PLANT breeders are constantly faced with the problem of identifying superior material based on subjective evaluation. Due to the masking of heritable by non-heritable variations, this type of evaluation often leads to less than maximum gains. The selection index technique provides an objective approach to the evaluation of breeding material. Estimates of population parameters, which are easily obtained from measurements on the various attributes, are used in indexing the lines. Based on the information used in its construction, the index provides for maximum theoretical gain.

Smith (9) and Hazel (5), using slightly different approaches, constructed specific selection indices which gave maximum genetic advance from selection. Manning (7) in cotton, Robinson et al. (8) in corn, and Brim et al. (3) in soybeans evaluated specific selection indices and found them of value in the identification of superior genotypes.

The major limitations to specific index selection are (a) obtaining reliable parameter estimates from limited evaluation of the materials involved, and (b) the laborious task of constructing an index for each population in each generation. Hanson and Johnson (4) modified specific index theory to an average or a general selection index. This approach utilized average estimates of population parameters within a crop species in index construction. Selection advance based on the average index was highly correlated with the advance of specific indices.

The purpose of this study was to compare the effectiveness of general, average, and specific selection indices in identifying high-yielding genotypes of soybeans. A general index was constructed by utilizing parameter estimates from unrelated populations; an average index was constructed by pooling parameter information from the populations in this study; and each specific index was constructed from estimates of a particular population.

MATERIALS AND METHODS

Four soybean populations of random F4-derived lines were evaluated in the F4 and F5 generations. The parentages of the populations were:

<table>
<thead>
<tr>
<th>Population</th>
<th>Parentage</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>C1105 × A4-3159</td>
</tr>
<tr>
<td>2</td>
<td>'Lindarin' × A4-3159</td>
</tr>
<tr>
<td>3</td>
<td>A4-3159 × AX29-267-1-1-2 × A4-3202</td>
</tr>
</tbody>
</table>

The 4 F4 populations were grown in 1959, and visually classified into 3 maturity groupings—early, midseason, and late. In 1960 the F4 lines were grown in single rows 40 inches wide and 8 feet long. Fifty F4 lines were grown in each of the 3 maturity groups within each environment. These lines remained in the same population throughout the study. The maturity classification of comparisons with three check varieties: 'Blackhawk' (early), 'Hawkeye' (midseason), and 'Ford' (late).

A bulk sample from each F4 line was evaluated in the F4 generation (1961) in two replications at the Agronomy Farm, Ames, Iowa, (environment 1). A bulk sample from each F4 line was evaluated in the F5 generation (1962) with 2 replications at 2 locations—Squaw Creek Bottom, Ames, Iowa (environment 2) and the Agronomy Farm, Ames, Iowa (environment 3). Environment 2 was planted 2 weeks prior to those of environment 1 and 3, and, in addition, received approximately 3 inches of water by overhead irrigation on July 7. Plants of environments 1 and 2 received mild moisture stress in August and September. In both environments, plot size was 10 feet long, after end trimming, with rows 40 inches wide.

The seven attributes evaluated on a plot basis in all environments were:

- Seed yield—Air dried to uniform moisture content, pounds per acre
- Maturity—Days after August 31 when 95 to 100% of pods had turned brown
- Plant height—Inches from ground level to the tip of the main stem at maturity
- Lodging score—Scored at maturity: 1 (nearly all plants erect) to 5 (nearly all plants prostrate)
- Seed size—Grams per 100 seed
- Oil and protein percent—Dry weight basis
- Test weight—Air dried to uniform moisture content, pounds per bushel

The experimental design for all environments was a factorial arrangement of whole plots (population × maturity groups). Each whole plot contained 2 replications corresponding to the lines of a particular population. Locations and years were considered equal.

Whole plot analyses of the data were made individually, and combined for all environments. Subplot data were analyzed for environment 1 and for environments 1, 2, and 3 combined.

Estimates of phenotypic and genotypic variances for the combined data were obtained from the square which had the expectation: