AN ALLOZYMIC POLYMORPHISM IN PEA MALATH DEHYDROGENASE IS SPECIFIED BY A LOCUS ON CHROMOSOME 1

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Polymorphism in the malate dehydrogenase (L-malate NAD oxido reductase EC 1.1.1.37; MDH) phenotype has been previously reported in pea (4,5,7) and attributed to genetic differences among the lines examined. However genetic tests confirming this assumption have not been published, although the genetic basis of MDH polymorphism has been established in Zea mays (6), He1ianthus annuus (1), and Cucurbita pepo (2). In this communication we present data demonstrating that the variation observed in one region of the MDH zymogram exhibits Mendelian segregation. Comparison of the MDH segregation pattern with segregation at other loci indicate that the locus responsible for the MDH variation is located on chromosome 1.

To obtain the MDH phenotype, leaf extracts were subjected to horlzontal starch gel electrophoresis using a histidine buffer system at pH 6.5 as described previously (9). The assay solution (25 ml) contained the following: 0.1M Tris-HCl pH 8.5, 1 5 mg L-malate, 5 mg NAD, 3 mg MTT and 0.5 mg PMS. Assays for other isozyme systems have been described (9). The parental lines used for the genetic analysis were A1078-234, B777-248, A1078-239 (all obtained from Dr. G.A. Marx) and PI 358612 (obtained from the NW Regional Plant Introduction Station at Geneva).

The variation observed in the MDH phenotype is shown in Fig. 1. Line PI 3586 12 (and B777-248) displayed an MDH band with an R of about 0.25 (MDH-4 in Fig. 1), whereas the other 2 lines lacked this band. Crosses between lines possessing the MDH-4 isozyme and those lacking such a band gave Fl plants exhibiting a discernable, although often slightly less intense, MDH-4 band. In segregating F2 populations we did not attempt to differentiate between the heterozygous and homozygous MDH-4 "plus" phenotypes but divided the plants into 2 categories, those exhibiting the MDH-4 band and those lacking it.

The MDH segregation data from 2 different crosses closelv fits a 3:1 ratio expected for monogenic control (Table !). We suggest **that this** locus tentatively be designated Mdh. There are probably other loci coding MDH isozymes but further characterization of the MDH system is required before more appropriate locus designations can be made.

Joint segregation analysis revealed non random assortment between Mdh and 2 isozyme loci on chromosome 1 (Table 2). Both Aat-p and Est-3 have been mapped near A (3,8) and our data indicate that Mdh also should display linkage with this morphological marker. Mdh segregated independently of D Idh, and I, the other chromosome 1 markers segregating in one or both of the crosses listed in Table 1 (data not shown).

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Table 1. Segregation of the MDH-4 phenotype in F2 populations.

Original Cross	N	No. plants with stated phenotype: Band present	Band absent	X^2 (3:1)
A1078-234 x B777-248	65	46	19	0.62
A1078-239 x PI 358612	59	46	13	0.28

Table 2. Joint segregation data for Mdh and selected other loci segregating in the cross A1078-239 x PI 358612.

Loci	N	Number of plants with designated phenotype* +/F(+)	+/H	+/S(-)	-/F(+)	-/H	-/S(-)	X^2	Recomb. fract.
Mdh : Est-3	59	6	29	11	9	3	1	17[1]	20+ 6
Mdh : Aat-p	59	6	29	11	7	4	2	9.9[1]	25+ 6
Mdh : D	59	32		11	14		2	1.2[2]	----

*Phenotype designations: + = wild type or band present; - = mutant or band absent; F = homozygous for fast allozyme; H = heterozygous; S = homozygous for slow allozyme.

[1]Expected ratio: 3:6:3:1:2:1.

[2]Expected ratio: 9:3:3:1.

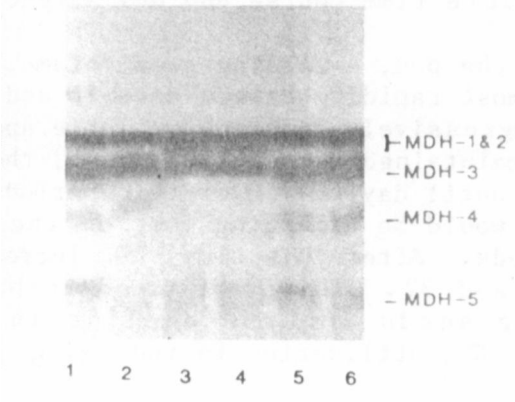

Fig. 1. Malate dehydrogenase phenotypes from leaf extracts of the hybrid produced from the cross A1078-239 x PI 358612 (lanes 1 and 2), of the Al078-239 parent (lanes 3 and 4), and of the PI 358612 parent (lanes 5 and 6). Migration is toward the anode at top of figure.