Research Notes: Glycine Germplasm Resources

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The low whole plant quality of the soybeans was not only a reflection of high stem fiber but also a reflection of high leaf fiber. The better quality of the wild soybean was due to the young growth which finally occurred at the end of the summer as rabbit pressure eased. Rabbits and deer selectively browsed the soybeans and neglected the protepeas in both 1974 and 1975. The apical, meristemic regions of the growing soybean plant are apparently quite acceptable even though the rest of the plant is highly fibrous.

Use of the leafy, small-vined *G. soja* in 1975 was an effort to improve protein while retaining the *in vitro* digestibility of *Zea mays* silage. Perhaps other soybean types, possibly the edible or non-pubescent types, may have less plant fiber.

Reference

J. J. Faix
C. J. Kaiser
F. C. Hinds

UNIVERSITY OF ILLINOIS
Department of Agronomy
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1) Determination of sugar content of individual soybean seeds.

In order to investigate the possibility of single seed selection for sugar content in soybeans, a technique has been developed for analysis of 20-40 mg samples of soybean meal. The method described by Hymowitz et al. (1972) has been modified to serve this purpose.

A portion of a soybean seed is ground for 5 min in a ball mill (Spex Industries, Inc.). A 40 mg sample of meal is weighed and wrapped in 7½ cm Whatman filter paper (No. 50). The package is then bound tightly with wire. Lipids are extracted by refluxing for 24 hr with petroleum ether (bp 30-60°C) in a Soxhlet extraction apparatus. The defatted meal is then transferred to a 16 x 125 mm screw-capped culture tube and .5 ml (2.5 mg) of gentiobiose solution is added as an internal standard. The volume is brought to 5 ml
with 80% ethanol and the tube is shaken on a Super Mixer (Matheson Scientific). The sample is heated in a 75°C water bath for 1 hr, being shaken every 10 min. The solution is then transferred to a 50 ml beaker. The meal is washed four times with 5 ml of 80% ethanol, the washings being combined with the original transfer. The sugar solution is evaporated to low volume (about 3 ml) and transferred to a clean culture tube. Protein is precipitated with 6 drops of lead acetate, and 6 mg of sodium bicarbonate is added to remove excess lead. The sample is then centrifuged at 2000 g for 15 min and decanted into a 15 x 45 mm shell vial. The pH is adjusted to 5.7-6.3 with 3.4 M acetic acid and the sample is then evaporated to complete dryness. Derivitization and GLC settings are as described by Hymowitz et al. (1972) with the following exceptions: carrier flow rate, 30 cc/min; carrier makeup, 90 cc/min; column temperature rise from 150-330°C over an 8 min rise time, preceded by a hold time of 2.4 min at 150°C.

Reference

S. J. Openshaw
T. Hymowitz
H. H. Hadley

2) Inheritance of a second SBTI-A2 variant in seed protein of soybeans.

The soybean trypsin inhibitor (SBTI-A2) is a seed protein that exhibits different electrophoretic forms. Hymowitz and Hadley (1972) demonstrated that two different electrophoretic forms of SBTI-A2 represent the expression of two codominant alleles at a single locus. They assigned the symbol Ti1 to the allele controlling the most commonly occurring electrophoretic form Rf 0.79/10% (Rf = mobility relative to the dye front in a 10% polyacrylamide gel anodic system) and Ti2 to the allele controlling the electrophoretic form found at Rf 0.75/10%. A third electrophoretic form of SBTI-A2 Rf 0.83/10%

was recently located in seed of PI 246.367 and PI 196.172 (Hymowitz, 1973). Data reported herein is concerned with the inheritance of Rf 0.83/10% electrophoretic form.

We crossed T245 (Rf 0.75, Ti2) with PI 246.367 (Rf 0.83). The F1 seed had both electrophoretic forms. The pooled F2 seed segregated 1 Rf 0.75 : 2 both forms : 1 Rf 0.83 (89:162:74, expected 81.5:163:81.5, x^2 = 0.54). We crossed 'Harosoy' (Rf 0.79, Ti1) with PI 246.367 (Rf 0.83). The F1 seed had both electrophoretic forms. The pooled F2 seed segregated 1 Rf 0.79 : 2 both forms : 1 Rf 0.83 (42:101:57, expected 50:100:50, x^2 = 0.33). In both crosses the data were pooled since the x^2 analysis among families showed no heterogeneity.

From these data, we conclude that a gene, here designated Ti3, controls the electrophoretic form Rf 0.83/10% and that it has two codominant alleles Ti1 and Ti2 with which it forms a multiple allelic series controlling the three electrophoretic forms of SBTI-A2.

References

James H. Orf
Theodore Hymowitz

3) The gene symbols Sp1^a and Sp1^b assigned to Larsen and Caldwell's seed protein bands A and B.*

Larson (1967), using acrylamide gel electrophoresis, described two seed proteins in soybean seed and noted they were variety specific. The inheritance of these proteins (although the proteins were not characterized) was reported as being controlled by two codominant alleles at a single locus (Larsen and Caldwell, 1968); gene symbols were not assigned. The letters "A" and "B" were used to designate the two different seed protein bands.

Our studies using polyacrylamide gel electrophoresis revealed that the seed protein band called "A" by Larsen and Caldwell (1968) occurs at Rf 0.36/10% (Rf = mobility relative to the dye front in a 10% polyacrylamide gel anodic system) and the seed protein band called "B" occurs at Rf 0.42/10%.

We crossed 'Cloud' (Rf 0.42) with 'Amsoy' (Rf 0.36). The F₁ seed had both electrophoretic forms. The pooled F₂ seed segregated 1 Rf 0.36 : 2 both forms : 1 Rf 0.42 (35:77:30, expected 35.5:71:35.5, $\chi^2 P = .51$). We propose the gene symbol base $Sp$ for seed protein with subscript numbers to designate different proteins and superscript letters for codominant alleles controlling different forms of a protein. Thus, we propose $Sp₁^a$ for the electrophoretic form Rf 0.36 and $Sp₁^b$ for the electrophoretic form Rf 0.42. $Sp₁^a$ should be the same gene for the "A" protein band studied by Larsen and Caldwell in Amsoy, and $Sp₁^b$ probably corresponds to their gene for the "B" protein band.

References

James H. Orf
Theodore Hymowitz
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<th>Collection #</th>
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<td>E. E. Hartwig</td>
<td>Delta Branch Experiment Station, Stoneville, Mississippi 38776</td>
<td>1400</td>
<td>Genetic types, varieties, <em>Glycine</em> spp. world-wide southern collection</td>
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<td>U.S.A.</td>
<td>T. Hymowitz</td>
<td>Department of Agronomy, University of Illinois, Urbana, Illinois 61801</td>
<td>2800</td>
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<td>B. B. Singh</td>
<td>Department of Plant Breeding, G. B. Pant University, Pantnagar, Uttar Pradesh</td>
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<td>S. Korea</td>
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<td>France</td>
<td>R. M. Ecochard</td>
<td>Ecole Nationale Superieure Agronomique, 145 Av. de Muret, Toulouse</td>
<td>500</td>
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<td>14) Japan</td>
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<td>15) Japan</td>
<td>J. Fukui</td>
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<td>Ministry of Agriculture Causeway, Salisbury</td>
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Additional Collections
- Bulgaria, National Institute of Agriculture, Sofia
- Romania, Agricultural Experiment Station, Fundulea
- Indonesia, Institute Pertanian, Bogor
- Philippines, College of Agriculture, University of the Philippines, College, Laguna
- Hungary, Agricultural Experiment Station, Iregszemcse
- Australia, CSIRO, Division of Plant Industry, P.O. Box 1600, Canberra City, A.C.T. 2601

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