Although the indeterminate and the determinate types of soybean have been known to differ in physiological and ecological characteristics (NAGATA 1960 a, b, c; THSENG and HOSOKAWA 1971), the genetic behavior of such habit has not been clarified completely. But the introduction of the indeterminate habit into determinate varieties to make the "half-indeterminate type", seems to be a promising method to create a new subject of soybean breeding in Japan. Consequently, in order to raise such variety effectively, it is indispensable to obtain the information of the inheritance mode of these characters.

This study is devoted to the analysis of the inheritance mode of the several agronomic characters in the early segregating generations from the some crosses between indeterminate and determinate varieties.

Materials and Methods

Four F2 populations i.e., Harosoy × Tokachi-nagaha, Harosoy × Kitami-shiro, Kogane-jiro × Shinsei and Isuzu × Toiku No. 122, and seven parental varieties were used for experiments. Harosoy and Kogane-jiro are known as an indeterminate variety, and Tokachi-nagaha, Kitami-shiro, Shinsei and Toiku No. 122 are determinate variety.

In 1969, the P1, P2, F2 plants were grown in the farm of Tokachi Agriculture Experimental Station, Hokkaido.

The experimental designs were as follows:
1) Two crosses, Harosoy × Tokachi-nagaha and Harosoy × Kitami-shiro, were designed following a completely randomized block with six replications. Each replication contained two plots of P1, P2, and ten
### Table 1. Total F₂ variance, error variance, and heritability in four F₂ populations

<table>
<thead>
<tr>
<th>Character</th>
<th>F₂, Harosoy × Tokachi-nagaha</th>
<th>F₂, Harosoy × Kitami-shiro</th>
<th>F₂ Kogane-jiro × Shinsei</th>
<th>F₂, Isuzu × Toiku No. 122</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>$\sigma_F^2$</td>
<td>$\sigma_e^2$</td>
<td>$h^2$</td>
<td>$\sigma_F^2$</td>
</tr>
<tr>
<td>Days to first flowering</td>
<td>64.817</td>
<td>1.426</td>
<td>97.8</td>
<td>130.367</td>
</tr>
<tr>
<td>Plant height</td>
<td>734.572</td>
<td>26.445</td>
<td>96.4</td>
<td>1074.492</td>
</tr>
<tr>
<td>Node no. in main stem</td>
<td>13.714</td>
<td>0.741</td>
<td>94.6</td>
<td>18.442</td>
</tr>
<tr>
<td>Branch number</td>
<td>5.940</td>
<td>0.791</td>
<td>86.8</td>
<td>5.296</td>
</tr>
<tr>
<td>Pod number</td>
<td>3045.235</td>
<td>228.493</td>
<td>92.5</td>
<td>2761.325</td>
</tr>
<tr>
<td>Seed number</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>Seed weight</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>Ratio of node no.*</td>
<td>164.685</td>
<td>13.011</td>
<td>92.1</td>
<td>204.012</td>
</tr>
</tbody>
</table>

* Increment of node number after first flowering in percent of the total node number.
plots of F₂. Each plot consisted of 12 plants, 10 of them being used for taking records. All the plants were planted in 60 × 60 cm spacing.

2) Other two crosses, Kogane-jiro × Shinsei and Isuzu × Toiku No 122, were also designed following a completely randomized block with four replications. Each replication contained one plot of P₁ and P₂, and four plots of F₂. Each plot consisted of 20 plants, 15 of them being used for taking records. All the plants were space-planted at 60 × 20 cm.

Results

1. Genetic parameter in F₂ population (Table 1)

In spite of the difference in the planting density, experimental error in all characters seemed to be small enough to inference that the phenotypic values of F₂ plants were made up almost only of the genotypic effects.

The heritability values in broad sense were estimated by the following formula:

\[
\text{Genetic variance (} V_a \text{)} = V_{F_2} - \frac{1}{2}(V_{P_1} + V_{P_2})
\]

\[
\text{Heritability (} h^2 \text{)} = \frac{V_a}{V_{P_1}}
\]

Where \( V_{F_2} \) is phenotypic variance in F₂ population, \( V_{P_1} \) and \( V_{P_2} \) are phenotypic variance in P₁ and P₂ populations, respectively.

The heritability values estimated from the F₂ population of indeterminate × determinate crosses were rather high in all characters, especially most of them from wide spaced experiment exceeded over 90%. On the other hand, the heritability values estimated from the F₂ population crossing from the determinate × determinate were very low.

2. Days to first flowering (Fig. 1)

In both populations, the ranges of F₂ variation exceeded the parental difference by more than twelve times. The F₂ mean exceeded the parental mean about ten days. There were two peaks of distributions; one of them located at the class of 100–120 days was bigger, and another one located at the class of 60–70 days was small.

3. Plant height (Fig. 2)

The distributions of plant height observed in each of the three F₂ populations derived from the crosses between indeterminate and determinate varieties were continuous showing the deviation from the normal distributions. On the other hand, F₂ populations derived from the crosses among deter-
Fig. 1. $F_2$ distribution of days to first flowering (cross figures indicate the parental mean with $\sigma_d$).

Fig. 2. $F_2$ distribution of plant height (cross figures indicate the parental mean with $\sigma_d$).
determinate varieties showed the normal distribution. The ranges of variation in F2 populations were greatly wider in the crosses between indeterminate and determinate varieties, and the mean of F2 populations overwhelmingly exceeded the parental means. In the F2 population from the crosses between the determinate varieties, mean value was equal to the parental mean and noticed that amount of F2 population plants lower than both the low and high parents is very few.

4. Node number in main stem (Fig. 3)

In three crosses, Harosoy × Tokachi-nagaha, Harosoy × kitami-shiro and Kogane-jiro × Shinsei, the variation in the F2 populations were so big that the node number of plants in the largest classes were more than four times as much as another extreme value. Seeing the distributions of the F2 populations, the former two populations were somewhat deviated from normal distributions, while the distribution of the later population is normal. The ranges of F2 variations in all crosses were much wider than the parental differences, and these mean values exceeded the parental means.

In the population of Isuzu × Toiku No. 122, the parental mean was about equal to the F2 mean and the range of F2 variation was equal to the parental

Fig. 3. F2 distribution of node number in main stem (cross figures indicate the parental mean with \( \sigma_2 \).)
difference.

5. **Branch number (Fig. 4)**

In all of the three crosses between indeterminate and determinate varieties, F₂ distributions were typically normal and the ranges of F₂ variation were apparently wider than the parental differences. The parental means, F₂ means showed the almost same value.

In the population of Isuzu × Toiku No. 122, more than half of the plants exceeded the values of lower parents and none of the plants in F₂ than the highest value in the parental varieties.

![Graph showing branch number distribution](image)

**Fig. 4.** F₂ distribution of branch number (cross figures indicate the parental mean with σ_e).

6. **Pod number (Fig. 5)**

About four populations, F₂ distributions were normal, especially the F₂
population of Isuzu × Toiku No. 122 showed the typical normal distribution, and none of these plants had a lower value than the lowest value in parental varieties. The ranges of \( F_2 \) variation of the crosses between indeterminate and determinate varieties were extremely wider than the parental difference, especially in the population of Harosoy × Tokachi-nagaha, where the range exceeded the parental difference by more than four times.

7. **Seed number (Fig. 6)**

In \( F_2 \) populations derived from crosses Kogane-jiro × Shinsei and Isuzu × Toiku No. 122, the ranges of variation were much wider than the parental differences, only five plants in population of Isuzu × Toiku No. 122 showed the lower seed number than values of lower parents, and the distribution of the population of Isuzu × Toiku No. 122 was deviated from the normal, but the variation was continuous.
In the population of Isuzu × Toiku No. 122, the mode of F₂ distribution was an extremely skewed one, and the mean value was smaller than the parental mean. On the other hand, the mean of F₂ in Kogane-jiro × Shinsei was equal to the parental mean.

![Graph showing F₂ distribution of seed number per plant](image)

**Fig. 6** F₂ distribution of seed number per plant (cross figures indicate the parental mean with $\sigma_x$).

8. **Seed weight (Fig. 7)**

In both populations, the ranges of F₂ variation were greatly wider than the parental differences, while F₂ distribution of Kogane-jiro × Shinsei was a typically normal.

The F₂ mean of Isuzu × Toiku No. 122 exceeded the parental mean, but in the population of Kogane-jiro × Shinsei, the F₂ mean and each parental means were not so much different, as the value was 24.17, 24.91 and 25.01, respectively.
Fig. 7. $F_2$ distribution of seed weight per plant (cross figures indicate the parental mean with $\sigma_e$).

Fig. 8. $F_2$ distribution of ratio of node number (cross figures indicate the parental mean with $\sigma_e$).
9. Ratio of node number (Fig. 8)

To describe the growth habit, the authors took the increment of node number after first flowering in per cent of total node number (Sanbuichi 1967; Thseng and Hosokawa 1971).

In both populations, the distributions of F₂ populations were normal, the ranges of F₂ variation were not so much bigger than the parental differences and F₂ means were smaller than the parental means. There were only 1% plants located at the tail of distribution of higher parent and 10% plants at lower parent, generally about 60% plants showed the values ranging from 35% to 55% in the F₂ distributions.

Discussion

To study the variations on three F₂ populations in the crosses between indeterminate and determinate varieties revealed that many of the characters are similar in inheritance mode and transgressive segregation in F₂ distribution. Also the variations of F₂ populations apparently showed that the distributions are normal or far normal, and continuous, and no character is conditioned monogenically. These results as mentioned above, seem to support that the indeterminate and determinate varieties are controlled by a different genetic basis, and its may be roughly said that the inheritance of F₂ plants are under the control of various gene effects, and with intra and inter-allelic interaction or additive effects, and poly-genic effects in all characters. Thus, the analysis of the effective number of genes and their effects will be a very important problem for breeding for which indeterminate and determinate varieties are used as the parents of the hybridizations.

Thseng and Hosokawa (1971) reported that the node number in main stem at first flowering was not correlated with its increment after first flowering in the F₂ hybrids of indeterminate × determinate variety, and the heterosis of ratio of node number was not found in F₁ plants. In this study, it is indicated that many plants located between indeterminate and determinate variety in the F₂ distribution of ratio of node number.

Selection of the "half-indeterminate" plants seems to be possible in soybean breeding. This will be discussed in the following paper.

Summary

Three F₂ populations obtained from the crosses between indeterminate and determinate varieties, and one F₂ population of determinate × determinate variety, and their parents were used to investigate the inheritance modes of
the F₂ plants for several agronomic traits.

The environmental variance, estimated by the variation of each parental variety, was so small enough that the heritability values estimated by the formula (total F₂ variance—environmental variance/total F₂ variance), and heritability value was very higher in the populations of the crosses between indeterminate and determinate variety.

The inheritance modes of the F₂ distributions were more or less normal in all characters given, i.e., plant height, node number in main stem, branch number, pod number, seed number, seed weight and ratio of node number.

Days to first flowering was only exceptional character whose distribution was found by two peaks in the inheritance mode.

Ratio of node number, 60 percents of the F₂ plants distributed in the centre of the parents.

The F₂ mean exceeded the parental mean in days to first flowering, plant height, node number in main stem, branch number, pod number, seed weight, except the ratio of node number.

Acknowledgements

The authors wish to express their hearty thanks to Dr. T. KUSUNOKI, Director, Mr. M. SAITO, Head of the Soybean Laboratory, Mr. K. SASAKI, Mr. T. TSUCHIYA and Mr. S. SAKAI of the Tokachi Agriculture Experimental Station, who encouraged them to carry out this work and helped them with valuable suggestions. Likewise, the authors are also grateful to Dr. C. TSUDA, for his interest in this work and discussions.

Literature cited


