

Bluegrass billbug feeding response to perennial triticeae grasses

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Abstract

In a 4-year field study, 25 perennial triticeae grasses, representing a wide range of genomes and genome combinations, were evaluated as potential hosts for the bluegrass billbug (*Sphenophorus parvulus* Gyllenhal [Coleoptera: Curculionidae]). Root-sample data suggested that Russian wildrye (*Psathyrostachys juncea* [Fischer] Nevski) was unsuitable for billbug reproduction. Numbers of immatures varied significantly among remaining entries. Rhizomatous entries were more tolerant of billbug injury than caespitose entries. Plant mortality rates were frequently 50% or higher for self-pollinated caespitose entries with the SH genome complement (*Elymus* spp.). Losses to billbugs among the remaining species, particularly those with the J, N, and P genomes, were insignificant. Billbugs did not discriminate between native and introduced grasses, as resistant and susceptible entries were identified in both groups. The results obtained here may aid in selecting triticeae grasses for reseeding in areas where billbugs have damaged stands in the past.

Key Words: *Acremonium* endophyte, Curculionidae, rangeland insects, *Sphenophorus parvulus*

Improved range grasses are desirable for revegetating degraded rangelands in the western U.S. Perennial triticeae species (wheatgrasses, wildryes, and their relatives) and interspecific hybrids are continually being evaluated. Superior cultivars are usually chosen on the basis of forage production and seedling establishment in semiarid environments. While revegetation success continues to improve, the genetic potential for insect resistance in many forage grasses remains underutilized. An alternative to the breeding of insect-resistant germplasm may be to use plant materials that are inherently resistant.

In the past little emphasis has been placed on plant diversity in revegetation projects. When rangelands are converted to monocultures by seeding operations, insect outbreaks may be favored. For example, monocultures of grass such as crested wheatgrass (*Agropyron* spp.) have been heavily damaged by a black grass bug (*Labops hesperius* [Hemiptera: Miridae Uhler]) over large areas of the Intermountain region (Bohning and Currier 1967, Jensen 1971).

In the last 10 years the bluegrass billbug (*Sphenophorus parvulus* Gyllenhal [Coleoptera: Curculionidae]), a common pest on lawn grasses throughout much of the northern half of the U.S. (Tashiro and Personius 1970, Kindler and Kinbacher 1975, Lindgren et al. 1981), has caused considerable damage in evaluation nurseries composed of range wheatgrasses (Asay et al. 1983). Bluegrass billbugs are not restricted to *Poa* spp. as hosts, as their name implies, for they have been reported on more than 40 other grasses (Satterthwait 1931, Ahmad and Funk 1983, Asay et al. 1983, Johnson-Cicalese and Funk 1990). These insects are often

associated with quackgrass (*Elytrigia repens* [L.] Nevski) (Nielson 1985) and are commonly found along roadsides and in ditchbanks where quackgrass is present. Research has focused primarily on the billbug's impact on turf grasses, but its seasonal history on range grasses has also been documented (Hansen 1987).

Adult insects are dark gray and 6 to 8 mm long. Females are slightly larger than males. Like most weevils, billbugs have chewing mouthparts located at the end of the prominent snout. In the spring adult females lay eggs inside the grass stem near the crown. After hatching, the white larvae feed inside the stems and migrate to the crown and root system, where they feed on the roots and rhizomes for several weeks and sever many culms. Because of their limited mobility the legless larvae usually complete their development on a single plant, although multiple plant feeding may occur in dense stands where roots of adjacent plants intertwine. Most of the larvae produced in a season will complete their life cycle by fall, but the new adults will generally remain inactive in the soil until the following spring. Infested plants appear stunted and drought-stressed despite adequate soil moisture. The characteristically dry severed stems of damaged plants are easily pulled from the soil. Host grasses may be killed within 1 to 2 years after an infestation or they may simply exhibit poor vigor for several seasons. Billbugs are often accidentally distributed when soil and sod are moved by man. Natural dispersal is probably quite slow as the adults rarely fly.

Our objective was to compare bluegrass billbug survival and reproduction on 25 perennial triticeae grasses representing a broad range of genomic compositions. The genomic system of classification groups species into genera with a similar genomic formula (Barkworth and Dewey 1985). The genomic formula consists of letters, each representing a diploid set of 7 pairs of chromosomes. Genomes of 2 species are assigned the same letter if they show meiotic pairing in the interspecific hybrid, but different letters if pairing is minimal. Consideration of genomic formulae has led to a recent reclassification of perennial triticeae grasses that is based on phylogenetic considerations as well as traditional morphological characteristics. Our second objective was to compare plant mortality rates among the grass entries after 4 years of billbug infestation.

Methods

Twenty-five perennial triticeae entries, including experimental species and hybrids, were selected on the basis of genomic composition and economic importance (Table 1). Plants were grown from seed in a greenhouse and were transplanted to the field 3 km south of Logan, Ut., at 4 months of age in May 1986. This location was chosen because a natural infestation of billbugs was already present. Plants were spaced on 1.0-m centers to ensure that billbug larvae would develop on a single plant. Each plot consisted of 10 plants of an entry. Plots were arranged in a randomized complete

Table 1. Perennial triticeae grasses used in the bluegrass billbug feeding study.

Entry	Origin ¹	Genomic formula ²	Growth habit ³
<i>Agropyron cristatum</i> (L.) Gaertner cv. Fairway	I	P	C
<i>A. desertorum</i> (Fischer ex Link) Shultes cv. Nordan	I	PP	C
<i>A. cristatum</i> X <i>A. desertorum</i> cv. Hycrest	I X I	PP	C
<i>Elymus canadensis</i> L.	N	SH	C
<i>E. caninus</i> (L.) L.	I	SH	C
<i>E. fibrosus</i> (Schrenk) Tzvelev	I	SH	C
<i>E. glaucus</i> Buckley	N	SH	C
<i>E. lanceolatus</i> (Scribn. and Smith) Gould cv. Critana	N	SH	R
<i>E. lanceolatus</i> ssp. <i>wawawaiensis</i> ⁴ cv. Secar	N	SH	C
<i>E. sibiricus</i> L.	I	SH	C
<i>E. trachycaulus</i> (Link) Gould ex Shinnery cv. San Luis	N	SH	C
<i>Elytrigia repens</i> (L.) Nevski X <i>Pseudoroegneria spicata</i> (Pursh) A. Löve RS-1	I X N	SSX ⁵	R
<i>Et. repens</i> X <i>P. spicata</i> RS backcross	I X N	SSX	R
<i>Et. repens</i> X <i>P. spicata</i> RS-MC	I X N	SSX	R
<i>Et. repens</i> X <i>P. spicata</i> RS-N	I X N	SSX	R
<i>Et. repens</i> X <i>A. desertorum</i> RD	I X I	PPSSX	R
<i>Leymus cinereus</i> (Scribner and Merrill) A. Löve cv. Magnar	N	NNXX	C
<i>Pascopyrum smithii</i> (Rybd.) A. Löve cv. Rosana	N	SHNX	R
<i>Psathyrostachys juncea</i> (Fischer) Nevski cv. Bozoisky-Select	I	N	C
<i>Pseudoroegneria spicata</i> ssp. <i>inermis</i> (Scribn. & J.G. Smith) A. Löve cv. Whitmar	N	S	C
<i>P. spicata</i> P-7845	N	SS	C
<i>P. spicata</i> X <i>E. lanceolatus</i> SL	N X N	SSH	R
<i>P. stipifolia</i> (Czern. ex Nevski) A. Löve (2n = 14)	I	S	R
<i>P. stipifolia</i> (2n = 28)	I	SS	R
<i>Thinopyrum intermedium</i> (Host) Barkw. & D.R. Dewey cv. Greenar	I	SJJ	R

¹N = Native, I = Introduced.

²Each letter represents a distinct genome of 7 pairs of chromosomes.

³C = Caespitose, R = Rhizomatous.

⁴Latin binomial not yet published.

⁵X indicates an unidentified genome.

block design with 4 replications as blocks. Soil between plants was cultivated as necessary to control weeds and prevent rhizomatous entries from spreading to adjacent plots. All plots were mowed and raked in the fall. Adult billbugs were observed feeding on the test plants within 1 month after planting.

Data collection began in October 1987. A 10 × 10 × 20-cm deep soil-root sample was dug from each of 2 plants randomly selected per plot in all 4 replications. Soil was separated from the roots and sieved through a 3-mm wire screen to isolate billbug life stages. Pupae, larvae, and adults from the current year, all designated as immatures, and adults from previous seasons were counted. Current year adults were identified by their reddish-brown color and clean appearance while previous season adults were grey in color and exhibited exoskeletal wear. This sampling procedure was repeated in October 1988 and September 1989. Analysis of variance was used to compare numbers of adult and immature billbugs among entries. Replications were considered random and entries fixed. Means were separated using the Bayes L.S.D. test (Smith 1978) and were deemed significantly different at k ratio = 100. In October 1989 billbug-related plant mortalities were determined in each plot, and the mean percentage of dead plants was calculated over the 4 replications.

Results and Discussion

The grasses used in this study were transplanted into a cultivated field that was previously a stand of hybrid wheatgrass, *Elytrigia repens* × *Agropyron desertorum* (Fischer ex Link) Shultes (RD). This hybrid served as an adequate host for the bluegrass billbug; many adult insects were present at the beginning of the study. Billbug distribution among test plants varied considerably over the 3-year sampling period. The feeding adults did not appear to be conditioned to the RD hybrid, which was also one of the test entries. Although adults and immatures were collected from 22 of the 25 entries, over 50% of the total number of billbugs at the fall 1987 sampling were from RS-1, RS-MC, 'San Luis' slender wheat-

grass, *E. sibiricus* L., and *E. caninus* (L.) L. (Table 2). Billbug reproduction was very low in the plots during 1988, possibly due to the dry spring and summer. Only a single larva was found that year over all entries in the experiment (data not shown). Most of the adults collected in 1988 were of the 1987 generation, also suggesting a current year reproduction failure. The effect of April-June precipitation on billbug reproductive success is unclear, particularly in the arid western states. Short growing seasons in dry regions may limit the range of this insect. In 1989 billbug numbers increased to 1987 levels but their distribution among entries differed from 1987. Sampling data from 1987 probably provided the best indication of host preference as equal numbers of healthy plants were available to the insects. In the third year of the study, billbug distribution among entries was no longer strictly indicative of host preference. By this time differences in plant availability resulting from differential mortality from billbug damage were present.

Low numbers of immatures collected from some entries suggest that these grasses are not suitable for billbug development. For example, larvae were not collected from 'Bozoisky-Select' Russian wildrye during the 3-year sampling period, while relatively few immatures were obtained from 'Fairway' crested wheatgrass and *P. stipifolia* (Czern. ex Nevski) A. Löve (2n = 14). Remaining entries could be considered marginal to excellent hosts. The presence of current-year adults in root samples indicates that billbugs were able to complete their life cycles on particular host plants. For this reason, the higher billbug densities were found on the most susceptible entries. Many individual grasses were severely damaged or killed by billbugs in 1987. Surviving plants from highly susceptible entries were often in such poor condition that the insects apparently abandoned them for healthier plants in 1988 and 1989. Plant mortality by the fall of 1989 was as high as 80% for some entries (Table 2).

Resistance to the bluegrass billbug has been associated with the presence of a fungal endophyte (*Acremonium* spp.) in perennial

Table 2. Number of billbugs collected from fall root samples and plant mortality of 25 perennial triticeae grasses. Means followed by the same letter in each column are not significantly different as determined by the Bayes L.S.D. (k ratio = 100).

Entry	Billbugs per plant				Plant mortality
	1987		1989		
	adults	immat.	adults	immat.	
	----- (no.) -----				-- (%) --
Fairway	0.1 c	0.1 c	0.1 de	0 d	3 e
Nordan	0.4 c	0.1 c	0.5 bcde	0.6 cd	0 e
Hycrest	0.3 c	0.8 c	0.1 d	0.1 de	0 e
<i>E. canadensis</i>	0.5 bc	0.8 c	0.6 bcde	0.9 bcd	25 c
<i>E. caninus</i>	1.6 abc	0.9 c	0.1 de	0.3 d	45 b
<i>E. fibrosus</i>	0.6 bc	0.8 c	0.1 de	0 d	80 a
<i>E. glaucus</i>	0.1 c	1.1 c	0.1 de	0.1 d	50 b
<i>Critana</i>	0.5 bc	0.5 c	0.8 bcde	0 d	5 de
<i>Secar</i>	0.6 bc	0.1 c	0.4 cde	2.9 a	18 cd
<i>E. sibiricus</i>	2.9 a	1.4 bc	0.1 de	0.3 d	78 a
<i>San Luis</i>	1.1 bc	1.0 c	1.6 ab	0.1 d	85 a
<i>RS-1</i>	2.1 ab	3.0 a	0.4 cde	0.5 cd	10 de
<i>RS backcross</i>	0.1 c	0.6 c	0.6 bcde	0.5 cd	3 e
<i>RS-MC</i>	0.3 c	2.8 ab	1.3 bcd	2.1 abc	3 e
<i>RS-N</i>	0.5 bc	0.5 c	0.4 cde	0.5 cd	5 de
<i>RD</i>	0.5 bc	0.8 c	1.5 abc	1.4 abcd	13 cde
<i>Magnar</i>	0.3 c	0.6 c	0 e	0 d	8 de
<i>Rosana</i>	0 c	1.0 c	0 e	0.5 cd	0 e
<i>Bozoisky-Select</i>	0.1 c	0 c	0 e	0 d	3 e
<i>Whitmar</i>	0.5 bc	0.3 c	2.5 a	2.5 ab	18 cd
<i>P-7845</i>	0 c	0.3 c	0.5 bcde	1.3 abcd	8 de
<i>SL</i>	0.4c	0.3 c	0.3 de	0.3 d	8 de
<i>P. stip.</i> (2n = 14)	0.1c	0 c	0.4 cde	0.8 bcd	8 de
<i>P. stip.</i> (2n = 28)	0 c	0.3 c	0.5 bcde	0.1 d	3 e
Greenar	0 c	0.5 c	0.3 de	0.5 cd	0 e
Bayes L.S.D.	1.7	1.6	1.2	1.8	14

ryegrass, *Lolium perenne* L. (Ahmad et al. 1986). In a controlled feeding study, adult billbug mortalities were higher on endophyte-infected tall fescue (*Festuca arundinacea* Schreb.) than on endophyte-free tall fescue (Johnson-Cicalese and White 1990). Stem samples from each entry in our study were examined for the presence of fungal endophytes but none were found.

Large numbers of billbugs on a plant did not necessarily result in its deterioration or mortality. No significant correlation was found relating entry mortality with billbug infestation rate. Rhizomatous entries survived billbug injury better than caespitose entries. After 3 years of exposure to billbugs, 30% of the plants of caespitose entries were killed, compared to 5% of the plants of rhizomatous entries. This difference suggests that a spreading growth habit may be an effective defense mechanism against billbugs. Since larval mobility is very limited, it is probably that billbugs prefer the high stem and root densities associated with bunchgrass crowns. Billbugs did not discriminate between native and introduced species. Highly resistant and highly susceptible entries were identified in each category.

Similar to results of Asay et al. (1983), most entries of SH genomic formula, as noted in Table 1, were highly susceptible (Table 2). However, 'Critana' thickspike wheatgrass (*Elymus lan- ceolatus* [Scribn. and Smith] Gould) had the lowest mortality rate in the SH group. Unlike most *Elymus* spp., thickspike wheatgrass is cross-pollinating, rhizomatous, and a long-lived perennial (Barkworth and Dewey 1985). With the exception of SH entries, there were no significant differences in mortality rates among the genomic groups. The effect of an individual genome on a wheatgrass' degree of resistance is unclear, but the combination of the S and H genomes, as commonly found in *Elymus*, apparently is associated with susceptibility. Crested wheatgrasses (*Agropyron* spp.), Russian wildrye (*Psathyrostachys juncea* [Fischer] Nevski),

and bluebunch wheatgrass (*Pseudoroegneria spicata* [Pursh] A. Löve) and related *Pseudoroegneria* species were relatively unaf- fected. The P, J, and N genomes were associated with resistance but reaction of combinations of genomes was not predicted by reaction of the individual constituent genomes.

The effect of long-term billbug infestation on a tolerant wheat- grass is unknown. It is possible that stem production, seed yields, and overall vigor are reduced while damage inflicted to the root system may affect drought tolerance. The impact of the bluegrass billbug on the grasses tested here may differ in a rangeland envi- ronment where management practices, precipitation, and soil type may vary. The presence of natural enemies would also be an important factor in billbug success on rangeland. Further host preference studies of this insect may aid range managers when selecting forage grass species for revegetation.

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Efficacy of fenbendazole against gastrointestinal nematodes in white-tailed deer

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Abstract

We provided fenbendazole to captive (N = 77) and free-ranging (3 study areas) white-tailed deer (*Odocoileus virginianus*) in Louisiana to determine effects on gastrointestinal nematode burdens. Fenbendazole reduced gastrointestinal nematode burdens of captive and free-ranging white-tailed deer. Mean eggs per gram of feces from captive deer decreased $P < 0.01$ and $P < 0.01$, respectively) 89% and 84% after provision of fenbendazole in doses approximating 0.47 and 0.62 g/deer, respectively. Doses approximating 0.42-0.46 g/deer did not affect ($P = 0.61$) eggs per gram of feces collected from free-ranging deer. Mean eggs per gram of feces collected from free-ranging deer was affected by fenbendazole treatment ($P = 0.04$) and decreased an average of 86% (SE = 1.9) on the 3 study areas after provision of fenbendazole in doses approximating 1.67-1.82 g/deer. Eggs per gram of feces collected from the distal colon and abomasal parasite counts from abomasa of free-ranging deer harvested on the study areas were associated positively ($r = 0.706$, $P < 0.001$), were affected by fenbendazole treatment ($P < 0.01$ and $P < 0.01$, respectively), and decreased 66% (SE = 5.1) and 52% (SE = 7.4), respectively, after provision of fenbenda-

zole in doses approximating 1.67-1.82 g/deer. A reduction in the cross-transmission of gastrointestinal parasites common to deer and livestock might be possible through fenbendazole treatment of deer.

Key Words: anthelmintic, disease, Louisiana, *Odocoileus virginianus*, parasites

Domestic livestock and white-tailed deer (*Odocoileus virginianus*) share common range in much of the United States, increasing the potential for crossinfection of endoparasites among these ruminants (Beaudion et al. 1970). Prestwood and Pursglove (1981) reported that 32 species of gastrointestinal nematodes have been recorded in white-tailed deer, several of which also infect livestock (Anderson 1962, Prestwood et al. 1973, Prestwood et al. 1975, Prestwood et al. 1976, Davidson et al. 1980, McGhee et al. 1981, Conti and Howerth 1987). Livestock operations often utilize some control program against gastrointestinal parasites and fenbendazole has been demonstrated to be an effective drug for treatment of gastrointestinal parasites in domestic ruminants (Fraser 1986). Free-ranging deer could potentially serve as a reservoir for gastrointestinal nematodes (Dunn 1968, McGhee et al. 1981) and lead to reinfection of treated livestock.

Most species of gastrointestinal nematodes are nonpathogenic or mildly pathogenic in free-ranging white-tailed deer under normal circumstances (Prestwood and Pursglove 1981). However, heavy infection combined with malnutrition led to mortality and

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