HERITABILITIES OF CERTAIN YIELD CHARACTERS OF THE COCONUT PALM

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In the genetic improvement of an economic character like yield, it is necessary to understand the contribution of the environment and the genotype to the phenotype of the individual. The concept of 'heritability' which is a ratio of the genetic variance to the phenotypic variance is useful in evaluating the genetic value of a desired character and consequently an appropriate programme of selection (Lush, 1949).

Selection of high-yielding coconut palms (Cocos nucifera L.) for seed collection has been a common practice in most coconut growing countries. Different authors have listed a number of criteria for selection of seed-bearers, and in most cases these characters have been taken on an empirical basis (Prudhomme, 1906; Sampson, 1923; Jack, 1930). In the absence of any progeny trials or similar studies it would not have been possible to give a fair assessment of the selection criteria. Pieris (1934, 1937) has worked out correlations between ten characters of the coconut palm including yield, and has specified standards for selection of seed palms. According to him, the size of nut is not important, provided large numbers are present, a medium sized nut is the best, palms with extra large nuts should be avoided; the weight per husked-nut should be high. The number of nuts per palm and their weight provide the best standards of selection.

The object of the present study is to assess the heritability of four important characters of the coconut palm and their genetic correlations, and study their relative importance in a selection programme. The characters concerned are: (i) the flowering-period, (ii) yield of nuts, (iii) yield of copra (i.e. total weight of husked nuts) and (iv) weight per husked-nut.

Material

The data presented have been taken from a progeny trial planted in November 1934 with open-pollinated seednuts collected from 9 high-yielding mother palms of the tall variety of coconuts. The mother palms have been selected for high yield of copra on the lines advocated by Pieris (1937) and the seednuts or the seedlings have not been selected before transplantation. There are altogether 278 progeny in the 9 families, and the number of seedlings per family has varied between 10 and 64. The design of the trial is full randomisation with unequal replications.

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Four characters have been considered, viz. the flowering-period of the palm, the number of nuts produced per palm, the total weight of husked-nuts, and the mean weight per husked-nut. The flowering-period is the time taken from transplanting a seedling to the appearance of the first spathe. The other characters represent the harvests gathered during the four years, 16 to 19 years after planting. The yield of copra per palm has been calculated as 32 per cent of the total weight of husked-nuts (Pieris, 1935).

**Methods of Statistical Analysis**

The tall variety of the coconut palm grown on a plantation scale in Ceylon is predominantly out-breeding. On the assumption that random pollination takes place in a population of coconut palms, the mean squares and the mean products are partitioned into within and between families components, and the genetic and non-genetic variances and covariances are estimated. The analysis of variance and covariance and partitioning into within and between families components are shown in Table I.

<table>
<thead>
<tr>
<th>Source</th>
<th>Degree of Freedom</th>
<th>Variances</th>
<th>Co-variances</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Mean squares</td>
<td>Expected components</td>
</tr>
<tr>
<td>Total</td>
<td>( \sum_{i=1}^{x} y_i - 1 )</td>
<td>( M_1 )</td>
<td>( \sigma_w^2 + k \sigma_n^2 )</td>
</tr>
<tr>
<td>Between families</td>
<td>( x - 1 )</td>
<td>( M_2 )</td>
<td>( \sigma_w^2 )</td>
</tr>
<tr>
<td>Within families</td>
<td>( \sum_{i=1}^{x} (y_i - 1) )</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

In the above table, \( x \) stands for the number of families, \( y_i \) the number of individuals in the \( i \)-th family and \( k \) is a coefficient related to \( y \). If the number of individuals in each family is the same, then \( k = y \), but since it varied from family to family in this experiment, \( k \) is computed by using Crump’s formula (1946) as follows:

\[
k = \frac{1}{x - 1} \left\{ \sum y_i - \frac{1}{\sum y_i} \sum_{i=1}^{x} y_i^2 \right\}
\]

where \( x \) = number of families, \( y_i \) = number of individuals in the \( i \)-th family, and \( \sum y_i \) = total number of individuals investigated.

\( \sigma_w^2 \) and \( \sigma_{w \times w} \) are between individuals within families variance and covariance, and \( \sigma_n^2 \) and \( \sigma_{n \times n} \) are between families variance and covariance.

\( \sigma_w^2 \) (or \( \sigma_{w \times w} \)) is expected theoretically to include environmental variance (or covariance between two characters) and three quarters of the genetic variance (or...