INHERITANCE OF THE BLOOMLESS OR SPARSE-BLOOM CHARACTER IN SOME LINES OF SORGHUM

BY

BALAJI MANMOHAN NUKAL

Bachelor of Science

Oklahoma State University

Stillwater, Oklahoma

1982

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, 1985

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Thesis Approved:

Dale E. Weibel
Thesis Adviser

Charles M. Taliaferro

Charles E Denman

Norman N. Durham
Dean of the Graduate College

ACKNOWLEDGMENTS

I wish to express my appreciation to my major advisor, Dr. Dale E. Weibel, for the guidance, counsel, and understanding provided throughout the course of my graduate study. Appreciation is also extended to members of my advisory committee, Dr. Charles M. Taliaferro, and Professor Charles E. Denman, for their advice and assistance in this study.

The encouragement and help I got from Gary Strickland, Ketema Belete, and other members of the Sorghum Project is deeply appreciated.

To my parents Mr. and Mrs. N.M. Reddi, I wish to express my deepest gratitude and appreciation for their encouragement, understanding, and support throughout the course of my education.

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CHAPTER I

INTRODUCTION

Grain sorghum, Sorghum bicolor (L.) Moench, is the fifth largest cereal crop in the world on the basis of acreage grown. The sorghum plant is covered by a grayish epicuticular wax known as the "bloom". The bloom occurs in two intensities: 1) heavy bloom - the plants have a thick layer of wax on the leaf sheath, boot, internode, and the undersurface of the leaf blade; 2) sparse-bloom - the wax is found at the top of the leaf sheath, internode, and the basal portion of the undersurface of the leaf blade. A third condition known as bloomless is said to exist when no wax is present on the plant.

In 1968 the greenbug, Schizaphis graminum (Rondani), mutated to a form that infested sorghum, and caused damage exceeding $20,000,000 to the U.S. sorghum crop that year. Resistant sorghums were soon found, and the resistance was bred into hybrids to combat the insect. Bloomless sorghum exhibited a high degree of nonpreference for the insect. Recently the greenbug again mutated to a new biotype which made most of the previous sources of resistance useless. However, the newly mutated insects continued to express a high degree of nonpreference for bloomless sorghum, showing it to be the most reliable form of resistance. Greenbugs show more nonpreference to sparse-bloom plants than to bloom types, but less than to the bloomless plants.

At present genes at two loci are known to condition the bloomless character, and at least three loci are known to be involved in condition-

ing the sparse-bloom character. A fourth sparse-bloom gene could also be present (20). The purpose of this study was to determine the inheritance of the bloomless or sparse-bloom character, if present, in ten lines of sorghum, and to determine the inheritance of the fourth sparse-bloom line from the earlier study.

CHAPTER II

LITERATURE REVIEW

Grain sorghum, Sorghum bicolor (L.) Moench, belongs to the tribe Andropogoneae, and family Gramineae. There are five basic races of cultivated sorghum, namely bicolor, guinea, caudatum, kafir, and durra. The classification is based on five fundamental spikelet types as described by Harlan and de Wet (10). Worldwide among the major cereal crops, sorghum ranks fifth in area sown, following wheat, rice, maize, and barley (15).

Bloom on Sorghum

In 1930 Martin (14) noted that the superiority of sorghum over corn under conditions of drought stress may be in part due to the wax which covers parts of the sorghum plant. In 1937 Ayyangar et al. (2) reported that all sorghums develop a waxy bloom. The amount of this waxy bloom present allows sorghums to be seperated into types with heavy bloom and sparse bloom. In the heavy-bloomed condition there is a heavy deposit of wax on the leaf sheath, boot, internode, and the whole abaxial surface of the leaf blade. In the sparse-bloom condition plants show bloom at the top of the leaf sheath, top of the internode, and the base of the abaxial leaf blade surface. Inheritance of the character is controlled by a single gene, H and h, where the heavy bloom condition is dominant over the sparse-bloom condition.

Ayyangar and Ponnaiya (3) in 1941 reported the occurrence of a

bloomless condition in an African variety named 'Vigage'. Crosses between bloom and bloomless resulted in completely bloom F_1 plants. The F_2 populations segregated into a ratio of 3 bloom : 1 bloomless, indicating complete dominance of the bloom. When bloomless types were crossed with sparse-bloom types the F_1 plants were heavily bloomed, but the F_2 populations segregated into a 9 bloom : 3 sparse-bloom : 4 bloomless ratio. They concluded that a gene designated Bm is responsible for bloom, while its allele bm was responsible for the bloomless condition where the gene H had no expression. Allele h governed the sparse-bloom condition.

Blum (5) found that excessive deposition of epicuticular wax in sorghum is an effective component of drought resistance as it decreased net radiation in the field, and decreased cuticular transpiration. Blum (4) compared near isogenic lines of bloom and bloomless in the sorghum cultivar 'R Combine Kafir-60' (RCK-60). He found that the leaf sheaths of the normal (bloom) genotypes were covered with a meshwork of very fine waxy filaments. The covering of waxy filaments extended to the basal portion of the abaxial surface of the leaf blade in the normal genotypes. No waxy filaments were observed on the leaf sheaths or leaf blades of the bloomless genotypes. In both genotypes however the two surfaces of the leaf blade were covered with a homogeneous-amorphous layer of wax. Reflectance of solar radiation in the visible and near infra-red region over the adaxial leaf blade surface was found to be 4 to 5% greater in the bloom type than in the bloomless type.

Cannon and Kummerow (6) observed that the plant waxes of sorghum were laid down throughout the growth of the plant, with a constant level being reached about the time that the grain heads became apparent. The

waxes laid down on different parts of the plant differed from each other in quantity and in chemical composition. Ebercon et al. (7) using a colorimetric method for the analysis of epicuticular wax content of sorghum leaves, observed that the transition from bloom to bloomless genotype in nearly isogenic lines of Combine Kafir-60 caused a reduction by nearly one-half in the epicuticular wax content of the leaf blade.

Maunder et al. (17) found 38.4% more disease activity in bloomless lines as compared to their isogenic bloom lines in a charcoal rot nursery. Under conditions of stress the bloomless plants showed a greater leaf diffusive resistance. They speculated on the seemingly greater resistance to water loss in bloomless plants as being the result of quicker or greater closure of the stomata. Lambright and Maunder (12) recorded a higher degree of resistance to stomatal diffusion in bloom lines under conditions of stress in a controlled greenhouse environment.

Ross (22) compared the yields of near-isogenic bloom and bloomless lines of R Combine Kafir-60 at two different planting rates. In both cases the bloom line yielded significantly more than it's near-isogenic bloomless line. Webster and Schmalzel (26) in a trial involving isogenic lines of normal vs bloomless R Combine Kafir-60 and 'Redbine-60' recorded data showing that the normal lines as an average yielded 15% more than the bloomless lines.

Results of yield tests involving bloom, sparse-bloom, and bloomless near-isohybrids under severe moisture stress and a low yield level at Perkins showed an advantage for the bloomless hybrids (27). Yousefi (35) on analyzing data collected at three locations over 3 years

observed that in general, bloom hybrids yielded more than their bloomless near-isohybrids. The bloomless and sparse-bloom traits did not affect midbloom, plant height, threshing percent, or test weight to any great extent.

Peterson (19) crossed five bloomless and four sparse-bloom lines in a partial diallel system to determine the number of genes involved. Based on the F_1, F_2, and backcross data, he concluded that two of the bloomless lines had the same gene for the character, and that the sparse-bloom lines were conditioned by genes independent of each other and of the bloomless genes. Peterson et al. (20) in further studies found only two different bloomless genes which they designated $\underline{bm_1}$, and $\underline{bm_2}$. The sparse-bloom condition was controlled by at least three different genes designated $\underline{h_1}$, $\underline{h_2}$, and $\underline{h_3}$. A fourth sparse-bloom line was found to possess a gene different from $\underline{h_2}$ and $\underline{h_3}$, but it was not crossed to $\underline{h_1}$. This fourth sparse-bloom line was designated as gene $\underline{h_4}$.

The Greenbug on Sorghum

The greenbug, Schizaphis graminum (Rondani), is of European origin, and was first reported in the U.S. during 1882 in Virginia. Prior to 1968 two biotypes, A and B, had been reported as serious pests of small grains. During the summer of 1968 a widespread infestation of the greenbug was reported on sorghum, and the estimated loss to sorghum was well in excess of $20,000,000 with Kansas, Oklahoma, Nebraska, and New Mexico reporting the most damage (1).

In 1961, Wood (32) reported the discovery of a new greenbug biotype in the greenhouse. This new biotype differed from the field strain in its ability to thrive on the previously resistant wheat variety

Dickinson Sel. 28-A. Wood (33) designated the field strain as biotype A, and called the greenhouse strain biotype B. Harvey and Hackerott in 1969 (11) reported that the greenbug attacking sorghum was a new biotype designated as biotype C. They seperated biotype B and C by using seedling 'Piper' sudangrass which is resistant to biotype B but susceptible to biotype C. Wood et al. (34) reported that both biotype A and biotype B differed from biotype C morphologically and ecologically. Biotype C could reproduce and survive at higher temperatures than either biotype A or B.

Hackerott et al. (9) rated 648 sorghum cultivars and breeding lines for plant injury and screened greenbug populations under natural infestation in the field. The entries classified as tolerant were 'Sudan-grain', 'Shallu Grain', some waxy endosperm types, and derivatives of the three. Some derivatives of the grassy type (S. virgatum) were also found to have less greenbug damage. The F_2 segregation ratio of crosses between resistant and susceptible indicated that resistance to the insect was controlled by more than one dominant gene. Hackerott and Harvey (8) found that tolerance was the main component of resistance in the sorghum cultivar 'KS30' under greenbug infestation in the field.

Wood (33) studied the preference, fecundity, and longevity of the three biotypes on resistant and susceptible sorghums, and found marked differences between them. Weibel et al. (31) rated the F_1 and F_2 populations of crosses between resistant and susceptible sorghum lines for their reaction to biotype C of the greenbug. The F_1 plants gave an intermediate score between the resistant and susceptible parent. Data from the F_2 population indicated that resistance was controlled by a

single incompletely dominant factor. Weibel et al. (28) compared crosses among resistant Shallu Grain (SA7536-1), 'IS809', and PI264453 for resistance to greenbug biotype C and concluded that they had a somewhat similar form of resistance. The differences appeared to be of degree rather than of number.

Starks and Burton (23) seperated greenbugs into four biotypes: A, B, C, and D based on morphology and preference of host plants. Biotype D gave the same reaction on plants as biotype C but was more resistant to organophosphorous insecticides. Weibel et al. (29) counted the greenbugs on near-isogenic bloom and bloomless lines 3 and 4 weeks after emergence. Fewer greenbugs were counted on the bloomless plants, indicating nonpreference at an early stage of plant development. Weibel et al. (30) rated the damage by greenbugs to five pairs of adjacent bloom and bloomless plants in five F_3 segregating rows of four crosses at the heading stage of development. They concluded that less leaf damage on the bloomless plants was due to fewer greenbugs.

Peiretti et al. (18) studied parental, F_1, and F_2 sorghum populations involving the bloomless trait for their reaction to greenbugs. The sorghum entries used in the study were RWD3xWeskan (bloomless), Shallu Grain (resistant), IS809 (resistant), and 'RS610' (susceptible hybrid). They reported that: the tolerance to damage of Shallu Grain and IS809 was inherited independently of the bloomless trait; the bloomless plants did not exhibit greenbug tolerance as did Shallu Grain and IS809, except where the two traits were combined in an F_2 plant; bloomless plants showed slightly more of an antibiotic effect on greenbugs than the susceptible check, and; bloomless plants 50 to 70 days old exhibited as much nonpreference to the greenbugs as the resistant

parents. Martin (16) found the rate of reproduction of the greenbug to be lower on bloomless plants than on their near-isogenic bloom types, however the difference was not significant.

Starks and Weibel (25) evaluated four bloomless and three sparse-bloom entries for resistance to the greenbug in the field. The results suggested that the resistance in the bloomless and sparse-bloom lines may not be effective in the seedling stages of the plant or against the apterous form of the greenbug. Nonpreference was thought to be the mechanism of resistance.

In November, 1979 a collection of greenbugs from Bushland, Texas was discovered to be of a new biotype by Porter et al. (21). They evaluated biotype C tolerant and susceptible lines of sorghum for resistance to the new biotype. They found sorghum lines possessing biotype C resistance from (S. virgatum) to be susceptible, but sorghums PI220248 and 'Capbam' were resistant to the new biotype (biotype E). Starks et al. (24) screened biotype C resistant lines for their reaction to biotype E. They reported that PI220248, PI264453, and Capbam showed a useable level of resistance to biotype E, and that bloomless appeared to maintain its resistance and was effective against biotype E. Legako (13) carried out a study to determine the nature of inheritance of biotype E resistance in PI220248. He found that resistance to biotype E of the greenbug in PI220248 could be the result of a single dominant gene.

Bloomless hybrids performed better than their respective bloom near-isohybrids under severe greenbug attack at Goodwell (27,35).

CHAPTER III

MATERIALS AND METHODS

Ten lines known to possess the bloomless or sparse-bloom phenotype of unknown inheritance were used in the study (Table I). Each of these ten lines was crossed to two bloomless lines and four sparse-bloom lines whose inheritance was known (Table II). Crosses were also made between h_4 and all the sparse-bloom lines for the completion of an earlier study by Peterson et al. (20).

The known bloomless lines used were RWD3xWeskan ($\underline{bm}_1$), and RCK-60 or Redbine-60 ($\underline{bm}_2$). The known sparse-bloom parents were Redlan derivative ($\underline{h}_1$), RedlanxWiley or 'OK11' ($\underline{h}_2$), 'Martin' ($\underline{h}_3$), and RedlanxCalico ($\underline{h}_4$).

The crosses were made in the field at Puerto Rico in the winter of 1983-84. The F_1 plants were grown in the greenhouse at Stillwater, Oklahoma in the spring of 1984. There were two plants per pot and two pots of each cross with the parents used in the cross planted in adjacent pots. The F_1 plants were classified for their development of bloom when they were 6 weeks old.

Remnant seed from crosses made in Puerto Rico in 1982 was used to obtain F_2 populations of the crosses between bloomless ($\underline{bm}_1$) and each of the introductions from Yemen. The F_2 populations were planted in the field at the Perkins Agronomy Research Station on September 4, 1984. The soil type was a Teller loam. An attempt was made to plant at least six rows of each cross with seed from more than one source when possible.

TABLE I

SORGHUM PARENTAL LINES OF UNKNOWN INHERITANCE FOR THE BLOOMLESS OR SPARSE-BLOOM CHARACTER

PARENT	SOURCE
MN960	MISSISSIPPI
THEIS	MISSISSIPPI
WILEY	MISSISSIPPI
AOK24xPI264453	OKLAHOMA
PI 465901	YEMEN ARAB REPUBLIC
PI 465902	YEMEN ARAB REPUBLIC
PI 465904	YEMEN ARAB REPUBLIC
PI 474712	YEMEN ARAB REPUBLIC
PI 474713	YEMEN ARAB REPUBLIC
PI 474714	YEMEN ARAB REPUBLIC

TABLE II

BLOOMLESS AND SPARSE-BLOOM SORGHUM PARENTAL LINES

PARENT	GENETIC DESIGNATION
RWD3xWESKAN	$\underline{bm}_1$
R COMBINE KAFIR-60	$\underline{bm}_2$
REDBINE-60	$\underline{bm}_2$
REDLAN DERIV.	h_1
REDLANxWILEY	h_2
OK11	h_2
MARTIN	h_3
REDLANxCALICO	h_4

Experimental rows were 9.14 m long and 91.4 cm apart. Plants were thinned after emergence to one plant approximately every 10 cm. Fertilizer was broadcast pre-plant at the rate of 160 kg N/ha in the form of urea (46-0-0). The experimental area was irrigated once with approximately 10 cm of water being applied.

Approximately 6 weeks after planting the plants were classified as either bloom, bloomless, or sparse-bloom based on visual observation.

The chi-square (x^2) goodness of fit test was used as the statistical test of the segregation ratio.

CHAPTER IV

RESULTS AND DISCUSSION

Crosses Involving MN960

Bloom F_1 plants were produced in all crosses except in the $\underline{h_2}$xMN960 cross. The F_2 populations of the crosses bloomless($\underline{bm_1}$)xMN960 and the bloomless($\underline{bm_2}$)xMN960 segregated into bloom, sparse-bloom, and bloomless types. The F_2 populations of crosses between MN960 and three sparse-bloom lines ($\underline{h_1}$, $\underline{h_3}$, and $\underline{h_4}$) segregated for bloom and sparse-bloom. No segregation was observed in the F_2 population of the cross $\underline{h_2}$xMN960, and all plants showed a sparse-bloom phenotype, while the population appeared to be segregating for other characters. The classification of F_2 populations of crosses involving MN960, with chi-square and probability values is given in Table III.

Expected numbers were obtained based on the assumption of a 9 bloom: 3 sparse-bloom : 4 bloomless segregation ratio or a 9 bloom : 7 sparse-bloom segregation ratio. The cross $\underline{bm_1}$xMN960 did not satisfy the expected segregation ratio at the .05 probability level for acceptance, however the genes appear to be different. Expression of the sparse-bloom character in the F_2 is the result of a homozygous recessive condition at one of the sparse-bloom loci. The totally sparse-bloom F_2 of the $\underline{h_2}$xMN960 cross indicated that MN960 has a sparse-bloom genotype conditioned by the $\underline{h_2}$ locus.

TABLE III

CLASSIFICATION OF F_2 POPULATIONS OF CROSSES INVOLVING MN960 WITH CHI-SQUARE AND PROBABILITY VALUES

Cross		Number of plants in classes[1] Bm	h	bm	Total	Expected ratio	Values X^2	p
$\underline{bm}_1$x	(O)[2]	148	73	81	302	9:3:4	7.95	.05-.01
MN960	(E)[3]	170	57	76				
$\underline{bm}_2$x	(O)	148	52	67	267	9:3:4	.11	.95-.90
MN960	(E)	150	50	67				
$\underline{h}_1$x	(O)	30	21		51	9:7	.14	.30-.20
MN960	(E)	29	22					
$\underline{h}_2$x	(O).		262		262			
MN960								
$\underline{h}_3$x	(O)	178	130		308	9:7	.24	.20-.10
MN960	(E)	173	135					
$\underline{h}_4$x	(O)	72	57		129	9:7	.00	<.95
MN960	(E)	73	56					

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

[2] Observed

[3] Expected

Crosses Involving 'Theis'

The F_1 plants of crosses $\underline{bm_1}$xTheis, and $\underline{bm_2}$xTheis were completely bloomed. The F_2 populations of the two crosses segregated in a 9 bloom : 3 sparse-bloom : 4 bloomless ratio, thus indicating that the genes in Theis were different from both $\underline{bm_1}$ and $\underline{bm_2}$ (Table IV). The crosses between Theis and two sparse-bloom lines ($\underline{h_1}$ and $\underline{h_4}$) gave a bloom F_1 population which segregated in the F_2 generation into a ratio of 9 bloom : 7 sparse-bloom. This indicated that Theis has a sparse-bloom genotype controlled by a gene different from either $\underline{h_1}$ or $\underline{h_4}$. The cross $\underline{h_2}$xTheis gave sparse-bloom F_1 plants with no segregation in the F_2 generation. This suggested that the sparse-bloom condition in Theis is controlled by the gene $\underline{h_2}$. The cross $\underline{h_3}$xTheis was not studied.

Crosses Involving 'Wiley'

The crosses between Wiley and the two bloomless lines resulted in bloom F_1 plants with the F_2 populations segregating into a ratio of 9 bloom : 3 sparse-bloom : 4 bloomless (Table V). This suggested that Wiley has a sparse-bloom genotype. Bloom F_1 plants were produced when Wiley was crossed to the sparse-bloom lines $\underline{h_1}$, $\underline{h_3}$, and $\underline{h_4}$. The F_2 populations of the crosses with $\underline{h_1}$ and $\underline{h_4}$ segregated in a 9 bloom : 7 sparse-bloom ratio. The F_2 population of the cross $\underline{h_3}$xWiley was too immature for accurate classification, but appeared to be segregating into bloom and sparse-bloom types. The cross $\underline{h_2}$xWiley resulted in sparse-bloom F_1 plants with no segregation in the F_2 generation. This

TABLE IV

CLASSIFICATION OF F_2 POPULATIONS OF CROSSES INVOLVING THEIS WITH CHI-SQUARE AND PROBABILITY VALUES

Cross		Number of plants in classes[1] Bm	h	bm	Total	Expected ratio	Values X^2	p
$\underline{bm}_1$x	(O)[2]	156	69	85	310	9:3:4	4.70	.10-.05
Theis	(E)[3]	174	58	78				
$\underline{bm}_2$x	(O)	128	51	56	235	9:3:4	1.35	.70-.50
Theis	(E)	132	44	59				
$\underline{h}_1$x	(O)	173	134		307	9:7	.00	<.95
Theis	(E)	173	134					
$\underline{h}_2$x	(O)		345		345			
Theis								
$\underline{h}_4$x	(O)	168	141		309	9:7	.37	.70-.50
Theis	(E)	174	135					

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

[2] Observed

[3] expected

TABLE V

CLASSIFICATION OF F_2 POPULATIONS OF CROSSES INVOLVING WILEY WITH CHI-SQUARE AND PROBABILITY VALUES

Cross		Number of plants in classes[1] Bm	h	bm	Total	Expected ratio	Values X^2	p
$\underline{bm}_1$x	(O)[2]	129	59	55	243	9:3:4	4.94	.10-.05
Wiley	(E)[3]	137	46	61				
$\underline{bm}_2$x	(O)	89	31	39	159	9:3:4	.06	<.95
Wiley	(E)	89	30	40				
$\underline{h}_1$x	(O)	146	118		264	9:7	.06	.95-.90
Wiley	(E)	149	116					
$\underline{h}_2$x	(O)		308		308			
Wiley								
$\underline{h}_3$x	(O)	+	+					
Wiley								
$\underline{h}_4$x	(O)	56	59		115	9:7	2.37	.20-.10
Wiley	(E)	65	50					

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

[2] Observed

[3] Expected

showed that the gene controlling the development of wax in Wiley was at the $\underline{h_2}$ locus.

Crosses Involving AOK24xPI264453

Bloom F_1 plants were produced in all crosses except one. The F_2 population of the cross $\underline{bm_2}$xAOK24xPI264453 segregated into a 9 bloom: 7 bloomless ratio (Table VI), confirming that AOK24xPI264453 possessed a bloomless genotype controlled by a gene other than $\underline{bm_2}$. The F_2 populations of all crosses with the sparse-bloom lines segregated in a 9 bloom : 3 sparse-bloom : 4 bloomless ratio indicating independent inheritance. Bloomless F_1 plants were derived from the cross with $\underline{bm_1}$ with no segregation in the F_2 generation. This indicated that the $\underline{bm_1}$ locus was responsible for the bloomless condition in AOK24xPI264453.

Crosses Involving Six Introductions from Yemen

The F_1 plants of crosses between these six lines and the known parental lines were classified for their development of wax (Table VII). Bloom F_1 plants were observed in all crosses except in those with the lines possessing the sparse-bloom genes designated $\underline{h_1}$ and $\underline{h_4}$, where sparse-bloom F_1 plants were observed. This suggested that: 1. the six lines are homozygous recessive at both the $\underline{h_1}$ and $\underline{h_4}$ loci, or; 2. the $\underline{h_1}$ and $\underline{h_4}$ genes are the same.

F_2 populations of $\underline{bm_1}$ crossed with each of the six lines were available for study (Table VIII). In every case bloom F_1 plants resulted and the F_2 populations segregated in a 9 bloom : 3 sparse-bloom : 4 bloomless ratio. This supported the conclusion that a sparse-bloom condition existed in each of these lines. An evaluation of the F_2

TABLE VI

CLASSIFICATION OF F_2 POPULATIONS OF CROSSES INVOLVING AOK24xPI264453 WITH CHI-SQUARE AND PROBABILITY VALUES

Cross		Number of plants in classes[1] Bm	h	bm	Total	Expected ratio	Values χ^2	p
$\underline{bm}_1$x AOK24xPI453	(O)[2]			335	335			
$\underline{bm}_2$x AOK24xPI453	(O)	160		125	285	9:7	.00	<.95
	(E)[3]	160		125				
$\underline{h}_1$x AOK24xPI453	(O)	135	51	71	257	9:3:4	1.51	.30-.20
	(E)	145	48	64				
$\underline{h}_3$x AOK24xPI453	(O)	108	49	50	207	9:3:4	3.35	.20-.10
	(E)	116	39	52				
$\underline{h}_4$x AOK24xPI453	(O)	72	28	33	133	9:3:4	.49	.90-.70
	(E)	75	25	33				

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

[2] Observed

[3] Expected

TABLE VII

F_1 CLASSIFICATION OF CROSSES FROM PI474712, PI474713, PI474714, PI465901, PI465902, AND PI465904

Cross	F_1 Bloom	Cross	F_1 Bloom
PI474712 x		PI465901 x	
$\underline{bm}_1$	Bm[1]	$\underline{bm}_1$	Bm
$\underline{bm}_2$	Bm	$\underline{bm}_2$	Bm
$\underline{h}_1$	h[2]	$\underline{h}_1$	h
$\underline{h}_2$	Bm	$\underline{h}_2$	Bm
$\underline{h}_3$	Bm	$\underline{h}_3$	Bm
$\underline{h}_4$	h	$\underline{h}_4$	h
PI474713 x		PI465902 x	
$\underline{bm}_1$	Bm	$\underline{bm}_1$	Bm
$\underline{bm}_2$	Bm	$\underline{bm}_2$	Bm
$\underline{h}_1$	h	$\underline{h}_1$	h
$\underline{h}_2$	Bm	$\underline{h}_2$	Bm
$\underline{h}_3$	Bm		
$\underline{h}_4$	h		
PI474714 x		PI465904 x	
$\underline{bm}_1$	Bm	$\underline{bm}_1$	Bm
$\underline{bm}_2$	Bm	$\underline{bm}_2$	Bm
$\underline{h}_1$	h	$\underline{h}_1$	h
$\underline{h}_2$	Bm	$\underline{h}_2$	Bm
$\underline{h}_3$	Bm	$\underline{h}_3$	Bm
$\underline{h}_4$	h	$\underline{h}_4$	h

[1] Bm=bloom

[2] h=sparse-bloom

TABLE VIII

CLASSIFICATION OF F_2 POPULATIONS OF CROSSES INVOLVING bml WITH PI465901, PI465902, PI465904, PI474712, PI474713, AND PI474714

Cross		Number of plants in classes[1] Bm	h	bm	Total	Values X^2	p
EXPECTED RATIO 9:3:4							
$\underline{bm}_1$ x	(O)[2]	21	7	9	37	.01	<.95
PI465901	(E)[3]	21	7	9			
$\underline{bm}_1$ x	(O)	112	60	65	237	9.42	.01-.001
PI465902	(E)	133	44	59			
$\underline{bm}_1$ x	(O)	92	39	48	179	1.87	.50-.30
PI465904	(E)	101	34	45			
$\underline{bm}_1$ x	(O)	98	48	55	201	5.28	.10-.05
PI474712	(E)	113	38	50			
$\underline{bm}_1$ x	(O)	107	41	48	196	.61	.90-.70
PI474713	(E)	110	37	49			
$\underline{bm}_1$ x	(O)	116	48	57	221	1.65	.50-.30
PI474714	(E)	124	41	55			

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

[2] Observed

[3] Expected

populations will be necessary to reach a definite conclusion about the nature of inheritance of the sparse-bloom condition in these six lines.

Sparse-bloom x Sparse-bloom Crosses

In an earlier study (20) the sparse-bloom line $\underline{h}_4$ was not studied in crosses with the line $\underline{h}_1$. Hence, $\underline{h}_4$ was studied in combination with $\underline{h}_1$, $\underline{h}_2$, and $\underline{h}_3$ (Table IX). In crosses with $\underline{h}_2$ and $\underline{h}_3$ the F_1 plants were completely bloom, and the F_2 populations segregated in a 9 bloom : 7 sparse-bloom ratio. In the cross $\underline{h}_1 x \underline{h}_4$ the F_1 plants showed a sparse-bloom phenotype and there was no segregation in the F_2 generation. This indicated that the genes designated as $\underline{h}_1$ and $\underline{h}_4$ are the same.

TABLE IX

CLASSIFICATION OF F_2 POPULATIONS OF SPARSE-BLOOM X SPARSE-BLOOM CROSSES WITH CHI-SQUARE AND PROBABILITY VALUES

Cross		Number of plants in classes[1] Bm	h	Total	Values X^2	p
EXPECTED RATIO 9:7						
$\underline{h}_3 \times \underline{h}_4$	(O)	70	57	127	.03	.90-.70
	(E)	71	56			
$\underline{h}_2 \times \underline{h}_4$	(O)	73	60	133	.05	.90-.70
	(E)	75	58			
$\underline{h}_1 \times \underline{h}_4$	(O)		225	225		

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

[2] Observed

[3] Expected

CHAPTER V

SUMMARY AND CONCLUSIONS

The purpose of this study was to: 1. determine the inheritance of the bloomless or sparse-bloom character in ten lines of sorghum known to possess the condition, and; 2. determine the inheritance of the gene designated $\underline{h}_4$.

Each of the ten lines of unknown inheritance for the bloomless or sparse-bloom character was crossed to six lines whose inheritance for the character was known, and the sparse-bloom line $\underline{h}_4$ was crossed to the three other known sparse-bloom lines. The F_1 and F_2 progenies of these crosses were classified to obtain phenotypic segregation ratios. The F_1 plants were classified in the greenhouse, and the F_2 populations in the field. Statistical analysis was done using the chi-square test for goodness of fit.

The lines MN960, Theis, and Wiley produced sparse-bloom F_1 plants in crosses with $\underline{h}_2$ and there was no segregation in the F_2 generations. In all other crosses these lines produced bloom F_1 plants which segregated in the F_2 generation. This indicated that these three lines possessed a sparse-bloom genotype controlled by the gene $\underline{h}_2$.

The lines AOK24xPI264453 in a cross to $\underline{bm}_1$ gave bloomless F_1 plants with no segregation in the F_2 generation. All other crosses produced bloom F_1 plants which segregated in the subsequent generation. It can be concluded that AOK24xPI264453 possesses a bloomless genotype

controlled by the gene $\underline{bm}_1$.

The F_2 populations of six introductions from Yemen (PI465901, PI465902, PI465904, PI474712, PI474713, and PI474714) were studied for only one cross, namely that with $\underline{bm}_1$. In each case bloom F_1 plants segregated into a 9 bloom : 3 sparse-bloom : 4 bloomless ratio in the F_2 generation, suggesting that these lines possess a sparse-bloom genotype. The classification of the F_1 plants from crosses between these six lines and the other lines of known genetic inheritance shows a sparse-bloom resulting each time in crosses with $\underline{h}_1$ and $\underline{h}_4$. All other crosses gave bloom F_1 plants. This indicated that these lines possess the $\underline{h}_1$ and/or $\underline{h}_4$ gene.

The cross $\underline{h}_1$ x $\underline{h}_4$ gave sparse-bloom F_1 plants that did not segregate in the F_2 generation. The crosses between $\underline{h}_4$ and the remaining sparse-bloom lines resulted in bloom F_1 plants that segregated into a 9 bloom : 7 sparse-bloom ratio in the F_2 generation. This indicated that the gene designated $\underline{h}_4$ is different from genes $\underline{h}_2$ and $\underline{h}_3$, but is similar to the gene $\underline{h}_1$.

Future studies will be needed to determine the inheritance of the crosses whose F_2 data were not included here.

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VITA \

BALAJI MANMOHAN NUKAL

Candidate for the Degree of

Master of Science

Thesis: INHERITANCE OF THE BLOOMLESS OR SPARSE-BLOOM CHARACTER IN SOME LINES OF SORGHUM

Major Field: Agronomy

Biographical:

Personal Data: Born in Hyderabad, India, April 8, 1961, the son of Manmohan N. and Sabita Reddi.

Education: Attended Andhra Pradesh Agricultural University, Hyderabad, India, from August 1978, until May, 1981; transferred to Oklahoma State University, August, 1981, and received a Bachelor of Science degree in Agronomy in December, 1982; completed the requirements for the Master of Science degree at Oklahoma State University, May, 1985.

Professional Experience: Employee of the Sorghum Breeding Project in the Agronomy Department at Oklahoma State University, January, 1983 - May, 1985.