PROGRESS IN THE IDENTIFICATION OF GENETIC VARIATION FOR TOLERANCE TO *CUCUMBER MOSAIC VIRUS* IN *PHASEOLUS VULGARIS* L.

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INTRODUCTION

Wisconsin continues to be the primary producer of processing snap beans in the U.S., however, beginning in 2000, dramatic increases in aphid-transmitted viruses have adversely impacted late-season snap bean production in the state. Based on statewide survey data collected in Wisconsin year-to-year fluctuations in aphid and virus pressure and in the number of species present have occurred (1;2;3). Coincidently, the combination of *cucumber mosaic virus* (CMV) and the soybean aphid (*Aphis glycines* Matsumura) vector has been detected each year in Wisconsin since 2000. Symptoms caused by CMV include leaf blistering, interveinal chlorosis, off-colored and twisted pods, plant stunting, and flower abortion. Snap bean cultivar evaluation trials have concluded that there are currently no commercial varieties available with resistance to CMV although some tolerance has been observed (4,5,6). We have screened germplasm for resistance to CMV and have identified Plant Introductions (PI) with tolerance to CMV.

A recombinant inbred line (RIL) population (H2-RIL) derived from a cross between a selection within PI 619437 (selection 2313.9.1000 – hereafter TL for tolerant line) and Hystyle (susceptible to CMV) has been developed and is currently being field evaluated to determine the inheritance of tolerance to CMV.

MATERIALS AND METHODS

Germplasm Evaluation & Parent Selection - An array of germplasm including PI accessions from the *Phaseolus vulgaris* L. core and reserve collections, several RIL populations as well as commercial snap bean cultivars were screened in replicated field trials from 2002-2007 (Table 1). Repeatable variation in symptomatology was observed in all years and locations with the exception of 2007. In 2002, individual plants selections were made within three PI accessions (PI 557487, PI 594325 and PI 619437) based on a symptomless phenotype and a negative CMV titer and screened repeatedly in the greenhouse in 2002 and 2003 to determine if the selections were resistant to CMV, tolerant or escapes. These selections were also field evaluated in 2004 and 2005 in replicated trials at Hancock Agricultural Research Station, Hancock, WI and in cooperation with Dr. Walt Stevenson, UW-Madison Dept. of Plant Pathology in three production field trials throughout Wisconsin with a previous history of high virus pressure (5,6). With the exception of 2007, TL remained symptomless over years and locations and was crossed with MV185, a commercial snap bean tolerant to CMV and to Hystyle to create two RIL populations. These populations (M2-RIL and H2-RIL) were screened in replicated trials in 2006 and 2007, respectively. Accession PI 309881 was planted each year as the resistant check (hereafter RL for resistant line).

Symptomatology & ELISA - Visual symptomatology ratings were taken twice each growing season. Composite leaf samples were harvested from each plot at approximately 60 days after planting and screened using Enzyme Linked Immunosorbant Assay (ELISA) for the presence of CMV and *alfalfa mosaic virus*.

RESULTS & CONCLUSIONS

Unlike previous years, both RL and TL had virus symptoms and a positive CMV titer in 2007. The conflicting results from previous years and 2007 must be studied further. Resistance and tolerance may have been defeated due to a new strain of CMV, excessive inoculum and aphid pressure or environmental conditions such as temperature. Nevertheless, breeding for tolerance to CMV in snap beans may be an acceptable strategy until resistant varieties can be developed.

Table 1. Summary of germplasm screened from 2002-2007 and corresponding results.

Year	Germplasm Evaluated	Results
2002	▪ *170 P. vulgaris PI accessions previously reported as having a degree of virus resistance to an array of viruses* ▪ 60 Eagle x Puebla 152 RIL (EP-RIL) ▪ 10 commercial cultivars	▪ *Within the 170 PI accessions, seed was harvested from 77 individual plant selections having a symptomless phenotype and a – CMV titer. These selections were screened in the greenhouse and narrowed to 32.* ▪ Repeatable variation in EP-RIL for aphid preference ▪ 10 commercial cultivars with a +CMV titer and virus symptoms
2003	▪ **423 PI accessions from *P. vulgaris* core collection & commercial checks** ▪ *32 symptomless selections from 2002* ▪ *RL as resistant check*	▪ **16 of 423 accessions and MV185 with a symptomless phenotype and all 16 with a +CMV titer** ▪ *32 selections narrowed to 12 (TL symptomless and a +CMV titer)* ▪ *RL symptomless and a –CMV titer*
2004	▪ **16 symptomless PI accessions from 2003 core collection & commercial checks** ▪ *12 symptomless selections from 2003* ▪ *RL as resistant check*	▪ **All 16 PI accessions and MV185 symptomless and a +CMV titer** ▪ *4 of 12 selections symptomless and a +CMV titer at 4 WI locations (TL symptomless and a +CMV titer)* ▪ *RL symptomless and a – CMV titer*
2005	▪ **200 random PI accessions from the *P. vulgaris* reserve collection** ▪ 32 pre-1950 commercial cultivars ▪ **16 symptomless core collection accessions from 2004 & commercial checks** ▪ *Of the 12 selections from 2004, TL with best symptomatology ratings to date* ▪ *RL as resistant check*	▪ **All reserve collection accessions with a +CMV titer and visual symptoms** ▪ All pre-1950 cultivars with a +CMV titer and visual symptoms ▪ **2 of 16 PI core collection accessions with better than or the same virus symptomatology ratings as MV185 at 4 WI locations** ▪ *TL symptomless and a +CMV titer at 4 WI locations, chosen as parent of RIL populations* ▪ *RL symptomless and a –CMV titer*
2006	▪ MV185 x 2313.9.1000 (M2-RIL) (Symptomless x Symptomless) 131 F3 families, parents and checks ▪ *RL as resistant check*	▪ Repeatable variation in M2-RIL for virus symptomatology ▪ *Selection TL symptomless and a +CMV titer* ▪ *RL symptomless and a –CMV titer*
2007	▪ Hystyle x 2313.9.1000 (H2-RIL) (Susceptible x Symptomless) – 90 F_3 families, parents and checks ▪ *RL as resistant check*	▪ No repeatable variation in H2-RIL for symptomatology ▪ *Selection TL with symptoms and a +CMV titer* ▪ *RL with symptoms and a +CMV titer*

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LITERATURE CITED

1) German, T.L., A. Thompson, and D.K. Willis. 2004. Statewide distribution of virus problems on processing beans. *In*: Proceeding of the 2004 Wisconsin Fertilizer, Aglime & Pest management Conference. 43:291-293.
2) Grau, C.R., A. Mondjana and W.R. Stevenson. 2001. Status of virus-like problems on processing snap beans in Wisconsin during 2000. *In:* 2001 Midwest Food Processors Association, Inc. Processing Crops Manual and Proceedings. 13:43-48.
3) Grau, C.R., W.R. Stevenson and A.M. Mondjana. 2002. Viruses causing losses on processing beans in the Midwest. *In:* 2002 Midwest Food Processors Association, Inc. Processing Crops Manual and Proceedings. 14:15-23.
4) Stevenson, W.R. and C.R. Grau. 2004. Evaluation of processing bean cultivars and advanced breeding lines for reaction to the current virus complex. *In:* 2004 Midwest Food Processors association, Inc. Processing Crops Manual and Proceedings. 16:43-50.
5) Stevenson, W.R., B. Lockhart and C.R. Grau. 2005. Evaluating snap bean cultivars for their reaction to aphid transmitted viruses. In: 77th Annual Convention and Processing Crops Conference Proceedings CD.
6) Stevenson, W.R., C.R. Grau and T.L. German. 2006. Reaction of snap bean cultivars and advanced breeding lines to aphid transmitted viruses. In: 78th Annual convention and Processing Crops Conference Proceedings CD.