

BIOMETRICAL STUDIES ON CHARACTERS ASSOCIATED WITH YIELD IN OILSEED RAPE (*Brassica napus*)

A. E. ARTHUR and M. A. FORD

Brassica and Oilseeds Research Department, John Innes Centre, Norwich, NR4 7UH, UK.

ABSTRACT

Information about the range and type of variation of a number of metrical characters associated with yield in oilseed rape (*Brassica napus*) was obtained using recombinant doubled haploid lines derived from two contrasting crosses and their reciprocals. These lines were grown in four different environments in the field. The measured variation was partitioned into the major sources: between environments, between genotypes, the interaction between the two, and error or residual. Statistically significant differences were found for all sources of variation and it was found that, for some characters, up to 20% of this variability was either due to differences between environments or to the effects of genotype-environment interactions. Statistical analyses provided information to facilitate the mapping of the quantitative trait loci involved in the control of these characters.

INTRODUCTION

The efficiency and effectiveness of the improvement of crop plants is greatly assisted by an improved understanding of the genetic systems controlling and influencing characters of commercial, biological and scientific interest (Thurling, 1991). However, many of these traits are quantitatively inherited, that is, they are controlled by a number of genes of small, cumulative effects rather than single, major genes. The elucidation of the quantitative trait loci (QTLs) associated with these quantitative genes in any species is dependent upon the availability of numerous genetic markers scattered throughout the genome. The mapping of QTLs or even genes of major effects in the brassicas is made difficult because of the lack of such morphological markers. However, as saturated genomic maps of Restriction Fragment Length Polymorphisms (RFLPs) are becoming increasingly available for the brassicas (Lydiate *et al.*, 1993, Ferreira *et al.*, 1994), it is now feasible to search these genomes for QTLs associated with particular traits. This enables us to locate the quantitative genes on these genomic maps and analyse the contributions made by different regions of the genome to the traits under investigation.

## EXPERIMENTAL

Recombinant doubled haploid lines derived from two contrasting crosses of *Brassica napus* - winter oilseed rape crossed with a resynthesised line obtained from a cross between *B. oleracea* and *B. rapa*, and the same winter line crossed with a spring oilseed rape cultivar, and their reciprocals (Parkin *et al.*, 1992) - were used to investigate a range of plant characters showing quantitative variation. The lines were grown in extensively replicated field trials in two growing seasons, 1992 and 1993, in two contrasting environments in 1992 (*viz.* spring planted with and without artificial vernalisation) and two in 1993 (autumn planted and spring planted). The characters assessed included time to and node number at flowering, plant height, and traits associated with yield such as pod and pedicel length and orientation, seed number and size. The data were subjected to statistical analyses to determine the contribution and significance of the major sources of variation associated with genotypes, environments (summarising the effects of planting times, treatments and years), the interaction between the two (the genotype-environment interaction) and residual or error variation.

## RESULTS

Highly significant differences were found for all the major sources of variation examined, including those associated with the different years and environments, amongst the genotypes in each of the two reciprocal families used, and for the interaction between environments and genotypes.

However, the relative contributions of the components of variation derived from these sources of variation to the total, phenotypic variation varied greatly amongst the characters assessed. The proportion of the total variation accounted for by differences between genotypes ranged from almost 60% down to less than 20%. Traits with the highest values included pod and beak length, and pod diameter, and those with the lowest genetic contributions were pedicel length, and seed number and weight per pod. Indeed, pedicel length gave consistently high values for the contribution from different environments, indicating that this character is likely to be highly influenced by different environmental conditions. Characters showing high percentage values for the genotype-environment interaction components included beak length and seed weight, and the lowest values were found for pod and pedicel length. In most cases, a significant proportion of the total variation, up to 60% in some cases, was accounted for by the residual or error component, indicating that there was considerable variation amongst the replicate plots, and the individual plants within them, throughout the experimental areas for each treatment in each year.

Traits with high interaction components, and those with high residual components, are particularly difficult to work with since their performances are unpredictable and will vary from environment to environment and year to year. Thus, characters with the highest genetic and the lowest interaction and residual components were selected for further detailed studies and analysis of the QTLs as these are likely to be more reliable and easier to resolve than those with high interaction and/or residual components.

Data for these characters are now being subjected to various statistical analyses to determine any association between the trait means and the RFLP markers used to construct, and therefore already located on, the genomic map. Various methods have been developed for achieving this but essentially all provide information about the extent to

which the markers used in the mapping are associated with regions of the genome that explain significant variation for the trait in question (see eg Kearsey and Hyne, 1994, Martinez, 1994). These regions are likely to contain important genes that control the expression of these traits. Despite the numerous complexities of the statistical analyses and those concerning the location of the markers on the maps, regions of the genome associated with some of these quantitative traits can be identified.

The presence of significant genotype-environment interactions and their effect on results from experiments and trials has been the cause of concern for researchers and breeders for many years. The refinement of procedures to study and map QTLs offers new opportunities to examine the nature of these interactions and provide breeders with information on the genetic control of the ability of genotypes to adapt to, and perform in, different environments.

This brings closer the attractive possibility of manipulating the genes associated with quantitative traits in similar ways to those now well established for genes of larger effects. However, because of the complicated genetic properties of quantitative variation, considerable effort will be required to bring the manipulation of QTLs to the level applied to the major genes, but this can be greatly facilitated by an improved understanding of the underlying nature of the genetic systems involved through biometrical studies of the traits of interest.

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