FURTHER STUDIES ON THE INHERITANCE OF SOME BLOOMLESS AND SPARSE-BLOOM MUTANTS IN SORGHUM

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1973

Submitted to the faculty of the Graduate College
of the Oklahoma State University
in partial fulfillment of the requirements
for the Degree of
MASTER OF SCIENCE
May, 1979

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ACKNOWLEDGMENTS

Sincere appreciation is expressed to Dr. Dale E. Weibel, the author's major adviser, for his guidance, understanding, and assistance throughout the graduate study. Sincere gratitude is also extended to Dr. M. B. Kirkham and Dr. J. Q. Lynd for their willingness to give their time and assistance by serving as committee members.

Special thanks is expressed to the Agronomy Department of Oklahoma State University for providing the facility which made this study possible.

I am indebted to my brother, Mr. Foong, and my sister, Miss Wimon, for their financial support, encouragement, and understanding throughout the course of this study.

Deep gratitude and appreciation is extended to my father, Mr. Tan Jok Phi, and my mother, Mrs. Cheng Seil Mai, for their generous assistance and encouragement across the sea.

Thanks is also expressed to Sue Heil for her carefulness of typing this thesis.

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CHAPTER I

INTRODUCTION

The greenbug, Schizaphis graminum (Rondani), is a major pest of sorghum in the USA. It has mutated into three biotypes (A, B, and C), and only biotype C attacks sorghum. In 1968 the outbreak of greenbugs attacked several million acres of sorghum in the Western United States. The estimated loss in sorghum due to infestation of the greenbug was in excess of $20,000,000.

The biotype C greenbug has shown nonpreference for "bloomless" sorghum especially as the age of the plant increases. The waxy substance or bloom that covers sorghum stems and leaves occurs at three intensities:

1) Heavy bloom (plants covered with thick layer of wax at internode, leaf sheath, and base of blade).

2) Bloomless (plants with the absence of wax).

3) Sparse-bloom (intermediate between bloom and bloomless, mostly covered with light layer of wax on leaf sheath and internode).

The purpose of this genetic study of the bloomless and sparse-bloom characters in sorghum was to determine the nature of the inheritance of the characters to facilitate breeding procedures, and further to determine the number of genes involved in the bloomless and sparse-bloom lines available for study.

CHAPTER II

REVIEW OF LITERATURE

Greenbugs, Schizaphis graminum (Rondani), traditionally a pest of grain sorghum (Sorghum bicolor L. Moench) in the USA, were first investigated by Webster (31) in 1884 at Oxford, Indiana. Because of the lack of economic importance, it was not given any special attention until 1968. The outbreak of this insect on sorghum in the Midwest and Southwest area caused losses of grain valued in excess of $20,000,000 (30). Since then it has been considered a major pest of sorghum, and the character and biotype of this greenbug has been studied extensively while searching for resistant germplasm in sorghum.

Biotypes of the Greenbug

Since the reproduction of aphids is primarily parthenogenetic, the opportunity for intraspecies variation should be less than in sexual species. However, several aphid biotypes have been discovered. In 1961 Wood (35) reported the existence of a new greenbug biotype that was able to destroy the resistant wheat lines Dickinson Sel. 28A and C. I. 9058. But it was found only in the culture maintained in the greenhouse, so he called it "greenhouse strain" while the previous strain was called "field strain". Later the greenhouse strain was designated as biotype B and the field strain as biotype A (36). Harvey and Hackerott (8) in 1969 recognized that biotype C preferred

sorghum and sudangrass while biotype B preferred barley, wheat and rye. They also reported that the outbreak which occurred in 1968 was caused by biotype C strain. Wood et al. (36) in 1969 pointed out the difference among these three biotypes. He noted that biotype A and B were similar in morphological and ecological characteristics, but both differ from biotype C. Biotype A and C both feed in phloem sieve-tubes of the leaf vascular bundles while biotype B appeared to feed in the parenchyma cells of plants. All wheats were susceptible to biotypes A, B and C except Dickinson Sel. 28A and C. I. 9058 which were resistant to biotype A. Biotype C not only infested small grain and sorghum, but it reproduced and survived in higher temperatures than biotypes A and B. Saxena and Chada (22) confirmed the feeding habit of biotype A and biotype B. The damage to plant tissue by biotype A was found mainly in the phloem which appeared completely collapsed, and no distinction could be made between the phloem parenchyma and sieve tube elements. Biotype B damaged only the mesophyll cells of the leaves. Wood (38) in 1971 studied the reaction of these three different biotypes of greenbug on resistant and susceptible selections of sorghum by evaluating the host preference, fecundity, longevity, and antibiosis. He found that all three biotypes showed a high degree of nonpreference to all the resistant entries, while there was a wide difference in performance among biotypes for fecundity and longevity. Biotype A did not survive on the resistant species, biotype B performed slightly better than A, but biotype C survived and reproduced on the resistant species almost as well as on susceptible species. Antibiosis studies showed that greenbugs cultured on susceptible entries were about three times the weight of those reared

on resistant species. He indicated that these markedly different reactions of the biotypes to resistant and susceptible sorghum can, therefore, be used to separate the three biotypes. Harvey and Hackerott (9) used seedings of barley, rye, wheat, and sudangrass to test for resistance to biotype B and biotype C. They found that Piper sudangrass, Caribou selection rye, and C. I. 9058/7 Bison wheat were resistant to biotype B but susceptible to biotype C. Only Dicktoo barley and Insave F. A. rye were resistant to both biotype B and biotype C. Starks et al. (23) compared the nonpreference of biotype B and C on Deer broomcorn and on RS610. They found that biotype B showed nonpreference for Deer over RS610 while biotype C showed no difference in preference for Deer and RS610.

Recently Starks and Burton (26) separated greenbugs into four biotypes: A, B, C, and D, on field crops. Biotype A and B had the same appearance and the same host species (wheat, barley, oat, and rye). They differed from biotype C and D in that C and D attacked sorghum. Plant species resistant to C were also resistant to A except C. I. 1579 and C. I. 1580 of oats which were susceptible to B. Biotype D gave the same reaction on plants as biotype C but had as much as thirty fold more resistance to some organophosphorus insecticides than biotype C.

Greenbug Resistance in Sorghum

Painter (15) proposed that resistance as seen in the field consists of three components: 1) Preference and nonpreference of the insect for the host plant, 2) Antibiosis, and 3) Tolerance. Hackerott et al. (6) rated 648 cultivars and breeding lines from diverse sorghum

types for plant injury and greenbug populations in a natural heavy greenbug infestation in the field. They also surveyed 157 entries for resistance to greenbug in the greenhouse by mass infestation and evaluated the seedling survival and injury. They reported that varieties tolerant to greenbug attack in the field were Sudan-grain, Shallu, some waxy endosperm lines and derivatives of these three types. PI 38108, T. S. 1636 (both S. virgatum derivatives), and Sudan-grain were resistant in the greenhouse, while Leoti, certain Shallu and waxy endosperm types, and some grassy sorghums including sudangrass were classified as intermediate.

For the inheritance study they evaluated the seedling survival from the resistant parent H3411 (S. virgatum derivative), the susceptible parent KS8A, and their F_1 and F_2 progenies. They also studied the F_2 population of H3411 x Sudan-grain (both are resistant). They found that in the cross of resistant x susceptible, the F_1 and the resistant parent survived 100% while the susceptible parent was killed. The F_2 population segregated into resistant and susceptible plants in the ratio of 9:7. But the F_2 population of two resistant sources did not segregate for resistance. From this segregation they concluded that resistance was controlled by dominant genes at more than one locus and that all sources of resistance appeared to trace to S. virgatum. They also suggested that tolerance was an important component of resistance in S. virgatum. Wood et al. (37) screened 263 sorghum varieties for greenbug tolerance and found only one entry (SA 7536-1) with high tolerance to all three greenbug biotypes. The antibiotic effect study showed that SA 7536-1 was a very poor greenbug host. Studies also indicated that SA 7536-1 had nonpreference. Weibel et al.

(32) found that the F_1 of a susceptible x a resistant line gave an intermediate score between the parents. The F_2 segregating population showed that the inheritance of resistance probably was controlled by a single incompletely dominant factor. They anticipated no difficulty in transferring resistance to adapted lines. Teetes and Johnson in 1973 (27) determined the number of greenbugs on grain sorghum required to cause damage and yield loss. They reported that greenbug population levels of about 1300-1500 per plant resulted in the loss of more than three leaves at the bloom stage and also caused significant yield loss. A medium population density which killed two or three leaves per plant did not significantly decrease the yield. Teetes et al. (29) in 1976 determined that under natural greenbug infestation 700 greenbugs per plant caused no significant leaf damage or yield loss on resistant varieties. However when greenbug populations reached about 2500 per plant, yield and seed size were decreased. Also they found no benefit from using insecticides on resistant sorghum under natural greenbug infestation. They reported that the economic threshold should be based on damage and not on greenbug numbers for both resistant and susceptible sorghums. Harvey and Hackerott (10) reported that greenbug infestations in the seedling stage significantly reduced grain and forage yields in a susceptible cultivar but not in a resistant one or in the heteroresistant F_1 hybrid. Teetes et al. (28) compared the leaf damage, grain yields, and seed weights of three greenbug resistant hybrids with a susceptible hybrid. They were compared under both natural and artificial greenbug infestation, and under both insecticide treated and untreated conditions. They found that under natural infestation, the susceptible hybrid suffered greater leaf damage and

grain yield reduction than the resistant hybrids, but there was no difference in kernel weight. Under artificial infestation grain yield and kernel weight were reduced both in the resistant hybrids and the susceptible hybrid with the susceptible hybrid being reduced more. The insecticide treated and nontreated condition showed no difference in grain yield and kernel weight for the resistant hybrids, but higher grain yield and kernel weight were obtained from the treated susceptible hybrid. They concluded that hybrids with resistance incorporated from one parent should not sustain yield loss from natural greenbug population levels, and that in their test the use of an insecticide treatment under field conditions did not increase the yield of resistant hybrids. Starks and Wood (25) compared the damage of a resistant sorghum variety (IS 809) with a susceptible variety (Wheatland) at 12, 24, 36 and 48 days of age. They found that IS 809 was not affected by the greenbug infestation in any growth stage, while the susceptible Wheatland was severely damaged and killed even when the infestation was begun at 36 or 48 days. Very little additional growth took place when the infestations were done at 12 and 24 days. Johnson et al. (11) using two resistant lines (IS 809 and SA 7536-1), three of their F_1 hybrids with greenbug-susceptible A-lines, three susceptible hybrids, and one susceptible line (SD 100), tested for yield under natural infestation by comparing plots treated and untreated with disulfoton insecticide. They found that the increase in grain yield of treated plots was larger, but not significantly larger, for the susceptible hybrids than for the resistant hybrids. They indicated that the resistance of the resistant lines and their F_1 hybrids made with susceptible A lines was sufficient to survive under a natural greenbug

infestation.

Kofoid et al. (12) studied the relationship of greenbug resistance to various agronomic traits by testing 100 greenbug-resistant and 100 greenbug susceptible S_2 progenies derived from a sorghum random mating population. In the absence of greenbug infestation no differences existed between these two populations for any of the traits studied. The presence of a greenbug infestation resulted in a greater mean for height, grain yield, grain weight per plant, grain weight per head, and live leaves per plant in the resistant populations. Starks and Schuster (24) used 10 selections that showed some degree of resistance in previous tests to determine the components of resistant (nonpreference, antibiosis, and tolerance). They found that only five entries (PI 229828, IS 809, Shallu Grain, PI 302178, and PI 226096) appeared to possess a comparatively high degree of all three components of resistance. PI 308976 had an intermediate level of all three components while entries PI 264453 and Piper sudangrass were intermediate for nonpreference to both apterate and alate forms of the greenbug. The last two entries (PI 220248 and PI 302231) showed relatively less tolerance.

Greenbugs On Small Grains

Chada et al. (2) reported in 1951 the screening of the domestic and U. S. Department of Agriculture world collections of small grain varieties and hybrid lines in searching for greenbug resistant germplasm. There were more than 18,860 varieties and strains in the tests. They reported that in wheat, only Dickinson Sel. 28A and C. I. 9058 were found resistant to greenbugs. In barley they found that Omugi,

Kearney, and Dobaku survived and produced grain while the others were killed. In oats Andrew, New Nortex, Russian No. 77 (CI 2898), and PI 183990 seemed to be more resistant than the rest.

Painter and Peters (14) screened more than 2,000 foreign wheat introductions with Pawnee as a susceptible check for greenbug resistance and reported that most of the strains were more susceptible than Pawnee. Only 4% of the strains carried some resistance. They also screened the F_1 and F_2 populations of Dickinson crossed with three susceptible winter wheats (Pawnee CI 11669 x Dickinson Sel., Chiefkan-Oro-Tenmarq CI 12578 x Dickinson Sel., and Concho CI 12517 x Dickinson Sel.). They found that among 872 F_2 plants exposed to the greenbug, 207 plants survived the infestation which was quite close to 3:1 ratio. They then suggested that there was a single major genetic factor difference for this type of reaction to the greenbug in wheat. Wood et al. (34) in 1960 crossed two resistant wheat lines DS 28A and CI 9058, with the susceptible varieties Ponca, Concho, and Crockett to determine the genetics of greenbug resistance. They found that resistance was conditioned by a single recessive gene pair, gb gb. They also reported that resistance could be readily transferred from DS 28A and CI 9058 to other strains of wheat. Porter and Daniels (18) reported in 1963 a study of the inheritance and heritability of greenbug resistance in F_1, F_2, F_3, F_4, and backcross generations of the cross Concho times Dickinson Sel. 28A. They found that the heritability of greenbug resistance in wheat was greatly influenced by the environment. If the environmental factors were minimized by replication, resistance was highly heritable. So they concluded that resistance from DS 28A could be transferred to a

commercial winter wheat variety by commonly used breeding methods, if factors contributing toward greenbug resistance do not in addition contribute toward undesirable agronomic characteristics.

Gardenhire (3) in 1964 used "Russian 77" (Avena sativa), a greenbug resistant line of oats, to cross with "New Nortex" (Avena byzantina C. Koch), and Texas Sel. 2, to study the inheritance of greenbug resistance in oats. Based on data from the segregating population in F_2 and F_3 generations, he hypothesized that the inheritance of greenbug resistance in the oat variety Russian 77 was conditional by a single gene pair. Gardenhire (4) in 1965 crossed four strains of greenbug susceptible barley, R 244-1, R 431, Cebada Capa, and Rogers to the resistant strains Omugi or a selection from Cordova x Omugi to determine the inheritance of greenbug resistance in barley. He concluded from the segregation of F_1, F_2, and F_3 populations that resistance from Omugi barley was controlled by a single dominant gene, and that there was no association between the gene for greenbug resistance and the genes conditioning green-seedling, powdery mildew resistance, leaf rust resistance, and orange lemma. In 1973 Gardenhire et al. (5) used primary trisomic and tertiary trisomic homozygous translocations in "Will" cultivar of barley to study the linkage group of the gene for greenbug resistance. They found that the resistant gene was on linkage group 1 located on the centromere bearing segment of chromosome 1 in the T1-6a translocation. Hackerott and Harvey (7) conducted a growth chamber study of the reaction of biotype C greenbug to "Gahi" pearl millet, "White wonder" foxtail millet, "Turghai" proso millet, and "Combine Kafir-60" grain sorghum. They found that the greenbugs survived, reproduced well, and caused more damage to grain

sorghum than any of the three millets. Among these three millets greenbugs appeared more numerous on pearl millet and next on foxtail millet.

Bloomless Sorghum

In 1937 Rangaswami Ayyangar et al. (19) reported that all sorghum types, when examined under the microscope, had a very light basic layer of wax on the leaves, leaf sheaths and internodes which was invisible to the naked eye. Over this basic layer there was a more conspicious waxy covering visible to the naked eye in all sorghums. The degree of this waxy substance makes it possible to separate sorghum into types with heavy bloom and sparse-bloom. The heavy bloom condition was dominant to the sparse-bloom which was controlled by a single gene h h. In 1941 Rangaswami Ayyangar and Ponnaiya (20) found that an African variety from Tanganyika named Vigage was devoid of this waxy substance. When they crossed this bloomless cultivar with a heavy bloom variety all F_1 plants had heavy bloom, and in the F_2 generation the plants segregated into heavy bloom and bloomless in the ratio of 3:1. In the cross between bloomless and sparse-bloom, all F_1 plants also showed the heavy bloom condition, while in the F_2 population the plants segregated into 9 heavy bloom:3 sparse-bloom:4 bloomless. From this segregation pattern they designated Bm as the gene responsible for the production of bloom in sorghum, while the bm allele gave an absolutely bloomless condition. The gene H had no visible expression. This segregation also indicated the possibility of two alleles involved in this character with a recessive epistatic effect of one gene. Peiretti (16) studied greenbug resistance in sorghum as related to the bloomless

character since bloomless sorghums exhibit a high degree of nonpreference to greenbugs. He studied a bloomless line (RWD3-Weskan), a normal resistant line (Shallu Grain), their F_1, F_2, and a susceptible check (RS 610). He reported that the bloomless character was regulated by a single recessive pair of genes with the expression of bloom being dominant to bloomless. The bloomless trait from RWD3-Weskan (nonpreference) was inherited independently from alleles which regulated the expression of tolerance to damage from Shallu Grain, and the tolerance to damage was regulated by a single pair of alleles with partial or no dominance. Amini (1) also studied the nature of the resistance of bloomless sorghum to greenbug. He confirmed the nature of the inheritance of the bloomless character, and also reported that the bloomless type of resistance from RWD3-Weskan (nonpreference) and the normal type of resistance from IS 809 (tolerance) were regulated by independent factors. There appeared to be no difficulty in combining them to improve the resistance character. From a nonpreference study he concluded that the bloomless sorghum appeared to increase in nonpreference with the increase in the age of the plants and they were not significantly different from plants with IS 809 resistance at 50 and 70 days of age. Weibel et al. (33) counting the number of greenbugs on bloom and bloomless sorghums found that there were fewer greenbugs on bloomless plants at three and four weeks after emergence. This indicated the nonpreference of greenbugs at an early stage of plant development. They found that the numbers of greenbugs increased on the plants with bloom but not on the bloomless plants as the age of plant increased. Martin (13) studied the antibiosis of bloomless sorghum and showed that the rate of reproduction of the greenbug was

lower on the bloomless sorghums than on their respective near isogenic bloom sorghums. This difference seemed to increase as the age of plants increased. Ross (21) compared the yield of normal Combine Kafir-60 with a near isogenic bloomless line of the same variety and reported that bloomless sorghum produced highly significantly less yield than normal sorghum. Peterson (17) crossed five bloomless and four sparse-bloom lines in a partial diallel cross system to determine the number of genes involved. From the segregation of F_1, F_2, and backcross populations he concluded that among the bloomless x bloomless crosses only one cross appeared to have the same locus involved. The crosses among sparse-bloom x sparse-bloom all indicated separate loci were involved and all bloomless x sparse-bloom crosses indicated that different loci were involved.

CHAPTER III

MATERIALS AND METHODS

Parents

Five bloomless, four sparse-bloom, and two bloom sorghum lines were used in this study. The bloomless lines were RWD3 x Weskan-431122, Redbine-60, R Combine Kafir-60, Brooks, and Cyto. 13 x Tan Sugar Drip-1311 (Table I). The bloomless RWD3 x Weskan-431122 and Cyto. 13 x Tan Sugar Drip-1311 appeared as mutants in early generation breeding rows in the Oklahoma breeding program. Bloomless Redbine-60 originated in the DeKalb breeding program at Lubbock, Texas. Bloomless R Combine Kafir-60 was developed in the Kansas breeding program at Hays, Kansas, and bloomless Brooks was developed or discovered by the late J. S. Brooks as a genetic stock in Oklahoma.

The four sparse-bloom lines consisted of Redlan derivative, Redlan x Wiley-1221122, Martin, and Redlan x ROKY10-Calico-11 (Table I). The Redlan derivative and Redlan x ROKY10-Calico-11 appeared as mutants in segregating rows in the Oklahoma breeding program. Redlan x Wiley 1221122 originated from the sparse-bloom Wiley parent in the Oklahoma program. Martin was developed in the Kansas breeding program at Hays, Kansas.

The bloom sorghums were BOK8 and Redlan. BOK8 was developed by J. B. Sieglinger at Woodward from the cross between Dwarf Kafir x

TABLE I

PARENTAL LINES OF BLOOMLESS, SPARSE-BLOOM, AND BLOOM SORGHUM WITH APPROPRIATE GENETIC DESIGNATION

Pedigree	Genetic Designation[1]
RWD3 x Weskan-431122	bm_1
Redbine-60	bm_2
R Combine Kafir-60	bm_3
Brooks	bm_4
Cyto-13 x Tan Sugar Drip-1311	bm_5
Redlan Derivative	h_1
Redlan x Wiley-121122	h_2
Martin	h_3
Redlan x ROKY10-Calico-11	h_4
Redlan	Bm_R
BOK8	Bm_O

[1] bm - bloomless; h - sparse-bloom; Bm - bloom.

Sedan Red Kafir-8-2 for the purpose of combining earliness with dwarfness and standability. In 1966 the Oklahoma Agricultural Experiment Station released the A-line and B-line as an early parent variety. Redlan originated from the cross between Kafir x Milo-8-2-6 (C. I. No. 1090) and Standard Blackhull Kafir (C. I. No. 71) made in 1936 at Woodward with the objective of developing a better kafir. It was released as a dwarf red kafir in 1948.

All the parental lines were designated for their genetic trait with letters plus a number. The bloomless lines were assigned the letters "bm" for bloomless with numbers from 1 to 5 (bm_1 - bm_5). The sparse-bloom lines were assigned the letter "h" for sparse-bloom and numbers from 1 to 4 (h_1 - h_4). The bloom lines were given the letter "Bm" for bloom and the subscript of "R" for Redlan and "O" for BOK8.

The number which was assigned to each trait was a temporary designation and may be withdrawn or reassigned when the number of dictinctly different genes for the bloomless and sparse-bloom have been determined.

Growing of Parents and Making of Crosses

During the summer of 1977 four bloomless lines (bm_2 - bm_5) and two sparse-bloom lines (h_1 and h_4) were planted in the field at the Perkins Agronomy Research Station. From these parental lines six crosses among bloomless lines, and four crosses between bloomless and sparse-bloom lines were made (Table II and III). All parental lines were grown in pots with three plants per pot in the greenhouse at Oklahoma State University during the summer of 1977. All of the bloomless and sparse-bloom lines were crossed to one or both of the

bloom lines Redlan and BOK 8 by hand emasculation of the bloomless and sparse-bloom parents (Tables IV and V). Peterson (17) studied the remaining combinations of the diallel.

Growing of the F_1 Generation

All F_1 seeds obtained either from the greenhouse or from the field were grown in pots with three plants per pot, in the greenhouse during winter 1977-1978. Heads were bagged before flowering to ensure the production of F_2 selfed seed. Plants were irrigated as needed to facilitate the expression of the bloom character in the plants. Visual classification of the plants for the bloom, sparse-bloom, and bloomless characteristics was made and recorded. The plants reached their highest concentration of bloom about 6-7 weeks after planting.

Growing of the F_2 Generation

All F_2 seeds which were obtained from the greenhouse were planted in rows at the Perkins Agronomy Research Station, Perkins, Oklahoma, on June 16, 1978. The experimental rows were 7.6 meters long and 91.4 centimeters apart. Each population consisted of seed from at least two F_1 generation plants. One to six rows were sown for each population. The total number of plants in each population ranged from 23 to 441.

The soil was a Teller loam, a member of the fine loamy, mixed, thermic family of Udic Arginstolls. Fertilizer was applied at the rate of 133 kg N per hectare of 45-0-0 and 114 kg K_2O per hectare broadcast preplant. Sprinkler irrigation was supplied when necessary.

Three weeks after planting plants were thinned to one plant approximately every 15 centimeters. During the early head stage (about 6-7 weeks after planting), all plants were classified by visual observation as bloom, bloomless or sparse-bloom.

Statistical Analysis

Populations were put into four groups according to the crosses (bloomless x bloomless, bloomless x sparse-bloom, bloomless x bloom, and sparse-bloom x bloom). The Chi-square (x^2) goodness of fit test was used as the statistical test of the segregation ratios.

TABLE II

SUMMARY OF F_1 PLANT REACTION FROM BLOOMLESS x BLOOMLESS CROSSES

Crosses	F_1	Crosses	F_1
bm_2 x bm_4	-[1]	bm_3 x bm_5	-
bm_3 x bm_2	-	bm_5 x bm_2	-
bm_3 x bm_4	-	bm_5 x bm_4	-

[1] - = bloomless

TABLE III

SUMMARY OF F_1 PLANT REACTION FROM BLOOMLESS x SPARSE-BLOOM CROSSES

Crosses	F_1	Crosses	F_1
bm_2 x h_4	+[1]	bm_4 x h_1	+
bm_3 x h_4	+	bm_4 x h_4	+

[1] + = bloom

TABLE IV

SUMMARY OF F_1 PLANT REACTION FROM BLOOMLESS x BLOOM CROSSES

Crosses	F_1	Crosses	F_1
$bm_1 \times Bm_R$	+[1]	$bm_4 \times Bm_R$	+
$bm_1 \times Bm_0$	+	$bm_4 \times Bm_0$	+
$bm_2 \times Bm_R$	+	$bm_5 \times Bm_R$	+
$bm_3 \times Bm_0$	+		

[1] + = bloom

TABLE V

SUMMARY OF F_1 PLANT REACTION FROM SPARSE-BLOOM x BLOOM CROSSES

Crosses	F_1	Crosses	F_1
$h_1 \times Bm_R$	+[1]	$h_3 \times Bm_0$	+
$h_2 \times Bm_R$	+	$h_4 \times Bm_R$	+
$h_2 \times Bm_0$	+	$h_4 \times Bm_0$	+
$h_3 \times Bm_R$	+		

[1] + = bloom

CHAPTER IV

RESULTS AND DISCUSSION

Bloomless x Bloomless Crosses

All of the crosses of bloomless x bloomless produced F_1 plants that were bloomless which apparently resulted from homozygous recessive bmbm alleles in each parent (Table II). In the F_2 generation all plants were bloomless also (Table VI) while segregation for plant height and for date of first bloom were evident. Based on this lack of segregation for bloomlessness, it was concluded that the same gene was involved in the bm_2, bm_3, bm_4, and bm_5 mutants. Peterson (17) found that the crosses between bm_1 and bm_2, bm_3, bm_4, or bm_5 all produced bloom F_1 plants and all segregated in F_2 in a ratio of 9 bloom:7 bloomless, indicating bm_1 to be different from the other bloomless mutants. Only one cross between bm_5 x bm_2 produced all bloomless F_1 and all bloomless F_2, indicating that the same loci were involved. The present study substantiated the similarity of bm_5 and bm_2.

Bloomless x Sparse-bloom Crosses

All of the F_1 plants produced from bloomless x sparse-bloom crosses had bloom (Table III), which resulted from one dominant Bm allele and one recessive bm allele at one locus, and one dominant H

TABLE VI

THE CLASSIFICATION OF F_2 PLANTS OF BLOOMLESS x BLOOMLESS CROSSES

Crosses	Number of Plants		
	Bm[1]	bm[1]	Total
bm_2 x bm_4	--	185	185
bm_3 x bm_2	--	198	198
bm_3 x bm_4	--	233	233
bm_3 x bm_5	--	162	162
bm_5 x bm_2	--	192	192
bm_5 x bm_4	--	183	183

[1]Bm = bloom; bm = bloomless

allele together with one recessive h allele at the second locus (BmbmHh). The analyses of F_2 plant types are presented in Table VII. The populations were classified into three categories on the basis of the level of the presence of the waxy substance on the plant:the presence of heavy bloom as bloom, lighter bloom as sparse-bloom, and the absence of bloom as bloomless. These observed numbers were compared with the expected values under the segregation ratio of 9 bloom:3 sparse-bloom:4 bloomless. Two distinct loci were involved with complete dominance at each locus, but the bm gene when homozygous recessive, is epistatic to the h gene.

The expression of the bloom character in F_2 plants required at least one dominant Bm allele at one locus, and one dominant H allele at the other locus. The genotype of this plant would be Bm_H_. To induce the expression of the sparse-bloom character it was necessary to have homozygous recessive hh alleles at one locus and at least one Bm allele at the second locus. The genotypes would be hhBmBm or hhBmbm. The homozygous recessive bmbm alleles at one locus induced the expression of the bloomless trait regardless of any other allele at the second locus (two gene interaction with the homozygous recessive bmbm alleles epistatic to the homozygous hh genes). The possible genotypes would be bmbmHH, bmbmHh, or bmbmhh.

The cross of bm_2 (Redbine-60) x h_4 (Redlan x ROKY10-Calico) produced 107 individual plants in the ratio of 67 bloom:14 sparse-bloom:26 bloomless. The x^2 analysis obtained the probability level of 0.50-0.25. Since a x^2 test of 0.05 or larger indicates a good fit, this indicated a good fit of the observed to the expected ratio and that two separate loci were involved in bm_2 and h_4.

TABLE VII

THE CLASSIFICATION OF F_2 PLANTS OF BLOOMLESS x SPARSE-BLOOM CROSSES WITH CHI-SQUARE AND PROBABILITY VALUES

Crosses		Number of Plants				Values	
		Bm[1]	h[1]	bm[1]	Total	x^2	P
Expected ratio 9:3:4							
bm_2 x h_4	(O)[2]	67	14	26	107	1.624	.50-.25
	(E)[3]	60.18	20.06	26.75			
bm_3 x h_4	(O)	73	30	46	149	3.60	.25-.10
	(E)	83.81	27.93	37.25			
bm_4 x h_1	(O)	108	34	70	212	7.34	.05-.025
	(E)	119.25	39.75	53.00			
bm_4 x h_4	(O)	124	42	58	224	0.103	.95
	(E)	126.00	42.00	56.00			

[1]Bm = bloom; bm = bloomless; h = sparse-bloom

[2]O = observed value

[3]E = expected value

The F_2 plants from the cross bm_3 (R Combine Kafir-60) x h_4 (Redlan x ROKY10-Calico) segregated into the ratio of 73 bloom:30 sparse-bloom:46 bloomless. The chi-square test indicated a probability level of 0.25-.10; therefore, $\underline{bm}_3$ and $\underline{h}_4$ were different loci.

The cross of bm_4 (Brooks) x h_1 (Redlan derivative) produced 212 F_2 plants segregating into a ratio of 108 bloom:34 sparse-bloom:70 bloomless. When compared to the expected ratio, the probability level was 0.05-.025, below the .05 level. More bloomless and less bloom plants were observed than expected. This could be lack of penetrance: when the bloom phenotype is not expressed but the gene is present. However, there was segregation for plant height and blooming date. Therefore, based on this segregation it was concluded that two separate loci were involved in $\underline{bm}_4$ and $\underline{h}_1$.

From the cross between bm_4 (Brooks) x h_4 (Redlan x ROKY10-Calico) 224 F_2 plants were obtained and were classified into a segregation ratio of 124 bloom:42 sparse-bloom:58 bloomless which was almost the same as the expected values. The probability level of .95 indicated a strong fit to the hypothesis of two separate loci for $\underline{bm}_4$ and $\underline{h}_4$ mutants.

Bloomless x Bloom Crosses

The summary of F_1 plants between bloomless x bloom crosses is given in Table V. All F_1 plants had bloom which resulted from the heterozygous Bmbm alleles. The classification of F_2 plants may be found in Table VIII with chi-square and probability values. The observed values were obtained under the assumption of a single

TABLE VIII

THE CLASSIFICATION OF F_2 PLANTS OF BLOOMLESS x BLOOM CROSSES WITH CHI-SQUARE AND PROBABILITY VALUES

Crosses		Number of Plants			Values	
		Bm[1]	bm	Total	x^2	P
Expected ratio 3:1						
bm_1 x Bm_R	(O)[2]	256	90	346	0.19	.75-.50
	(E)[3]	259.50	86.50			
bm_1 x Bm_0	(O)	80	42	122	5.78	.02-.01
	(E)	91.50	30.50			
bm_2 x Bm_R	(O)	188	43	231	5.02	.02
	(E)	173.25	57.75			
bm_3 x Bm_0	(O)	135	45	180	0	1
	(E)	135.00	45.00			
bm_4 x Bm_R	(O)	146	46	192	0.11	.75-.50
	(E)	144.00	48.00			
bm_4 x Bm_0	(O)	136	42	178	0.18	.75-.50
	(E)	133.50	44.50			
bm_5 x Bm_R	(O)	19	4	23	0.71	.50-.25
	(E)	17.25	5.75			

[1] Bm - bloom; bm = bloomless

[2] O = observed value

[3] E = expected value

completely dominant gene for bloom.

The expression of the bloom trait in F_2 plants required at least one Bm allele, (BmBm or Bmbm), while the bloomless expression required homozygous recessive bmbm alleles, (bmbm).

The cross betweem bm_1 (RWD3 x Weskan) x Bm_R (Redlan) produced an F_2 population of 256 bloom and 90 bloomless plants. A probability level of 0.75-.50 indicated a good fit to the expected 3:1 ratio, and the control of the expression of bm_1 by a single recessive gene. The F_2 population of bm_1 x Bm_0 (BOK8) produced 80 bloom and 42 bloomless plants, which when compared to the expected number resulted in a chi-square value and probability level of 0.02-.01, which was significant at .05 level. Fewer bloom and more bloomless plants were observed than expected. This could be the result of a small population of 122 plants or a chance population which failed to fit. Since there was segregation for plant height and other agronomic traits, it was concluded that a single recessive gene controlled bm_1.

The cross of bm_2 (Redbine-60) x Bm_R (Redlan) resulted in more bloom and less bloomless plants in the observed numbers than expected numbers. With a probability level of 0.02, the hypothesis must be rejected. However, there was segregation for bloomlessness and the population seemed adequate in size. Therefore, it was assumed that bm_2 was controlled by a recessive gene.

The observed numbers were exactly equal to the expected number for the cross of bm_3 (R Combine Kafir-60) x Bm_0 (BOK8). This indicated bm_3 was controlled by a single recessive gene.

The cross of bm_4 (Brooks) to either Bm_R (Redlan) or Bm_0 (BOK8) resulted in the same probability level of 0.75-.50. The observed

number closely agreed with the expected number of 3 bloom:1 bloomless ratio. A single recessive gene controlled $\underline{bm}_4$.

A small population of 23 plants was produced from the cross of bm_5 (Cyto-13 x Tan Sugar Drip) x Bm_R (Redlan). It resulted in a probability level of 0.50-.25. This indicated that the control of bm_5 was by a single recessive gene. However, this conclusion was based on a small population. The assurance of this conclusion would be greater if a larger population had been observed.

Sparse-bloom x Bloom Crosses

The summary of F_1 plants from the cross between sparse-bloom and bloom were given in Table V. All F_1 plants showed the bloom character which resulted from the heterozygous $\underline{Hh}$ alleles. The classification of F_2 plants is presented in Table IX with the chi-square and probability values. The observed values were obtained from the identification of bloom and sparse-bloom plants based on the heavy presence and lighter presence of waxy substance on the leaf sheaths. The expected values were obtained under the assumption of the segregation of 3 bloom:1 sparse-bloom. The expression of bloom in F_2 required at least one dominant $\underline{H}$ allele, ($\underline{HH}$ or $\underline{Hh}$). The sparse-bloom condition was induced by homozygous recessive $\underline{hh}$ alleles.

The cross of h_1 (Redlan derivative) x Bm_R (Redlan) produced 214 F_2 individual plants which were classified into 147 bloom and 67 sparse-bloom. This ratio gave a probability level of 0.05-.02, significant at .05 level. Too many sparse-bloom or too few bloom plants were observed than expected. Possibly some plants were misclassified from bloom to sparse-bloom. However, segregation for plant

TABLE IX

THE CLASSIFICATION OF F_2 PLANTS OF SPARSE-BLOOM x BLOOM CROSSES WITH CHI-SQUARE AND PROBABILITY VALUES

Crosses		Number of Plants			Values	
		H[1]	h	Total	x^2	P
Expected ratio 3:1						
h_1 x Bm_R	(O)[2]	147	67	214	4.50	.05-.02
	(E)[3]	160.50	53.50			
h_2 x Bm_R	(O)	27	4	31	2.41	.25-.10
	(E)	23.25	7.75			
h_2 x Bm_O	(O)	337	104	441	0.47	.50-.25
	(E)	330.75	110.25			
h_3 x Bm_R	(O)	215	63	278	0.81	.50-.25
	(E)	208.50	69.50			
h_3 x Bm_O	(O)	121	45	166	0.39	.75-.50
	(E)	124.50	41.50			
h_4 x Bm_R	(O)	54	24	78	1.38	.25-.10
	(E)	58.50	19.50			
h_4 x Bm_O	(O)	126	32	158	1.89	.25-.10
	(E)	118.50	39.50			

[1] H = bloom; h = sparse-bloom

[2] O = observed value

[3] E = expected value

height and first blooming date were observed confirming that an F_2 population was being studied. It was concluded that the sparse-bloom mutant, $\underline{h}_1$, was controlled by a single recessive gene.

The cross of h_2 (Redlan x Wiley) x Bm_R (Redlan) produced a small F_2 population which indicated that the sparse-bloom mutant, $\underline{h}_2$, was a single recessive gene. However, the population was small and further study with a larger number of plants would be more convincing. From another cross of the same mutant, h_2 x Bm_0 (BOK8), 441 plants were classified into 337 bloom:104 sparse-bloom. When compared to the expected number this fit the 3:1 ratio with a probability level of 0.50-.25 indicating that the $\underline{h}_2$ allele was a single recessive gene.

The cross between h_3 (Martin) x Bm_R (Redlan) produced 278 plants with 215 bloom and 63 sparse-bloom. The chi-square test probability level of 0.50-.25 indicated the single recessive nature of the $\underline{h}_3$ mutant.

The cross of h_3 to Bm_0 (BOK8) produced 121 bloom and 45 sparse-bloom individuals with a probability level from the chi-square test of 0.75-.50. This was supportive evidence that $\underline{h}_3$ was a single recessive gene.

The cross of h_4 (Redlan x ROKY10-Calico-11) to either Bm_R (Redlan) or Bm_0 (BOK8) produced the same chi-square probability level of 0.25-.10, though different population sizes were obtained. This indicated a good fit of the data with the hypothesis of one recessive gene controlling the sparse-bloom mutant, $\underline{h}_4$.

CHAPTER V

SUMMARY AND CONCLUSIONS

The purpose of this study was to determine the number of genes involved in the inheritance of the bloomless and sparse-bloom mutants in sorghum. Five bloomless and four sparse-bloom parental lines with temporary genetic designations were crossed in a partial diallel cross. Ten of the thirty-six possible crosses were obtained. Crosses of each of the bloomless and sparse-bloom mutants were also made to either Redlan or BOK8, the two bloom parental lines. Crosses were grouped into four categories: bloomless x bloomless, bloomless x sparse-bloom, bloomless x bloom, and sparse-bloom x bloom. All inheritance studies were conducted in the field using F_2 segregating populations. The chi-square goodness of fit test was calculated for the statistical analyses.

Among the six bloomless x bloomless crosses, all F_1 and F_2 populations were bloomless. This indicated the same genes involved among $\underline{bm}_2$, $\underline{bm}_3$, $\underline{bm}_4$, and $\underline{bm}_5$.

Among four bloomless x sparse-bloom crosses observed all F_1 plants had bloom and all F_2 populations segregated in a ratio of 9 bloom:3 sparse-bloom:4 bloomless. This indicated that different loci were involved in the bloomless and sparse-bloom mutants. Only one cross (bm_4 x h_1) did not fit the 9:3:4 ratio statistically but from a practical standpoint it can be assumed that two different loci were

involved.

Among the seven crosses of bloomless x bloom that were studied, all F_1 plants had bloom, while the F_2 populations of plants segregated in a ratio of 3 bloom:1 bloomless. This indicated that a single recessive gene controlled the expression of the bloomless mutants. There were two crosses (bm_1 x Bm_O, bm_2 x Bm_R) that did not fit the 3:1 ratio, but another cross of bm_1 did fit and it can be assumed that both mutants were controlled by single recessive genes.

Among seven crosses of sparse-bloom x bloom examined, all F_1 plants had bloom and the F_2 generation plants segregated in a 3:1 ratio of bloom:sparse-bloom. A single recessive gene was indicated to control the sparse-bloom mutants. There was only one cross (h_1 x Bm_R) that did not fit the 3:1 ratio. However, the segregation indicated single gene inheritance of the mutant.

Conclusion:

1. The same locus controlled the bloomless character in $\underline{bm}_2$, $\underline{bm}_3$, $\underline{bm}_4$, and $\underline{bm}_5$ bloomless mutants. Therefore, these mutants of bloomless sorghum should all be designated $\underline{bm}_2$.

2. The expression of the sparse-bloom and bloomless mutants tested herein appeared to be controlled by different loci.

3. The bloomless characteristic was regulated by a single recessive gene pair in all mutants.

4. The sparse-bloom condition was controlled by a single recessive gene in all mutants.

LITERATURE CITED

(1) Amini, Iraj. 1976. A study of greenbug resistance in a progeny from "bloomless" sorghum. (Master's Thesis, Oklahoma State University.)

(2) Chada, H. L., I. M. Atkins, J. H. Gardenhire and D. E. Weibel. 1961. Greenbug resistance studies in small grains. Texas Agric. Exp. Sta. Bul. 982.

(3) Gardenhire, James H. 1964. Inheritance of greenbug resistance in oats. Crop Sci. 4:443.

(4) Gardenhire, James H. 1965. Inheritance and linkage studies on greenbug resistance in barley (Hordeum vulgare L.). Crop Sci. 5:28-29.

(5) Gardenhire, James H., N. A. Tuleen, and K. W. Stewart. 1973. Trisomic analysis of greenbug resistance in barley, Hordeum vulgare L. Crop Sci. 13:684-685.

(6) Hackerott, H. L., T. L. Harvey, and W. M. Ross. 1969. Greenbug resistance in sorghum. Crop Sci. 9:656-658.

(7) Hackerott, H. L., and T. L. Harvey. 1970. Resistance in greenbug in three millet species. Agron. J. 62:574-575.

(8) Harvey, T. L., and H. L. Hackerott. 1969a. Recognition of greenbug biotype injurious to sorghum. J. Econ. Entomol. 62: 776-779.

(9) Harvey, T. L., and H. L. Hackerott. 1969b. Plant resistance to a greenbug biotype injurious to sorghum. J. Econ. Entomol. 62:1271-1274.

(10) Harvey, T. L., and H. L. Hackerott. 1974. Effect of greenbugs on resistant and susceptible sorghum seedlings in the field. J. Econ. Entomol. 67:377-380.

(11) Johnson, J. W., D. T. Rosenow, and G. L. Teetes. 1974. Response of greenbug-resistant grain sorghum lines and hybrids to a natural infestation of greenbugs. Crop Sci. 14:442-443.

(12) Kofoid, K. D., W. M. Ross, H. L. Hackerott, T. L. Harvey, and S. D. Kindler. 1976. Evaluation of greenbug resistance in S_2 progenies of grain sorghum. Crop. Sci. 16:265-267.

(13) Martin, L. K. 1977. A study of antibiosis and nonpreference mechanisms of greenbug resistance of bloomless sorghum. (Master's Thesis, Oklahoma State University.)

(14) Painter, R. H., and D. C. Peters. 1956. Screening wheat varieties and hybrids for resistance to the greenbug. J. Econ. Entomol. 49:546-548.

(15) Painter, R. H. 1968. Insect resistance in crop plants. The Macmillan Co., New York, N. Y. p. 25.

(16) Peiretti, R. A. 1975. Some aspects of greenbug resistance in sorghum as related to bloomless character. (Master's Thesis, Oklahoma State University.)

(17) Peterson, G. C. 1978. Inheritance of some bloomless and sparse-bloom mutants in sorghum. (Master's Thesis, Oklahoma State University.)

(18) Porter, K. B., and Norris E. Daniels. 1963. Inheritance and heritability of greenbug resistance in a common wheat cross. Crop Sci. 3:116-118.

(19) Rangaswami Ayyangar, G. N., V. Panduranga Rao, A. Kunhikoran Nambiar, and B. W. X. Ponnaiya. 1937. The occurence and inheritance of waxy bloom on sorghum. Proceedings of the Indian Academy of Sci. 5:4-15.

(20) Rangaswami Ayyangar, G. N., and B. W. X. Ponnaiya. 1941. The occurence and inheritance of a bloomless sorghum. Current Sci. 10:408-409.

(21) Ross, W. M. 1972. Effect of bloomless (blbl) on yield in Combine Kafir-60. Sorghum Newsl. 15:121.

(22) Saxena, P. N., and Harvey L. Chada. 1971. The greenbug Schizaphis graminum. 1. Mouth parts and feeding habits. Ann. Entomol. Soc. Amer. 64:897-904.

(23) Starks, K. J., D. E. Weibel, and E. A. Wood, Jr. 1972. Nonpreferences of a biotype of the greenbug for a broomcorn cultivar. J. Econ. Entomol. 65:623-624.

(24) Starks, K. J., and D. J. Schuster. 1973. Greenbug components of host-plant resistance in sorghum. J. Econ. Entomol. 66: 1131-1134.

(25) Starks, K. J., and E. A. Wood, Jr. 1974. Greenbug damage to growth stages of susceptible and resistant sorghum. J. Econ. Entomol. 67:456-457.

(26) Starks, K. J., and R. L. Burton. 1977. Greenbugs: determining biotypes, culturing and screening for plant resistance with

notes on rearing parasitoids. USDA Tech. Bul. 1556.

(27) Teetes, G. L., and J. W. Johnson. 1973. Damage assessment of the greenbug on grain sorghum. J. Econ. Entomol. 66:1181-1186.

(28) Teetes, G. L., J. W. Johnson, and D. T. Rosenow. 1975. Response of improved resistant sorghum hybrids to natural and artificial greenbug populations. J. Econ. Entomol. 68:546-548.

(29) Teetes, G. L., J. W. Johnson, and D. T. Rosenow. 1976. Damage assessment of greenbug resistant sorghum hybrids. Sorghum Newsl. 19:128.

(30) USDA. 1969. The greenbug situation on sorghum - 1968. Coop. Econ. Ins. Rept. 19(5):63-65.

(31) Webster, F. M. 1907. The spring grain-aphis (Toxoptera graminum Rond.) USDA Bur. Entomol. Cir. 85.

(32) Weibel, D. E., K. J. Starks, E. A. Wood, Jr., and R. D. Morrison. 1972. Sorghum cultivars and progenies rated for resistance to greenbug. Crop Sci. 12:334-337.

(33) Weibel, D. E., K. J. Starks, and R. A. Peiretti. 1976. Greenbug damage ratings of bloom and bloomless plants in F_3 segregating rows. Sorghum Newsl. 19:119.

(34) Wood, E. A., Jr., B. C. Curtis, and A. M. Schlehuber. 1960. Genetic of greenbug (Toxoptera graminum Rond.) resistance in two strains of common wheat. Agron. J. 52:599-602.

(35) Wood, E. A., Jr. 1961. Biological studies of a new greenbug biotype. J. Econ. Entomol. 54:1171-1173.

(36) Wood, E. A., Jr., H. L. Chada, and P. N. Saxena. 1969. Reaction of small grains and grain sorghum to three greenbug biotypes. Okla. Agric. Expt. Sta. Prog. Rep. P-618.

(37) Wood, E. A., Jr., H. L. Chada, D. E. Weibel, and F. F. Davies. 1969. A sorghum variety highly tolerant to the greenbug: Schizaphis graminis (Rond.). Okla. Agric. Expt. Sta. Prog. Rep. P-614.

(38) Wood, E. A., Jr. 1971. Designation and reaction of three biotypes of the greenbug cultured on resistant and susceptible species of sorghum. J. Econ. Entomol. 64:183-185.

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