



Mapping QTL Associated with White Mold in Common Bean

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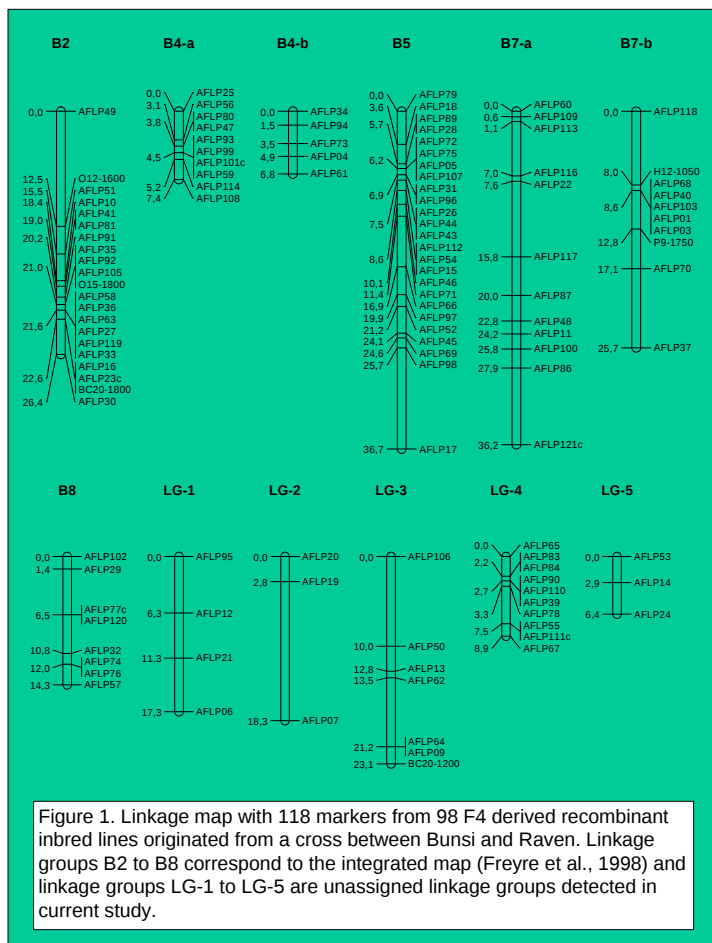


Introduction

White mold, caused by *Sclerotinia sclerotiorum*, is a serious disease of common bean (*Phaseolus vulgaris*) that results in substantial yield loss and reduced seed quality. Resistance to white mold in bean is a quantitative trait, complexly inherited, and highly influenced by environment, making selection for resistance difficult. Field resistance to white mold is partial and involves physiological resistance and morphological avoidance mechanisms. QTL associated with white mold resistance have recently been reported in diverse bean genotypes (Park et al., 2001; Miklas et al., 2001; Kolkman et al., 2003). The present work was undertaken to identify and map additional QTL associated with white mold resistance in common bean.

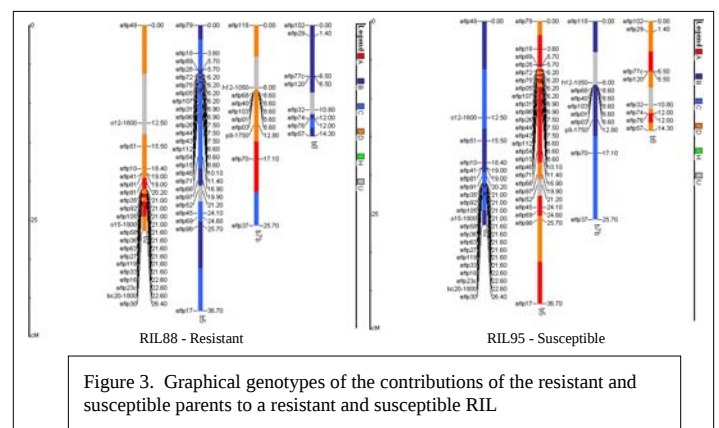
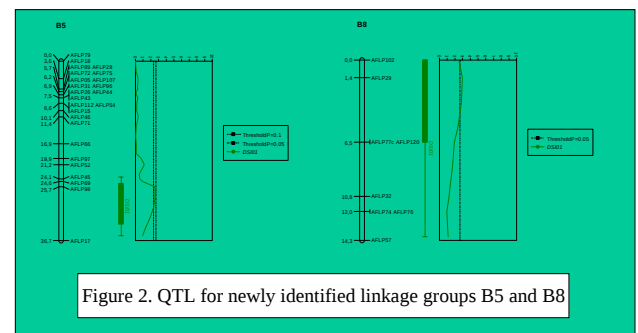
Results and Discussion

The 28 AFLP primer combinations were tested and the resulting 124 molecular markers (118 AFLP and 6 RAPD) mapped to 12 linkage groups. Linkage groups were compared against the integrated map (Freyre et al., 1998) and seven linkage groups were anchored to the integrated map (Fig.1). QTL for resistance to white mold were found on bean linkage groups B2, B4, B5, B7, and B8. The QTL for resistance on linkage groups B2 and B7 support the results found by Kolkman and Kelly (2003). The QTL on linkage groups B5 and B8 are newly identified (Fig. 2). Graphical genotypes of resistant and susceptible RILs confirm the contributions of each parent and provide breeders with a visual aid in selecting for resistance to white mold in common bean (Fig. 3).



Materials and Methods

This study was conducted in a population of 98 F_{4:7} recombinant inbred lines (RIL) derived from the cross between Bunsu and Raven. Bunsu is an indeterminate navy bean, with physiological resistance and a porous plant canopy. Raven is a susceptible indeterminate black bean with upright architecture. The phenotypic data was collected in 2001 and 2002 in field plots naturally infected when the plants had reached physiological maturity. Thirty plants per plot were rated from 0 to 4, where 0 = no disease present, 1 = 1 to 25%, 2 = 26 to 50%, 3 = 51 to 75%, and 4 = 76 to 100% of the plant with white mold symptoms (Hall and Phillips, 1996). The disease was also rated on a scale of 1 to 9 (WM1-9) as described by Miklas et al. (2001). Bulk segregant analysis (BSA) approach using AFLP markers with 256 primer pair combinations (EcoR1 + ANN and MSE1 + CNN) were first tested on the parents and resistant and susceptible bulks to detect useful associated markers and 28 primer pairs were identified as polymorphic. Candidate markers were first tested on the RILs included in the bulks and subsequently on the recombinant population. The markers were analyzed by Joinmap (Stam, 1993) and single marker analysis and composite interval mapping was conducted on QTL Cartographer (Basten et al., 2001).



References

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