

Two Cycles of Recurrent Selection for Pyramiding Common Bacterial Blight Resistance in Common Bean

R.W. Duncan^a, S.P. Singh^b and R.L. Gilbertson^a

^a Department of Plant Pathology, University of California, Davis

^b University of Idaho, Kimberly, Idaho

Abstract

Common bacterial blight (CBB) is an important disease in common bean (*Phaseolus vulgaris* L.) and resistance is the best method of management.

Recurrent selection (RS) has not been used to improve resistance to CBB in common bean. Thus, the potential and number of recurrent selection cycles needed to increase CBB resistance is not known.

Here, we demonstrate that each cycle of RS increases the frequency of resistant genotypes and that parents with intermediate levels of resistance can be used to generate materials with a high level of CBB resistance.

Introduction

Common bacterial blight is one of the most important diseases of common bean and is caused by *Xanthomonas campestris* pv. *phaseoli* (*Xcp*) and *X. campestris* pv. *phaseoli* var. *tuscans* (*Xcpf*).

Most CBB resistance has been introgressed into common bean from tepary and scarlet runner bean.

More than 20 quantitative trait loci (QTL), most with minor effects have been associated with CBB resistance.

Recurrent selection (RS) has been used in common bean to improve plant architecture, seed yield and white mold resistance, but not for increasing levels of CBB resistance.

Thus, evaluating RS for determining the number of recurrent selection cycles necessary and the resistance levels needed in the selected parents will be useful for future CBB resistance breeding programs.

Objectives

Assess RS as a method to increase levels of CBB resistance in common bean and determine the effect of intermating genotypes with differing levels of CBB resistance.

Materials and Methods

An initial double-cross (Wilkinson 2 / DRK 2 // DRK 1 / VAX 3) for CBB resistance was made (C₀S₀ - Cycle 0, Selfing 0). Wilkinson 2 and VAX 3 are the donors of CBB resistance.

Trifoliolate leaves were inoculated with *Xcp* (1x10⁸ cfu/ml).

Plants with resistant [R, 1<4] or intermediate [I, 4<7] CBB scores (on a 1-9 scale, Figure 1), identified 21 days post-inoculation, were selected for intermating.

Resistant plants were intermated with other resistant plants (R x R) or intermediate plants (R x I), and intermediate plants were intermated (I x I) to produce three subpopulations within each RS cycle.

Two recurrent selection cycles were produced by intermating (C₀, C₁ and C₂) and each selfed twice (S₂), and then a third time (S₃). Each RS cycle had three subpopulations (R x R, R x I and I x I) (Figure 1).

Email Address: rwduncan@ucdavis.edu

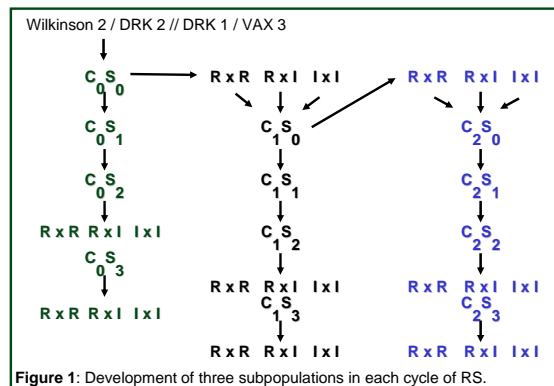


Figure 1: Development of three subpopulations in each cycle of RS.

The three subpopulations in each cycle of RS were organized in a randomized complete block design and evaluated for CBB resistance using direct selection.

The replicated comparison was also repeated in the S₃ generation.

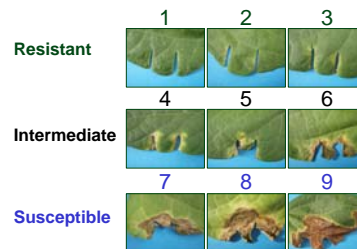


Figure 2: Disease symptoms of common bacterial blight on the 1-9 rating scale.

Results and Discussion

Each cycle of recurrent selection decreased the mean disease severity within each S₂ and S₃ subpopulation (Figures 3 and 4).

The mean disease severity decreased from the S₂ to S₃ generations because of increasing the level of homozygosity (Figures 3 and 4).

Figure 3. S₂ mean disease severity for common bacterial blight in a recurrent selection program with three subpopulations within each cycle (Letters denote significant LSD 0.05).

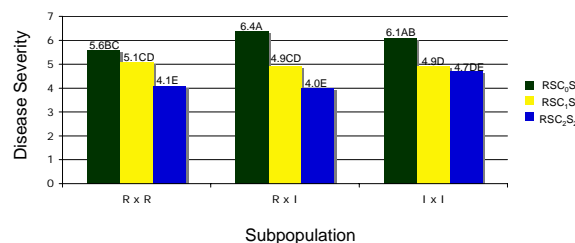
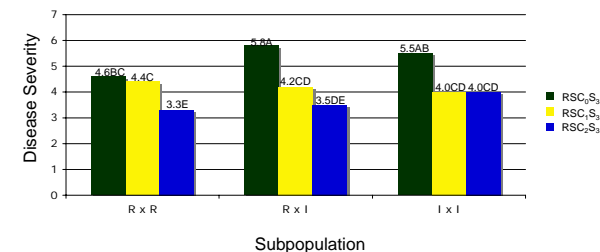


Table 1. The total number of recombinants with resistant (R), intermediate (I), and susceptible (S) mean common bacterial blight scores selected in the recurrent selection cycles RSC₀S₂, RSC₁S₂, RSC₂S₂, RSC₀S₃, RSC₁S₃ and RSC₂S₃.

Subpopulation	R x R	R x I	I x I
C ₀ S ₂	12I	1S, 6I	6I, 4S
C ₁ S ₂	3R, 8I, 1S	1R, 6I	3R, 7I
C ₂ S ₂	6R, 6I	3R, 4I	3R, 7I
C ₀ S ₃	2R, 10I	7I	2R, 7I, 1S
C ₁ S ₃	5R, 7I	4R, 3I	7R, 3I
C ₂ S ₃	9R, 3I	5R, 2I	5R, 5I

Figure 4. S₃ mean disease severity for common bacterial blight in a recurrent selection program with three subpopulations within each cycle (Letters denote significant LSD 0.05).



The effect of subpopulation was minimal due to the nature of CBB resistance and the effect of selfing (Figures 3 and 4).

In the S₂ generation, at least one RS cycle was necessary to produce a family with a CBB-resistant mean (Table 1).

The number of resistant families increased in each cycle of RS in all three subpopulations (Table 1).

The number of resistant families also increased during selfing from the S₂ to S₃ generations.

Conclusions

The results show that RS is a successful breeding methodology for improving resistance to CBB in a diverse double-cross population.

At least one cycle of recurrent selection is required to produce a family having a resistant mean CBB score.

Selfing was critical to recover the highest levels of CBB resistance and, thus, RS to the S₃ generation maybe required to produce enough resistant genotypes to allow for selection of desirable market classes.

With RS, it is possible to pyramid a high level of CBB resistance using parents with intermediate levels of CBB resistance.

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