THE GENETIC CONTROL OF PETALLESS FLOWERS AND UPRIGHT PODS

A.KELLY, M.FRAY, E.A.ARTHUR AND D.J.LYDIATE

John Innes Centre, Norwich, Norfolk, NR4 7UH

A.KELLY, M.FRAY, E.EVANS

University of Newcastle, Newcastle-Upon-Tyne, NE1 7RU

ABSTRACT

RFLP analysis has been used to position the genes which control flower morphology in three distinct apetalous variants of oilseed rape and pod angle in two additional variants with upright pods. One apetalous phenotype is determined by an epistatic interaction between recessive alleles at a pair of homoeologous loci. Another apetalous type is controlled by an interaction between alleles at three loci. Mapping these genes will allow marker aided selection to accelerate the production of near-isogenic lines in which the physiological effect and the potential benefits of these novel morphologies can be investigated accurately.

INTRODUCTION

A number of characters have been identified in having physiological advantages, amongst these a petalless variant that is more efficient because of reduced reflection of photosynthetically active radiation (normally caused by petals). The upright pod variant that allows better distribution of light throughout the canopy and both have the potential to increase yield.

Analysis of the real significance of these traits in near-isogenic lines has been hampered by the difficulty of transfering multiple genes and the unavailabilty of near-isogenic substitution lines where the exact measure of the character can be established. One reason that multiple genes are involved is because of the amphidiploid nature of *Brassica napus* where intergenomic complementation between genes controlling a single character occurs because of the two genomes.

In order to successfully introduce several genes controlling one character into a defined background it will be neccessary to develop novel marker assisted breeding methods.

RFLP markers have been used to map the genes and they have identified loci controlling almost all of the variants and in each case multiple loci have been detected. Current computer assisted methods for identifying QTL's are heavily biased towards identification of loci with additive interactions between alleles. The most prominant interaction in the identified loci has been epistatic and has therefore made the identification of loci more taxing.

In future it will be necessary to develop computer software that is specifically

designed to look at the measure of significance of loci with epistatic interactions and also to devise breeding strategies that cope with the simultaneous introgression of beneficial alleles at several loci if genetic mapping and RFLP selection is going to realise its full potential in oilseed rape.

EXPERIMENTAL

Stap genes

The first to be analysed was the stap variant that had petals which developed into stamen like structures. An associated effect was a change in leaf morphology i.e. reduced size and leaf shrivelling. All variation in the stap phenotype is controlled by 2 loci, stap-1 and stap-2 (fig 1.), which have homoeologous locations on one linkage group of *B.napus* C genome and another on the A genome. Epistatic interactions between these two loci is such that only plants with homozygous recessive alleles at both loci exhibit the stap phenotype. Changes in flower and leaf morphology appeared to be completely linked with one another because they were pleiotropic effects of the same gene. This gene has been shown to be homologous to a gene in *arabidopsis* which when mutated causes a similar change in both flower and leaf morphologies.

Apet genes

The second to be analysed was the apet variant which had flowers with reduced numbers of petals but no obvious pleiotropic effects. Over 90% of the variation of petals per flower can be explained by three loci, apet-1, apet-2 and apet-3 (fig 1.). There are both additive and epistatic interactions between these loci but the epistatic interaction was the most significant. Apet-1 and apet-2 can be considered to be the major loci controlling flower morphology and apet-3 a modifier loci that has the most significance in the most extreme phenotype. There is some homoeology between the regions containing the apet-1 and apet-2 loci although the most prominant A genome homeologues of the C genome chromosome N15 are N5 and N6.

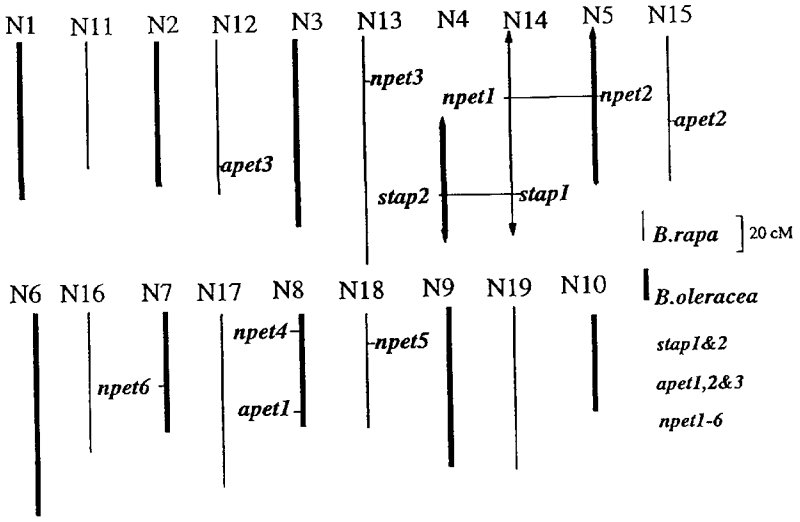
Npet genes

The third to be analysed was the npet variant which produced completely petalless flowers again with no obvious signs of any pleiotropic effects. The genetic evidence suggests between four and six loci are required for the expression of the npet phenotype, npet-1 to npet-6 (fig 1.). Npet-1 and npet-2 appear to be the major loci that are acting epistatically while up to four other modifier genes may also be present that have an additive effect on the character. The two major loci are shown to be on homoeologous chromosomes of *B.napus*.

Upright pods

Mapping loci controlling pod angle is more provisional because this character is less inheritable. The provisional studies suggest that alleles for upright pods are dominant over alleles for horizontal pods and that additive interactions between two loci can be identified in each of the three popualtions where genes for upright pods have been mapped. However the relevant loci differ popualtion to population and have not been assigned conclusive locations on the *Brassica napus* chromosomes.

Figure 1. Positions of petalless loci



Simultaneous Introgression of desirable alleles at multiple loci

The number of genes controlling these will have severe ramifications on the ease of which the petalless character can be introduced into elite genetic backgrounds. For example only 1 plant in 8 in an introgression backcross population will be heterozygous at each of the three petalless loci controlling the apet phenotype and only 1 in 16 of a similar population will be heterozygous at all 4 loci for the npet phenotype.

To introgress multiple genes successfully will require the development of markers which can rapidly screen the initial introgression backcross population to identify a sub-population that is still heterozygous at all the relevant loci. PCR-based markers should be the most efficient for this selection process. Once the sub-population has been identified it could be analysed using convential RFLP markers that are very efficient at identifying the individual with the best background genotype i.e.that of the recurrent parent.

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