Resistant Turfgrasses for Improved Chinch Bug Management on Golf Courses

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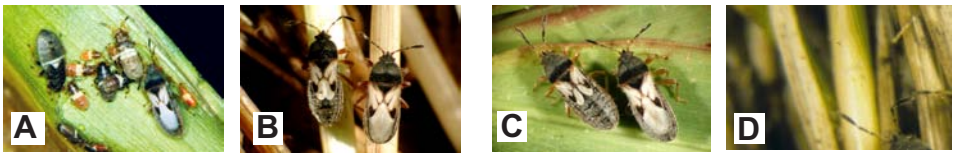
Objectives:

1. Evaluate selected cool- and warm-season turfgrasses for resistance to chinch bugs in the *Blissus* complex.
2. Investigate the biochemical and physiological responses of buffalograss to chinch bug feeding.
3. Identify genes conferring resistance to chinch bugs.

Start Date: 2003
Project Duration: five years
Total Funding: $50,000



The Blissus *complex:* B. l. leucopterus *(A),* B. l. hirtus *(B),* B. insularis *(C), and* B. occiduus *(D).*

The overall goal of this research is to identify chinch bug-resistant turfgrasses, investigate the mechanisms of this resistance, and identify specific genes contributing to the resistance. This information is fundamentally important for formulating plant breeding strategies and subsequently developing chinch bug-resistant germplasm through conventional breeding and biotechnological techniques. Know-ledge of specific resistance mechanisms would be valuable for identifying biochemical and physiological markers for use in germplasm enhancement programs, and for characterizing plant defense strategies to insect feeding.

Of the 100 buffalograss genotypes evaluated in greenhouse and field studies, four have been categorized as highly resistant ('Prestige', NE 184, NE 196, and NE PX 3-5-1) and 24 as moderately resistant. Of the resistant buffalograsses studied, 'Prestige' exhibited the highest level of resistance even though it often became heavily infested with chinch bugs. Subsequent choice and no-choice studies characterized the four resistant buffalograsses as tolerant.

Studies have also been conducted to determine if there is a relationship between chinch bug resistance and ploidy level. Fifteen diploid, tetraploid, and hexaploid genotypes have been evaluated for chinch bug resistance under greenhouse conditions. The genotypes 'Density' (diploid), 196 (hexaploid), and 'Legacy' (hexaploid) were identified as moderately resistant, whereas, NE 2990 (tetraploid) and NE 2838 (hexaploid) were moderately susceptible. No correlation was found between level of chinch bug resistance and ploidy level. A diploid population is being developed from crosses between 'Density' (diploid female) and NE 2781 (diploid male). The parents and progeny from this population will be used to develop a buffalograss genetic linkage map to identify genetic markers associated with chinch bug resistance.

The impact of chinch bug feeding on the physiological responses of resistant and susceptible buffalograss has been evaluated through gas exchange and chlorophyll fluorescence measurements at specific time intervals using established procedures. These studies have demonstrated that resistant plants can generate energy for recovery from chinch bug feeding. Susceptible plants appear unable to maintain compensatory photosynthesis and, as a consequence, suffer substantially more tissue damage from chinch bug feeding.

Enzyme kinetics studies documented a loss of catalase activity in susceptible buffalograsses in response to chinch bug feeding, while resistant buffalograsses showed an increase in peroxidase activity. These findings support our working hypothesis that an initial plant defense response to chinch bug feeding is to elevate the levels of specific oxidative enzymes, such as peroxidase, to help detoxify peroxides that accumulate as a result of plant stress. Native gels stained for peroxidase have identified differences in the isozyme profiles of resistant and susceptible buffalograsses.

A final objective of this research was to identify specific genes conferring resistance to *B. occiduus* through the development of cDNA subtractive libraries for resistant and susceptible buffalograsses. Thirty-two transcripts were found to be differentially expressed between resistant and susceptible buffalograsses in response to chinch bug feeding. These differentially expressed genes were classified into the following categories: photosynthesis, signal transduction, and defenses against stress and pathogens.

From these 32 transcripts unique to the resistant buffalograss, three transcripts (catalase, GRAS, and glutathione-S-transferase) were selected for qRT-PCR analysis to document the expression of these genes in response to chinch bug feeding over time. Results from the qRT-PCR assays documented the up-regulation of these three defense-related transcripts and provide insights into possible pathways of plant resistance mechanisms during the continuum of the tolerance response.

Summary Points

- Warm-season grasses with resistance to chinch bugs in the *Blissus* complex have been identified.
- Commercial production of 'Prestige' provides consumers with a high quality buffalograss with improved chinch bug resistance.
- Documenting gas-exchange and oxidative enzyme responses specific to tolerant buffalograsses will provide insights into the biological pathways impacted by aphid feeding and help to elucidate plant tolerance mechanisms.
- Subtractive cDNA buffalograss libraries will allow comparison of gene expression between tolerant and susceptible buffalograsses and serve to identify genes differentially expressed in response to chinch bug feeding.
- Ultimately, this research will facilitate development of improved turfgrasses with resistance to chinch bugs.