skdh : Est	45	3	6	1	2	17	7	1	1	7	13.8	27 ± 6	
Aldo-p : Est	44	7	3	0	1	23	1	0	0	9	60.2	6 ± 3	
<u>Senator x Table Queen</u>													
Gpi-c2 : Aat-p2	35	7	2	0	3	14	0	0	3	6	33	12 ± 4	
<u>Blackjack x Early Prolific</u>													
Skdh : Aldo-p	54	9	3	2	4	16	5	0	7	8	22.1	24 ± 5	

\* Phenotypic designations: F = fast; H = heterozygous; S = slow.