

## Soybean Linkage Studies: y18 and y20

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### Introduction

[Amberger et al., \(1992\)](#) reported that the Chinese cultivar Jilin 3 (PI 427099 [GRIN]) was very conducive to generate variants from tissue culture. Among the progeny of a chimeric foliage plant (LA55-1) identified in the R3 generation, were plants with green foliage, chimeric foliage, and yellow viable, and yellow lethal plants. The yellow viable mutant was allelic to y20 [Soybase] and the yellow lethal mutant was allelic to y18 [Soybase]. These data will be reported elsewhere. Our objective was to determine linkage relationships of these two mutants with morphological and isoenzyme mutants in soybean.

### Materials and Methods

Cross-pollinations were made between the yellow viable mutant and heterozygous yellow lethal mutant plants and cultivar BSR 101 [GRIN] ([Tachibana et al., 1987](#)) at the Bruner Farm near Ames, Iowa. The F1 seed were planted at the University of Puerto Rico-Iowa State University soybean nursery near Isabela, Puerto Rico. F2 seed were sampled for isoenzymes and the F2 seedlings transplanted to the Bruner Farm.

The traits evaluated were: malate dehydrogenase (E.C.1.1.1.37 [PBD]), phosphoglucomutase (E.C.5.4.2.2 [PBD]), isocitrate dehydrogenase (E.C.1.1.1.42 [PBD]), aconitase (E.C.4.2.1.3 [PBD]), alcohol dehydrogenase (E.C.1.1.1.1 [PBD]), flower color (*w1* locus [Soybase]), and leaflet morphology (*Na* locus). Starch gel electrophoresis procedures of [Cardy and Beversdorf \(1984a, b\)](#) were used to assay for the isoenzymes. The computer program 'Linkage 1' was used to analyze the data and to estimate linkage intensity ([Suiter et al., 1983](#)).

### Results and Discussion

The yellow viable mutant was allelic to y20 and completely linked to *Mdh1-n* [Soybase] and will be reported elsewhere. The seven linkage tests between the

yellow viable mutant and the isozyme and morphological traits showed no linkage, i.e., they were independent ([Table 1](#)). Twenty-one additional linkage tests were done between all possible loci pairs. The only linkage detected was between flower color (*w1* locus) and alcohol dehydrogenase (*Adh1* locus [[Soybase](#)]) with  $23.7 \pm 4.1$  percentage recombination ([Table 1](#)).

The lethal yellow mutant was allelic to *y18* and will be reported elsewhere. Similarly, seven linkage tests between the lethal yellow mutant and the isozyme and morphological trait hypocotyl color (pleiotropic effect of flower color) showed no linkage ([Table 2](#)). The lethal yellow mutant died before expressing leaflet morphology so the *Na* trait could not be determined. Of the twenty-one additional linkage tests, linkage was detected only between the *w1* and *Adh1* loci with  $18.6 \pm 1.9$  percentage recombination ([Table 2](#)).

The *y20* and *Mdh1-n* loci were completely linked and confirmed previous reports ([Chen and Palmer 1996, 1998](#)). The linkage intensities for *w1-Adh1* from both cross-combinations are similar to those summarized by [Palmer and Hedges \(1993\)](#).

## References

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**Table 1.** F2 linkage of yellow viable plants crossed with BSR 101. (Between 283 to 297 F2 seeds or seedlings were classified for linkage for each comparison). Values are given as percentage recombination with standard errors.

	<b>MDH<sup>a</sup></b>	<b>Mdh1<sup>b</sup></b>	<b>Pgm</b>	<b>ldh1</b>	<b>Aco4</b>	<b>Adh1</b>	<b>W1</b>
<b>Mdh1<sup>b</sup></b> [ <a href="#">Soybase</a> ]	45.3±6.6						
<b>Pgm</b> [ <a href="#">Soybase</a> ]	48.3±3.6	47.4±3.5					
<b>ldh1</b> [ <a href="#">Soybase</a> ]	47.9±3.5	44.0±3.5	48.4±2.9				
<b>Aco4</b> [ <a href="#">Soybase</a> ]	49.1±3.6	46.4±3.5	49.6±2.9	47.5±2.9			
<b>Adh1</b> [ <a href="#">Soybase</a> ]	48.4±6.8	48.9±6.9	45.8±3.5	47.8±3.5	48.4±3.6		
<b>W1</b> [ <a href="#">Soybase</a> ]	46.8±6.9	45.5±6.8	47.8±3.6	47.1±3.6	46.8±3.6	<b>23.7±4.1</b>	
<b>Na</b>	49.9±7.1	48.3±7.0	49.0±3.6	49.2±3.6	44.9±3.6	43.6±6.6	47.7±6.9

<sup>a</sup>MDH is a mobility variant, gene symbols not assigned; [Palmer et al. 1992](#).

<sup>b</sup>All *Mdh1-n* plants were yellow viable plants.

**Table 2.** F2 linkage of heterozygous lethal yellow plants crossed with BSR 101. (Between 950 to 1020 F2 seeds or seedlings were classified for linkage for each comparison). Values are given as percentage recombination with standard errors.

	<b>MDH<sup>a</sup></b>	<b>Lethal yellow</b>	<b>Pgm</b>	<b>ldh</b>	<b>Aco4</b>	<b>Adh1</b>	<b>W1</b>
<b>Lethal yellow</b>	49.1±3.7						
<b>Pgm</b>	48.9±1.9	47.4±1.0					
<b>ldh</b>	49.4±1.9	47.8±1.9	49.8±1.6				
<b>Aco4</b>	48.4±1.9	48.4±1.9	48.4±1.5	49.8±1.6			
<b>Adh1</b>	47.7±3.7	49.4±3.8	46.0±1.9	47.8±1.9	49.6±1.9		
<b>W1</b>	49.4±3.8	49.6±3.8	46.2±1.9	49.9±1.9	48.0±1.9	<b>18.6±1.9</b>	
<b>Na</b>	50.0±3.9	ND	49.3±2.0	48.1±2.0	49.9±2.0	50.0±3.9	49.6±3.9

ND: Not determined, seedlings died before expressing leaflet phenotype.

<sup>a</sup>MDH is a mobility variant, gene symbols not assigned; [Palmer et al. 1992](#).