APPLICATION OF MOLECULAR MARKERS IN THE GENETIC ANALYSIS OF QUANTITATIVE TRAITS.

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SUMMARY

Breeding goals are more easily attained with knowledge on the inheritance of agronomically important traits. The present study aims at gaining insight in the inheritance of quantitative traits in non-inbred allogamous crops and a better understanding of the effects of multi-allelism.

Cooking type, tuber shape, flesh colour, complex fysio resistance to *Phytophthora infestans* and earliness were analyzed by single marker analysis of variance and by using MapQTL™. In our material the majority of the genetic variation for these traits could be explained by a single DNA-marker locus. Our findings suggest that quantitative traits are the result of multiple alleles in conjunction with multiple loci.

INTRODUCTION

Quantitative traits are characterized by a continuous distribution of the trait value. They are supposed to be under control of a number of genetic loci (QTLs), each making a small contribution and sensitive to environmental conditions. However, this concept was challenged by Sirks (1929), who proposed multiple alleles at a single locus, each allele making its own contribution to the trait value. Epistasis and interactions between multiple alleles were further described by Rasmusson (1934). With the advent of molecular marker techniques the presence of multi-allelism for quantitative traits could be demonstrated (Van Eck *et al.*, 1994). In this presentation other multi-allelic traits will be presented.

MATERIALS AND METHODS

In the offspring derived from diploid non-inbred parents the segregation of the two maternal and the two paternal alleles of a marker locus can be observed. In case both parents are heterozygous up to four different alleles may occur at a single marker locus or QTL. Those multi-allelic loci segregate in a 1:1:1:1 ratio (*ab* × *cd* → *ac, ad, bc, bd*). In this way the four allele combinations found in the descendants at marker loci flanking a Locus involved in a Quantitative Trait (QTL) can be determined. Details on plant material and map construction are described by Jacobs *et al.* (1995). Quantitative traits were analyzed using single marker analysis of variance and by using the cross-pollinator version of the computer program MapQTL™ developed by Van Ooijen & Maliepaard (1996).

RESULTS AND DISCUSSION

For the traits mentioned high heritability estimates (h^2) were found. Marker analysis demonstrated that in our material the majority of the genetic variation of each trait could be explained by a single DNA-marker locus. The major QTL which has been detected for cooking type (*Co*) was mapped on chromosome *8*, flesh colour (*Y*) on *3*, earliness (*El*) and resistance to *Phytophthora* (Pi_{comp}) on *5*, and tuber shape (*Ro*) on *10*. The proportion of the genetic variance explained by a single marker locus (R^2) is indicated in table 1. These unexpected results suggests that quantitative traits may have a simple (oligogenic) hereditary basis. Apparently the simple inheritance was not recognized earlier because of the many possible allele combinations and their interactions (especially when studying tetraploids).

The presence of multiple alleles could be demonstrated at the major-QTLs *El*, Pi_{comp} and *Ro* by using the complete classification of allele combinations of flanking molecular markers. The *Y* locus involved in flesh colour is commonly regarded as a quantitative trait, despite great differences within the phenotypic classes yellow and white. The *Or* allele involved in orange flesh colour is considered to be a third allele at locus *Y* (Brown *et al.*, 1994).

A graphical representation describing the allele interactions found at the *El* locus is shown in Fig 1.

Table 1: Heritability estimates and proportions of the genetic variance explained by informative marker loci of five quantitative traits.

Trait locus	symbol	h^2 (%)	R^2 (%)	informative marker	Chromosome
Flesh colour	*Y*	76	99	*Y* phenotypic classes	*3*
Earliness	*El*	86	93 (vin TOT)	RFLP GP21	*5*
Resistance to *Phytophthora*	Pi_{comp}	na 90%	na 64%	RFLP GP21	*5*
Cooking type	*Co*	39	74	ACA/CAC-208.4	*8*
Tuber shape	*Ro*	80	75	*Ro* phenotypic classes	*10*

na = accurate estimates not available, but resemble the estimates for *El*.

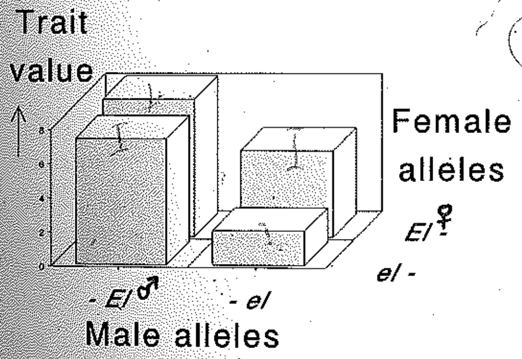

Fig. 1: Allele interactions at the *El* locus. The effects of female alleles ($El^♀$ and *el*) is surpassed by the effect of the male allele $El^♂$.

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