A GENE CODING ISOCITRATE DEHYDROGENASE IS LINKED WITH D ON CHROMOSOME 1

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NADP-speclf1c Isocltrate dehydrogenase (1DH) has been shown to be a polymorphic enzyme in many plant species. Polymorphism for this enzyme also occurs in peas, although each line typically exhibits only one of these forms. Three distinct mobility classes have been observed in the approximately 200 pea lines we have tested for their IDH phenotype. Two of these variants, here designated "slow" and "fast", are relatively common while a third much faster migrating form has been found In only two lines (John Innes #JI73 and USDA #PI343972).

The genetic bases of the two common variants was investigated in several F2 populations from the following crosses:

(1) B78-288 x A1078-236
(2) A1078-234 x B777-248
(3) C82-243 x A171-235-(2)
(4) B77-254 x A78-237

IDH phenotypes were determined by starch gel electrophoresis using a N-3(aminopropy1)-morpholine/cltric acid buffer system at pH 6.1 (1). The assay mixture consisted of 25 ml 0.1 M Tris-HCl pH 7.1 containing 1 mM $MnCl_2$, 15 mg sodium isocitrate, 5 mg NADP, 4 mg 3-(4,5-dimethylthlazolyl-2)-2,5-diphenyltetrazolium bromide (MTT), and 0.5 mg phenozine methosulfate.

Segregation data (Table 1) indicate that the two forms are coded by distinct alleles at a single locus we designate Idh. The alleles exhibit codomlnant expression; however, the individual bands cannot be distinguished in the heterozygote but appear as a wide blur. Analysis of the joint segregation at Idh and D was performed in the first three crosses, the fourth not exhibiting segregation at D. The tight linkage observed (Table 2) indicates that Idh is situated on chromosome 1 very close to D. Some F plants could not be confidently scored for D-d or, in a few cases, for Idh, and were therefore excluded from the analysis. Note also that populations 1 and 2 differ from 3 in their cis/trans relationship.

Table 1. Segregation in F_2 of allelic forms at Idh.

Cross[1/]	N	IDH phenotype			Chi-square
		slow	heterozygous	fast	(1 : 2 : 1)
1	40	9	20	11	0.02
2	68	11	44	13	6.0
3	20	6	11	3	1.1
4	84	20	45	19	0.45

[1/] Numbers refer to those given in text.

Table 2. Joint segregation of Idh and D. Dominance at D locus indicated by (+) and recessivity by (-).

Cross[1/]	Phenotype						Estimated	St
	-/slow	-/het	-/fast	+/slow	+/het	+/fast	% recomb.	Err
1	9	1	0	1	19	10	5	3.
2	11	2	1	0	19	12	9	4.
3	0	0	2	6	9	0	no detectable recombinants	

1/ Numbers refer to those given in text.

The IDH phenotype may be determined using small tissue samples from seeds or young seedlings and this advantage together with the codominant expression of alleles should make Idh an excellent genetic marker for chromosome 1.

1. Clayton, J. W. and D. N. Tretiak 1972. J. Fish. Res. Bd. Can. 29: 1169-1172.