Indian J. Genet., 51 (4): 438–444 (1991)

ISOZYME VARIATION IN MUSKMELON (*CUCUMIS MELO* L.)

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(Received: April 5, 1990; accepted: May 21, 1991)

ABSTRACT

Isozyme variation in 32 melon varieties was studied for the enzyme systems esterase (EST), peroxidase (PRX), glutamate oxaloacetate transaminase (GOT), and glutamate dehydrogenase (GDH). Three out of the 14 loci scored, were dimorphic with two alleles at each locus. The remaining 11 loci were monomorphic. While both the alleles at the PRX_2 locus were fairly well distributed in the collections studied, the variant alleles GOT_{2b} and EST_{1b} were confined to Indian nondessert and semiwild collections (Phut and Kachri, respectively). Acc. 566, catalogued as *C. melo* var. *callosus*, was unique in possessing all the variant alleles identified in the present study.

Key words: *Cucumis melo*, isozyme variation, genetic distance, wild *Cucumis* ssp.

The variations in morphological characters in muskmelon (*Cucumis melo* L.) are wide [1]. In the present study, varieties of *C. melo* from India and other countries were studied for morphological and isozyme variations.

MATERIALS AND METHODS

Thirty two melon varieties representing dessert and nondessert types from all over the world listed below were included in this study.

A.	Indigenous dessert/varieties	Source
1.	Lucknow Safeda	Uttar Pradesh
2.	Bhagpat Melon	"
3.	Allahabadi Kajra	"
4.	Chittidar	"

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5.	Durgapura Madhu	Rajasthan
6.	Hara Gola (Tonk type)	Rajasthan (Tonk region)
7.	Pusa Madhuras	New Delhi
8.	Pusa Sharbati	"
9.	Hara Madhu	Punjab
10.	Punjab Sunehri	"
11.	Kharri	Madhya Pradesh (Narmada river bed)
12.	Sharbat-e-Anar	Andhra Pradesh

B. Indigenous nondessert and semiwild types

13.	Nakkadosakaya (cooking type)	Andhra Pradesh
14.	Budamkaya (cooking type)	"
15.	Vellarikkai (salad and cooking)	Tamil Nadu
16.	*C. melo* var. *callosus* (Acc. 566)	"
17.	Kakri (long melon, salad type)	New Delhi
18.	Phut (snap melon)	"
19.	Kachri (semiwild)	Rajasthan
20.	Mudikode local (cooking type)	Kerala

C. Exotic dessert varieties

21.	Perlita	USA
22.	Campo	"
23.	Planter's Jumbo	"
24.	Gulf Stream	"
25.	Georgia 47	"
26.	Top Mark	"
27.	Siberian Honey Dew	"
28.	Tehkizil	U.S.S.R.
29.	Zolotistaya	"
30.	Pakistan Collection	Pakistan
31.	Sarda	Afghanistan
32.	Bokor	Hungary

Polyacrylamide gel electrophoresis was carried out using vertical slab gel. The methodology for enzyme assay was as given below:

Enzyme assayed	*Sample*	*Gel concentration*	*Gel buffer*	*Electrode buffer*	*Staining technique (reference)*
Peroxidase (PRX)	Root and hypocotyl region of 4-5-week-old seedlings	7% acrylamide	Tris-chloride pH 9.0	Tris-glycine pH 8.3	[2]
Esterase (EST)	3-4 days old seedlings	"	"	"	[3]
Glutamate oxaloacetate transaminase (GOT)	"	9.5% acrylamide	"	"	[3]
Glutamate dehydrogenase (GDH)	"	8% acrylamide	Tris-chloride pH 8.0	"	[3]

The loci were represented by a numerical subscript, eg. EST$_1$, PRX$_2$, etc. The numbering was done in the ascending order from the fastest to the slowest moving anodal loci.

The alleles were named using small letters of the English alphabet, eg. PRX$_{2a}$, EST$_{1b}$, etc. The standard allele was always given the letter a and the variants—the subsequent letters.

RESULTS

PEROXIDASE

In the peroxidase system of *C. melo*, four major groups were detected. These were allotted to four loci, viz., PRX$_1$, PRX$_2$, PRX$_3$ and PRX$_4$ (Fig. 1), while PRX$_1$, PRX$_3$ and PRX$_4$ proved to be monomorphic, PRX$_2$ showed 2 variant alleles. Of these, one produced 5 isozymes in the PRX$_2$ cluster (PRX$_{2a}$) whereas the other (PRX$_{2b}$) produced only 4 isozymes in the cluster. Genetic studies confirmed the monogenic nature of inheritance of the character with complete dominance for the 5-banded type in F$_1$.

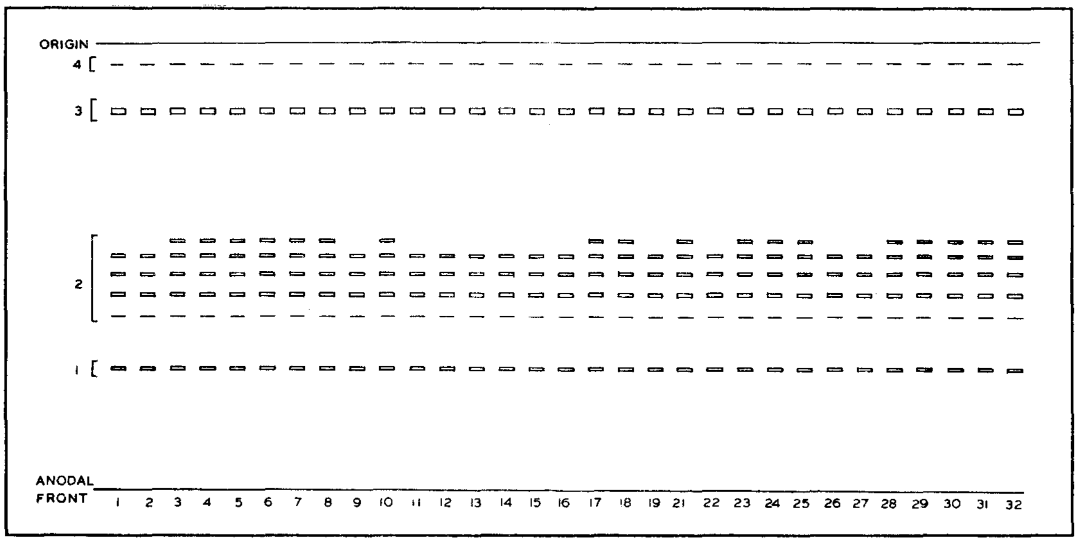

Fig. 1. **Peroxidase isozyme pattern in *Cucumis melo.***

GLUTAMATE OXALOACETATE TRANSAMINASE

The GOT zymogram of *Cucumis melo* showed four isozymes in all the varieties. These four isozymes were allotted to four loci: GOT1, GOT2, GOT3 and GOT4 (Fig.2).

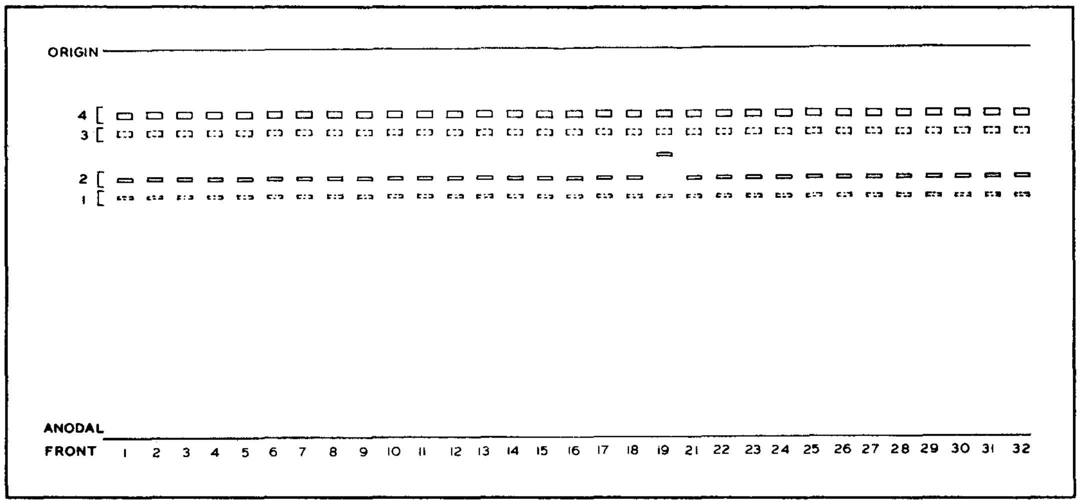

Fig. 2. **GOT isozyme pattern in *Cucumis melo.***

While GOT_1, GOT_3 and GOT_4 were found to be monomorphic, two alleles were identified at GOT_2. Most of the indigenous and all the exotic varieties had the standard allele GOT_{2a}, Phut (snapmelon), an Indian nondessert type, had a variant allele (GOT_{2b}) in homozygous condition. Also, Acc. 566 (*C. melo* var. *callosus*) had GOT_{2b} in heterozygous condition with GOT_{2a}. The heterozygotes showed codominance for the alleles. This variant allele at GOT_2 was not found to be present in the 125 varieties of *C. melo* studied by Esquinas-Alcazar [5]. He reported melons to be monomorphic for GOT zymogram.

ESTERASE

Four isozymes of esterase were identified and were alloted to four different loci, EST_1, EST_2, EST_3 and EST_4 (Fig. 3). While EST_2, EST_3 and EST_4 were monomorphic in the *C. melo* collections studied, two alleles were identified at EST_1: EST_{1a} was the standard allele present in most of the melon varieties, and EST_{1b} was found in Kachri and Acc. 566, the two semiwild collections from India. Kachri was homozygous for EST_{1b}, whereas Acc. 566 was heterozygous for this locus. The alleles were codominant in the heterozygote.

GLUTAMATE DEHYDROGENASE

In the GDH zymogram, two isozymes were observed in *Cucumis melo*. There was no variation in different collections for the GDH system (Fig. 4).

DISCUSSION

The study on four enzyme zymograms in 32 collections of *Cucumis melo* showed very little variation within the species. Out of the 14 loci surveyed, 11 were monomorphic and the remaining 3 loci were dimorphic with 2 alleles at each locus.

The varieties were grouped into two different classes based on the variation at PRX_2 locus. Neither of the alleles belonged to any specific geographical locality. Even the only two accessions from Russia were divided into the two different classes. The dessert or nondessert types also did not aggregate in any one particular group. The cantaloupes of U.S.A. and the indigenous dessert types were also divided between the two classes.

Variant alleles found at EST_1 and GOT_2 loci, on the other hand, were less frequent. They were confined to one or two accessions. It was interesting to note that the Indian melons showed more variation at the isozyme loci studied. Esquinas-Alcazar [4] also pointed out that melons from India showed more diversity at the isozyme loci.

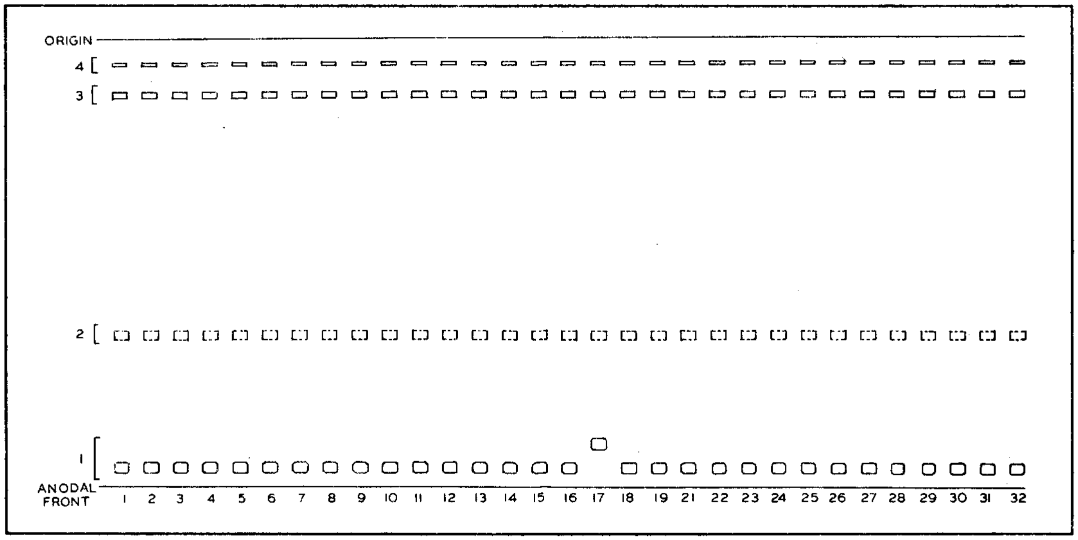

Fig. 3. Esterase isozyme pattern in *Cucumis melo.*

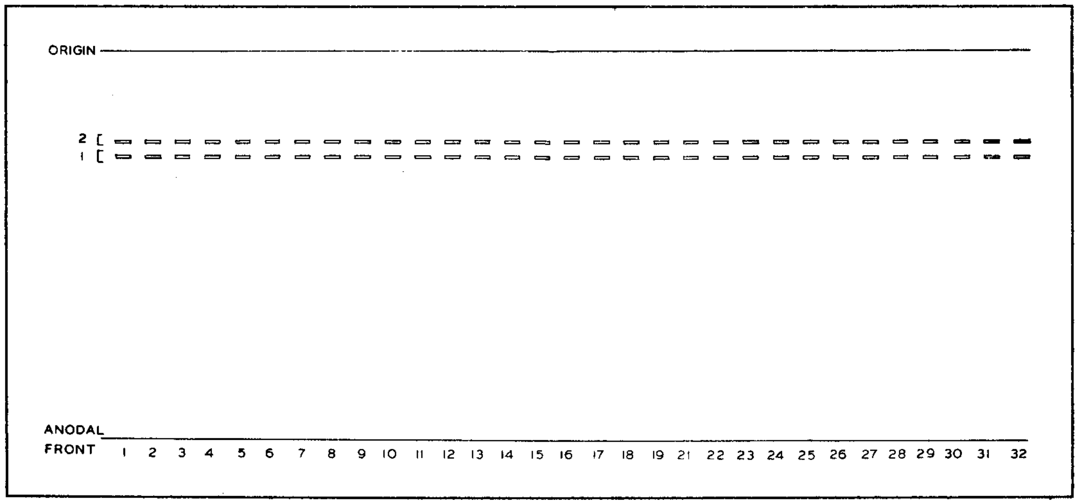

Fig. 4. GDH isozyme pattern in *Cucumis melo.*

ACKNOWLEDGEMENTS

The authors are grateful to Dr. K. R. Sarkar, Division of Genetics, and Dr. I. M. Santha, Division of Biochemistry, IARI, New Delhi, for their valuable suggestions during the course of the work. The financial assistance provided to the first author by the Indian Agricultural

Research Institute, New Delhi, in the form of a Senior Research Fellowship is gratefully acknowledged. The results reported in this communication formed part of the thesis for the Ph.D. degree of the Indian Agricultural Research Institute by the first author.

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