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Selection for resistance to *Cochliobolus sativus* in tall fescue (*Festuca arundinacea* Schreb.) *

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Summary. *Cochliobolus sativus* (Ito and Kurib.) Drechsl. ex Dastur is a major foliar pathogen of tall fescue (*Festuca arundinacea* Schreb.) which can greatly reduce the quantity and quality of forages available for animal consumption. A greenhouse screening program was initiated to determine the inheritance of resistance to *C. sativus* in tall fescue over several cycles of mass selection. Resistance to *C. sativus* in four tall fescue cultivars was increased with 2–3 cycles of mass selection. Realized heritabilities were low to moderate (0.04 to 0.58) indicating that environmental influences on the expression of resistance are quite high. Variances were unchanged by selection, indicating that further improvement should be possible. However, progress with mass selection can be expected to be slow. Lesion size was decreased in each cultivar by selecting for lesion coverage. Lesion size, being independent of inoculum load and therefore less subject to environmental variation, should be considered as an additional selection criteria to improve the rate of progress.

Key words: *Cochliobolus sativus* – *Drechslera sorokiniana* – *Helminthosporium sativum* – Resistance – Forage quality

Introduction

Cochliobolus sativus (Ito and Kurib.) Drechsl. ex Dastur (imperfect stage: *Bipolaris sorokiniana* (Sacc. in Sorok.) Shoem.) (= *Drechslera sorokiniana* (Sacc.) Subram. and Jain) (= *Helminthosporium sorokinianum* Sacc. ex Sorokin. syn. *H. sativum* P. K. and B.) is a major foliar disease of tall fescue (*Festuca arundinacea* Schreb.) (Linscombe 1982; Linscombe et al. 1983; Smith et al. 1984).

Infection by *Cochliobolus* sp. and related genera has been shown to decrease forage yield and digestibility (Allinson and Washko 1972; Cook 1975; Gross et al. 1975; Jessen et al. 1983; Mower and Millar 1963). Smith et al. (1984) reported that *C. sativus* infection of tall fescue increased fiber content and reduced soluble cell contents, digestibility, and dry matter yield. Development of cultivars with high levels of resistance to *C. sativus* would greatly reduce losses associated with this pathogen.

Linscombe (1982) found variation in the levels of resistance to *C. sativus* among plant introductions and cultivars of tall fescue in both greenhouse and field studies. Diallel analysis revealed significant general combining ability (GCA) but not specific combining ability (SCA) for resistance to *C. sativus* (Linscombe et al. 1983). The authors further reported a significant improvement in the level of resistance in four cultivars with a single cycle of mass selection.

The objective of this study was to determine the inheritance of resistance to *C. sativus* over several cycles of mass selection.

Materials and methods

Isolation and preparation of the pathogen

Cochliobolus sativus was isolated from tall fescue plants growing on the Animal Research Center at Mississippi State, MS. The organism was streaked on petri plates on potato dextrose agar and incubated for a minimum of 21 days at 28 °C (Hodges 1972). Inoculum was collected by flooding the Petri plate with 10 ml of distilled water and scraping the fungal mat with a sterilized loop. The resulting conidial-mycelial suspension was then filtered through cheese cloth into a 1,000 ml Erlenmeyer flask. Spore concentration was monitored with a hemocytometer to maintain an inoculum density of approximately 3×10^6 conidia per flat. This inoculum density produced infection levels similar to those ob-

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Table 1. Mean percent lesion coverage ratings, variances, means of selected population, and realized heritabilities of four tall fescue cultivars subjected to several cycles of mass selection for resistance to *C. sativus*

Generation	Mean percent lesion coverage	Variance	Mean of selected population	Realized heritability
	'Alta'			
Parental	2.96	0.82	1.71	0.19
1	2.72	0.75	1.89	0.18
2	2.57	0.70	1.00	0.38
3	1.98	0.87		
LSD (0.05) =	0.22			
	'Kentucky 31'			
Parental	2.95	0.84	1.00	0.08
1	2.79	0.71	1.83	0.56
2	2.25	0.73	1.00	0.22
3	1.98	0.80		
LSD (0.05) =	0.35			
	'MSF 72-1'			
Parental	2.97	0.96	1.46	0.26
1	2.57	0.70	1.90	0.39
2	2.31	0.79	1.00	0.12
3	2.17	0.70		
LSD (0.05) =	0.44			
	'MSF 77-1'			
Parental	2.87	0.86	1.95	0.58
1	2.34	0.73	1.00	0.04
2	2.29	0.71		
LSD (0.05) =	0.34			

Table 2. Mean lesion size of four cultivars and synthetic populations of tall fescue derived from mass selection for resistance to *C. sativus*

Generation	'Alta'	'Kentucky 31'	'MSF 72-1'	'MSF 77-1'
Parental	3.21	2.86	3.06	2.99
1	3.03	2.93	2.88	2.72
2	2.82	2.55	2.42	2.52
3	2.12	2.21	2.52	–
LSD (0.05)	0.28	0.36	0.31	0.51

served under field conditions (Smith 1986). Distilled water was added to the conidial suspension to bring it up to the desired volume. Tween 20 was used as a surfactant at a rate of 0.1 ml/100 ml of conidial suspension. This spore suspension was applied with a hand-held mist sprayer.

Forage grass preparation

Four cultivars, 'Alta', 'Kentucky 31', 'MSF 72-1', and 'MSF 77-1' were screened for resistance to *C. sativus* using mass selection techniques. Cultivars were seeded in 38 × 58 cm wooden flats containing a sand-peat moss mixture. Approximately 2 weeks after emergence, all flats were thinned to 40 plants per flat. Plant material was then screened for resistance using a greenhouse procedure similar to that described by Linscombe (1982). At approximately 6 weeks of age plant material was clipped back to one tiller per plant and inoculated with *C. sativus*. Plants were placed in a mist chamber (ca. 28 °C and 70% R.H.) for 3 days and then removed to a greenhouse bench for an additional 3 days. The last fully expanded leaf on each plant was then individually scored using a subjective scoring system of 1–5 with 1 representing 0–20% of the leaf area covered by lesions, 2 representing 21–40% coverage, 3 representing 41–60%, 4 representing 61–80%, and 5 representing 81–100%. All populations were rated for lesion size in the last cycle of selection with plants rated in class 1 having lesions with a diameter of 1 mm or less, 2 having lesions of 1 to 2 mm, 3 having lesions of 2 to 3 mm, 4 having lesions of 3 to 4 mm, and 5 having lesions larger than 5 mm in diameter.

The first cycle of selection was made by Linscombe et al. (1983) who screened approximately 100 plants each of the cultivars 'Alta', 'Kentucky-31', and 'MSF 72-1'. In the second and third cycles of selection approximately 160 plants of each of the three cultivars were evaluated. Two cycles of mass selection were performed on the cultivar 'MSF 77-1', with approximately 160 plants being screened in each cycle. Plants selected from each population were transplanted to the field into separate crossing blocks in the fall of each year. A 3 m border row of rye (*Secale cereale* L.) was planted around each block to serve as an isolation mechanism. Bulked progenies from each population were then planted in the greenhhouse for each subsequent cycle of selection.

Populations from each cycle of selection and each parental cultivar were planted in the greenhouse in the fall of 1984. Five flats of each population, containing approximately 40 plants per flat, were evaluated for lesion coverage and lesion size in a randomized complete block design with 5 replications. A realized heritability of resistance to *C. sativus* was calculated for each cultivar and cycle of selection using the formula:

$$H = \frac{G - \bar{X}_{pop}}{\bar{X}_{sel} - \bar{X}_{pop}}.$$

Where:

$\bar{X}_{pop}$ = mean of the source population,

$\bar{X}_{sel}$ = mean of the individuals selected from the source population,

G = mean of the population derived from mating the selected individuals.

A least significant difference was utilized to determine difference among selection cycles.

Results and discussion

There were significant differences among generations for resistance to *C. sativus* within each cultivar (Table 1). Within each cultivar the level of resistance in the second and third generations was increased compared to their parental populations. Realized heritabilities were low to moderate and differed among cultivars and generations. Low heritability values were indicative of large environmental influences on the expression of resistance, which can reduce the rate of progress from selection.

Linscombe et al. (1983) reported significant differences for lesion coverage between pre- and post-selected populations for the cultivars 'Alta', 'Kentucky 31', and 'MSF 72-1'. These results differ somewhat from those of the current study. In the current study the first cycle synthetic populations of 'Alta' and 'MSF 77-1' were significantly more resistant than the base populations, however no differences were noted between parental and first cycle synthetic populations for 'Kentucky 31' and 'MSF 72-1' (Table 1). Linscombe et al. (1983) also reported higher heritability values (0.62 to 0.76) than those observed in the current study (0.04 to 0.58). Linscombe et al. (1983) carried out their evaluations in a greenhouse with temperatures of approximately 18 °C. Evaluations in the present study were conducted in a greenhouse at approximately 28 °C, which is the optimum temperature for vegetative growth of *C. sativus* (Tinline and Dickson 1958). This resulted in higher lesion coverage scores and lower heritability values than those reported by Linscombe. This discrepancy further indicates that environmental effects on the expression of this trait are quite high and improvement using mass selection may be slow. These data also suggest that resistance to *C. sativus* may be broken down by higher temperatures.

Cultivars did not respond to selection in the same manner over generations (Table 1). Within 'Alta', there was a steady reduction in lesion coverage score with the third cycle population being significantly lower than the parental and previous synthetic populations. Response to selection was similar in all cycles of selection for 'Kentucky 31', 'MSF 72-1', and the first and second cycles of 'MSF 77-1'. First and second cycle synthetic populations of 'MSF 77-1' corresponded to the second and third cycle synthetic populations of 'Alta', 'Kentucky 31', and 'MSF 72-1' in that both represented the first and second cycles of selection at 28 °C. The two Mississippi cultivars are thought to have some 'Kentucky 31' parentage, which could explain the similarity of response to selection in these three cultivars.

Although the rate of gain being achieved by mass selection was low, there was no reduction in the amount of variation within each cultivar indicating that sufficient variation still existed for further improvement through selection.

Lesion size has been reported to be positively correlated with lesion coverage (Linscombe 1982). Significant differences among generations for lesion size rating were observed in the cultivars 'Alta', 'Kentucky 31', and 'MSF 72-1' (Table 2). Within these cultivars, lesion size was decreased by selecting for decreased lesion coverage. This trait is independent of inoculum load and therefore less subject to environmental effects. Simultaneous selection for lesion size and coverage in future evaluations might help manage the environmental variation currently being encountered and thus increase the rate of progress from selection.

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