Final Project Report to the NYS IPM Program,
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Title: Evaluation and enhancement of virus-resistant snap beans

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Abstract:

Aphid-transmitted viruses have caused devastating yield losses in snap bean production regions of NY in the last 5 years. Cucumber mosaic virus (CMV) appears in almost 100% of infected fields; however, bean yellow mosaic virus and clover yellow vein virus are also prevalent. Chemicals are ineffective, as aphids do not life-cycle on snap beans, leaving host-plant resistance as the only viable approach to managing these viruses.

Background and justification:

During 2001, yield-losses associated with aphid-transmitted bean viruses were incurred in several snap bean growing areas in western NY. These viruses were linked to the appearance of a new aphid vector in Eastern States, the Asian soybean aphid. These problems have persisted for the 2002-2005 seasons, with 2005 proving to be the most devastating yield losses. Left unchecked, the virus problems threaten the very future of snap bean production in NY State.

The most important virus appears to be cucumber mosaic virus (CMV), which is detected through ELISA in close to 100% of virus infected bean fields. Additionally, bean yellow mosaic virus (BYMV) and clover yellow vein virus (CYVV) are also prevalent, with alfalfa mosaic virus (AMV) and other potyviruses being detected to a lower extent.

Control of the viruses through pesticides is impractical, as the aphid vectors do not life cycle on snap beans, but move onto the crops from other plantings, such as, soybean or alfalfa. The only practical solution to these problems is the incorporation of host-plant resistance into snap beans. Resistance to CMV has been identified in scarlet runner bean accessions, and moved into common bean breeding lines. This resistance is controlled by at least 2 genes, and may be incomplete, but sufficient for protection of plants. BYMV resistance has been reported in Great Northern types, and CYVV resistance has been reported in cv. ‘Kentwood’ and in black bean cv. ‘Black Knight’ (the latter two viruses are reportedly controlled by single genes). Introgression of these resistance genes into a snap bean background is vital in helping to assure the future viability of the snap bean industry in NY State.

Objectives:

[1] To stabilize CMV resistance in a snap bean background.

[2] To transfer BYMV and CYVV resistance into a snap bean background.

[3] To field-test breeding lines and eventually pyramid resistance genes for the viruses.

Procedures:

[1] CMV resistance has been introgressed into a common bean background from two sources of scarlet runner bean. Materials derived are now determinate, and mostly have white flowers, as they are moved into a snap bean background. Combination of the two sources has increased the level of CMV resistance in lines that will be crossed to snap bean varieties to develop populations segregating CMV resistance, and to backcross CMV resistance into a snap bean type. Using greenhouses, it is possible to evaluate 4 generations of snap bean in 12 months, enabling accelerated introduction of virus resistance into snap beans. Plants are evaluated following a leaf-rub inoculation of the virus using a phosphate based buffer. Plants are rated for viral symptoms 7 and 14 days after inoculation for host-plant resistance. Standard breeding methodologies will be employed to transfer the resistance genes.

[2] BYMV and CYVV resistance genes have previously been reported in varieties including 'Kentwood' and 'Black Knight'. The resistance genes for both viruses are single gene, and in a common bean background, consequently, they can be transferred relatively quickly. Similar leaf-rub inoculations will be used on F2 populations derived from crosses between the resistant sources and snap bean. This will both confirm the single gene segregation of the virus resistance genes, and initiate transfer into a snap bean background. The two genes will potentially be combined and selected for in the same background using molecular markers identified for the genes.

[3] Resistant lines determined through greenhouse screenings and selection will be field tested for ability to yield normally in virus infected field plots. Eventually, the resistance genes to CMV will be combined with breeding lines exhibiting resistance to BYMV and CYVV in order to pyramid resistance to the viral diseases.

Results and discussion:

[1] Resistance to CMV was identified in scarlet runner bean accessions, and transferred into snap bean breeding lines following interspecific crosses with bridge line 5-593. Segregating populations indicate that this resistance is controlled by at least 2 genes, and is incomplete, but would likely be sufficient for protection of plants if transferred into commercial cultivars. Several interspecifc hybrids were recovered from crosses with ELISA negative scarlet runner bean accessions in 2003-2005, and have been used to make backcrosses to snap bean cultivars for transfer of CMV resistance. These populations have been evaluated for the control of CMV resistance from these sources, and to transfer the resistance into commercial snap bean types.

Backcross populations created from these crosses were developed and evaluated from several sources (Table 1). Two sources are being focused on for breeding line development and selection (PI 361328 and PI 273666). Combining the two sources has resulted in a higher level of resistance, indicating that not all the genes in the two populations were allelic. Populations have since been developed, inoculated and selected for CMV resistance in greenhouse trials, and lines have been identified that exhibit high levels of resistance to CMV when progeny tested (Table 2). An additional source has also been developed from a separate scarlet runner bean accession that is currently being combined. Breeding lines have now recovered determinacy, white flower traits, and are approaching a snap bean type. Preliminary work also demonstrated the direct effect of CMV in yield reduction of snap bean. Transfer into a commercial background could provide a significant contribution to preventing yield losses from this virus.

Table 1: Populations segregating CMV resistance

Label	Pedigree
8/05 C49 F_2	(Hystyle x {5-593 x [Hystyle x (5-593 x PI361328)]}) x [5-593 x (5-593 x PI273666)]
8/05 C50 F_2	[5-593 x (5-593 x PI273666)] x [Hystyle x ({Hystyle x [(5-593 x PI361328)]})]
8/05 C51 F_2	Cornell 501 x (Hystyle x {[(5-593 x PI3613238)]})
8/05 C52 F_2	Cornell 501 x (Hystyle x {[(5-593 x PI3613238)]})
8/05 C53 F_2	Cornell 501 x (Hystyle x {[(5-593 x PI3613238)]})
8/05 C54 F_2	Cornell 501 x (Hystyle x {5-593 x [Hystyle x (5-593 x PI361328)]})
8/05 C55 F_2	Cornell 501 x [5-593 x (5-593 x PI273666)]
8/05 C56 F_2	Cornell 501 x [5-593 x (5-593 x PI273666)]

Table 2: Pedigrees of CMV resistant breeding lines developed in 2006

Line	Background
CMVR1-3 x Hystyle	(Hystyle x {5-593 x [Hystyle x (5-593 x PI361328)]}) x [5-593 x (5-593 x PI273666)]/Hystyle
CMVR1-5 x Hystyle	(Hystyle x {5-593 x [Hystyle x (5-593 x PI361328)]}) x [5-593 x (5-593 x PI273666)]/Hystyle
CMVR1-9 x Hystyle	(Hystyle x {5-593 x [Hystyle x (5-593 x PI361328)]}) x [5-593 x (5-593 x PI273666)]/Hystyle
CMVR8-2 x Hystyle	(Hystyle x {5-593 x [Hystyle x (5-593 x PI361328)]}) x [5-593 x (5-593 x PI273666)]/Hystyle
CMVR15-5 x Hystyle	[5-593 x (5-593 x PI273666)] x Hystyle x ({Hystyle x [(5-593 x PI361328)]})/Hystyle
CMVR21-5 x Hystyle	[5-593 x (5-593 x PI273666)] x Hystyle x ({Hystyle x [(5-593 x PI361328)]})/Hystyle
CMVR28-3 x Hystyle	[5-593 x (5-593 x PI273666)] x Hystyle x ({Hystyle x [(5-593 x PI361328)]})/Hystyle
CMVR28-8 x Hystyle	[5-593 x (5-593 x PI273666)] x Hystyle x ({Hystyle x [(5-593 x PI361328)]})/Hystyle
CMVR30-4 x Hystyle	[5-593 x (5-593 x PI273666)] x Hystyle x ({Hystyle x [(5-593 x PI361328)]})/Hystyle
(CMVR8 x Hystyle)-2 x Hystyle	(Hystyle x {5-593 x [Hystyle x (5-593 x PI361328)]}) x [5-593 x (5-593 x PI273666)]/Hystyle
(CMVR8 x Hystyle)-3 x Hystyle	(Hystyle x {5-593 x [Hystyle x (5-593 x PI361328)]}) x [5-593 x (5-593 x PI273666)]/Hystyle
(CMVR18 x Hystyle)-1 x Hystyle	[5-593 x (5-593 x PI273666)] x Hystyle x ({Hystyle x [(5-593 x PI361328)]})/Hystyle
(CMVBU5-8) x Hystyle	[5-593 x (5-593 x PI273666)] x Hystyle x ({Hystyle x [(5-593 x PI361328)]})/Hystyle
(CMVBU8-2) x Hystyle	[5-593 x (5-593 x PI273666)] x Hystyle x ({Hystyle x [(5-593 x PI361328)]})/Hystyle
(CMVBU8-6) x Hystyle	[5-593 x (5-593 x PI273666)] x Hystyle x ({Hystyle x [(5-593 x PI361328)]})/Hystyle
{(C39xC37)F3 6-4} x Hystyle	[{Hystylex(5-593xPI361538)}⊗⊗] x [{5-593x(5-593xPI317596)}⊗⊗]/Hystyle
{(C39xC37)F3 51-1} x Hystyle	[{Hystylex(5-593xPI361538)}⊗⊗] x [{5-593x(5-593xPI317596)}⊗⊗]/Hystyle
{(C39xC37)F3 51-4} x Hystyle	[{Hystylex(5-593xPI361538)}⊗⊗] x [{5-593x(5-593xPI317596)}⊗⊗]/Hystyle
{(C39xC37) F3 64-3} x Hystyle	[{Hystylex(5-593xPI361538)}⊗⊗] x [{5-593x(5-593xPI317596)}⊗⊗]/Hystyle

[2] BYMV resistance has been reported in Great Northern types and previously transferred into breeding lines including B-21 and SP-17B. CYVV resistance has been reported in the cultivars 'Kentwood', 'Clipper', 'Black Knight'. Crosses were made between all five of these sources and 'Hystyle' for the transfer of resistance into snap bean. Separate populations were developed for BYMV and CYVV, BYMV appearing to segregate as a single dominat gene in F_2 populations, and CYVV as a single recessive gene. Selections were made from these segregating populations and were crossed to 'Hystyle'. Additionally backcrosses of the F_1 hybrids were created, and self-pollinated to enable evaluation of resistance in segregating populations. Resistance to these viruses will be selected and backcrossed into 'Hystyle' as a recurrent parent, where they will then be combined for pyramiding with CMV resistant lines. CYVV has been associated with the internal necrosis of snap beans, often referred to as 'chocolate pod'. BYMV is a perrenial problem in common beans. Incorporation of these resistance genes into snap bean will make a significant contibution to stabilizing yields with CMV resistance.

[3] CMV resistant breeding lines did not exhibit traits that were homologous enough to have effective field evaluation with commercial cultivarsin 2006. It is anticipated that side by side field trials will be possible in 2007 or 2008, at which point the advanced breeding lines will be close to commercial snap bean type. CYVV and BYMV resistance genes introgressed separately will be combined with the CMV resistant materials at this point (parallel backcrossing prior to gene pyramiding providing a more efficient approach to combinining virus resistance genes in snap bean). The losses associated with CMV have been estimated at $1million per year since 2001 in processing snap bean alone. The incorporation of this resistance into commercial snap beans for New York State will contibute significantly to yield stability and viability of snap bean production in the state.

Project Location:

Geneva, NY