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The Construction of Genetic Map of Faba Bean (Vicia faba L.) Using RAPD Markers

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ABSTRACT

Fifty seven individuals of recombinant inbred lines (RILs) of faba bean (Vicia faba L.) descended from the cross between 34Morocco x Kristall25 have been analyzed for RAPD markers. A total of 77 markers were assayed segregating in the 57 RI lines and grouped into 14 linkage groups, with total length of 973.2 cM.

Key words : Vicia faba, Recombinant inbred line, RAPDs, Linkage groups

INTRODUCTION

Preliminary analysis of genetic linkage in faba bean includes the study of morphological traits (Cabrera and Martin, 1989) and was followed by the establishment of linkage maps based on morphological, isozyme, RFLP and RAPD markers (Van de Ven *et al.*, 1991). Torres *et al.* (1993) reported, that when two F2 populations (20 F2 individuals derived from the cross Vf6 x Vf173 and 44 F2 plants from the cross Vf6 x Vf35) were analyzed using isozyme, RFLP and RAPD, 11 independently assorting linkage groups were identified in this population. Satovic *et al.* (1996) analysed 13 F2 families of faba bean descending from a trisomic plant. They have been analyzed for morphological, isozyme and RAPD markers. The study revealed a total of 10 linkage groups, six of which have been precisely assigned to specific chromosomes. The most recent map in faba bean has been reported by Vaz Patto *et al.* (1998). The map consist of 14 linkage groups with total length of 984.5 cM. The main objective of the present study was to construct genetic map.

MATERIALS AND METHODS

For the construction of a linkage map a population of recombinant inbred lines (RILs) derived from the cross 34Morocco x Kristall25 was used. The 34Morocco is a bean pure line BPL228/ILB141 from ICARDA, Syria. Kristall25, developed at Hohenheim, Germany, is an inbred line from the German cultivar Kristall. These parents were chosen because of their large genetic and phenotypic difference (Schill *et al.*, 1997).

The F2 plants from the cross 34Morocco x Kristall25 and from the cross Kristall25 x 34Morocco were self-pollinated and advanced to the F7 generation using single-seed descent. The final population consists of 253 lines including reciprocal lines. A random sample of 57 lines was characterized based on RAPDs.

Segregation data were analyzed with MAP-MAKER/EXP 3.0 computer program (Lander *et al.*, 1987; Lincoln *et al.*, 1993), with a LOD score 3.0 and with 0.4 theta (40 Haldane cM; Haldane, 1919) as critical distance between two linked markers.

RESULTS

The 48 selected primers amplified a total of 115 polymorphic bands (data not shown) with an average of 2.3 polymorphic bands per primer. Fragment sizes ranged from about 550 bp to 2400 bp. With linkage criteria LOD >3.0 and a distance of less than 40 cM, 77 RAPD marker loci were classified into 14 groups (Figure 1). There were 38 unlinked markers. These markers were omitted.

The size of the 14 linkage groups ranged from 6.3 cM to 278.7 cM. The total length of map is 973.2 cM. The largest linkage group contains 16 loci (linkage group 3). The distance between markers ranges from 1.9 cM to 38.5 cM, with an average of 14.66 cM.

DISCUSSION

A total of 77 markers were found segregating in 57 RI F7-sample lines (Figure 1). The total map distance defined among linked markers was 973.2 centiMorgan. A comparison of the present genetic map with the hitherto published maps shows that its total length resembles the map of Vaz Patto *et al.* (1998) with a map length of 984.5 cM. However these maps are still small when compared to the expected size of the *Vicia faba*

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