

GENETICS OF ISOZYME VARIATION IN *CUCUMIS MELO* L.

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ABSTRACT

Of the 14 isozyme loci scored in *Cucumis melo*, 11 were monomorphic and 3 polymorphic with two alleles at each locus. Genetical studies proved monogenic nature of inheritance of the alleles at all the three loci. While PRX_{2a} was completely dominant over PRX_{2b}, the two alleles at GOT₂ and EST₁ showed codominant reaction.

Key words: Isozymes, inheritance, *Cucumis melo*,

MATERIALS AND METHODS

Isozyme variation in 32 melon (*Cucumis melo* L.) varieties was studied for four enzyme systems [1]. Of the 14 loci scored, 11 were monomorphic while the remaining 3 (PRX₂, GOT₂ and EST₁) were polymorphic, with two alleles at each locus. The results of genetical studies on these variations are presented in Tables 1, 2 and 3.

A perusal of Table 1 indicated that the parent varieties were homozygous at the PRX₂ locus. In F₁, the Hara Madhu type (PRX_{2a}) showed complete dominance over that of cv. Phut (PRX_{2b}). There was no difference between reciprocal crosses. The χ^2 values for F₂

Table 1. Segregation in the progenies of a cross between the varieties Hara Madhu and Phut of *Cucumis melo* for the PRX₂ locus

Parents		F ₁				F ₂		BC ₁ (F ₁ x P)		χ^2 for 3:1 in F ₂	χ^2 for 1:1 in BC ₁
Hara Madhu (HM) PRX _{2a}	Phut (P) PRX _{2b}	(HM x P) PRX _{2a}	(HM x P) PRX _{2b}	(P x HM) PRX _{2a}	(P x HM) PRX _{2b}	PRX _{2a}	PRX _{2b}	PRX _{2a}	PRX _{2b}		
12	12	16	0	16	0	32	13	7	9	0.36	0.25

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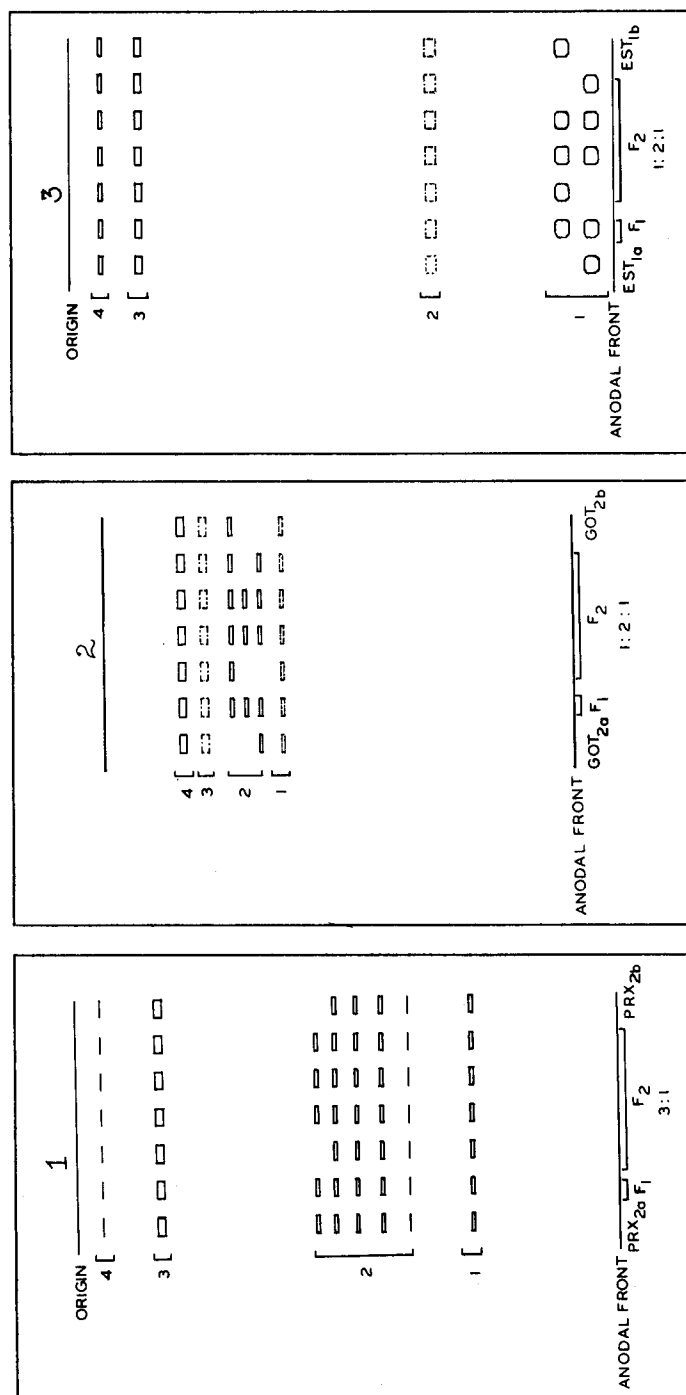
Fig. 1. Genetics of variation in *Cucumis melo* for (1) PRX2 (2) GOT2 (3) EST1.

Table 2. Genetic studies on variation at GOT₂ locus of *Cucumis melo*

Parents		F ₁								F ₂				BC ₁ F ₁ x Phut				χ^2	
Hara Madhu (GOT _{2a})	Phut (GOT _{2b})	Hara Madhu x Phut				Phut x Hara Madhu				A	B	AB	ABC	A	B	AB	ABC	1:2:1 in F ₂	1:1 in BC
A	B	A	B	AB	ABC	A	B	AB	ABC										
14	14	0	0	0	10	0	0	0	10	11	13	0	16	0	8	0		1.8	0

segregation and BC generations were calculated and found to fit a monogenic ratio (Fig. 1:1).

The variant isozyme for GOT₂ was found in the variety Phut. The standard isozyme was named GOT_{2a} and the variant, GOT_{2b}. In F₁, in addition to parental bands, a new band with intermediate mobility can be seen (Fig. 1:2). This indicated the dimeric nature of the GOT protein involved. The results of genetical analysis, as can be seen from Table 2, clearly indicate the monogenic nature of inheritance of alleles with codominance for the variants in the heterozygote.

Table 3. Segregation in the progenies of cross between the varieties Kachri and Hara Madhu of *Cucumis melo* for the EST₁ locus

Parent		F ₁			F ₂			χ^2 for 1:2:1
Hara Madhu	Phut EST _{1b}	EST _{1a}	EST _{1b}	EST _{1a/b}	EST _{1a}	EST _{1b}	EST _{1a/b}	
10	10	0	0	20	14	11	17	1.95

As can be seen from Fig. 1:3, the alleles at EST₁ (EST_{1a}, the standard, and EST_{1b}, the variant, found in var. Kachri) also are codominant. But unlike GOT, the EST protein is monomeric and no hybrid enzyme is formed in the heterozygote. The pattern of inheritance of the alleles fit a monogenic ratio (Table 3).

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REFERENCE

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