RESISTANCE OF COLONIAL BENTGRASS (*AGROSTIS TENUIS*) TO BROWN PATCH (*RHIZOCTONIA SOLANI*)

BY

PEIYU ZENG

A THESIS SUBMITTED IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE DEGREE OF

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MASTER OF SCIENCE THESIS

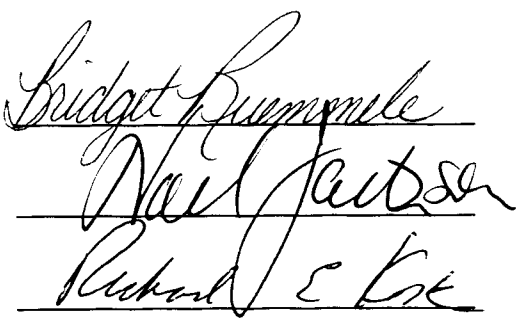
OF

PEIYU ZENG

APPROVED:

Thesis Committee

Major professor



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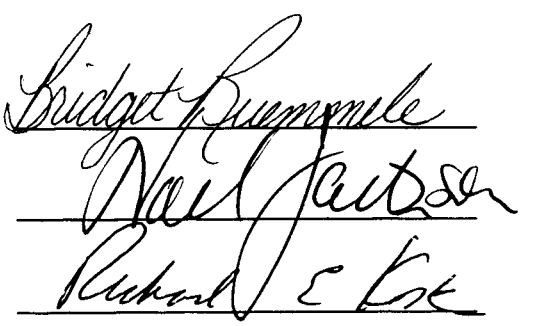

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ABSTRACT

Colonial bentgrass, a perennial cool-season turfgrass native to Europe, has been introduced to cool-humid regions throughout the world. This grass has considerable potential for improvement as a low maintenance species appropriate for use on greens, fairways, and roughs of golf courses and on roadside verges, parks, and home lawns. The potential for developing a Colonial bentgrass with low maintenance tolerance and improved disease resistance has not been fully researched.

The fungus, *Rhizoctonia solani* Kuhn., causes brown patch disease. Resistance to this disease is an important breeding criterion at the present time, since it attacks most grasses, being particularly injurious to putting green turf. *Rhizoctonia solani* is a complex species with many biotypes differing in pathogenicity, host range, distribution in nature, and appearance in culture. It is important to identify virulent strains of the fungus and confirm their pathogenicity before including them in any brown patch screening program.

Using the RAPD (Random Amplified Polymorphic DNA) technique based on PCR (Polymerase Chain Reaction) technology, differences among eight turf isolates of *R. solani* (RS1 to RS8) were demonstrated. The three most pathogenic isolates (RS4, RS5, and RS8) were identified for use in a large-scale brown patch screening procedure. RS4′, RS5′, and RS8′, recovered from inoculated grasses, were identical to the

original inoculum (RS4, RS5, RS8, respectively). To maximize the pathogenicity of RS4, RS5, and RS8, recovered isolates were utilized throughout the large-scale brown patch screening experiment.

In the screening experiments, the bentgrass germplasm differed in symptom response to each isolate. This suggests that genes for pathogenicity vary between *R. solani* isolates, making selection and identification of the isolates used in a breeding program critical. The research also suggested that genes for brown patch resistance exist in some Colonial bentgrasses. This research project provided a suitable, rapid, large volume, brown patch resistance screening procedure for Colonial bentgrass germplasm.

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PREFACE

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I. INTRODUCTION

Colonial bentgrass is a perennial cool-season turfgrass native to Europe. It has been introduced to cool-humid regions throughout the world, including naturalization in New Zealand and coastal areas in the northeast and northwest United States (Lewis, 1934). As one of the two most widely cultivated *Agrostis* species, Colonial bentgrass forms an upright, dense, fine-textured turf under close mowing (Sprague, 1933). The species has considerable potential for lower maintenance and improved golf turf performance, making it an appropriate species to investigate for use on greens, fairways, and low maintenance areas of golf courses in addition to roadways, parks, and home lawns.

Colonial bentgrass is susceptible to a large number of diseases, including dollar spot (*Sclerotinia homeocarpa* F. T. Bennett), brown patch (*Rhizoctonia solani* Kuhn), red thread (*Laetisaria fusiforms* McAlp.), *Typhula* blight (*Typhula* spp.), *Fusarium* patch (*Microdochium nivale* (telemorph *Monographella nivalis*) (Schaffnit) E. Muller), stripe smut (*Ustilago striiformis* (Westend.) Niessl), and leaf spot (*Helminthosporium* spp.) (North and Odland, 1934). During periods of hot, humid weather, brown patch is particularly severe. Some improved Colonial bentgrasses may be developed for better disease tolerance or resistance.

The potential for developing a Colonial bentgrass with low maintenance tolerance and improved disease resistance has

not been fully researched. Resistance to brown patch is an important breeding criterion at the present time. *Rhizoctonia solani* Kuhn. is the fungus which causes this disease. It attacks most grasses, being particularly injurious to putting green turf (Dickinson, 1930). *Rhizoctonia solani* is a complex species with many biotypes differing in pathogenicity, host range, distribution in nature, and appearance in culture (Adams and Butler, 1979). The object of this research was to identify virulent strains of the fungus, confirm their pathogenicity, and develop their use in screening programs for brown patch resistant germplasm.

II. LITERATURE REVIEW

A. COLONIAL BENTGRASS

Colonial bentgrass (*Agrostis tenuis* Sibth.) is one of the two most widely cultivated *Agrostis* species. It is a long-lived perennial, cool-season grass native to Europe, but has been introduced for turfgrass use throughout cool-humid climates of the world. Colonial bentgrass is naturalized in New Zealand and in the Pacific Northwest and New England regions of North America (Beard, 1973). Naturalized strains of Colonial bentgrass have been named brown bentgrass, browntop, New Zealand bentgrass, Northwest bentgrass, Prince Edward Island bentgrass, and Rhode Island bentgrass. No significant phenotypic differences have been found among the so-called strains. Colonial bentgrass has been identified as

Agrostis capillaris Huds. or *Agrostis vulgaris* With. (Beard, 1973).

Colonial bentgrass forms an upright, fine-textured, dense turf under close mowing (Sprague, 1933). Stems and leaves are fine-textured, and low-growing, with lower internodes being quite short. The low growth habit results in good tolerance to close mowing (Beard, 1973). Some cultivars, such as 'Astoria', may segregate into off-types due to inherent heterogeneity as the turf matures.

Colonial bentgrass ranges in color from greenish yellow to medium dark green. Its roots are fibrous, relatively shallow, and annual in nature (Stuckey, 1941). This species has minimal creeping tendency due to the presence of short rhizomes or stolon growth (Philipson, 1937). Propagation is primarily by seed. It is cross-pollinated, with a chromosome number of 28 (Aston and Bradshaw, 1963; Beddows, 1931; Bradshaw, 1959; Fryxell, 1957; Hanson and Carnahan, 1956; and Jones, 1956). The establishment rate is fairly good (DeFrance and Simmons, 1951), but recuperative potential is fair to poor (Beard, 1973).

Colonial bentgrass is adapted to a wide range of soil types, but does best on fertile, moist, fine-textured soils having a pH of 5.5 to 6.5 (Garner and Damon, 1929; Hanson and Carnahan; Hartwell and Damon, 1917; Juska and Hanson, 1959; Sprague, 1934; and Van Dersal, 1936). Colonial bentgrass tolerates fairway heights of 1 to 2.5cm and lower amounts of

water and fertilizer (80 to 150 kg ha-1 per year) better than creeping bentgrass (*Agrostis palustris*). It can utilize nitrogen at the lower soil pH and even persists on more acidic soils common to those in the New England region (Musser, 1948 and Sprague, 1934). With the emerging emphasis on developing resource-efficient turfgrass for golf turf use, Colonial bentgrass would be an appropriate species to investigate for use on greens, fairways, and low-maintenance areas of golf courses.

Brown patch, caused by *Rhizoctonia solani* Kuhn., is one of the most damaging diseases of Colonial bentgrass. Brown patch resistance is, therefore, an important criterion at the present time for any improved Colonial bentgrass.

The potential for developing a bentgrass with low maintenance requirements and improved disease resistance has not been fully researched. A brown patch screening program at Texas A&M University Research and Extension Center in Dallas revealed that some creeping bentgrass progeny from crosses resisted the disease better than their parents, resulting in the conclusion that breeding for brown patch resistance is feasible (Colbaugh, 1989).

B. BROWN PATCH (*RHIZOCTONIA SOLANI* KUHN.)

Rhizoctonia solani Kuhn. is the fungus which causes the disease commonly called large brown patch. It exists primarily as vegetative mycelia that are colorless when young, but turn yellowish or light brown with age. Mycelia consist

of long hyphal cells which produce branches that grow at approximately right angles to the main hyphae, are slightly constricted at the junction, and have a cross wall (septum) near the junction. *Rhizoctonia solani* attacks most grasses and is particularly injurious to putting-green turf. It develops a fine, white to brown, cobweb-like mass of mycelium on or within the turf. Hyphae enter grass leaves (directly or through the stomata) and break down leaf cells, causing leaves to shrivel and turn brown. Hyphae enter basal stems or crowns only during the severest attacks. The fungus forms sclerotia, or resting bodies, that are able to withstand unfavorable conditions (Dickinson, 1930).

Rhizoctonia solani is a complex species containing many biotypes differing in pathogenicity, host range, distributions in nature, and appearance in culture (Adams and Butler, 1979). One of the best ways to group isolates of this fungus is by anastomosis determination (anastomosis group, also known as AG). This scheme was described in Germany (Schultz, 1937), Japan (Watanabe and Matsuda, 1966), and the United States (Parmeter et al., 1969).

According to this scheme, hyphal fusion occurs only between isolates of the same AG. Each AG can be considered an evolutionary unit in the sense that each is a genetically isolated, non-interbreeding population. An appreciation of the AG concept in *Rhizoctonia solani* can make the difference between progress and failure in a breeding program for disease

resistance (Anderson, 1982).

C. RAPD-PCR TECHNIQUE

Molecular genetic markers permit analysis of genetic relationships and genetic diversity (Mullis et al., 1987; Saiki et al., 1988; and Ochman et al., 1988). PCR (Polymerase Chain Reaction) is an *in vitro* method for the enzymatic synthesis of specific DNA sequences. It uses two oligonucleotide primers of varying length (usually approximately 20 nucleotides in length) that specifically hybridize to opposite strands flanking the region to be synthesized. Repetitive cycles of DNA denaturation, primer annealing and extension of the annealed primers by DNA polymerase, produces an exponential amplification of the target DNA region. The specifically-amplified fragment termini are defined by the 5′ ends of the primers. Since the primer extension products also serve as templates for the next round of synthesis in each PCR cycle, the number of products approximately doubles after each cycle. DNA regions of interest can be amplified millions of times (Bassam et al., 1991).

The PCR technique is technically simple and quick to perform, but requires prior knowledge of the DNA sequence. A modification of the basic PCR technique not dependent on prior knowledge of the DNA sequence produces randomly amplified DNA sequences that allows for the detection of genetic polymorphisms. (Waugh and Powell, 1992).

The RAPD (Random Amplified Polymorphic DNA) assay uses PCR with a single short arbitrary primer to amplify target sequences. A single, short oligonucleotide primer binds to many different loci and amplifies random sequences from a complex DNA template, such as a plant genome. Theoretically, the number of amplified fragments generated by this approach depends on the length of the primer and the size of the target genome, and is based on the probability that a given DNA sequence (complementary to that of the primer) will occur in the genome on opposite DNA strands in opposite orientation within a distance that is readily amplifiable by PCR. The primers are generally of random sequence, biased to consist of at least 50% 'GC' content, and to lack internal inverted repeats. The products are easily separated by standard electrophoretic techniques and visualized by ultraviolet illumination of ethidium-bromide stained gels (Waugh and Powell, 1992). The nature of the fragments that are amplified is highly dependent on the primer sequence and on the DNA sequence of the genome being assayed. The primers differing by a single nucleotide give rise to different amplified bands, and genomic polymorphisms at one or both priming sites result in the disappearance of amplified bands. Thus, DNA amplification with random sequence primers is a highly sensitive method for discovering polymorphisms randomly distributed throughout the genome (Rafalski et al., 1991).

The main advantages of the RAPD technology include

suitability for work on anonymous genomes, applicability to problems where only limited quantities of DNA are available, efficiency, and low expense (Waugh and Powell, 1992).

III. MATERIALS AND METHODS

A. CULTURE OF COLONIAL BENTGRASS

Colonial bentgrasses from various sources (Appendices A-E) were vegetatively propagated in 36-cell (5.5cm X 5cm) growing flats (54cm X 27cm) containing 1:1:1 (volume) peat, perlite, and vermiculite and maintained in a greenhouse approximately 60 days. Plants were fertilized bi-weekly with 100 ppm 20-20-20 water-soluble fertilizer applied with regularly scheduled watering. The greenhouse was coated with semi-opaque whitewash during May through September to reduce ambient temperature. Day and night thermostat settings were 21C and 21C, respectively. Particularly during summer months, completely adequate heat reduction was difficult due to lack of evaporative cooling pads. This was more of a problem during the disease-inoculation phase when flats were covered by plastic domes (Sections III. D and G).

B. CULTURE AND INOCULUM PRODUCTION OF *RHIZOCTONIA SOLANI* KUHN.

Eight isolates of *Rhizoctonia solani,* from diseased turfgrass collected in New England (Table 1), were used in the pathogenicity experiment. Cultures of each isolate were grown in petri dishes (60mm X 15mm) containing 10ml sterilized

potato dextrose agar medium before transfer to 250ml flasks containing sterilized perennial ryegrass seeds and distilled water (1:1 ratio). The cultures were maintained at room temperature at least one week prior to inoculation of the Colonial bentgrasses.

C. ANASTOMOSIS GROUP (AG) IDENTIFICATION

Anastomosis grouping was demonstrated by placing a mycelial plug (3mm diameter) from actively-growing cultures (isolates RS1 to RS8) on a 1.5% water agar plate (100mm X 15mm), surrounded by 4 plugs of four available anastomosis group tester isolates (AG1, AG2-2, AG3, and AG4). Five replicates per isolate were examined. Hyphae were stained briefly with 1% aniline blue in 5% glycerin. The plate was placed directly on the microscope stage for observation at 40x and 100x for confirmation of anastomosis. Observation of at least three perfect fusions per replicate confirmed the AG identity of the isolates.

D. IDENTIFICATION OF THE THREE MOST PATHOGENIC *Rhizoctonia solani* ISOLATES

Four experiments (Appendices A-D) used two to ten genotypes of Colonial, creeping, and velvet bentgrass vegetatively propagated in 36-cell growing flats. Approximately 60 days after propagation, the grasses were cut to 1cm heights, and the turf plugs arranged in each flat in a randomized complete block design with four plugs per treatment. Inoculum of one of the eight isolates (Table 1)

was placed on each plug, except for controls which received no inoculation.

After inoculation with six *Rhizoctonia solani*-permeated perennial ryegrass seeds per plug, the flats were covered with plastic, domed covers to maintain high humidity. Flats were placed under greenhouse benches during the day to avoid overheating. Covers were removed 24 to 72 hours after inoculation. Disease ratings were recorded at intervals from 1 to 10 days during a one-month period, with the greatest frequency closest to inoculation date. Ratings ranged from 1 to 9, with 9 meaning the plug suffered no visible damage from the disease down to 1 being totally dead. The three most virulent brown patch isolates were identified from the eight original isolates for use in the large-scale screening trial for brown patch resistance (See III. G.).

E. RE-ISOLATION OF *RHIZOCTONIA SOLANI* FROM INOCULATED GRASS

Infected grass blades from each treatment were cut into 3 to 5mm pieces, sterilized with 10% NaHClO, then cultured on potato dextrose agar media. Recovered *Rhizoctonia solani* isolates were transferred to new media several times to obtain pure cultures. The three most damaging isolates selected from the original eight were readily recovered and their identity confirmed. They were used as the inoculum source for the large-scale brown patch resistance screening (See III. G.).

F. IDENTIFICATION OF MOLECULAR DIFFERENCES AMONG STRAINS OF *RHIZOCTONIA SOLANI* AND CONFIRMATION OF IDENTITY BETWEEN RE-ISOLATES FROM INOCULATED GRASSES AND THE ORIGINAL ISOLATES USED AS INOCULUM

Plugs of mycelium were transferred from potato-dextrose agar culture to potato-dextrose liquid medium. Mycelia were harvested and dried four days later.

Fungal genomic DNA was extracted from the dried mycelia of all eight original isolates of *Rhizoctonia solani* and also from the three re-isolates deemed most damaging. The method of Zolan, et al. (1986) was adopted. DNA samples were cleaned by spermidine precipitation.

RAPD assay conditions were essentially as described by Williams et al (1990), using 0.2mM each of dATP, dTTP, dGTP and dCTP, 0.1% gelatin, 45ng genomic DNA, 60ng of a single decamer primer (kit from Operon, Alameda, CA, USA and kit from UBC), 0.72 units of Taq polymerase, 1.5mM $MgCl_2$ and reaction buffer to a total volume of 12μl. The reaction mixture was overlaid with a drop of oil and was incubated in a GTC Genetic Thermal Cycler with LTM-2 Low Temperature Cooling Module (Precision Scientific) programmed for 44 cycles of 1 minute at 94C, 1 minute at 36C, and 2 minutes at 72C, followed by one cycle of 1 minute at 94C, 1 minute at 36C, and 5 minutes at 72C. Negative controls (the reaction mixture without genomic DNA), were analyzed by gel electrophoresis in 1.4% agarose in Tri-acid-EDTA buffer stained with ethidium bromide (Sambrook

et al., 1990). DNA samples of each isolate were analyzed in duplicate for this study.

Eleven primers were tested to identify those that would produce useful banding patterns for analysis. Primers included: UBC groups 302 (80% GC), 317 (70%), 331 (70%), 347 (60%), 338 (70%), 336 (70%), 359 (60%), 326 (50%), and 384 (70%); OPA17; and OPB17.

G. IDENTIFICATION OF COLONIAL BENTGRASS GENOTYPES WITH THE MOST BROWN PATCH RESISTANCE

Eight experiments utilized 11 to 64 Colonial bentgrass genotypes (Appendix E), propagated as in III. A. Genotype number varied with experiment depending on space availability in the greenhouse. Approximately 60 days after propagation, 36 plugs per genotype were trimmed to 1cm height and arranged in a randomized complete block design with nine replications per fungal treatment. Treatments included a non-inoculated control and one of the three most damaging *Rhizoctonia solani* isolates tested in III. D. After inoculation with eight *Rhizoctonia solani*-permeated perennial ryegrass seeds per plug, the flats were covered with plastic, domed covers to maintain high humidity. Flats were placed under greenhouse benches during the day to avoid overheating. Covers were removed 96 hours after inoculation. Reduction in plant quality due to disease damage was recorded at various intervals during at least a one-month period after inoculation. Plugs were rated 1 to 9, with a rating of '1'

equal to complete death and '9' equal to no damage from the disease. Analysis used the ANOVA procedure in SAS.

IV. RESULTS AND DISCUSSION

A. ANASTOMOSIS GROUP (AG) IDENTIFICATION

Anastomosis between the tester and the unknown isolates was observed in this study. Isolates of RS1, RS2, RS4, RS5, RS7, and RS8 fused with AG1 but not with AG2-2, AG3, and AG4. RS3 and RS6 fused with AG2-2 but not with AG1, AG3, and AG4. According to the current AG concept, these results indicated that RS1, RS2, RS4, RS5, RS7 and RS8 belong to the AG1, while RS3 and RS6 belong to the AG2-2.

B. IDENTIFICATION OF THE THREE MOST PATHOGENIC *RHIZOCTONIA SOLANI* ISOLATES

Four experiments were completed (Appendices A to D), with the following results typical in each experiment. Generally, mycelia were observed growing along the grass blades 24 hours after inoculation and incubation within plastic domes. Grasses yellowed and the mycelia became shrunken after 84 hours incubation. Twenty-four hours after uncovering plants, disease symptoms intensified. Some leaves dried as the spread of symptoms increased. Six days after the inoculation, the grass started regrowing slowly. Two weeks later, most grasses were fully recovered.

In the first experiment, each plug was inoculated with six fungus-infected perennial ryegrass seeds. Two of four

replications were covered for 24 hours and the remainder were covered 72 hours. The results showed that: a) the RS7 caused the most damage, followed in order by RS4, RS5, and RS8; b) grass leaves were withered, but crowns were not damaged; c) all plants began to recover one week after inoculation; and d) plants of replications 1 and 2 were more damaged than in replications 3 and 4, indicating the longer covering induced more damage.

Increased inoculum per plug and/or longer coverage after inoculation may be advantageous. Subsequent experiments used eight perennial ryegrass seeds per plug, with 84 hours coverage after inoculation.

RS2, RS4 and RS5 caused more damage than other isolates or the control in experiment 2, although the greatest damage apparently resulted from excessively high temperatures caused by the domed trays being exposed to continuous direct sunlight. In experiment 3, RS8 caused the most damage, followed by RS2, RS6, and RS7, in order. The most plant damage in experiment 4 resulted from inoculations with RS4, RS5, and RS8.

Statistical analyses indicated RS4, RS5, and RS8 affected Colonial bentgrass quality most. These isolates were selected for the large-scale brown patch screening procedure of 277 additional genotypes (See IV. D.).

C. IDENTIFICATION OF MOLECULAR DIFFERENCES AMONG STRAINS OF *RHIZOCTONIA SOLANI* AND CONFIRMATION OF IDENTITY

BETWEEN RE-ISOLATES FROM INOCULATED GRASSES AND THE ORIGINAL ISOLATES USED AS INOCULUM

Nine randomly chosen decamer primers from the UBC collection including 302 (80% GC), 317 (70%), 331 (70%), 347 (60%), 338 (70%), 336 (70%), 359 (60%), 326 (50%), and 384 (70%) and two from Operon (OPA17 and OPB17) were screened for their ability to generate RAPD marker DNA polymorphisms among the isolates of *Rhizoctonia solani*. Seven of these primers gave no bands in DNA samples of several isolates (Figure not shown). Four primers gave one or more unique band markers for each isolate, with three of them shown in Fig. 1 to 4. PCR products of each isolate had a unique banding pattern and each isolate and re-isolate pair produced the same banding pattern (Fig. 1 to 4).

RAPD patterns of the four primers produced unique banding patterns (Fig. 1 to 4). All eight isolates also had unique RAPD patterns (Fig. 1,2). The three re-isolates RS4′, RS5′ AND RS8′ had the same RAPD patterns as RS4, RS5, and RS, respectively (Fig. 2 to 4). With primer OPA17, the RAPD patterns of the three most pathogenic isolates showed more similarity to one another than to the other five isolates (Fig. 2).

Each of these isolates had unique sequences in its genome, suggesting that different pathogenic genes may affect each isolate. These genes may be involved in pathogenicity, host range, distribution in nature, and appearance in culture

(Adams and Butler, 1979). Traditionally, the isolates of *Rhizoctonia solani* have been grouped by anastomosis groups (AG). A more recent concept has been to classify isolates based on the pectic enzymes produced during growth on pectin (Sweetingham, Cruickshank and Wong, 1986). In this system, isolates are divided into pectic zymogram groups (ZG). It agrees with the division on the basis of the anastomosis behavior, except that some of the AG can be further subdivided into different ZG. Although the AG concept correlates to some extent with pathogenicity, several studies suggest that there is considerable variation between strains from the same AG, and that the pathogenicity of *Rhizoctonia solani* cannot be explained solely in the terms of AG or ZG (Vilgalys, 1987; Golshi,1987, Vilgalys and Gonzalez, 1990; Jabaji-Hare et al., 1990). The RAPD-PCR technique used in this study addressed this problem. In the current research, six of the eight isolates (RS1, RS2, RS4, RS5, RS7, and RS8) belong to AG1, and two of the eight isolates (RS3 and RS6) belong to the AG2-2. However, none of these caused the same symptom on genotypes. The results of RAPD-PCR showed each of these eight isolates has its own biotype. RAPD-PCR is a useful alternative to anastomosis grouping for identification of isolates of *Rhizoctonia solani*.

D. IDENTIFICATION OF COLONIAL BENTGRASS GENOTYPES WITH THE MOST BROWN PATCH RESISTANCE

Two hundred seventy-seven Colonial bentgrasses (Appendix E) were screened using the three most damaging isolates (RS4′, RS5′, and RS8′). Due to space limitations, genotypes were divided into eight experiments, with each experiment analyzed separately. Since the screening process conducted as part of an actual turfgrass breeding program would be performed on an on-going basis at different times of the year, decisions as to superior disease-resistant genotypes would be based on comparisons within each set of plants screened, rather than waiting until the last genotype has been screened (which may be several years after the first testing). Two experiments (6 and 8) produced data sets too large to be analyzed using PC-SAS. These experiments were split approximately in half for analysis and reporting.

In experiment 1, 11 Colonial bentgrass genotypes were evaluated for response to each isolate. Eight days after inoculation, RS5′ generally caused the most damage, followed by RS4′ and RS8′. Plugs inoculated by RS8′ began recovery soonest. Nine days after inoculation, RS5′-treated plugs still displayed the most severe symptoms, followed by RS4′ and RS8′.

Genotypes responded differently to each isolate of *Rhizoctonia solani*. For example, RS8′ caused extreme damage on genotype 3 (see Appendix E, 'G3'), but genotype 2 suffered

more damage from RS4′ and RS5′ than RS8′ (Table 2). This finding indicates that resistance to different isolates of *Rhizoctonia solani* may be controlled by different genes. One variety may carry certain gene(s) resistant to RS8′, but sensitive to other isolates, while other varieties could carry gene(s) resistant to RS4′, RS5′, or other isolates. Figure 2 shows six representative genotypes from the 11 genotypes used in this experiment. Genotypes 11 and 5 showed more resistance to the three isolates than genotypes 4, 6, 2 and 7 (Fig. 5). Quality ratings of genotypes 11 and 5 indicate that these genotypes were significantly more resistant than the other nine genotypes (Table 2).

Thirty-six Colonial bentgrass genotypes were tested in experiment 2. Five and six days after inoculation, RS4′ generally caused the most plant damage, while RS5′ induced the least damage. Two days later, genotypes inoculated with RS8′ had recovered faster than those inoculated with RS5′. RS4′ still incited the worst symptoms, while the RS8′ caused the least damage. Genotypes 18 and 33 were significantly more resistant to the three isolates of *Rhizoctonia solani* than the other genotypes (Table 3).

In experiment 3, thirty-two Colonial bentgrass genotypes were assessed for brown patch resistance. Six days after inoculation, RS8′ caused the most damage and RS5′ induced the least. Twelve days after inoculation, genotypes inoculated with RS8′ recovered faster than those inoculated with RS4′.

RS5′ affected quality the least. Based on statistical analysis (Table 4), genotypes 54 and 55 were more resistant to the three isolates of *Rhizoctonia solani* than 25 other genotypes. Genotypes 50, 51, 56, 73, and 75 also expressed better resistance than most other genotypes (Table 4).

Twenty-eight Colonial bentgrass genotypes were evaluated in experiment 4. On genotype 80, RS4′ induced the most damage, plugs of the same genotype inoculated with RS5′ and RS8′ recovered after thirty days. Most plugs of genotype 92 inoculated with RS4′ recovered from disease symptoms, while most of the plugs inoculated with RS5′ and RS8′ still showed extreme disease symptoms after several days. These results suggest that genotype 80 may carry gene(s) resistant to RS5′ and RS8′, while genotype 92 may carry gene(s) resistant to RS4′.

Five and nine days after inoculation, RS8′ caused the most damage averaged across all 32 genotypes; RS5′ caused the least damage. Twelve days after inoculation, genotypes inoculated with RS8′ recovered faster than those by RS4 and RS5, with RS4′ inducing the worst symptoms on genotypes. Genotypes 81, 83, 98 and 99 were significantly more resistant to fungal inoculation than the genotypes tested in this experiment (Table 5).

Forty Colonial bentgrass genotypes were screened against RS4′, RS5′, and RS8′ in experiment 5. Averaged across all genotypes, RS5′ caused the worst damage, followed by RS8′ and

RS4'. Genotype 136 showed significantly more resistance to the three isolates than the other 39 genotypes (Table 6).

In experiment 6, 42 Colonial bentgrass genotypes were evaluated. Due to limitations with the statistical software, the data set was divided for analysis among isolates. RS8' induced the most damage averaged across genotypes 148 to 168, while RS5' caused the least damage. On genotype 169 to 189, RS8' caused the most damage, with RS5' inducing the least damage. Six representative genotypes from all 42 genotypes are shown in Figure 6. Genotypes 156, 167, 153, and 151 showed more resistance to RS4', RS5', and RS8' than genotypes 187 and 172. Genotypes 150 and 174 rated significantly higher for quality than 35 other genotypes in this experiment (Table 7). Genotypes 156, 157, 164, 166, and 182 were not significantly different from genotypes 150 and 174.

RS4', RS5', and RS8' were used to inoculate 24 genotypes in experiment 7. RS5' caused the most damage and RS8' caused the least damage when averaged across all genotypes. Figure 7 shows six representative genotypes, with genotype 199 and 202 more resistant to damage than genotypes 191, 193, 194, and 201. Statistical analysis of quality placed 14 genotypes in the most resistant group (genotypes 190, 195, 196, 198, 199, 202, 204, 205, 206, 207, 210, 211, 212, and 213) (Table 8).

In experiment 8, 64 Colonial bentgrasses were screened. As in experiment 6, the data set required division for statistical analysis. Among genotypes 214 to 245, RS4' caused

the most damage, while RS5′ caused the least damage. RS8′ caused the most damage on genotypes 246 to 277, compare to RS5′ and RS4′. Nine genotypes (224, 225, 227, 228, 244, 256, 258, 273, and 274 ranked in the highest statistical group for quality (Table 19).

E. GENERAL DISCUSSION

Each bentgrass germplasm responded differently to each isolate. This suggests that different genes for pathogenicity may exist in each isolate, and this makes the selection and identification of isolates used in a breeding program critical. Although the traditional method of the anastomosis grouping can distinguish groups of fungal isolates, the RAPD-PCR is another useful technique for distinguishing within the groups of isolates. Due to the ability to naturally cross pollinate, Colonial bentgrass is heterozygous, producing genetic variation necessary for plant improvement. In these experiments, some genotypes appeared strongly resistant to the three most aggressive isolates of *Rhizoctonia solani*, while others were extremely sensitive. This suggests that genes for resistance to *Rhizoctonia solani* exist in some genotypes.

V. SUMMARY

1. RS1, RS2, RS4, RS5, RS7 and RS8 belong to the AG1, while RS3 and RS6 belong to the AG2-2.

2. RS4, RS5, and RS8 were the most aggressive disease-

causing isolates selected for the large-scale brown patch screening procedure.

3. Each of the eight isolates had a unique genetic composition as determined by RAPD analysis.

4. The three isolates, RS4′, RS5′ and RS8′ were recovered successfully from inoculated plants and appeared to have the same genetic composition as RS4, RS5, and RS8, respectively, based on RAPD analysis.

5. By using the large-scale brown patch screening method described in III G., resistance could be selected for on the basis of the response of each genotype to inoculation by *Rhizoctonia solani* isolates. This technique provided a suitable, rapid, large volume screening procedure for selecting brown patch-resistant Colonial bentgrass germplasm.

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VII. TABLES

Table 1. Cultures[1] of *Rhizoctonia solani* used in brown patch screening in greenhouse. Eight isolates of *Rhizoctonia solani* obtained January 19, 1994 from the collection of Dr. Noel Jackson:

Isolate	Group	Grass type	Collection source
RS1	AG1	creeping bentgrass	Penncross sod
RS2	AG1	creeping bentgrass	D. Wallace sod
RS3	AG2-2	velvet bentgrass	Turf farm
RS4	AG1	Kentucky bluegrass	New England Turf
RS5	AG1	perennial ryegrass	Segregansett G.C.
RS6	AG1	creeping bentgrass	Turf farm
RS7	AG2-2	unknown	Turf farm
RS8	AG1	tall fescue, cv. ISI-ATK	URI cultivar test plots

[1] Cultures of each isolate were grown in 100mm X 15mm petri dishes containing 10ml sterilized potato dextrose broth. After retransfers on 19, 22, 28 January and 4 February, pure cultures with no contamination were obtained.

Table 2. Quality ratings (1-9, 9 = no disease symptoms) of the eleven genotypes used in experiment 1 testing the ability of three isolates of *Rhizoctonia solani* (RS4', RS5', and RS8') to induce disease in Colonial bentgrass germplasm. Each mean is an average of all three isolates.

GENO-TYPE	DAY 7	DAY 8	DAY 9	DAY 10	DAY 11	DAY 13
G1	4.4ab[1]	4.7ab	4.4cd	4.5cde	4.9de	5.4de
G2	3.9cde	4.2abc	4.3de	4.3de	4.6f	4.9ef
G3	3.6e	3.7c	3.7f	3.8f	4.1g	4.9f
G4	4.5ab	4.9a	4.3de	4.4cde	5.1cd	5.4bcd
G5	4.7a	4.9a	4.7b	5.1ab	5.9a	6.3a
G6	4.1bc	4.7ab	4.5cd	4.6cd	4.7efg	5.2d-g
G7	3.6de	4.2abc	4.1e	4.2e	4.5f	4.8fg
G8	4.0cd	4.4abc	4.5cd	4.7cd	5.4bc	5.8b
G9	3.9cde	4.4abc	4.6bc	4.8bc	5.4b	5.7bc
G10	3.9cde	3.9cde	4.5cd	4.6cd	4.6f	4.9ef
G11	3.9cde	3.9cde	5.4a	5.4a	6.1a	6.6a

[1] Means within a column followed by the same letter are not significantly different using the Waller-Duncan mean separation test (k-ratio = 100).

Table 3. Quality ratings (1-9, 9 = no disease symptoms) of the 36 genotypes used in experiment 2 testing the ability of three isolates of *Rhizoctonia solani* (RS4', RS5', and RS8') to induce disease in Colonial bentgrass germplasm. Each mean is an average of all three isolates.

GEN.	DAY 5	DAY 6	DAY 7	DAY 8	DAY 9	DAY 12	DAY 14	DAY 15	DAY 16	DAY 25	DAY 27
G12	3.8 c-f[1]	3.8 a-d	3.8 a-d	3.8 d-g	3.8 f-l	4.3 d-j	4.0 h-l	4.3 f-l	5.2 f-m	6.0 g-k	6.1 g-j
G13	4.0 ab	3.8 a-d	3.8 a-e	4.4 a	4.6 a	5.1 ab	5.0 a-d	5.0 a-d	6.0 a-d	7.0 abc	7.2 ab
G14	4.0 a	3.9 a	4.0 ab	4.3 ab	4.4 ab	4.9 bc	5.1 abc	5.1 ab	5.6 d-h	6.4 c-g	6.4 c-h
G15	3.5 g-m	3.5 f-m	3.5 e-j	3.8 e-i	3.8 f-l	4.4 c-h	4.6 a-f	4.7 b-g	5.8 a-e	6.9 a-e	6.9 b-f

G16	3.2 nop	3.3 lmn	3.2 klm	3.3 lm	3.4 mn	3.9 j-m	3.8 i-l	4.0 i-m	5.1 g-m	5.9 ghi	6.3 fgh
G17	3.5 g-m	3.4 h-m	3.5 g-k	3.9 c-f	4.1 c-g	4.4 c-h	4.3 e-i	5.0 a-d	5.6 d-j	6.3 d-i	6.6 b-g
G18	3.4 h-n	3.6 c-i	3.6 d-h	3.9 c-f	3.9 d-h	4.6 b-e	4.6 b-f	4.8 b-f	6.4 ab	7.4 ab	7.7 a
G19	3.8 a-c	3.9 a	3.9 a-c	4.1 abc	4.4 abc	4.8 bcd	5.0 abc	5.0 a-d	6.2 abc	7.0 abc	7.3 ab
G20	3.6 c-j	3.4 g-m	3.4 g-k	3.5 h-m	3.5 k-n	4.0 g-n	3.9 i-l	3.9 i-m	4.6 mn	5.3 klm	5.3 kl
G21	3.7 c-g	3.5 e-l	3.6 d-i	3.7 f-k	3.9 e-k	4.3 d-j	4.5 d-h	4.5 d-j	5.2 f-m	6.3 c-h	6.4 e-h
G22	3.4 i-o	3.3 j-n	3.5 g-k	3.5 h-m	3.5 k-n	4.0 h-n	3.9 h-l	4.0 i-m	5.1 h-m	5.8 g-l	5.9 g-k

G23	3.8 c-f	3.5 d-k	3.6 d-i	3.7 e-j	3.9 d-l	4.5 c-f	4.6 b-g	4.7 b-h	5.8 b-f	6.2 e-i	7.2 abc
G24	3.4 i-o	3.4 i-n	3.4 h-m	3.4 j-m	3.5 j-n	3.8 k-n	4.0 h-l	4.1 i-m	4.6 mn	5.4 j-n	5.5 i-l
G25	3.3 j-p	3.4 h-m	3.4 h-l	3.5 h-m	3.6 h-n	4.0 h-n	3.9 i-l	4.1 i-m	4.9 k-n	5.8 g-l	5.9 g-k
G26	3.3 l-p	3.3 k-n	3.3 i-m	3.3 lm	3.4 n	3.6 n	3.6 kl	3.7 lm	4.3 n	4.9 n	5.0 l
G27	3.8 c-f	3.8 abc	3.8 a-e	3.9 c-f	4.2 b-e	4.5 c-g	4.8 a-e	4.9 b-e	5.7 c-g	5.8 g-l	6.0 g-k
G28	3.7 c-h	3.6 c-j	3.6 d-h	3.8 e-i	3.9 d-j	4.2 e-l	4.3 e-j	4.5 c-i	5.6 d-i	6.3 d-i	6.4 d-h
G29	3.5 e-l	3.4 h-m	3.4 h-l	3.4 j-m	3.5 k-n	3.8 k-n	4.1 g-l	4.0 i-m	4.8 ln	5.0 mn	5.3 k-l

G30	3.8 bcd	3.8 abc	3.8 a-e	4.1 b-d	4.3 a-d	4.5 c-g	4.8 a-e	4.7 b-h	5.5 d-k	5.7 h-m	5.8 h-k
G31	3.3 k-p	3.3 ln	3.3 j-m	3.4 lm	3.5 lmn	3.9 i-n	3.8 i-l	3.9 j-m	4.8 lmn	5.6 i-n	5.8 h-k
G32	3.6 c-i	3.5 f-m	3.5 g-k	3.9 c-f	4.1 b-g	4.9 bc	5.1 ab	5.1 abc	6.3 ab	7.3 ab	7.2 abc
G33	3.6 d-k	3.5 f-m	3.5 f-j	4.0 c-e	4.2 b-f	4.5 c-g	4.7 a-e	4.9 b-e	6.4 a	7.5 a	7.7 a
G34	3.1 p	3.1 n	3.1 m	3.3 m	3.4 n	3.6 n	3.6 l	3.5 m	4.6 mn	5.2 mn	5.5 i-l
G35	3.5 g-m	3.3 j-n	3.4 h-m	3.6 g-l	3.8 g-m	3.7 mn	4.1 g-l	4.1 h-l	5.0 j-m	5.7 g-m	5.9 g-k
G36	3.2 m-p	3.2 mn	3.2 klm	3.3 lm	3.5 lmn	3.7 mn	3.7 kl	3.7 lm	4.6 mn	5.3 lmn	5.4 j-n

G37	3.8 b-e	3.5 f-m	3.5 f-j	3.7 f-k	3.6 h-n	4.0 g-n	4.5 c-g	4.7 b-h	5.8 b-f	6.8 a-e	7.1 a-d
G38	3.5 g-m	3.1 n	3.2 lm	3.3 m	3.3 n	3.9 i-n	3.8 i-l	4.0 i-m	4.8 lmn	5.4 j-n	5.8 h-k
G39	4.0 ab	3.9 ab	4.0 a	4.1 bcd	4.3 a-d	4.1 f-m	5.2 a	5.2 ab	6.1 a-d	6.7 b-f	7.2 ab
G40	3.6 c-j	3.7 b-h	3.7 c-g	3.8 d-h	3.9 e-k	4.5 c-g	4.6 b-f	4.7 b-h	5.4 e-l	5.8 g-l	6.2 f-i
G41	3.5 e-l	3.3 k-n	3.3 j-m	3.4 k-m	3.6 i-n	3.7 lmn	3.8 jkl	4.0 i-m	5.0 i-m	6.0 f-j	6.3 fgh
G42	3.2 op	3.3 k-n	3.3 j-m	3.4 klm	3.6 i-n	3.8 k-n	4.0 h-l	4.1 i-m	5.0 j-m	5.6 i-n	5.8 h-k
G43	3.7 c-g	3.8 a-e	3.7 c-g	3.9 c-f	4.1 bcd	4.6 bg	4.8 a-e	5.1 ab	6.0 a-d	6.9 a-d	7.2 ab

G44	3.6 c-i	3.7 a-g	3.8 b-f	3.8 e-h	3.8 f-k	4.2 f-k	4.5 c-g	4.9 b-e	5.4 d-k	6.3 c-h	6.4 c-h
G45	3.5 g-m	3.5 f-m	3.4 h-m	3.8 d-i	4.0 c-g	4.1 f-m	4.0 h-l	4.2 g-l	4.7 mn	5.3 k-m	5.8 h-k
G46	3.7 c-g	3.7 a-f	3.7 c-g	3.9 c-f	4.2 b-e	5.1 ab	5.0 a-d	5.5 a	6.4 ab	7.1 ab	7.3 ab
G47	3.5 f-l	3.6 c-j	3.4 h-m	3.7 f-k	3.9 d-h	4.0 g-n	4.1 f-k	4.2 g-l	5.5 d-j	6.7 b-f	7.0 a-e

[1] Means within a column followed by the same letter are not significantly different using the Waller-Duncan mean separation test (k-ratio = 100).

Table 4. Quality ratings (1-9, 9 = no disease symptoms) of the 32 genotypes used in experiment 3 testing the ability of three isolates of Rhizoctonia solani (RS4, RS5, and RS8) to induce disease in Colonial bentgrass germplasm. Each mean is an average of all three isolates.

GEN.	DAY 5	DAY 6	DAY 7	DAY 8	DAY 9	DAY 12	DAY 14	DAY 16	DAY 19	DAY 25
G48	3.3 b-e[1]	3.3 b-f	3.4 a-e	3.5 abc	3.6 a-e	3.7 b-g	3.9 a-h	4.1 a-f	4.3 cde	4.4 b-f
G49	3.4 abc	3.5 ab	3.5 abc	3.7 a	3.8 abc	3.8 a-d	3.9 a-f	4.1 a-f	4.3 cde	4.4 b-f
G50	3.4 a-d	3.4 a-d	3.5 abc	3.6 ab	3.7 a-d	4.0 abc	4.1 abc	4.4 abc	4.5 a-d	4.8 abc
G51	3.2 c-g	3.3 c-g	3.4 a-e	3.5 abc	3.6 a-f	3.8 a-d	3.9 a-g	4.1 c-h	4.3 c-f	4.5 a-e

G52	3.3 b-f	3.3 c-g	3.3 b-g	3.4 b-f	3.6 b-g	3.7 b-h	3.8 b-i	4.0 c-i	4.3 c-f	4.5 b-f
G53	3.2 e-i	3.2 f-j	3.2 d-h	3.3 c-h	3.3 e-k	3.4 f-l	3.6 e-l	3.8 e-k	3.9 e-h	4.0 d-k
G54	3.4 ab	3.4 abc	3.5 ab	3.7 a	3.8 ab	4.0 ab	4.2 ab	4.6 a	4.9 ab	5.1 a
G55	3.5 a	3.5 a	3.6 a	3.6 ab	3.9 a	4.1 a	4.3 a	4.6 ab	4.9 a	5.1 a
G56	3.1 e-i	3.2 e-i	3.4 a-d	3.5 abc	3.6 a-e	3.8 a-f	4.0 a-d	4.2 a-e	4.4 b-e	4.8 ab
G57	3.0 i	3.0 j	3.0 hi	3.1 h	3.2 ijk	3.2 h-l	3.5 g-m	3.6 g-k	3.9 e-h	4.1 d-j
G58	3.1 e-i	3.1 f-j	3.2 d-h	3.3 c-h	3.5 c-i	3.6 d-i	3.8 b-i	4.1 c-h	4.3 c-f	4.4 b-f

G59	3.1 e-i	3.1 f-j	3.3 c-g	3.4 b-f	3.4 c-j	3.5 e-k	3.7 d-k	3.9 c-j	4.1 d-g	4.2 b-h
G60	3.0 hi	3.0 j	3.1 hi	3.1 h	3.1 jk	3.1 kl	3.2 lm	3.3 k	3.4 h	3.4 k
G61	3.1 ghi	3.1 g-j	3.1 ghi	3.2 fgh	3.3 f-k	3.4 g-l	3.4 i-m	3.5 ijk	3.9 e-h	4.0 d-k
G62	3.0 i	3.0 j	3.0 i	3.1 h	3.1 jk	3.2 jkl	3.3 j-m	3.3 k	3.5 g-k	3.6 ijk
G63	3.0 hi	3.1 ij	3.1 ghi	3.2 d-h	3.3 g-k	3.3 i-l	3.4 j-m	3.5 ijk	3.7 gh	3.8 g-k
G64	3.0i	3.0j	3.0hi	3.1h	3.1jk	3.2kl	3.2lm	3.3k	3.4h	3.5k
G65	3.0 i	3.1 g-j	3.2 e-i	3.2 d-h	3.4 d-j	3.5 e-k	3.6 e-m	3.7 f-k	3.9 e-h	4.1 d-i
G66	3.0 i	3.0 j	3.0 hi	3.1 h	3.1 jk	3.2 kl	3.3 k-m	3.3 k	3.4 h	3.5 jk

G67	3.2 d-h	3.3 c-g	3.3 b-g	3.4 a-e	3.6 b-g	3.7 c-h	3.8 b-i	3.9 c-j	4.1 d-g	4.3 b-g
G68	3.1 ghi	3.1 f-j	3.2 e-i	3.2 d-h	3.3 e-k	3.5 d-j	3.7 c-j	4.0 c-i	4.0 d-g	4.2 c-h
G69	3.0 hi	3.1 hij	3.1 ghi	3.2 e-h	3.2 h-k	3.4 g-l	3.5 g-m	3.5 ijk	3.7 gh	3.8 g-k
G70	3.1 f-i	3.1 g-j	3.1 ghi	3.2 e-h	3.3 g-k	3.4 f-l	3.5 g-m	3.5 ijk	3.7 gh	3.8 g-k
G71	3.2 e-i	3.1 f-j	3.2 e-i	3.3 c-h	3.3 e-k	3.4 f-l	3.5 f-m	3.6 g-k	3.9 e-h	3.9 e-k
G72	3.0 i	3.0 j	3.0 hi	3.1 gh	3.2 ijk	3.3 jkl	3.4 j-m	3.4 jk	3.8 fgh	3.9 e-k
G73	3.2 e-i	3.3 d-h	3.3 b-f	3.4 a-e	3.6 a-e	3.8 a-e	4.0 a-e	4.3 a-d	4.6 abc	4.8 ab

G74	3.1 ghi	3.1 hij	3.1 f-i	3.2 fgh	3.3 e-k	3.4 g-l	3.6 e-m	3.8 e-k	3.9 e-h	4.1 d-i
G75	3.2 e-i	3.3 d-h	3.3 b-g	3.4 a-e	3.6 b-g	3.7 b-g	3.9 a-h	4.0 c-h	4.4 b-e	4.6 a-d
G76	3.2 e-i	3.3 d-h	3.3 c-g	3.4 b-g	3.4 c-j	3.6 d-j	3.7 c-j	3.9 d-j	4.0 d-g	4.1 d-i
G77	3.1 ghi	3.1 ij	3.0 hi	3.1 h	3.1 k	3.1 l	3.2 m	3.3 k	3.6 gh	3.7 h-k
G78	3.1 e-i	3.1 f-j	3.2 e-i	3.2 d-h	3.4 e-k	3.4 f-l	3.6 e-l	3.8 d-j	4.1 d-g	4.1 d-i
G79	3.3 b-f	3.4 a-e	3.4 a-e	3.5 a-d	3.5 b-h	3.7 c-i	3.9 a-g	4.1 c-h	4.3 c-f	4.5 b-f

[1] Means within a column followed by the same letter are not significantly different using the Waller-Duncan mean separation test (k-ratio = 100).

Table 5. Quality ratings (1-9, 9 = no disease symptoms) of 28 plants in experiment 4 testing the ability of three isolates of Rhizoctonia solani (RS4, RS5, and RS8) to induce disease in Colonial bentgrass germplasm. Each mean is an average of all three isolates.

GEN.	DAY 5	DAY 6	DAY 7	DAY 8	DAY 9	DAY 12	DAY 14	DAY 17	DAY 18	DAY 24	DAY 26	DAY 30
G80	4.6 ab[1]	4.5 b	4.3 bcd	4.4 bcd	4.5 cde	4.8 cd	5.1 cd	5.9 bcd	5.3 e-h	5.4 cd	5.8 bcd	6.7 bc
G81	4.7 ab	4.8 a	4.7 a	4.7 ab	5.1 a	5.5 a	6.0 a	6.6 a	5.9 bcd	6.0 bc	6.5 a	7.4 a
G82	4.6 ab	4.5 ab	4.4 abc	4.3 cde	4.5 cde	4.8 c	5.1 cd	6.3 abc	5.8 cde	4.9 d-g	5.7 cd	6.6 bc
G83	4.8 a	4.7 ab	4.7 a	4.6 ab	4.8 ab	4.9 bc	5.4 ab	6.4 ab	6.5 ab	5.3 d	6.4 ab	7.2 ab

G84	3.5 klm	3.4 i-l	3.4 l-o	3.4 j-m	3.4 j-o	3.6 i-m	3.8 h-l	4.2 i-l	4.1 lmn	4.3 hij	4.3 f-i	5.2 ef
G85	3.6 j-m	3.5 h-k	3.5 j-m	3.5 ijk	3.6 il	3.6 h-l	3.7 h-l	3.8 k-n	3.8 h-r	4.1 ijk	3.8 ijk	4.2 h-k
G86	3.6 jkl	3.5 h-l	3.5 j-m	3.4 i-l	3.5 j-m	3.6 h-l	3.9 g-j	4.0 jkl	4.0 mno	3.9 jkl	4.1 g-j	4.1 i-l
G87	3.6 jkl	3.5 g-j	3.5 jkl	3.6 ijk	3.7 ijk	3.8 g-j	3.9 g-j	4.1 i-l	3.9 m-q	4.0 ijk	3.9 h-k	4.8 f-i
G88	3.6 jk	3.4 jkl	3.5 j-m	3.3 klm	3.4 k-o	3.4 j-m	3.5 i-l	3.5 lmn	3.5 o-q	3.7 klm	3.9 ijk	3.9 j-m
G89	3.6 jk	3.6 g-j	3.5 j-n	3.5 i-l	3.6 j-m	3.8 g-k	4.0 ghi	4.2 i-l	4.1 l-o	4.2 ijk	4.2 f-i	4.4 g-j
G90	3.7 h-k	3.7 ghi	3.6 i-l	3.7 g-j	3.9 ghi	4.0 e-h	4.0 efg	4.4 h-k	4.6 i-l	4.6 f-i	4.8 ef	5.3 ef

G91	4.2 cde	4.1 d	4.1 def	4.1 def	4.4 def	4.7 cd	5.1 cd	5.7 cde	5.7 c-f	5.1 def	5.8 bcd	6.3 cd
G92	4.0 d-g	4.0 def	3.9 e-h	3.9 fg	4.0 gh	4.1 efg	4.3 efg	4.9 gh	4.8 h-k	4.8 e-h	5.2 de	5.1 efg
G93	4.1 d-g	4.0 de	4.0 d-g	3.9 fgh	3.9 ghi	3.9 f-i	3.9 ghi	4.4 hij	4.4 j-m	4.4 g-j	4.6 e-i	4.9 f-i
G94	4.3 cd	4.4 bc	4.4 abc	4.8 a	4.7 bcd	4.8 cd	5.1 cd	5.5 def	5.4 d-g	5.4 d	5.8 cd	5.8 de
G95	4.1 def	4.2 cd	4.2 cde	4.1 ef	4.1 fg	4.4 de	4.7 de	5.1 fg	5.0 g-j	5.2 de	5.6 d	5.7 de
G96	4.3 cde	4.1 d	4.1 def	4.3 cde	4.6 de	5.0 bc	5.3 bc	5.9 bcd	6.1 bc	6.3 ab	6.3 abc	6.6 bc
G97	3.9 e-h	4.0 def	3.9 f-i	3.9 fg	4.2 efg	4.3 def	4.6 def	5.2 efg	5.1 f-i	5.0 de	5.7 cd	6.2 cd

G98	4.1 def	4.2 d	4.2 cde	4.3 cde	4.4 def	4.7 cd	5.1 cd	5.8 cde	5.8 cde	6.0 b	6.3 abc	6.9 abc
G99	4.4 bc	4.4 bc	4.5 ab	4.5 abc	5.0 a	5.3 ab	5.8 ab	6.5 a	6.7 a	6.8 a	6.9 a	7.3 ab
G100	3.9 f-i	3.7 fgh	3.7 h-k	3.6 hij	3.6 j-m	3.7 g-l	3.9 g-j	4.2 i-l	4.3 k-n	4.4 ghi	4.9 ef	4.9 fgh
G101	3.8 g-j	3.8 efg	3.7 h-k	3.7 ghi	3.7 hij	3.9 ghi	4.1 fgh	4.6 ghi	4.4 j-m	4.4 g-j	4.7 efg	5.0 fg
G102	3.8 g-j	3.7 fgh	3.6 h-l	3.7 g-j	3.7 ijk	3.8 g-j	3.8 g-k	3.9 j-m	4.0 m-p	4.1 ijk	4.4 f-i	4.7 f-i
G103	3.5 klm	3.4 i-l	3.4 l-o	3.3 klm	3.5 j-m	3.7 g-l	3.9 g-j	3.9 j-m	3.9 m-p	4.0 ijk	4.2 f-i	4.2 h-k
G104	3.3 lm	3.3 kl	3.2 o	3.1 m	3.1 o	3.2 mn	3.3 kl	3.3 m	3.3 qr	3.3 m	3.3 k	3.5 klm

G105	3.3 m	3.3 kl	3.2 mno	3.2 lm	3.2 no	3.1 n	3.2 l	3.3 n	3.2 r	3.3 lm	3.4 jk	3.4 m
G106	3.5 klm	3.4 h-k	3.4 l-o	3.3 klm	3.3 l-o	3.3 k-n	3.4 jkl	3.4 mn	3.4 pqr	3.3 lm	3.4 jk	3.4 lm
G107	3.3 m	3.2 l	3.2 no	3.2 lm	3.5 mno	3.3 lmn	3.4 jkl	3.3 n	3.3 r	3.3 m	3.3 k	3.4 klm

[1] Means within a column followed by the same letter are not significantly different using the Waller-Duncan mean separation test (k-ratio = 100).

Table 6. Quality ratings (1-9, 9 = no disease symptoms) of 40 plants in experiment 5 testing the ability of three isolates of Rhizoctonia solani (RS4, RS5, and RS8) to induce disease in Colonial bentgrass germplasm. Each mean is an average of all three isolates.

GEN.	DAY 5	DAY 6	DAY 8	DAY 11	DAY 14	DAY 17	DAY 19	DAY 23	DAY 32
G108	3.6 f-l[1]	3.4 g-m	3.4 f-m	3.4 g-n	3.4 g-l	3.3 k-h	3.4 j-o	3.4 k-p	3.6 o-s
G109	3.5 g-n	3.4 g-n	3.4 g-m	3.4 h-n	3.4 g-l	3.4 h-m	3.5 g-n	3.6 h-o	4.0 j-q
G110	3.4 i-p	3.3 h-n	3.3 i-n	3.3 j-o	3.3 h-l	3.2 lmn	3.4 k-o	3.4 k-p	3.8 m-r
G111	4.1 bc	4.0 bc	3.9 bc	4.0 bc	4.1 bc	3.9 b-e	4.7 b	4.8 bc	5.3 bc

G112	3.2 op	3.1 mn	3.1 mn	3.1 no	3.1 jkl	3.1 mn	3.1 no	3.1 nop	3.3 rs
G113	3.3 l-p	3.2 k-n	3.3 h-n	3.3 i-o	3.3 h-l	3.4 h-m	3.4 h-o	3.5 j-p	3.9 l-q
G114	3.1p	3.1n	3.1mn	3.0o	3.1l	3.0h	3.0p	3.0p	3.1s
G115	3.2 nop	3.2 lmn	3.1 lmn	3.1 mno	3.1 jkl	3.1 mn	3.3 l-o	3.3 nop	3.4 qrs
G116	3.7 e-i	3.6 d-h	3.6 d-i	3.6 e-i	3.6 d-h	3.7 c-i	3.9 d-h	4.0 d-j	4.4 e-l
G117	3.4 k-p	3.3 j-n	3.3 h-n	3.3 j-o	3.3 h-l	3.3 i-n	3.4 i-o	3.5 i-o	4.1 i-p
G118	3.6 f-l	3.5 e-k	3.5 e-j	3.5 f-k	3.5 f-i	3.4 h-m	3.4 h-o	3.6 h-o	4.3 f-n
G119	4.0 b-e	3.9 bcd	3.9 bcd	3.9 b-e	4.2 b	4.3 b	4.7 b	4.9 b	5.5 b

G120	3.7 e-j	3.6 d-i	3.6 d-i	3.5 f-k	3.4 g-l	3.4 h-m	3.5 g-o	3.6 h-o	3.8 m-r
G121	3.5 g-n	3.5 e-l	3.5 e-k	3.4 g-m	3.9 e-h	3.6 d-h	3.9 d-h	4.0 d-j	4.6 d-k
G122	3.7 f-k	3.6 d-h	3.6 d-h	3.6 e-i	3.6 d-h	3.8 c-g	3.8 e-j	3.9 f-k	4.3 f-n
G123	3.6 f-l	3.6 e-j	3.5 e-j	3.5 f-l	3.4 g-j	3.5 g-l	3.6 g-m	3.6 h-o	4.2 h-o
G124	3.4 h-p	3.4 g-n	3.4 f-m	3.4 g-n	3.3 h-l	3.4 h-m	3.5 g-o	3.6 g-m	4.1 i-o
G125	3.5 g-o	3.5 e-l	3.4 e-l	3.5 f-l	3.5 f-i	3.6 e-k	3.9 d-g	4.0 e-h	4.8 c-f
G126	3.3 nop	3.5 e-k	3.4 e-l	3.5 f-k	3.5 f-i	3.6 d-j	3.9 d-g	4.0 d-i	4.8 c-n

G127	3.4 h-p	3.4 g-m	3.4 g-m	3.4 g-n	3.4 g-l	3.4 h-m	3.4 i-o	3.4 k-p	3.9 l-r
G128	3.5 g-n	3.5 e-l	3.4 g-m	3.4 g-n	3.7 d-g	3.6 d-j	3.9 e-i	4.0 d-j	4.6 d-j
G129	3.2 op	3.2 lmn	3.2 k-n	3.2 l-o	3.4 g-l	3.2 lmn	3.3 l-o	3.4 l-p	3.8 m-r
G130	3.3 l-p	3.3 i-n	3.3 h-n	3.3 i-o	3.4 g-l	3.3 i-n	3.5 g-n	3.6 g-n	3.9 k-r
G131	3.6 f-m	3.5 f-l	3.4 e-l	3.5 f-l	3.5 fgh	3.4 i-n	3.5 g-n	3.7 g-n	4.4 f-m
G132	4.3 b	4.2 b	4.1 b	4.1 b	3.9 bcd	4.0 bc	4.5 bc	4.6 bc	5.1 bcd
G133	3.7 f-k	3.6 e-j	3.5 e-j	3.6 e-j	3.6 d-h	3.7 c-i	3.8 e-k	3.8 f-l	4.4 f-h

G134	3.3 l-p	3.3 i-n	3.2 j-n	3.3 k-o	3.1 i-l	3.2 lmn	3.1 mno	3.2 nop	3.5 p-s
G135	3.7 e-j	3.7 d-g	3.7 c-f	3.6 d-h	3.5 f-i	3.9 c-e	4.0 c-f	4.1 e-g	4.6 d-i
G136	5.1a	4.9a	4.9a	5.0a	5.2a	5.4a	6.4a	6.8a	7.2a
G137	3.8 c-g	3.8 cde	3.8 cde	3.8 c-f	3.7 d-g	4.0 bcd	4.2 cde	4.3 c-f	5.0 b-e
G138	3.7 e-i	3.6 d-h	3.6 d-i	3.6 e-j	3.6 d-h	3.7 c-h	3.9 d-h	3.9 e-k	4.1 i-p
G139	3.6 f-m	3.5 e-k	3.4 f-l	3.4 g-m	3.5 f-i	3.5 f-l	3.6 f-l	3.8 f-l	4.2 g-o
G140	3.5 g-n	3.6 d-i	3.4 e-l	3.4 g-m	3.4 g-k	3.5 g-l	3.7 f-l	3.7 g-m	3.9 l-r
G141	3.4 j-p	3.3 h-n	3.3 h-n	3.3 h-o	3.3 h-l	3.3 j-n	3.4 i-o	3.7 g-m	4.0 j-q

G142	3.9 c-f	3.8 c-f	3.8 cde	3.8 c-f	3.9 b-e	4.0 bc	4.4 bc	4.4 cd	4.8 c-g
G143	3.8 d-h	3.8 c-f	3.6 c-g	3.7 c-g	3.8 c-f	3.8 c-f	4.2 cde	4.4 cde	5.2 bcd
G144	4.1 bcd	4.0 bc	3.9 bc	3.9 bcd	3.9 b-e	4.0 bc	4.3 bcd	4.6 bc	4.9 b-f
G145	3.6 f-m	3.5 e-l	3.5 e-k	3.4 g-m	3.4 g-k	3.4 g-l	3.7 f-l	3.7 g-m	4.1 i-o
G146	3.5 g-n	3.5 e-k	3.4 e-k	3.4 g-m	3.4 g-l	3.4 i-n	3.6 f-l	3.6 g-m	3.9 l-r
G147	3.2 p	3.1 mn	3.1 mn	3.1 no	3.1 kl	3.1 mn	3.1 o	3.1 op	3.4 qrs

[1] Means within a column followed by the same letter are not significantly different using the Waller-Duncan mean separation test (k-ratio = 100).

Table 7. Quality ratings (1-9, 9 = no disease symptoms) of 42 plants in experiment 6 testing the ability of the three isolates of Rhizoctonia solani (RS4, RS5, and RS8) to induce disease in Colonial bentgrass germplasm. Each mean is an average of all three isolates.

GEN.	DAY 5	DAY 6	DAY 9	DAY 13	DAY 15	DAY 19	DAY 23	DAY 30	DAY 60
G148	4.3fgh[1]	4.2ghi	3.6i	3.6j	3.7i	3.9hi	4.2i	4.9g	5.8c
G149	4.1h	3.9i	3.3i	3.3j	3.4i	3.4i	3.5j	3.6h	3.9d
G150	5.3a	5.1a	6.3a	6.0a	6.9a	6.8a	7.1a	7.7ab	8.1a
G151	4.8bcd	4.8bc	5.4bc	5.5cd	5.6e-h	5.9d-g	6.2e-h	6.8f	7.1b
G152	4.4efg	4.3efg	4.9efg	4.9hi	5.7d-h	5.8fg	6.3e-h	7.2def	8.2a
G153	4.4efg	4.3efg	4.6gh	4.9ghi	5.4gh	5.6g	6.1h	7.4a-d	8.0a
G154	4.9bc	4.9abc	5.5bc	5.6bc	6.0b-e	6.5abc	6.9abc	7.4a-d	8.2a
G155	5.0b	4.9abc	4.8fg	5.1e-i	5.9b-f	6.1c-f	6.6b-e	7.5a-d	8.3a
G156	5.0b	4.8bc	5.0d-g	5.4cde	5.8c-g	6.4abc	6.8a-d	7.5a-d	8.3a

G157	4.5ef	4.5def	5.2cde	5.5cd	6.1bc	6.5ab	6.7a-d	7.4a-d	8.2a
G158	5.3a	5.1ab	5.7b	5.9ab	6.3b	6.4abc	6.6b-f	7.3cde	8.2a
G159	4.4efg	4.4efg	4.8fg	5.2d-h	5.4gh	5.9efg	6.2gh	7.2c-f	8.2a
G160	4.4e-g	4.2gh	4.4h	4.9hi	5.4h	5.8fg	6.3e-h	7.3cde	8.1a
G161	4.3fgh	4.1ghi	4.7gh	5.0f-i	5.4h	5.9d-g	6.2fgh	7.4bcd	8.3a
G162	4.3e-h	4.3e-h	5.2c-f	5.3c-f	6.0bcd	6.3bcd	6.5b-g	7.4a-d	8.1a
G163	4.0h	4.1hi	4.6gh	4.8hi	5.6e-h	5.8fg	6.2fgh	7.3c-f	8.1a
G164	4.6cde	4.5de	5.3cd	5.3c-f	6.0c-f	6.5abc	6.9ab	7.7ab	8.3a
G165	4.5def	4.4efg	4.8fg	5.1e-i	5.5efg	5.9efg	6.4d-h	7.5a-d	8.3a
G166	4.5def	4.7cd	5.5b	5.5cde	6.1bcd	6.8a	6.9abc	7.8a	8.3a
G167	4.3fgh	4.2fgh	4.8gh	4.8hi	5.4gh	6.3b-e	6.6b-f	7.6abc	8.0a
G168	4.2gh	4.1ghi	4.8gh	5.3c-f	6.1bcd	6.0e-g	6.5c-g	7.5a-d	8.3a
G169	4.1bcd	4.3ab	4.6c	5.2bc	6.1a	6.0bc	6.5bc	7.5ab	8.1ab

G170	4.2b	3.9d-f	3.9h	4.5de	5.1de	5.4fg	5.9e	7.2bc	8.3a
G171	4.2bc	4.0cd	3.3ijk	3.2h	3.2k	3.3j	3.3hi	3.4f	3.4e
G172	4.0e-g	4.0cd	3.3ijk	3.2h	3.2k	3.3j	3.3hi	3.4f	3.4e
G173	4.5a	4.3ab	4.4cde	4.4de	5.0de	5.6def	6.1de	7.2bc	8.3a
G174	4.6a	4.4a	5.3a	5.3ab	5.8b	6.4a	6.9a	7.8a	8.3a
G175	4.2bc	3.8fg	3.5i	3.4g	3.5j	3.7i	4.1g	4.7d	5.3c
G176	4.1bcd	4.0def	4.2efg	4.3e	4.5h	4.7h	5.5f	7.1c	8.3a
G177	4.1bcd	4.0cde	4.2efg	4.3e	4.9ef	5.7de	5.9e	7.3bc	7.7b
G178	4.2b	3.8efg	3.2jkl	3.4g	3.1k	3.1j	3.2hi	3.3fg	3.4e
G179	3.8gh	3.8fg	3.3ijk	3.1h	3.1k	3.1j	3.2hi	3.3fg	3.4e
G180	3.9fgh	3.8gh	3.0l	3.0h	3.0k	3.0j	3.0i	3.0g	3.0e
G181	4.7b-f	3.9d-f	3.1kl	3.1h	3.1k	3.2j	3.4h	3.8e	4.1d
G182	4.2b	4.2bc	4.3ef	4.6d	5.4c	6.1b	6.6bc	7.5ab	8.3a

G183	4.1b-e	4.0cde	3.4ij	3.8f	3.8i	3.2j	3.3hi	3.3fg	3.4e
G184	4.0d-f	4.0def	4.3de	4.7d	4.7fg	5.8cd	6.4cd	7.4bc	8.3a
G185	3.9e-h	3.9d-f	4.0gh	4.3e	4.6gh	5.4efg	6.0e	7.3bc	8.3a
G186	4.2bc	4.3ab	4.9b	5.4a	6.0a	6.6a	6.7ab	7.5ab	8.3a
G187	3.8h	3.6h	3.3jkl	3.1h	3.1k	3.0j	3.0i	3.0g	3.0e
G188	4.0efg	4.2b	4.4cde	4.6d	5.2cd	5.3g	6.0e	7.3bc	8.3a
G189	3.8h	3.9def	4.3fgh	4.3e	4.5h	5.3g	5.9e	7.3bc	7.9ab

[1] Means within a column followed by the same letter are not significantly different using the Waller-Duncan mean separation test (k-ratio = 100).

Table 8. Quality ratings (1-9, 9 = no disease symptoms) of 24 plants in experiment 7 testing the ability of three isolates of Rhizoctonia solani (RS4, RS5, and RS8) to induce disease in Colonial bentgrass germplasm. Each mean is an average of all three isolates.

GEN.	DAY 5	DAY 6	DAY 8	DAY 10	DAY 12	DAY 15	DAY 19	DAY 28	DAY 57
G190	5.3a[1]	5.2a	6.1a	6.2a	6.3abc	6.4ab	7.1ab	7.9a-d	8.7a
G191	4.0hi	3.9hi	3.4h	3.4jk	3.4g	3.5i	3.7ij	4.0jk	4.3fg
G192	3.8i	3.7ijk	3.4h	3.4k	3.4g	3.5i	3.7ij	4.0jk	4.3fg
G193	4.2gh	4.0f-i	3.6h	3.6jk	3.6g	3.8i	4.1i	4.6i	5.1e
G194	4.9bcd	4.8bcd	4.3def	4.3h	4.3f	4.5h	4.9h	5.8h	6.9Dd
G195	4.4fg	4.3fg	4.6def	5.3de	6.4ab	6.4ab	7.1ab	7.9a-d	8.7a
G196	4.6ef	4.2fgh	4.6d	5.1ef	5.8cd	5.9b-e	6.6bcd	7.6a-e	8.5ab
G197	4.1h	4.0g-i	4.1efg	4.6f	4.6f	4.7gh	5.1hi	5.8h	6.8d
G198	4.9cd	4.6de	5.1c	5.5cde	6.2abc	6.3abc	6.8bc	7.4b-f	8.4ab

G199	5.3a	5.1a	5.6b	5.9abc	6.3abc	6.3abc	6.8bc	7.6a-e	8.4ab
G200	4.0hi	3.8ij	4.0fg	4.2hi	4.5f	4.7h	5.3gh	6.5g	7.6c
G201	3.6j	3.3l	3.4h	3.4k	3.4g	3.4i	3.5j	3.7k	3.9g
G202	5.4a	5.3a	3.3bc	6.0ab	6.6a	6.6a	7.4a	7.9abc	8.7a
G203	4.2gh	4.2fgh	4.4def	4.7fg	5.1e	5.2fg	5.9ef	6.9fg	7.9bc
G204	4.4fg	4.3ef	4.5d	4.8f	5.3e	5.5ef	6.2de	7.3def	8.3abc
G205	5.1abc	5.2a	5.7ab	5.7bcd	6.0bc	6.0bcd	6.8bc	7.9abc	8.8a
G206	5.2ab	5.1ab	5.6b	5.9ab	6.3abc	6.3abc	7.1ab	8.0ab	8.5ab
G207	4.8de	4.6de	5.6b	5.9ab	6.3abc	6.3abc	7.1ab	8.0a	8.5ab
G208	3.7j	3.6jkl	3.4h	3.6jk	3.7g	3.7i	4.0ij	4.4ij	4.8ef
G209	3.7j	3.6jkl	3.4h	3.5jk	3.6g	3.7i	4.0ij	4.6i	5.0ef
G210	5.1abc	5.0abc	5.1c	5.4de	5.9cd	6.1bcd	6.8bcd	7.5a-e	8.3ab
G211	4.4fg	4.2fgh	4.4de	4.9f	5.5de	5.8cde	6.4cd	7.4c-f	8.4ab

G212	3.6j	3.5kl	3.7gh	3.8ij	4.4f	4.8gh	5.6fg	7.3ef	8.4ab
G213	4.8de	4.7cd	4.5d	4.9f	5.5de	5.6def	6.3cde	7.6a-e	8.5ab

[1] Means within a column followed by the same letter are not significantly different using the Waller-Duncan mean separation test (k-ratio = 100).

Table 9. Quality ratings (1-9, 9 = no disease symptoms) of 64 plants in experiment 8 testing the ability of three isolates of Rhizoctonia solani (RS4, RS5, and RS8) to induce disease in Colonial bentgrass germplasm. Each mean is an average of all three isolates.

GEN.	DAY 5	DAY 6	DAY 7	DAY 8	DAY 12	DAY 14	DAY 20	DAY 22	DAY 30	DAY 37
G214	3.8 a-f[1]	3.5 d-g	3.4 k	3.4 j	3.6 g	3.8 h	4.0 l	4.3 m	4.6 l	5.1 m
G215	3.9 a-d	3.5 d-g	3.5 g-k	3.6 ghi	3.7 fg	4.0 efg	4.6 e-j	4.9 jkl	5.4 f-i	6.1 d-j
G216	3.6 g-l	3.5 d-g	3.8 b-g	3.8 c-g	4.0 a-d	4.0 c-g	4.7 c-h	4.8 l	5.1 jk	5.7 kl
G217	3.7 d-i	3.4 efg	3.4 jk	3.4 ij	3.9 c-g	3.8 gh	4.3 kl	4.9 kl	5.3 ijk	5.7 jkl

G218	4.0 a	3.8 ab	3.8 b-e	4.0 bc	4.1 a	4.3 ab	4.7 c-h	5.1 e-j	5.4 e-i	6.2 c-i
G219	3.7 e-i	3.8 ab	3.9 abc	3.8 c-g	4.1 abc	4.1 b-f	4.8 b-g	5.3 c-f	5.6 d-h	6.1 d-j
G220	3.8 a-f	3.6 b-f	3.6 e-j	3.7 ghi	3.8 efg	4.0 c-g	4.7 e-j	4.9 i-l	5.5 e-i	6.2 c-h
G221	3.6 h-k	3.6 b-e	3.8 b-g	3.8 d-h	3.9 c-g	4.2 a-e	4.8 a-e	4.8 l	5.4 f-i	6.3 c-g
G222	4.0 abc	3.7 abc	3.8 b-f	3.8 c-g	3.9 c-g	4.1 b-f	4.7 f-j	4.9 kl	5.3 ijk	6.1 c-i
G223	3.8 b-g	3.6 b-e	3.8 b-g	3.8 c-g	4.0 a-d	4.2 a-e	4.7 e-j	5.1 f-k	5.6 d-h	6.4 c-f
G224	3.9 a-e	3.9 a	4.1 a	4.1 ab	4.1 ab	4.3 a	5.0 ab	5.4 cde	5.7 b-e	6.4 a-d

G225	3.8 b-d	3.7 bcd	3.9 a-d	3.9 bcd	4.1 ab	4.2 a-d	4.8 a-f	5.4 cde	5.9 bc	6.8 ab
G226	3.6 f-k	3.6 b-e	3.8 b-e	3.9 b-e	3.9 a-e	4.1 b-f	4.9 a-d	5.3 c-f	5.6 c-g	6.3 c-f
G227	3.6 f-j	3.5 d-g	3.6 e-j	3.8 d-h	3.9 c-g	4.0 efg	4.7 e-j	5.3 cde	5.9 bc	6.8 ab
2228	3.4 jkl	3.4 fg	3.5 ijk	3.6 ghi	3.8 d-g	4.2 a-d	4.7 e-j	5.2 e-i	5.7 c-f	6.5 abc
G229	3.3 l	3.3 g	3.5 ijk	3.6 ghi	3.8 d-g	4.1 b-f	4.5 g-k	5.2 d-h	5.5 e-i	6.1 e-k
G230	3.6 f-j	3.5 d-g	3.5 h-k	3.8 c-g	4.1 ab	4.1 b-f	4.8 b-g	5.3 c-f	5.5 d-i	6.1 e-k
G231	3.7 d-i	3.5 c-g	3.5 h-k	3.7 e-h	3.9 a-e	4.1 a-e	4.6 e-j	5.3 c-f	5.4 ghi	5.9 g-l

G232	3.5 jkl	3.4 fg	3.4 jk	3.7 gh	4.0 a-d	4.0 c-g	4.5 h-k	4.9 kl	5.4 ghi	6.1 c-i
G233	3.9 abc	3.7 b-e	3.8 b-f	4.1 ab	4.1 a	4.1 a-e	4.6 e-j	5.3 cde	5.5 e-i	5.8 h-l
G234	3.8 a-f	3.6 b-e	3.8 b-e	3.7 fgh	3.8 d-g	4.1 a-e	4.4 jk	5.0 h-l	5.4 hij	6.2 c-i
G235	3.5 h-l	3.5 c-g	3.7 d-i	3.7 e-h	3.9 c-g	4.0 d-g	4.6 f-l	5.1 f-k	5.5 e-i	5.8 i-l
G236	3.8 c-h	3.7 abc	4.0 ab	4.0 bc	3.9 a-f	4.2 a-d	4.4 ijk	5.2 d-g	5.4 ghi	6.2 c-i
G237	3.9 abc	3.8 ab	4.1 a	4.3 a	4.0 a-d	4.2 abc	5.0 abc	5.3 c-f	5.6 d-h	6.2 c-i
G238	3.3 l	3.4 fg	3.4 jk	3.6 hij	3.8 d-g	4.1 a-e	4.8 d-g	5.4 bcd	5.9 bc	6.3 c-f

G239	3.5 i-l	3.6 b-f	3.8 b-g	3.9 b-e	4.1 abc	4.1 b-f	4.8 b-g	5.6 ab	5.9 bc	6.4 b-e
G240	3.4 kl	3.5 c-g	3.7 c-h	3.9 bcd	3.9 b-h	4.1 b-f	4.7 d-i	5.5 abc	5.8 bcd	6.1 e-k
G241	3.5 i-l	3.4 fg	3.6 f-k	3.8 c-g	4.0 a-e	3.9 fgh	4.3 k	5.0 g-l	5.1 k	5.6 l
G242	3.7 e-i	3.5 c-g	3.5 h-l	3.8 d-h	4.0 a-d	4.3 ab	4.8 a-f	5.4 cde	5.7 b-e	6.3 c-f
G243	4.0 ab	3.6 b-f	3.6 e-i	3.8 c-g	4.0 a-e	4.2 abc	4.7 d-i	5.2 d-g	5.6 c-h	6.3 c-f
G244	4.0 ab	3.7 abc	3.8 b-g	3.9 b-e	4.1 abc	4.3 ab	5.1 a	5.7 a	6.1 a	6.8 a
G245	3.9 a-e	3.7 bcd	3.7 c-h	3.9 bcd	4.0 a-d	4.0 c-g	4.6 e-j	5.3 c-f	5.5 e-i	6.2 c-h

G246	3.6 g-k	3.6 h-l	3.7 i-l	3.8 e-l	4.0 d-h	4.1 cde	4.7 c-i	4.9 klm	4.9 ln	5.4 m
G247	3.7 e-j	3.5 i-l	3.5 kl	3.6 lm	3.9 e-h	4.0 ef	4.6 g-k	4.9 jkl	5.1 klm	5.5 j-m
G248	3.9 c-g	3.7 e-j	3.7 g-l	3.6 klm	3.8 h	4.0 ef	4.5 h-m	5.0 g-k	5.6 c-g	6.2 c-f
G249	4.0 bcd	3.9 c-f	3.9 c-i	3.9 c-f	4.1 b-g	4.4 ab	4.7 e-i	5.3 b-e	5.6 c-g	6.1 def
G250	3.9 cde	3.9 c-f	4.0 b-f	4.0 b-f	4.2 a-d	4.4 a	5.1 a	5.4 abc	5.9 ab	6.4 bc
G251	4.3 a	4.0 a-d	4.0 d-f	4.1 a-d	4.1 b-g	4.3 abc	4.7 c-i	5.1 f-j	5.4 f-i	6.0 fgh
G252	4.3 ab	4.3 a	4.4 a	4.3 a	4.3 ab	4.4 a	4.9 a-d	5.4 abc	5.7 b-e	6.2 c-f

G253	4.2 ab	4.2 ab	4.2 abc	4.1 abc	4.2 a-d	4.3 a-d	4.9 a-f	5.4 a-d	5.6 c-g	6.0 fgh
G254	3.8 d-h	3.6 f-l	3.7 h-l	3.9 c-h	4.1 c-g	4.1 cde	4.6 g-k	5.2 d-h	5.4 ghi	6.0 f-i
G255	3.9 c-f	3.8 e-g	4.0 c-g	4.0 a-e	4.2 a-d	4.3 a-d	4.7 d-h	5.3 b-f	5.5 d-h	5.8 g-j
G256	3.9 c-f	3.9 b-e	4.0 b-e	4.0 c-g	4.1 b-f	4.3 abc	5.0 ab	5.4 ab	6.1 a	6.7 ab
G257	3.8 d-i	3.7 e-k	3.8 e-k	3.8 g-n	4.1 b-g	4.1 cde	4.6 h-l	5.1 f-j	5.4 ghi	6.0 f-i
G258	3.9 c-f	3.8 e-h	3.9 d-j	4.0 a-e	4.2 abc	4.3 a-d	4.9 a-d	5.1 e-i	5.8 bc	6.6 ab
G259	3.7 e-j	3.6 g-l	3.7 i-l	3.8 e-l	4.1 b-f	4.1 cde	4.4 j-l	4.9 jkl	5.5 e-i	6.1 efg

G260	3.7 f-j	3.8 e-h	4.1 bcd	4.0 a-e	4.2 a-d	4.3 abc	4.8 a-d	5.6 a	5.8 bc	6.4 bc
G261	4.1 abc	4.1 abc	4.3 ab	4.2 ab	4.4 a	4.3 a-e	4.7 c-i	5.3 b-f	5.4 ghi	5.7 k-l
G262	3.5 ijk	3.5 i-l	3.7 i-l	3.8 d-k	3.9 fgh	4.0 ef	4.3 klm	4.6 n	5.0 klm	5.9 h-k
G263	3.8 d-h	3.7 e-k	3.7 g-l	3.9 b-k	4.0 d-h	4.2 b-e	4.6 g-k	5.0 i-l	5.3 ijk	5.9 f-i
G264	3.8 d-h	3.6 f-l	3.7 i-l	3.9 d-j	3.9 e-h	4.1 cde	4.8 b-h	5.1 e-i	5.7 b-e	6.4 bc
G265	3.9 cde	3.8 e-i	3.8 e-k	3.9 c-h	4.2 a-e	4.1 cde	4.7 c-i	4.9 i-l	5.6 c-g	6.4 bc
G266	3.9 cde	3.7 e-j	3.8 e-k	3.9 b-j	4.0 b-h	4.1 cde	4.3 lm	4.9 jkl	5.4 ghi	6.1 ef

G267	3.6 h-k	3.5 i-l	3.6 kl	3.7 j-m	3.9 gh	4.0 ef	4.3 klm	4.9 jkl	5.3 hij	6.0 f-i
G268	3.7 f-j	3.7 e-k	3.8 f-k	3.9 d-k	4.1 b-g	4.1 def	4.5 i-m	4.6 n	5.0 klm	5.9 g-l
G269	3.5 ijk	3.4 l	3.6 kl	3.7 i-m	4.0 d-h	4.0 cde	4.6 e-j	5.1 e-i	5.6 c-g	6.3 cde
G270	3.4 k	3.4 kl	3.5 l	3.6 m	3.9 gh	3.9 f	4.3 klm	4.7 mn	4.9 m	5.4 klm
G271	3.5 ijk	3.4 kl	3.6 jkl	3.8 f-m	3.9 fgh	3.9 f	4.3 m	4.8 lmn	5.0 lm	5.4 lm
G272	3.5 jk	3.4 kl	3.5 kl	3.7 h-m	3.9 fgh	4.0 ef	4.3 c-i	5.1 e-i	5.6 c-g	6.4 bc
G273	3.7 e-j	3.7 e-k	3.8 e-k	3.9 c-i	4.1 b-g	4.1 cde	5.0 abc	5.2 c-g	5.7 bcd	6.6 ab

G274	4.0 bcd	3.9 c-f	3.9 c-h	3.9 c-i	4.2 a-d	4.1 cde	4.7 c-i	5.2 c-g	5.9 ab	6.8 a
G275	3.9 c-g	3.8 e-i	3.8 e-k	3.9 d-k	3.9 e-h	4.2 b-e	4.5 h-m	5.0 g-l	5.6 b-f	6.4 bc
G276	3.9 cde	3.8 efg	3.9 d-j	4.0 a-e	3.9 e-h	4.0 ef	4.0 d-h	5.3 b-e	5.6 b-f	6.4 bcd
G277	3.9 cde	3.9 b-e	3.9 c-h	4.1 a-d	4.0 c-g	4.1 cde	4.6 f-j	5.3 b-f	5.7 bcd	6.4 bc

[1] Means within a column followed by the same letter are not significantly different using the Waller-Duncan mean separation test (k-ratio = 100).

VIII. FIGURES

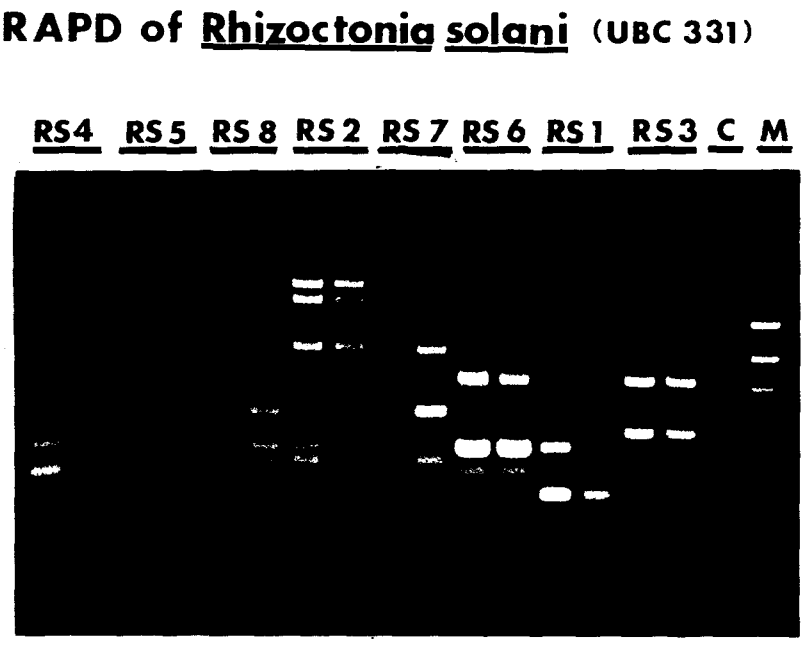

Figure 1. Random amplified Polymorphism DNA (RAPD) analysis of eight isolates of *Rhizoctonia solani* (RS1 to RS8) using UBC331 primer.

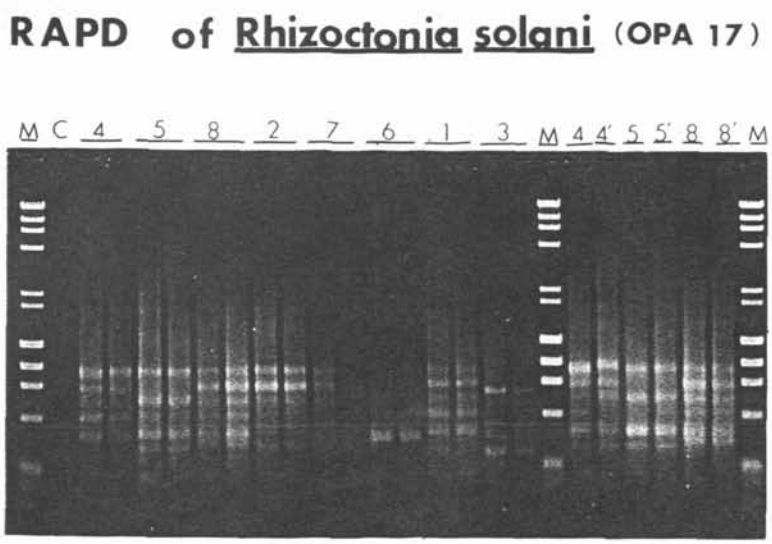

Figure 2. Random amplified Polymorphism DNA (RAPD) analysis of eight isolates of *Rhizoctonia solani* (RS1 to RS8) using OPA17 primer (left). The three most pathogenic isolates (RS4, RS5, RS8) and their re-isolates (RS4', RS5', and RS8', respectively) (right).

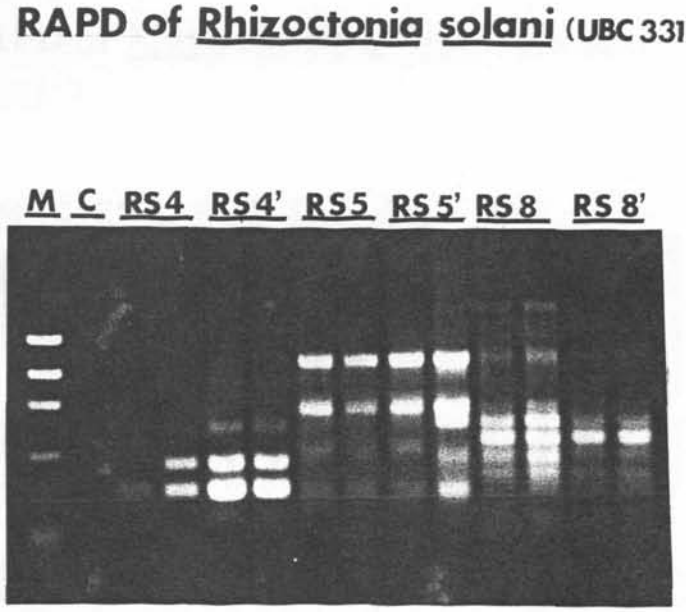

Figure 3. Random amplified Polymorphism DNA (RAPD) analysis of eight isolates of *Rhizoctonia solani* using UBC331 primer. The three most pathogenic isolates (RS4, RS5, RS8) of the eight original isolates (RS1 to RS8) and their re-isolates (RS4′, RS5′ and RS8′, respectively) from inoculated plants.

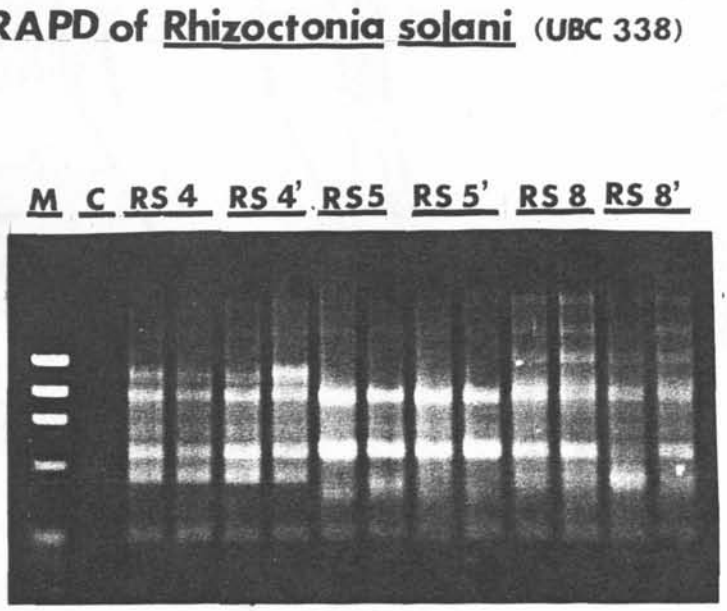

Figure 4. Random amplified Polymorphism DNA (RAPD) analysis of eight isolates of *Rhizoctonia solani* (RS 1-8) using UBC338 primer. The most pathogenic isolates (RS4, RS5, and RS8) of the eight original isolates (RS1 to RS8) and their re-isolates (RS4′, RS5′ and RS8′, respectively) from inoculared plants.

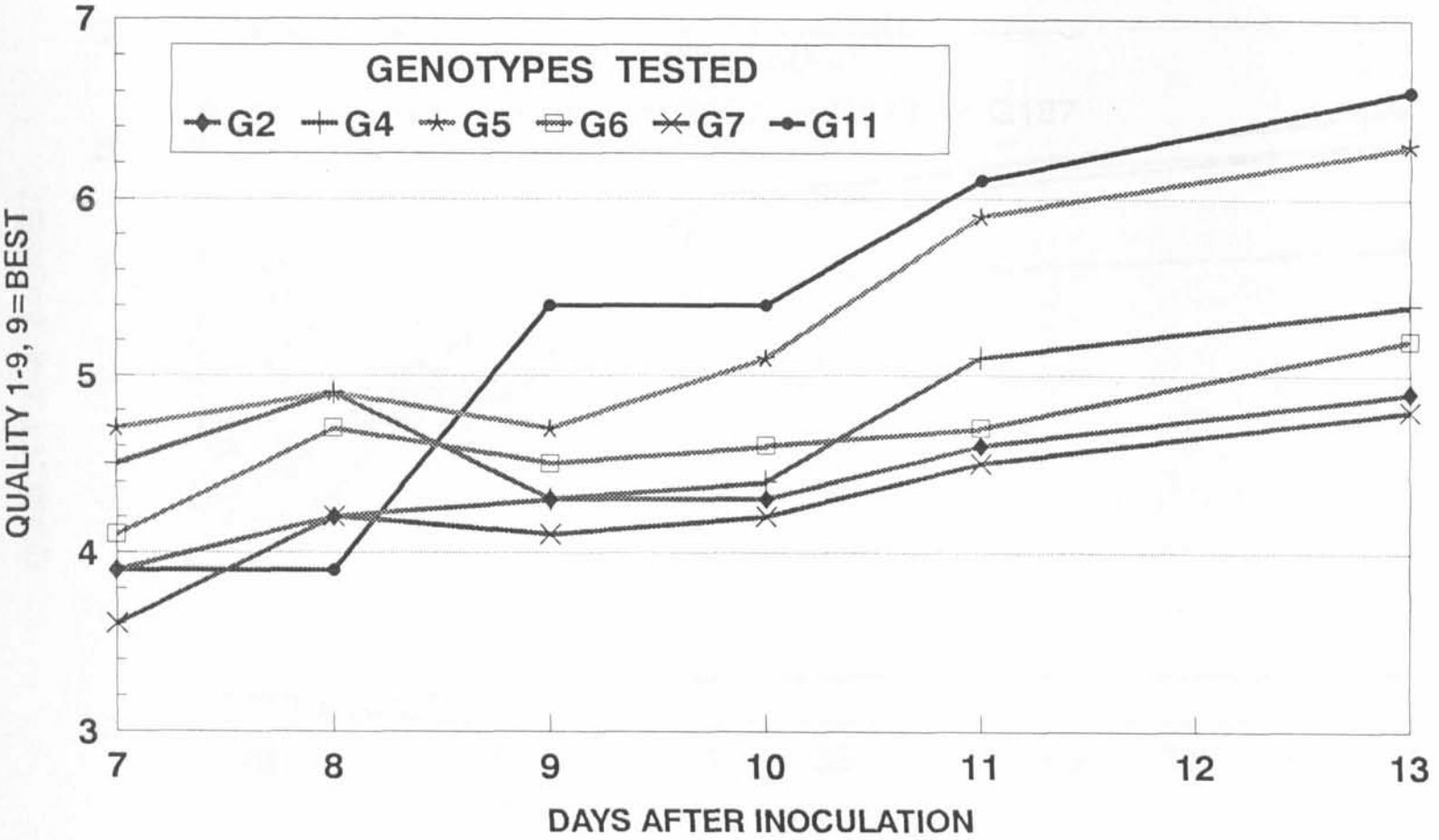

Figure 5. Quality ratings (1-9, 9 = no disease symptoms) of six representative genotypes (of 11 genotypes used in experiment 1) testing the ability of three isolates of Rhizoctonia solani (RS4', RS5', and RS8') to induce disease in Colonial bentgrass germplasm. Each mean is an average of all three isolates.

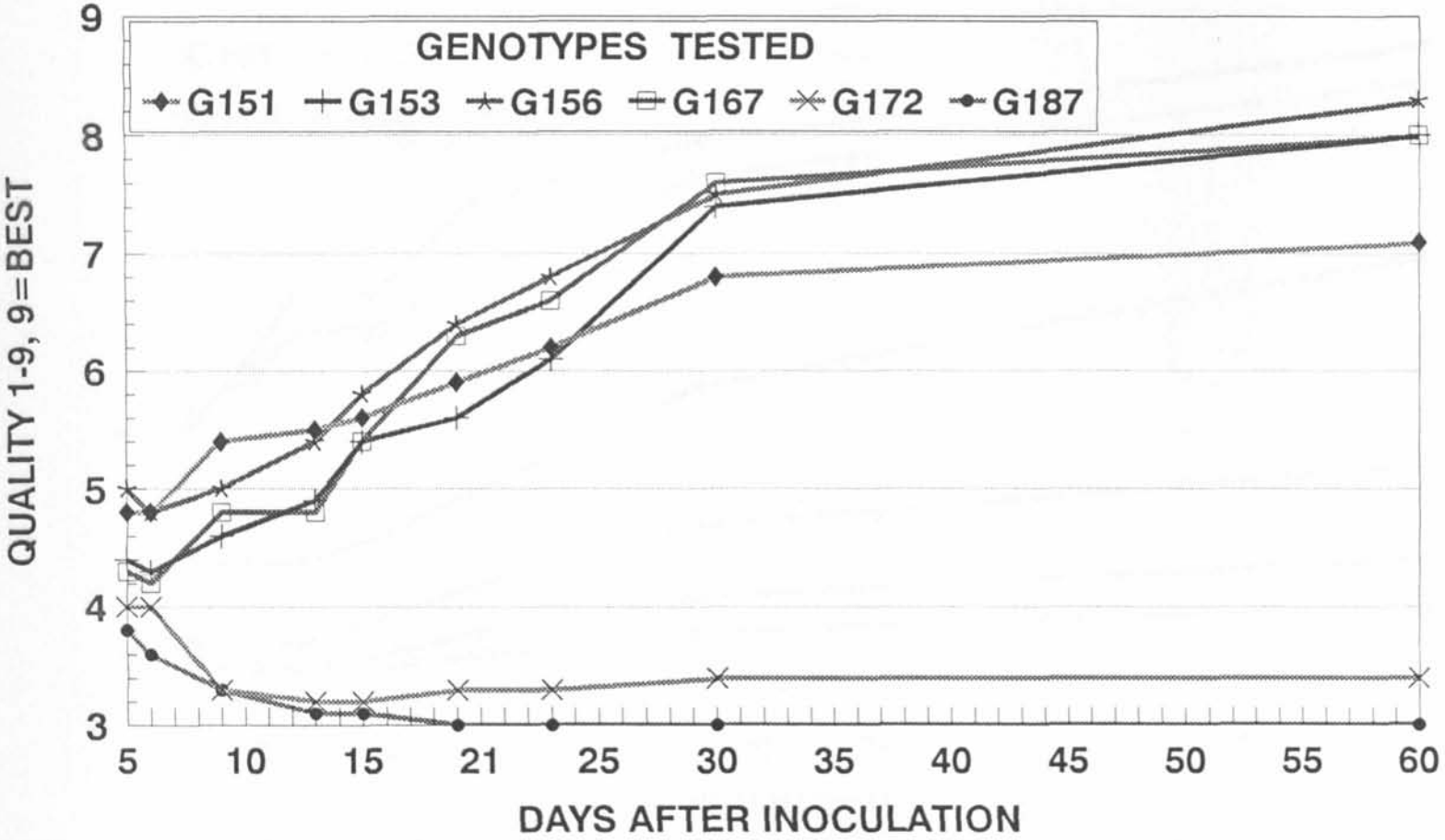

Figure 6. Quality ratings (1-9, 9 = no disease symptoms) of six representative genotypes (of 42 genotypes used in experiment 6) testing the ability of the three isolates of *Rhizoctonia solani* (RS4, RS5, and RS8) to induce disease in Colonial bentgrass germplasm. Each mean is an average of all three isolates.

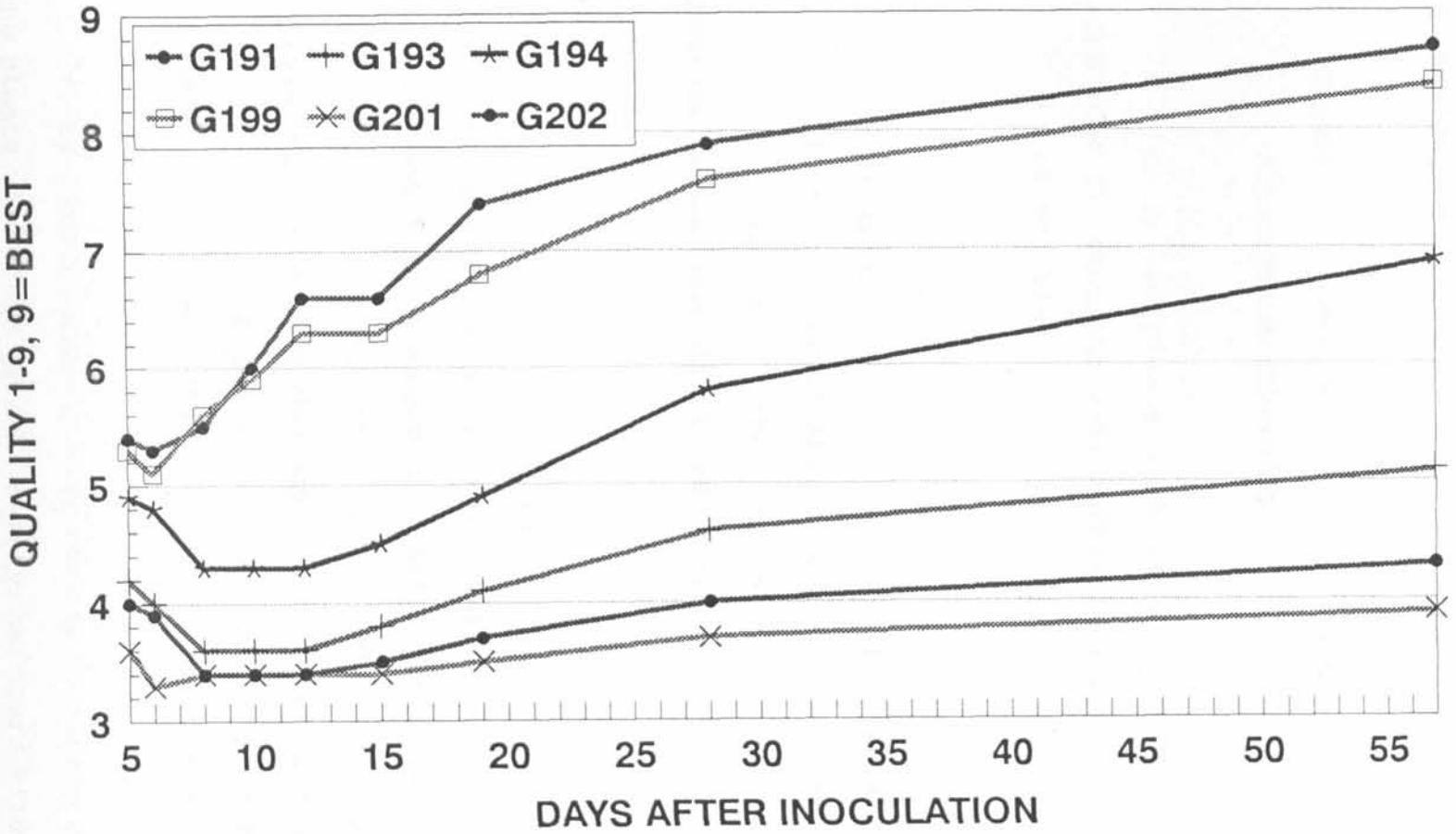

Figure 7. Quality ratings (1-9, 9 = no disease symptoms) of six representative genotypes (24 plants used in experiment 7) testing the ability of three isolates of Rhizoctonia solani (RS4, RS5, and RS8) to induce disease in Colonial bentgrass germplasm. Each mean is an average of all three isolates.

IX. APPENDICES

Appendix A. Summary for first preliminary experiment of brown patch screening.

1. Thirty-six plants each of eight bentgrasses were propagated 27 December 1993. They include:

a) URI 92-2
b) BAR FRIDAY 5
c) NEWPORT CC 20
d) 25
e) URI 92-35 17
f) 14-1
g) URI 92-14
h) 1137 BR 1445

2. Eight isolates of *Rhizoctonia solani* were inoculated in 250 ml erlenmeyer flasks containing sterilized perennial ryegrass seeds and distilled water (1:1 ratio) at room temperature 19 February.

3. Grasses were cut to 1 cm 19 February and arranged in a randomized complete block design with four plants per treatment. Treatments included the control or one of the eight isolates noted in Appendix 1. After inoculation with six perennial ryegrass seeds per plant, plants were placed inside plastic bags which were then sprayed 10 times with a hand mist sprayer. Bags were sealed to maintain high humidity and placed under the greenhouse bench during the day to avoid overheating. Bags were placed atop benches during the night.

4. By 1 March, mycelia grew well on the grass blades, yet the plants were still green. Twenty-two hours after bagging,

plants were removed from the bags. Some leaves turned brown, but crowns were not killed. Two of the four replications were re-bagged to assess for additional damage.

5. Two weeks after treatment, the following results were noted:

a) treatment 7 caused the most damage, with treatments 4, 5, and 8 the next worst, in order from most to least.

b) grass leaves were damaged; crowns were not damaged.

c) all grasses began to recover one week after inoculation.

d) plants of replications 1 and 2 were damaged more than replications 3 and 4, indicating the longer bagging induced more damage.

6. Conclusions: More inoculum per plant and/or longer coverage after inoculation may be advantageous.

Appendix B. Summary for second preliminary experiment of brown patch screening.

1. The following 13 bentgrasses were cloned 36 times 21 February:

a) URI 92-20
b) CAPE COD SALT POND 3
c) BGB 4
d) NEWPORT CC 5
e) HIGH FAIRWAY 16
f) 1 BR 1566 2
g) MT GROVE CEM STRATFORD 5
h) NEWPORT CC 36
i) VB 92-1 20
j) MEADOWEDGE 5
k) OAK HILL 90/22/92
l) 5849 BR 159 2
m) 17
+ 8 plants from Appendix A

2. The eight plants treated in the first preliminary experiment recovered and were retreated as a part of this second preliminary experiment.

3. Eight isolates of *Rhizoctonia solani* were inoculated in 250 ml erlenmeyer flasks containing sterilized perennial ryegrass seeds and distilled water (1:1 ratio) at room temperature 17 March.

4. Grasses were cut to 1 cm 1 April and arranged in a randomized complete block design with four plants per treatment. Treatments included the control or one of the eight isolates noted in Appendix A. After inoculation with eight perennial ryegrass seeds per plant, plants were placed under plastic covers made to fit the plant trays. From 1-4 April,

plants were placed under the greenhouse benches.

5. Mycelia grew well on the plants, with some lesions forming on leaves. Despite the damage, plants retained green color.

6. On 5 April, plants were returned to benches. Although the soil was still wet, plants wilted. The concern was that the plastic covers allowed temperatures to become excessive. Covers were removed to allow grass recovery.

7. Summary: Treatments 2, 4, and 5 caused more damage than other treatments or the control, although the most damage apparently resulted from excessively high temperatures.

Appendix C. Summary for third preliminary experiment of brown patch screening.

1. Nine bentgrasses were cloned 36 times 28 February.

2. Eight isolates of *Rhizoctonia solani* were inoculated in 250 ml erlenmeyer flasks containing sterilized perennial ryegrass seeds and distilled water (1:1 ratio) at room temperature 17 March.

3. Grasses were cut to 1 cm 8 April and arranged in a randomized complete block design with four plants per treatment. Treatments included the control or one of the eight isolates noted in Appendix A. After inoculation with eight perennial ryegrass seeds per plant, plants were placed under plastic covers made to fit the plant trays. During the day, plants were placed under the greenhouse benches to avoid overheating.

4. Covers were removed 11 April, 84 hours after treatments were initiated. Control plants were in good condition, indicating damage resulted from the inoculum rather than heat stress. Treatment 5 inoculum was contaminated by other fungi and had to be disregarded.

5. Conclusions: The amount of inoculum and treatment duration are acceptable. Treatment 8 caused the most damage, followed by treatments 2, 6, and 7, in order.

Appendix D. Summary for fourth preliminary experiment of brown patch screening.

1. The following 27 bentgrasses were cloned 36 times 5 March:

a) URI 92-20
b) 105 BR 1296 10
c) NEWPORT CC 114
d) 105 BR 1296 5
e) NEWPORT CC 26
f) URI 92-21 4
g) URI 92-23 4
h) URI 92-34 1
i) 104 BR 1296 7
j) URI 92-20 1
k) URI 92-19 3
l) URI 92-24 6
m) LIDO CC LI 3
n) 105 BR 1296 8
o) NEWPORT CC 29
p) URI 92-20 4
q) NEWPORT CC 113
r) NEWPORT CC 30
s) BERGEN PT LI 2
t) 105 BR 1296 6
u) BRANFORD CT CEM 6
v) URI 92-22 2
w) URI 92-19 1
x) 105 BR 1296 4
y) URI 92-22 4
z) 104 BR 1296 3
aa) NEWPORT CC 112

2. Eight isolates of *Rhizoctonia solani* were inoculated in 250 ml erlenmeyer flasks containing sterilized perennial ryegrass seeds and distilled water (1:1 ratio) at room temperature 11 April.

3. Grasses were cut to 1 cm 29 April and arranged in a randomized complete block design with four plants per treatment. Treatments included the control or one of the

eight isolates noted in Appendix A. After inoculation with eight perennial ryegrass seeds per plant, plants were placed under plastic covers made to fit the plant trays at 0700.

4. Covers were removed 3 May, 84 hours after initiation of treatments.

5. Plants were scored for quality every 1 or 2 days.

Conclusions of preliminary testing for the three most damaging brown patch isolates:

1. **#4 = Kentucky bluegrass from New England Turf.**
2. **#5 = perennial ryegrass from Segregansett G.C.**
3. **#8 = tall fescue from URI NTEP plots**

APPENDIX E. Colonial bentgrass genotypes used in large-scale brown patch screening.

G1 : BERGENPT LI 11
G2 : BERGENPT LI 7
G3 : PLATT BUR NE 3
G4 : URI 92-3 3
G5 : BERGENPT LI 15
G6 : BERGENPT LI 5
G7 : LAKEVIEW BRIDGEPORT 5-2
G8 : URI 92-28 1
G9 : BRANFORD CT CEM 7
G10: BERGENPT LI 9
G11: BRANFORD CT CEM 8
G12: 60 BR 16 03 2
G13: 1-1
G14: 31 BR 15 77 1
G15: 86 BR 16 27 1
G16: NEWPORT CC 106
G17: 86 BR 16 27 2
G18: CLEAR SM ZIPLOC 2
G19: 4 BR 15 64 1
G20: 53 BR 15 96 3
G21: 1-5
G22: 105 BR 12 96 5
G23: MEADOW EDGE LI 2
G24: 53 BR 15 96 4
G25: 1-4
G26: 1-2
G27: URI 92-29 1
G28: 60 BR 16 03 3
G29: 60 BR 16 03 4
G30: URI 92-11 2
G31: 15 BR 14 33 1
G32: TRINITY CEM PORTS MOUTH. R. 7
G33: URI 92-28 3
G34: 1-7
G35: 1-3
G36: 1-6
G37: 63 BR 16 06 1
G38: 63 BR 16 06 3
G39: MEADOW EDGE LI 20
G40: 31 BR 15 77 2
G41: 4 BR 15 64 2
G42: 53 BR 15 96 2
G43: 63 BR 16 06 4
G44: 53 BR 15 96 1
G45: 31 BR 15 77 3
G46: 63 BR 16 06 2
G47: 60 BR 16 03 1
G48: BRANFORD LI 3
G49: TOWN PARK OFF 84N LNDN CT 7

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G50:  NEWPORT CC  106
G51:  BROOKFIELD CEM ON9  2
G52:  NEWPOT CC   7
G53:  TOWN PARK OFF 84N LNDN CT  4
G54:  TOWN PARK OFF 84N LNDN CT  9
G55:  TRINITY CEM PORTS MOUTH.R.  2
G56:  TRINITY CEM PORTS MOUTH. R.  3
G57:  TOWN PARK OFF 84N LNDN CT  2
G58:  TOWN PARK OFF 84N LNDN CT  1
G59;  TOWN PARK OFF 84N LNDN CT  8
G60:  BP POLO 2ND  14
G61:  TOWN PARK OFF 84N LNDN CT 15
G62:  84 BR 76 25  3
G63:  NEWPORT CC  104
G64:  TOWN PARK OFF 84N LNDN CT  5
G65:  WOODSTOCK CT CEM  4
G66:  TOWN PARK OFF 84N LNDN CT  6
G67:  NOWPORT CC  II
G68:  NEWPORTCC  I
G69:  84 BR 16 25  2
G70:  LAKEVIEW CEM BRIDGEPORT 6-3
G71:  TRINITY PORTS CEM MOUTH R.9
G72:  84 BR 16 25  4
G73:  4 BR 15 64  3
G74:  86 BR 16 27  1
G75:  CEM WOODSHOLE  6
G76:  WOODSTOCK CT CEM  1
G77:  BROOKFIELD  CEM ON9  4
G78:  86 BR 16 27   3
G79:  4 BR 15 64   1
G80:  BP POLO 1ST  14
G81:  105 BR 12 96   9
G82:  BERGENPT LI  17
G83:  MT. GROVE CEM STRATPORT CT 6
G84:  BP POLO 2ND  13
G85:  EAST GREENWICH CC-POND  39
G86:  URI 92-14 1
G87:  BERGENPT LI  4
G88:  NEWPORT CC 64
G89:  URI 92-14  3
G90:  LAKEVIEW BRIDGEPORT  5-1
G91:  LAKEVIEW BRIDGEPORT 6-2
G92:  LOFTS SEED BAG 2
G93;  LOFTS SEED BAG 3
G94:  107 79 BR 157  6
G95:  GREENVALE 1-8
G96:  GREENVALE 1-4
G97:  BERGENPT LI  6
G98:  GREENVALE  2-4
G99:  LAKEVIEW CEM BRIDGEPORT 5-3
G100:  2854
G101:  2841
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G102; 2833
G103; URI 92-142
G104: 2856
G105: DARK GARBAGE BAG 4
G106: 2855
G107: 2840
G108: NEWPORT CC 20
G109: 2862
G110: 2827
G111: 2831
G112: 2839
G113; 2836
G114: 2834
G115: 2853
G116: 2849
G117: 2828
G118: 2850
G119: 2824
G120: 2860
G121: 2841
G122: 2853
G123; 2823
G124: 2933
G125: 2864
G126: 2869
G127: 2867
G128: 2830
G129: 2902
G130: UNKNOWN
G131: 2866
G132: 2852
G133: 2930
G134: 2942
G135: 2931
G136: URI 92-2
G137: 2935
G138: 2936
G139: 2943
G140: 2857
G141: 105 BR 12 '96 3
G142: 2905
G143: 2938
G144: 2922
G145: 2929
G146: 2928
G147: 105 BR 12 96 13
G148: NEWPORT CC 114
G149: 2904
G150: BERGENPT LI 5
G151: 2925
G152: BP POLO 1ST 23
G153: NORWICH CEM CANTER BURYTRAIC 3

G206: GREENVALE 2-6
G207: CAPE COD 7
G208: 2865
G209: 2847
G210: BERGENPT LI 1
G211: LAKEVIEW BRIDGEPORTS 6-1
G212: GREENVALE 2-2
G213: NO TAG #3
G214: 2835
G215: 2868
G216: BP POLO 2ND 19
G217: 2861
G218: 63 BR 16 06 4
G219: 2863
G220: NEWPORT CC 16
G221: 304
G222: 63 BR 16 06 4(?)
G223: 2932
G224: 2903
G225: 105 BR 12 96 7
G226: 105 BR 12 96 1
G227: 2843
G228: BP POLO 2ND 9
G229: 2858
G230: NEWPORT CC 29
G231: UNKNOWN
G232: 51 BR 15 94 5
G233: LOFTS SEED BAG 7-1
G234: HIGH FAIRWAY 9
G235: BERGENPT LI 4
G236: 63 BR 16 06 3
G237: 79 BR 16 20 2
G238: 53 BR 15 96 2
G239: 31 BR 15 77 3
G240: BP POLO 2ND 11
G241: 2846
G242: 2839
G243: GREENVALE 1-9
G244: 105 BR 15 94 2
G245: 51 BR 15 94 2
G246: BRANFORD CT CEM 12
G247: BRANFORD CT CEM 4
G248: BERGENPT LI 15
G249: NEWPORTCC 36
G150: 31 BR 15 77 1
G251: GREENVALE 1-7
G252: 105 BR 12 96 5
G253: 105 BR 12 96 11
G254: BRANFORD CT CEM 2
G255: BERGENPT LI 11
G256: NEWPORT CC 26
G257: BERGENPT LI 14

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G258:  105 BR 12 96  8
G259:  29 BR 15 96  3
G260:  29 BR 15 76  1
G261:  15 BR 14 33  5
G262:  BP POLO 2ND  18
G263:  29 BR 15 76  4
G264:  GREENVALE 2-8
G265:  7 BR 15 66  1
G266:  105 BR 12 96  16
G267:  NEWPORT CC  17
G268:  EAST GREENWICH CC-POND  31
G269:  51 BR 15 94  4
G270:  BP POLO 1ST  18
G271:  BRANFORD CT CEM 14
G272:  7 BR 15 66  2
G273:  105 BR 12 96  12
G274:  105 BR 12 96  8
G275:  105 BR 12 96  7
G276:  BERGENPT LI 8
G277:  LOFTS SEED BAG  8
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