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PHENOTYPIC AND GENOTYPIC VARIATION IN KIWIFRUIT

(Actinidia deliciosa (A. CHEV.) C.F. LIANG *et*
A.R. FERGUSON) SEEDLING POPULATIONS

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ABSTRACT

Kiwifruit breeding programmes in New Zealand have produced a large number of seedling populations. Effective methods are required to assess seedlings, and knowledge of phenotypic and genotypic variation would facilitate the design of breeding programmes.

1. Multivariate analyses of phenotypic data

Multivariate analyses were used to quantify the characters most powerful in distinguishing between seedlings and between crosses, and to examine their relationships. Seedlings and crosses were placed in order of their overall merit, and the best ones were determined. Bruno was a superior female parent for producing both floriferous male vines and productive female vines with high fruit vitamin C content, and D1-20 was the better male parent in all crosses. Multivariate analysis of variance and discriminant analysis were more suitable to sort cross combinations, while factor analysis was more efficient for screening single seedlings within a population. Factor patterns varied between crosses, and between years for the same cross.

Canonical correlation analysis proved a useful tool to obtain better understanding of the aggregates of useful vine characters and the relationship between them in fruit breeding.

2. Quantitative genetics studies

Relatively high heritability was shown for the beginning date of bloom (0.48) and flowering duration (0.50) in male vines, and total crop weight (0.46), percentage of shoots flowering (0.54), fruit elongation (0.65), and mean fruit weight (0.52) in female vines. For these traits, the selection of superior seedlings as parent could therefore lead to rapid genetic improvement to their subsequent generations. Hairiness of fruit (-0.07) and percentage soluble solids in fruit (-0.19) gave negative heritability value, thus could not be improved efficiently by individual selection. However, their broad sense heritability was reasonably high (0.22 and 0.37 respectively), showing there were some dominant and/or epistatic effects involved. This indicates a possible chance improvement may occur in a large seedling population. Fruit vitamin C content (0.22), fruit symmetry (0.30) and relative core size (0.13) gave moderate or low heritability values, indicating that individual selection may have only moderate success in improving these traits.

Simple recurrent individual selection was shown to be an effective breeding strategy for characters of high heritability. For characters of low heritability, the family selection methods yielded a greater rate of genetic gain. Selection indices were constructed to provide a technique for improving several traits simultaneously.

3. SDS-polyacrylamide gel electrophoresis of leaf proteins

Three regions of the protein profile were found useful for the characterisation of cultivars and seedlings. The banding patterns found in seedlings provided evidence that in the hexaploid kiwifruit the inheritance of these polypeptides occurred in a manner similar to that of a diploid. Hence the kiwifruit may have arisen as a diploidized polyploid and it is proposed the kiwifruit may be considered as allohexaploid.

Progressive changes of some bands with leaf growth and development may be of interest in the study of leaf development. The possible application of leaf protein analysis to kiwifruit breeding was discussed.

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