DEVELOPMENT OF ROOT-KNOT NEMATODE-RESISTANT SUGARBEET

M. H. Yu

U.S. Department of Agriculture, Agricultural Research Service, U.S. Agricultural Research Station, Salinas, California 93905, U.S.A.

ABSTRACT

Sugarbeet, *Beta vulgaris* L., is a favored host of *Meloidogyne* spp. Host-plant resistance to multiple species of root-knot nematodes was not found in the cultivated sugarbeet but was identified from wild *maritima* beets. The resistance has been introgressed into sugarbeet genotypes. Several breeding populations were planted in heavily infested field plots. Preliminary evaluations indicated that about 77% of plants in resistant families and 44% in backcrossed populations, produced healthy roots while the rest were with gall symptoms. In comparison, none of the susceptible control plants were free from galling; one-third of them died. Positive results were demonstrated by the improved taproot conformation and root weights. A phosphoglucomutase (PGM) isozyme marker for Mi-1 *Beta* and a cleaved amplified polymorphic sequence (CAPS) marker for M66 *Beta* were recently identified. The use of marker-assisted selections may facilitate sugarbeet root-knot nematode resistance breeding. Additional improvements on the breeding materials are needed to develop an elite sugarbeet cultivar.

INTRODUCTION

Root-knot nematodes, *Meloidogyne* spp., are important sugarbeet (*Beta vulgaris* L.) pathogens, which are difficult to control. These pests induce root gall symptoms that could severely limit sugarbeet yield and quality. Infestations may be accompanied by serious root rot, resulting from secondary invasion by other soil-borne pathogens, such as bacteria and fungi. Management of root-knot nematodes in sugarbeet fields is challenging because of the nematodes' wide host range and increasing restrictions on nematicide applications. At present, due to lack of highly effective and environmentally safe control measures, development of nematode resistant sugarbeet varieties has become increasingly important. The source germplasm with resistance to *M. incognita* (Kofoid and White) Chitwood Race 1 was discovered from noncultivated *B. vulgaris* ssp. *maritima* (L.) Arcang (sea beet) accessions (Yu, 1995). This resistance was determined to be effective against multiple species of *Meloidogyne*, such as *M. incognita*, *M. javanica* (Treub) Chitwood, *M. arenaria* (Neal) Chitwood, *M. hapla* Chitwood, *M. chitwoodi* Golden et al., and *M. fallax* Karssen, that have been investigated (Yu, et al., 1999). The characteristics of resistance to multiple species of root-knot nematode may facilitate sugarbeet breeding efficacy and increase their breeding value.

MATERIALS AND METHODS

Introgression of root-knot nematode resistance from wild beets to sugarbeet was carried out through hybridization and backcrossing to sugarbeet in the greenhouse. Selection against bolting habit (annuals), susceptibility to other pathogens, and improved root morphology was done from field plantings. Due to differential genotypic backgrounds, proportions of resistant progeny among breeding populations varied considerably.

All greenhouse processed breeding materials went through resistance screening. Seedlings were inoculated at four- to six-leaf stage with 800 newly hatched second-stage juveniles (J2) per plant. Seven days later, an additional 400 J2 juveniles were applied. The inoculated plants were cultured at 24 to 28 °C above heat pads, and examined for root gall and protuberance formations at about 40 days after the final inoculation. Individual plants with 0 (zero) or fewer than 10 gall (<2 mm diameter) counts were classified as resistant, and those with 11 or greater galls and protuberances observed were considered susceptible (Yu, 1995). The time consuming and labor intensive J2 inoculation test procedures, however, may soon be replaced by marker-assisted selection (MAS) methods. Field trials on the resistant sugarbeet breeding populations were conducted under heavily infested or noninfested soil conditions.

RESULRS AND DISCUSSION

The resistance from *B. maritima* suppressed *Meloidgyne* spp. reproduction, i.e., it reduced root gall formation in sugarbeet. Resistance was normally transmissible to sugarbeet through pollen, but the wild beet carried several undesirable characteristics. Nonetheless, promising sugarbeet plants with stable resistance transmission and improved root shape appeared from greenhouse and field evaluations. Agronomic features of sugarbeet crop were gradually restored into progeny genotypes. The intensity of sprangled root structures and easy bolting habits decreased with selection pressure and as the number of breeding generations increased. Sugarbeet-like taproots eventually developed.

The growth and production performance of several resistant sugarbeet breeding populations were observed in field plots infested with either *M. incognita* or *M. javanica* in Irvine and Parlier, and noninfested field plots in Salinas, California. The preliminary results indicated that under nematode infested and prolonged high temperature conditions, about 77% of progeny from inter-pollinated resistant plants produced healthy, non-galled taproots at harvest. In backcrossed populations, approximately 44% of plants expressed resistance. In both resistance-segregating groups, almost one-half of infected plants rotted or died. In comparison, none of the susceptible control plants were free from gall symptoms (i.e., 100% infected), in which one-third of plants died.

These results exhibited the strength and inheritance of root-knot nematode resistance transferred to sugarbeet. Positive results were demonstrated by the improved taproot conformation and root weights. Several root-knot nematode-resistant *Beta* germplasm lines have been developed and released, e.g., M6-2 and M1-3 (Yu, 2002). Resistant, homozygous cultures could enable sugarbeet

growers to plant them as trap crops, and researchers to expand their resistance breeding and biotechnological applications without the need for testing. The availability of wide variations in yielding capability among different breeding populations will provide opportunities for further sugarbeet improvements.

In this study, two series of root-knot nematode resistant sugarbeet genotypes, Mi-1 and M66, were generated. Both series of resistance seem to carry the same spectrum and strength to *Meloidogyne* spp. Phosphoglucomutase (PGM) was found to be a potentially useful isozyme marker of resistance in Mi-1 *Beta* and derived lines in starch gel electophoresis. Seven banding patterns were produced. All susceptible plants shared the banding pattern of the resistance strains, except for a single PGM band (Yu, et al., 2001). However, this isozyme marker was absent in the M66 series of sugarbeet. Molecular genetic tagging of resistance in M66 *Beta* was investigated using a random amplified polymorphic DNA (RAPD) technique. A cleaved amplified polymorphic sequence (CAPS) marker designated Nem06 that co-segregated with resistance to root-knot nematode was recently identified. Computer-assisted translation and comparison with sequences in public databases indicates that the marker DNA sequence encodes a protein with high sequence similarity to a plant transcription factor (Weiland and Yu, 2003). Application of marker-assisted selections should facilitate the breeding of sugarbeet resistance to root-knot nematodes.

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