MAPPING QUANTITATIVE TRAIT LOCI FOR *FUSARIUM* ROOT ROT IN COMMON BEAN (*Phaseolus vulgaris* L.)

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INTRODUCTION

The common bean is a primary protein source in the diet of many low-income populations. Bean root rots occur in most bean fields. Genetic resistance to *Fusarium* root rot caused by *Fusarium solani* f.sp. *phaseoli* is polygenic and is strongly influenced by environmental factors that confound the expression and detection of resistance mechanisms. Response to selection for root rot resistance is slow due to genetic complexity of the trait that makes it difficult to evaluate. Indirect selection for *Fusarium root rot* resistance based on DNA markers linked to the resistance QTL would facilitate improvement of *Fusarium* root rot, given the limitations of field selection. The study is aimed at identify significant QTL- simple sequence repeat (SSR) marker associations, which could be used to facilitate marker-assisted selection for *Fusarium* root rot resistance in common bean.

OBJECTIVES

1. To identify polymorphic SSR marker loci between *Fusarium* susceptible bean varieties K132, K20 and resistant MLB-49-89A.
2. To map quantitative trait loci conditioning resistance to *Fusarium* root rot in common beans.

Fig. 1: Symptoms of *Fusarium* root rot

MATERIALS AND METHODES

Three parents i.e., K20, K132 and MLB 49-89A were used to identify polymorphic SSR marker loci between susceptible and resistant parents. K20 and K132 are susceptible to while MLB49-89A is resistant to *Fusarium* root rot. I*n-silico* analysis was done to identify SSR's likely to be linked with the QTL's conditioning resistance to *Fusarium* root rot. 28 SSR's were identified and tested for polymorphism.

To map the QTL that condition resistance to *Fusarium* root rot , two mapping populations (Fig. 2) of $F_{4:5}$ recombinant inbred lines were developed by single seed descent from F_2 to the F_4 generation.. The two populations K132 X MLB49-89A and K20 X MLB49-89A had 81 and 100 lines respectively. The two populations have been planted for *Fusarium* root rot evaluation in the screen house using lattice design with two replications. Wooden trays with *Fusarium solani* disease inoculum (Fig. 3) were used as blocks within replications. Polymorphic SSR's will be used to genotype the two populations at the polymorphic marker loci. The phenotypic score data from screen house evaluations and the genotypic data will be used for QTL analysis .

Fig.2: Development of $F_{4:5}$ recombinant inbred lines using single seed descent from F_2 to the F_4 generation.

Fig. 3: Experimental layout in screen house for phenotypic evaluation for Fusarium root rot. The soil in the tray is inoculated with *Fusarium solani*

RESULTS

Among the 28 SSR's loci screened for fragment size polymorphism , 11 (39.3%) were polymorphic between the resistant (MLB49) and susceptible (K20 and K132). Table 1 is the list of the identified polymorphic SSR's markers and their linkage groups. Figure 4 shows a gel picture of one of the polymorphic markers.

SSR Marker	Linkage group	Reference
PV-at006	B2	3
Pv gccacc001	B2	3
PVBR 87,	B3	2
PVBR 109	B3	2
PVBR 235	B3	2
PVBR 255	B3	2
BM 139	B2	1
BM 156	B2	1
BM159	B3	1
BM 172	B3	1
BM 175	B5	1

Table 1: Eleven SSR's that are polymorphic and linkage group to which they belong.

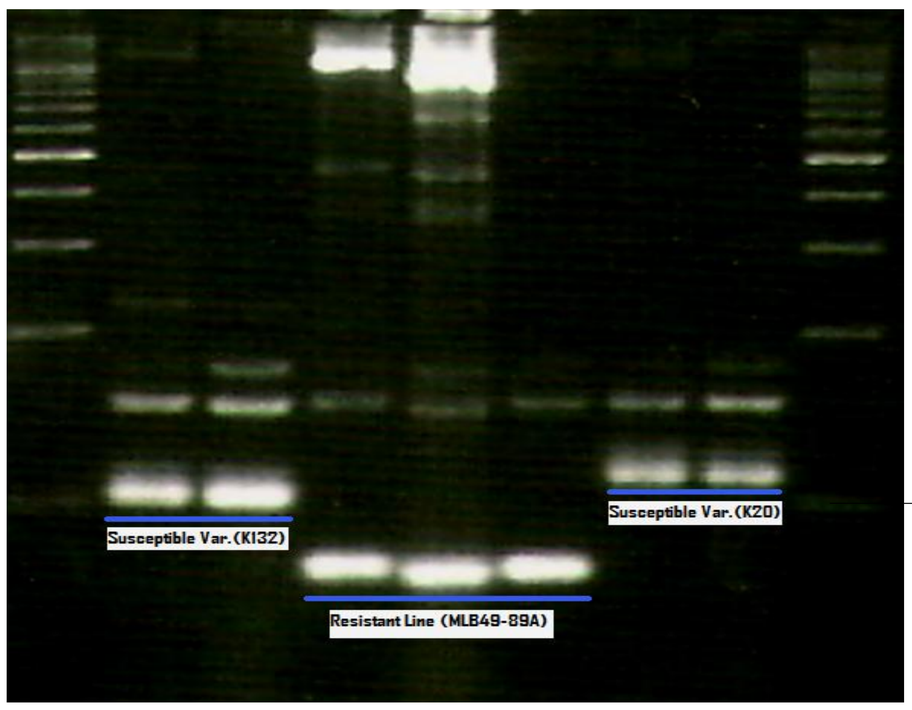

Fig. 4:SSR polymorphism between the resistant and susceptible Using SSR marker BM 172.

ONGOING WORK

The two mapping populations are being genotyped at the 11 polymorphic SSR loci and evaluated for *Fusarium* root rot resistance. The genotypic and phenotypic data is to be used for QTL analysis determine the number of QTL conditioning resistance to *Fusarium* root rot and their genomic locations

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