GENETICS OF SUICIDAL GERMINATION OF *Striga hermonthica* (Del.) Benth, BY COTTON (*Gossypium hirsutum* L.)

BY

BOTANGA CHRISTOPHER JOMIA
Bachelor of Agriculture (B. Agric.)
(Ahmadu Bello University, Zaria - Nigeria)

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DEPARTMENT OF PLANT SCIENCE
Faculty of Agriculture
Ahmadu Bello University, Zaria
Nigeria

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DECLARATION

I hereby declare that this thesis was written by me and is a record of my research work. It has not been presented in any previous thesis for a higher degree.

Botanga Christopher Jomia — Date: 30/06/98

The above declaration is confirmed by:

Dr. S.O. Alabi
Chairman,
Supervisory Committee — Date: 1/7/98

CERTIFICATION

This thesis entitled "GENETICS OF SUICIDAL GERMINATION OF *Striga hermonthica* (Del.) Benth, BY COTTON (*Gossypium hirsutum* L.)" by BOTANGA, Christopher Jomia meets the regulations governing the award of the degree of Master of Science (M.Sc.) of Ahmadu Bello University Zaria, Nigeria, and is approved for its contribution to scientific knowledge and literary presentation.

Dr. S.O. Alabi
Chairman,
Supervisory Committee

1/7/98
Date

Prof. S.T.O. Lagoke
Member,
Supervisory Committee

1/7/98
Date

Dr. C.A. Echekwu
Member,
Supervisory Committee

17/07/98
Date

Dr. S.O. Alabi
Head,
Dept. of Plant Science

1/7/98
Date

Dean,
Postgraduate School

25/2/99
Date

DEDICATION

This work is dedicated to my beloved parents; Mr. Godlove Botanga and Mrs. Rophina B. Botanga.

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ABSTRACT

The germination of "giant witchweeds" *(Striga hermonthica* (Del.) Benth), a noxious root parasite of many cereal crops, is stimulated by exudates from the roots of both host and non-host ("trap") plants. Forty genotypes of cotton *(Gossypium* spp.), a "trap" crop, were screened in the laboratory, using the cut root technique, to investigate the variability among these genotypes for their ability to stimulate the suicidal germination of S. *hermonthica* and to select materials for a genetic study.

The genotypes exhibited significant differences for the trait. *Striga* germination percentages ranged from 13.33 to 50.00% for the cotton genotypes compared with 47.33% for the sorghum variety CK60B, the susceptible control. Three cotton genotypes were selected based on their *Striga* seed germination stimulation and used as parents in crosses of the combination; low x high *Striga* germination stimulation. The $F_{1s,}$ F_2 s and parents for these crosses, (RASA(78)11b x SAMCOT-10 and RASA(78)11b x TX-CABS-1-83) were evaluated in separate experiments.

Broadsense heritability estimates for the trait from both crosses ranged from 71.8 to 78.5% indicating a high genetic influence for the trait. Gene number estimates gave values of less than 1. This was reflected by a discrete frequency distribution of the F_2 populations into two classes of high and low *Striga* seed germination stimulation, fitting into classical phenotypic ratio of 3:1.

These results tend to suggest that *Striga* germination stimulation by cotton (G. *hirsutum* L.) is a qualitative trait, and that the gene controlling this trait is monogenic and simply inherited, with high *Striga* germination stimulation dominant over low *Striga* germination stimulation. It should be possible to select and breed cotton genotypes that produce highly active germination stimulants in large amounts, while incorporating other good agronomic attributes.

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CHAPTER ONE

INTRODUCTION

The genus *Striga* of the family Scrophulariaceae composes of some 50 species, all holoparasites of tropical cereals and legumes (Butler, 1995). *Striga* species ("witchweeds") are noxious parasitic weeds that attack the roots of cereals and legumes, causing serious yield loss (Table 1). *Striga* and related parasitic weeds constitute the most important biotic constraint to food crop production in sub-Saharan Africa, causing between 10 and 100 percent loss in crop yield, while the rate of spread to areas not hitherto infested is alarming (Lagoke *et al.*, 1995). In Northern Cameroon and other areas in the Sahelian zone, *Striga* species cause great losses in the stable foods; sorghum (*Sorghum bicolor* L. Moench) and millet (*Pennisetum typhoides* [Burm.f.] Stapf)(Pieterse, 1985). In addition, *Striga* species in West Africa attack upland rice (*Oryza sativa* L.), maize (*Zea mays* L.), sugarcane (*Saccharum officinarum* L.) and cowpea (*Vigna unguiculata* (L.) Walp). In Northern Cameroon, two-thirds of the 600,000 ha cultivated land is severely infested by *Striga* (Njinyam, 1985). A severe infestation can result in complete loss of the crop and to abandonment of otherwise productive fields (Butler, 1995). A conservative estimate of crop losses due to *Striga* in Africa is 40 percent, representing an annual loss of cereal worth U.S. $7 billion (M'boob, 1986).

The *Striga* problem in Africa seems to be worsening due to intensive cultivation involving continuous monocropping of host crops in an attempt to produce sufficient food for the increasing population (Vogt *et al.,* 1991; Dogget, 1984; Butler, 1995; Berner *et al.*, 1996). Of the 23 species of *Striga* identified in Africa, *S. hermonthica* (giant "witchweed") is the most ubiquitous species, causing

much of the problems in the sahelian areas (Pieterse, 1985). *S. hermonthica* and *S. asiatica* (L.) Kuntze are the species which cause the most economically significant damage to cereals. *S. gesnerioides* (willd.) Vatke is the species most serious on cowpea and tobacco (Butler, 1995).

There is no single effective and economically feasible *Striga* control method available to the small scale African farmer (Lagoke *et al.*, 1991; Butler, 1995). The control methods identified include land preparation, hand pulling and hoe weeding, use of "trap" and "catch" crops, use of nitrogen fertilizer, seed treatment, chemical stimulants, biological control, herbicide application and the use of resistant varieties. Of these methods, the two most promising and culturally acceptable ones are suicidal germination ("trap cropping") and the use of resistant varieties, both of which are primarily concerned with manipulating *Striga* seed germination and seedling establishment (Sahai and Shivanna, 1982). It would appear that the major problem associated with the use of resistant varieties is the lack of universal resistance. This is probably due to the existence of different biotypes of *Striga* (Efron *et al.*, 1986). Aggarwal (1988), also reported that cowpea varieties resistant to *S. gesnerioides* in Burkina Faso were not necessarily resistant in other countries, attributing this to the presence of different strains or populations of *S. gesnerioides* in these places. *S. hermonthica* in particular is cross pollinated, and thus generates a great amount of variability through genetic recombination, making host variety improvement for resistance against the weed a difficult task (Olaniyan *et al.*, 1993).

Trap crops are those crops that induce germination of *Striga* seeds but are not parasitized, and consequently result in suicidal germination of *Striga* seeds. Cowpea, pigeon pea (*Cajanus cajan* (L.) Millsp), cotton, soyabean (*Glycine* max (L.) Merr) and groundnut (*Arachis hypogaea* L.) when grown in rotation with a susceptible host or as an intercrop, have been reported to induce abortive germination of *Striga* seeds, with a consequent reduction in infestation (Carson, 1985; Parkinson *et al.*, 1986; Mbwaga, personal comm., 1992). Cowpea is, however, susceptible to *S. gesnerioides*, but is a trap crop to *S. hermonthica*. The first indication of the possible use of trap crop was the synthesis of a potent germination stimulant, strigol (Cook *et al.*, 1972), a compound extracted from the roots of cotton (*Gossypium hirsutum*). In surveys conducted in the Republic of Benin and Togo, it was reported that the level of infestation was always lower in cereal crop planted after cotton (Parkinson, 1985).

No research work has been reported on the investigation of the genetic control of the stimulation of germination of *S. hermonthica* seeds by the cotton plant. Therefore, the objectives of this study are:

1. To investigate the variability among some cotton genotypes with respect to their ability to stimulate germination of *S. hermonthica* seeds.
2. To ascertain if this character *(Striga* seed germination stimulation) is under genetic control.
3. To determine the nature and mode of inheritance of *Striga* seed germination stimulation.

Table 1. The impact of *Striga* on grain production in Africa.

Country	Grain cultivation (1000 ha)	Infested area (1000 ha)	Grain production (1000 t)	Yield loss (1000 t)	Percent loss in production (1000 t)
Benin	555	186	399		
Gambia	116	87	158	10	6.3
Ghana	926	114	913	80	8.8
Cameroon	939	400	904	116	12.8
Nigeria	9655	3862	10560	056	10.0
Togo	577	200	387	14	3.6

Source: Ecology and Management of Parasitic Weeds - Training Manual (1996).

CHAPTER TWO

LITERATURE REVIEW

2.1Ecology and Distribution of *Striga hermonthica*

Ecologically, *Striga* is a native to the grasslands of the Old World tropics, reaching its greatest diversity in Sub-Saharan African (Ejeta, *et al.*, 1992). *Striga* problem is more widespread and serious in areas where both fertility and rainfall are low (Kiriro, 1991).

The origin of *S. hermonthica* is thought to be in the Nuba mountains of Sudan and partly Ethiopia, the origin of sorghum. Therefore the spread of *Striga* is linked to that of Sorghum (Anonymous, 1996). *S. hermonthica* is found widely in ecological zones from latitude 7° to 14°N (Obilana, 1981). In Africa, the countries affected by this species include; Benin, Burkina Faso, Cameroon, Chad, Cote d'Ivoire, Egypt, Ethiopia, Gambia, Ghana, Guinea, Kenya, Mali, Niger, Nigeria, Senegal, Sudan, Tanzania and Togo (Fig. 1). In Nigeria, *S. hermonthica* is the commonest species in the Nigerian savannas (Obilana, 1981).

2.2 *Striga* Biology and Life Cycle

Each *Striga hermonthica* plant is capable of producing 400,000 seeds depending on the species and growth conditions. The seeds are tiny, some 0.30 mm long and 0.15 mm wide. The seeds are not only numerous but can remain viable for as long as 20 years (Butler, 1995). The requirements of the seeds for germination include an after-ripening dormancy period of several months, pre-

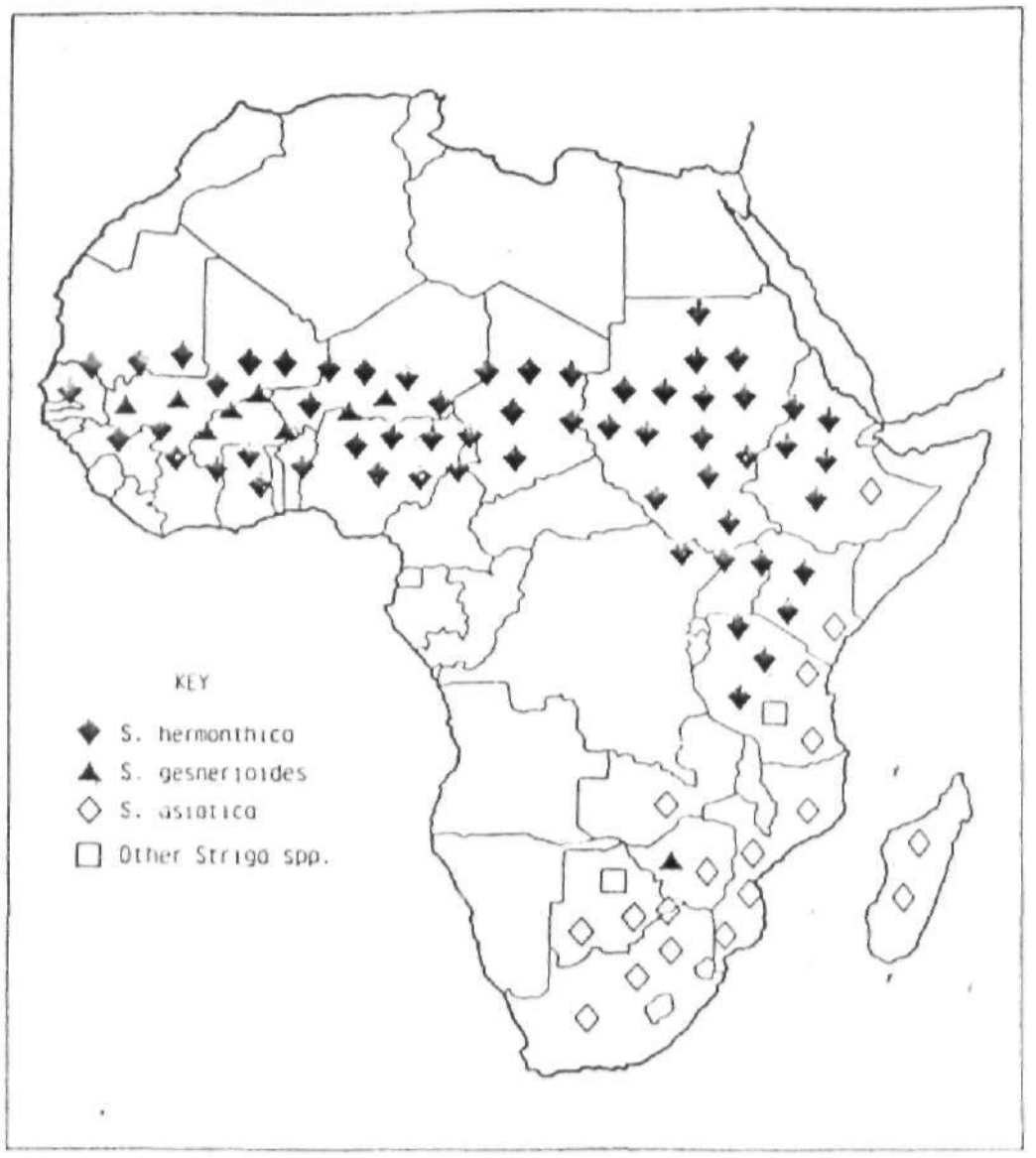

Fig. 1: Map of Africa showing regions with agriculturally significant *Striga* species.

Source: Pan African Striga Control Network (PASCON).

conditioning in moist conditions at an appropriate temperature for one to three weeks, and finally exposure to a specific chemical signal produced by the host root (Ramaiah *et al.*, 1983; Butler, 1995). After germination, a second host-derived chemical signal induces the elongating radicle to differentiate into a specialized structure, the haustorium, which the *Striga* seedling uses for attachment to and penetration into the host root (Butler, 1995). Approximately half the *Striga* life cycle is subterranean, living completely parasitically on the host, and much of the damage to the host occurs at this phase during which the parasite is in totality, a metabolic sink (Ramaiah *et al.*, 1983; Butler, 1995). Once above ground, the *Striga* plant develops chlorophyll and becomes green (except for *S. gesneroioides*), fixing some but not all of its own carbon. The flowers, which are purple, red, yellow or white depending upon the *Striga* species, develop rapidly and produce numerous seeds. *S. hermonthica* is a cross-pollinated species (Butler, 1995).

2.3 Variability for *Striga* Seed Germination Stimulant Production in some Trap Crop Varieties

Dejongh *et al.* (1993) observed inter-crop and intra-crop variability for stimulant production among some forty potential trap crop varieties of cowpea cotton and soyabean. Mean germination count as percentage of the control (GR 24) were within the range of 18.43 to 95.29%, 31.5 - 32.96%, and 0.00 to 64.18% for cowpea, cotton and soybean, respectively. It was further suggested that it would be possible to select and breed for trap genotypes that produce highly active germination stimulant in large amounts (Dejongh *et al.*, 1993).

2.4 *Striga*-derived Signals and their Effect on the Host

The mechanisms by which the damage occurs are not completely defined, but diversion of the host resources to the parasite accounts for only a small proportion of the damage. Diversion of water, minerals, energy and/or carbon from the host to the parasitic *Striga* necessarily diminishes host productivity. However, the degree to which host productivity is diminished by *Striga* is much greater than can be attributed to resource diversion from the host (Press *et al.*, 1987; Graves *et al.*, 1989). There have been suggestions that "toxins" produced by *Striga* inhibit host plant growth and development, diminishing the shoot/root ratio (Graves *et al.*, 1989). A small proportion of ^{14}C-labelled CO_2 taken up by photosynthetically active *Striga* plants is eventually transferred to the host plant (Rogers and Nelson, 1962), possibly accounting for the "toxin". It is possible that chemical signals are exchanged in both directions between *Striga* and the host (Butler, 1995).

2.5 Mechanism of Suicidal Germination

The germination of *Striga* is stimulated by several natural and synthetic compounds (Babiker *et al.*, 1993). Germination takes place after the seed would have undergone after-ripening, and pre-conditioning in a warm moist environment for several days and subsequent exposure to an exogenous germination stimulant (Sahai and Shivanna, 1982, Worsham, 1987). Babiker *et al.*(1993) observed that ethylene production preceded radicle protrusion and was detectable within three hours after treatment with germination stimulant. Furthermore, a key step in the conditioning process is the release of a restriction on the ethylene biosynthetic pathway, as *Striga* seeds have limited capacity to convert l-aminocyclopropane-1-

carboxylic acid (ACC), the immediate ethylene precusor, to ethylene. The role of endogenous ethylene is further substantiated by the decreased germination following simultaneous applications of germination stimulant and ethylene action inhibitors such as carbondioxide (CO_2), 2,5-norbornadiene (NBD) and silver thiosulphate (STS).

A germinating *Striga* seed develops a radicle but does not differentiate further unless it receives another chemical signal, also derived from the host root and transmitted through the soil around the root (Riopel, 1983). Unless this second signal is received within about 4 days of germination, the *Striga* seedling dies, but if the second signal is received, it rapidly responds by differentiating into a specialized attachment structure, the haustorium (Butler, 1995). Like germination, attachment is not host specific, as the resulting haustorium will attach to anything, including a glass plate (Riopel, 1983). Crop cultivars which produce *Striga* germination stimulant abundantly but fail to produce haustorial initiation factor would be uniquely useful as in addition to their resistance due to the failure of *Striga* to attach, they would also stimulate germination of many *Striga* seeds which would die (suicidal germination) and diminish the seed population in the soil (Butler, 1995). However several compounds from non-host sources have been shown to have activity as the *Striga* initiation signal (Riopel, 1983). These include 2,6-dimethoxybenzoquinone, a degradation product of lignin, which is found in surface abraded sorghum roots exposed to an enzyme produced by *Striga*, but not in undamaged roots. Preliminary findings suggest that the capacities for the production of the germination stimulant and the haustorial initiation factor are inherited completely independently, and that sorghum genotypes show relatively

little variability in their capacity to produce haustorial initiation factor, compared to their wide differences in capacity to produce the germination stimulant (Butler, 1995).

Once *Striga* is established on a host root, the vascular connections between host and parasite obviate any further need for host-parasite communication via chemical signals exuded into the soil (Butler, 1995). After establishment on the host root, the host plant provides the parasitic *Striga* plant not only moisture, mineral and photosynthate, but also additional chemical signals required for further growth and development (Cai *et al.*, 1993).

2.6 Genetics of Host-Plant Resistance to *Striga*

There is paucity of information on the genetics of host plant resistance. Even where available, the results are inconsistent due to a number of factors. Investigation of the genetics of host plant resistance to *Striga* have been hampered by the scarcity of resistant germplasm and the lack of reliable technique for evaluating germplasm (Ejeta *et al.*, 1992). Field evaluation of crop germplasm for *Striga* resistance in artificially or naturally infested experimental plots is cumbersome, unreliable, subject to a variety of confounding factors, and thus, inefficient. Genetic differences among host germplasm may also be obscured by diverse and shifting population of the parasite (Ejeta *et al.*, 1992).

Obilana (1984), defining resistance as "low total number of *Striga* per sorghum plant", reported gene action to be non-additive with over-dominance of susceptibility, and estimated that two to five genes control resistance. Ramaiah

(1987) reported that in three out of five sorghum parents studied, susceptibility was dominant over resistance, while in one parent resistance was dominant and in the other parent resistance was partially dominant. Hess and Ejeta (1992) reported that the gene controlling the production of *Striga* seed germination in sorghum is dominant and simply inherited. Vogler *et al.* (1996) also reported that low stimulant production in sorghum roots is a simply inherited recessive trait. This gene has now been mapped on the sorghum genome (Weerasuriya *et al.*, 1994). Using simple laboratory screening for the low stimulant trait, the resistance-conferring trait has been incorporated into highly productive sorghums well-adapted for African conditions (Butler and Ejeta, 1996).

In cowpea, Aggarwal *et al.* (1988) reported that genetic control varied with parental source background and the mechanism of resistance, as it is the case with sorghum. They reported a monogenic dominance in one set of crosses whereas in another set susceptibility was dominant and appeared to be controlled by two nuclear genes. Atokple (1988) showed that a single dominant gene conveys resistance to *Striga* in SUVITA-2 and KVx30-183-3G, and that genes from these two resistant parents are allelic because of the absence of segregation for susceptibility by the F_2 population of the two lines. Emechebe *et al.* (1991) reported that resistance to *Striga* in B301 appears to be dominant and simply inherited.

In pearl millet, few if any, genotypes have been found with a satisfactory level of resistance. Resistance where found was reported as dominant (Ramaiah, 1987).

CHAPTER THREE

MATERIALS AND METHODS

3.1 Origin and Description of Genetic Materials

Forty genotypes of cotton (*Gossypium* spp.) comprising of four varieties and thirty six advance breeding lines, obtained from the Fibre Research Programme of the Institute for Agricultural Research (I.A.R), Ahmadu Bello University, Zaria, Nigeria were screened in the Weed Science laboratory of the Department of Agronomy for their ability to stimulate the germination *S. hermonthica* seeds in 1996. The forty genotypes consisted of seven breeding lines of *G. barbadense* and thirty-three genotypes of *G. hirsutum* including four commercial varieties, ten eastern zone breeding lines, ten northern zone breeding lines, and nine exotic breeding lines.

Three genotypes of cotton were then selected on the basis of their performance with respect to their ability to stimulate *S. hermonthica* seed germination. These genotypes consisted of (RASA(78)11b (P_1), for low *Striga* seed germination stimulation, SAMCOT-10 (P_2) and TX-CABS-1-83 (P_3), for high germination stimulation. Crosses were made in each case between a low germination stimulant producer and a high germination stimulant producer; RASA(78)11b(P_1) x SAMCOT-10(P_2) and RASA(78)11b(P_1) x TX-CABS-1-83(P_3). These crosses were later advanced to the F_2 generation. The genetic background of the three parents (RASA(78)11b, SAMCOT-10 and TX-CABS-1-83) involved in these crosses are as follows:

1. **TX-CABS-1-183**: This is a high yielding multi-adversity resistant variety developed by the Texas Agricultural Experiment Station, U.S.A. The genetic background is similar to that of TX-CDP37HH-1-83, which was bred from the parent strains of TAMCOT SP21S and SP37 families. The cross (66N, B.v. 65, 418 Bgh 66-67) x (52, B.v.65, 437 Bgh 66-67) was made and individual plant selection began in the F_1 of the single cross. Individual selection was based on seed coat resistance to mold and to reduced rate of germination when held for eight days on 1.5 per cent water agar at 56°F; followed by an evaluation and selection for high seedling cotyledon resistance to a mixed inoculum of races 1,2,7 and 14 of Bacterial blight pathogen.

2. **SAMCOT-10**: This is a variety bred by the Institute for Agricultural Research Samaru, Zaria (Nigeria) from the cross (BJA 592 x ASA(68)63) x ASA(68)69. BJA 592 is a bacterial blight-resistant variety bred in Chad. ASA(68)63 is a derivative of (SA59/11 x Samaru 26J) x Albar 59/18. ASA(68)9 originated from the cross, Albar 51/474 x SA 55/44. Albar 58/18 and Albar 51/474 are bacterial blight resistant from Albar 51 in Uganda. Both SA 59/11 and SA 55/44 are materials derived by selection within the Nigerian Allen at Samaru. It was formerly designated as RASA(74)165.

3. **RASA(78)11b**. This is a line with genetic background much similar to that of SAMCOT-10, and was also bred by the Institute for Agricultural Research, Samaru (Zaria-Nigeria).

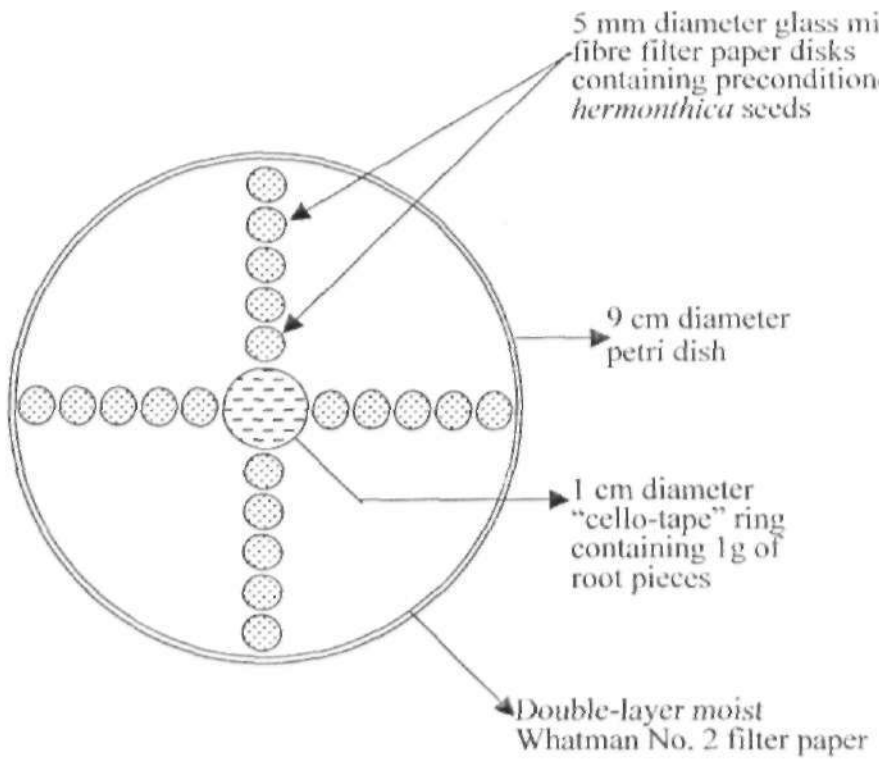

Fig. 2: Petri dish set-up for cut-root technique.

3.2 Screening Technique

Commencing in March 1996, forty genotypes of cotton were screened in the Weed Science Laboratory of the Department of Agronomy using the cut root technique developed by Van Mele *et al.*, 1992. The seeds of each cotton genotype was delinted using concentrated sulphuric acid, rinsed several times with tap water and then sun-dried. The seeds were surface sterilized by soaking in 1% sodium hypochloride (NaOCl) solution for five minutes and then rinsed several times with distilled water. The seeds were then placed in sterile petri dishes lined with moistened filter paper. The petri dishes were wrapped in aluminium foil and incubated at 28 °C for 48 hours to germinate. The germinating seeds were planted in sandy soils contained in small plastic pots (625ml by volume) and arranged in completely randomized design with three repetitions and grown in two sets for 14 and 21 days. Moist glass micro fibre filters (5.5 mm in diameter) were placed in petri dishes lined with a double layer moistened Whatman No. 2 filter paper of 9 cm diameter. *S. hermonthica* seeds, collected in 1991 at Hayan Ojo (Kaduna State, Northern Guinea savanna - Nigeria), were then spread one-layer thick on the moist glass micro fibre filter disks, wrapped with aluminium foil and incubated at 28°C on the same day that the germinating seeds were planted into small plastic pots. The plants were irrigated on a daily basis. At the end of 14 or 21 days, roots were obtained from the plants, washed free of soil and 1.0g of root pieces were placed in a cone (made of "cello-tape") at the center of the petri dishes lined with filter paper in 3 repetitions. Twenty disks of glass micro fibre filters (5 x 4) with preconditioned *S. hermonthica* seeds were placed in a diverging manner from the root core in the petri dishes (Fig. 2). The petri dishes were

covered and sealed with "cello-tape", wrapped in aluminium foil and incubated at 28°C for 3 days, after which germinated and ungerminated *S. hermonthica* seeds were counted with the aid of a microscope. Susceptible sorghum varieties SAR 35 and IS 1260 were used as control in the preliminary trial. A confirmatory trial was conducted with twelve (12) genotypes of cotton whose selection was based on the results of the preliminary trial. A susceptible sorghum variety, CK60B, was used as the control. The protocol for this confirmatory trial was the same as that described for the preliminary trial.

3.3 Greenhouse Technique/Cultural Practice

In September 1996, the selected parents were planted in soils (rich in organic matter) contained in plastic pots of 10 litres capacity, large enough to carry the crop to maturity in the greenhouse. Each pot contained 8.00 kg of soil. The three parents were planted in ten pots each so that a total of thirty plastic pots were used. Six to eight acid delinted seeds were planted per pot and later thinned to two plants per pot at two weeks after sowing (WAS). Tthe application of N-P-K fertilizer (20-10-10) was done 3 WAS. The fertilizer was applied at the rate of 5 grams per pot in 5cm deep holes and covered with soil. The pots were mulched after the second hand weeding at 5 WAS for insulation due to cold ambient temperature. At flowering, 9 WAS, emasculation and 'protective' selfing of the female and male parents, respectively, were carried out in the evenings, followed by crossing in the mornings. This lasted for five weeks. Insect pests, mainly aphids, were controlled using dimethoate (Rogor 40 EC) at the rate of one litre/ha following failure to achieve an effective control using Karate (one litre/ha).

Two sprays of diamethoate at two weeks interval gave an effective control. F_1 seeds were obtained from seed cotton harvested in two pickings in December 1996 and January 1997. The F_1 seeds from the two crosses were planted in March 1997, using 25 pots for each cross. Initially, six to eight undelinted seeds were planted per pot and later thinned to three plants which were selfed to obtain 75 F_2 plants from each cross. Insect pests, mainly red spider mites, which attacked the crop at 2 WAS were effectively controlled with two weekly sprays of dimethoate (Rogor 40 EC) at the rate indicated earlier. F_2 seeds were obtained from two pickings in July 1997.

3.4 Generation of Genetic Populations

Crosses were made between selected parents, with the high stimulant producing parents as males and the low stimulant producing parent as female. The F_1s were obtained by crossing the low stimulant producing parent by the high stimulant producing parents (pollinator parent), using the hand emasculation and pollination technique. The crosses made were: RASA (78)11b(P1) x SAMCOT-10(P_2) and RASA(78)11b(P_1) x TX-CABS-1-83(P_3). These crosses were advanced to the F_2 generation through controlled self-pollination. At the same time crosses were made to obtain fresh F_1s. The resulting genetic population; parents, F_1s and F_2 plants were evaluated (screened) in separate experiments in batches of twelve (12) genotypes in each experiment. The evaluation was on individual plant basis for *Striga* seed germination stimulation. Twelve (12) plants each for the parents and F_1s, and fifty (50) F_2 plants for each cross were evaluated, using CK60B, a highly susceptible sorghum variety as the control.

3.5 Statistical Analysis

Data analyses involved the analysis of variance (ANOVA). The statistical model used for the analysis was:

$$Y_{ij} = \mu + G_i + E_{ij}$$

where,

μ = population mean

G_i = genetic effect of the ith variety (genotype), and

G is assumed to be normally and independently distributed (NID)

($\mu = 0, \sigma^2G$)

E_{ij} = environmental influence or random error and this is also NID ($\mu = 0, \sigma^2E$)

i = 1,2,... n varieties (genotypes)

j = 1,2,... n replicates.

Separation of treatment means was done using the Duncan Multiple Range Test (DMRT). Numbers occurring in the segregating population (F_2) were tested using Chi-square (X^2) for goodness of fit to classical phenotypic ratio under the hypothesis of 3:1. Genotypes with means not significantly different from the high parent were considered to be high, while those not significantly different from the low parent were considered to be low. Broadsense heritability and genetic components were estimated using variances obtained from the analysis of variance with one way classification in a completely randomized design. The form of the general analysis of variance is presented in Table 2.

Table 2: Form of the general analysis of variance.

Sources of variation	Df	SS	MS	EMS
Among varieties	n-1	$\sum_i(Y_i...Y_n) - \frac{(N)^2}{n}$	M_1	$\sigma_e^2 + r\sigma_g^2$
Within varieties (error)	n(r-1)	$\sum_{ij}(Y_{ij}...Y_n) - \frac{(N)^2}{n}$	M_2	σ_e^2
Total	nr-1	$\sum_{ij}(Y_{ij}...Y_n) - \frac{(N)^2}{n}$		

$Y_{ij} = \sigma_p^2 = \sigma_g^2 + \sigma_e^2$

environmental variance = $\sigma_e^2 = M_2$

genotypic variance = $\sigma_g^2 = \frac{M_1 - M_2}{r}$

phenotypic variance = $\sigma_p^2 = M_2 + \left(\frac{M_1 - M_2}{r}\right)$

broadsense heritability = $h_B^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$

Broadsense heritability was also estimated using Weber and Moorthy (1952) formula;

$$Hx = \frac{\sigma^2 x F_2 - \sigma^2 x E}{\sigma^2 x F_2} \times 100$$

where,

Hx = Broadsense heritability for character x

$\sigma_x^2 F_2$ = Total variance observed in character x

$\sigma_x^2 E$ = Environmental variance in the expression of the character x, which is obtained as the geometric mean of the non-segregating population (P_1, P_2 and F_1).

Estimate of the minimum number of genes controlling *S. hermo nthica* germination stimulant production in cotton *(G. hirsutum)* were obtained using the following methods.

1. Wright (1921),

$$n = \frac{0.25(0.75 - h + h^2)D^2}{\sigma^2 F_2 - \sigma^2 F_1}$$

where

$$h = \frac{\bar{F}_1 - \bar{F}_2}{\bar{P}_2 - \bar{P}_1}$$

$$D = P_2 - P_1$$

where

n = number of genes

$\bar{F}_1$ = mean of the F_1 population

$\bar{F}_2$ = mean of the F_2 population

P_1 = mean of the smaller parent

P_2 = mean of the larger parent

$\sigma^2 F_1$ = variance of the F_1 population mean

$\sigma^2 F_2$ = variance of the F_2 population mean

The formula is expected to produce unbiased estimate for gene number if the following assumptions hold:

(a) No linkage exists between pertinent genes

(b) One parent supplies only plus factors and the other only minus factors among those in which they differ.

(c) All genes are equally important.

(d) The degree of dominance of all plus factors is the same for all.

(e) No interaction exists between pertinent non-allelic genes.

2. Castle and Wright 1921,

$$n = \frac{D^2}{8(\sigma^2F_2 - \sigma^2F_1)}$$

where,

n = number of genes

D = mean difference between the parents

σ^2F_1 = variance of F_1 population mean

σ^2F_2 = variance of F_2 population mean

Assumptions:

(a) No dominance

(b) Each gene has an equal effect

(c) Both parents are homozygous

The phenotypic and genotypic coefficients of variation for *Striga* germination stimulant production in the F_2 populations were calculated using the *formulae suggested by* Burton (1952)

$$GCV = \frac{\sigma^2GF_2^{1/2}}{\bar{x}} \times 100$$

$$PCV = \frac{\sigma^2F_2^{1/2}}{\bar{x}} \times 100$$

where,

GCV = genotypic coefficient of variance

PCV = phenotypic coefficient of variation

σ^2F_2 = total variance observed for the character in the F_2 population

σ^2GF_2 = genotypic variance for the character in F_2 population

$\overline{x}$ = F_2 mean for the character.

CHAPTER FOUR

RESULTS

4.1 *Striga* Seed Germination Stimulation by Cotton Genotypes

In general, higher *Striga* seed germination was recorded with combination of roots obtained from 3 weeks-old plants and *Striga* seeds preconditioned for the same period, than the corresponding 2 weeks crop growth stage and period (Tables 3 and 4). The mean percent germination at 2 and 3 weeks crop stages were 25.21 and 32.47%, respectively in the preliminary screening, and 31.40 and 36.23% for the confirmatory trial conducted with some selected genotypes. Generally, the Eastern zone breeding lines and the exotic breeding lines stimulated higher percentage of *Striga* seed germination compared to the Northern zone breeding lines (Tables 3 and 4).

In the preliminary evaluation, Bar 14/25(81)16, Bar XL7(7()35, SAMCOT-8, Y1422(7), RSA(79)4a, ASA(78)17b, ACSA(79)5f, ASA(74)80c, Y1422(79)30c and TAMCOT SP 21S stimulated *Striga* seed germination comparable to the maximum of 41.67% obtained with TX-CDP37HH-1-83 when cotton was planted for 14 days and *Striga* seeds incubated for the same period (Table 3). Bar XL7(7()36, Bar 14/25(87)14, SAMCOT-6, ASA(78)17f, Y1422(70)19g, BJA592(79)4f, ACSA(79)5c, TX-CABS-1-83 and TAMCOT SP 37 recorded a moderate *Striga* seed germination of at least 26.00%. All the other cotton genotypes and sorghum varieties were not significantly different from the least (13.33%) observed with ASA(75)13b (Table 3 and Appendix II). In a combination of 3 weeks-old plants and

Striga seeds preconditioned for a corresponding period, TX-CABS-1-83 recorded the highest *Striga* seed germination percentage of 50.00% which was comparable to that of SAMCOT-10, ACSA(79)5f and TX-CDP37HH-1-83 (Table 3). RASA(78)11b and the two sorghum genotypes (SAR 35 and IS1260) were not significantly different from the least percentage germination obtained, 1422(79)19g (13.33%) (Table 3 and Appendix II). All the other genotypes recorded a moderate *Striga* seed germination (>20.67%).

In the confirmatory laboratory screening trial, cotton genotypes stimulated *Striga* seed germination comparable to the susceptible sorghum control (CK60B) at 3 weeks crop growth stage and *Striga* seeds incubated for a corresponding period (Table 4). ACSA(79)8c, ASA(78)17b, SAMCOT-10, and TX-CABS-1-83 stimulated *Striga* seed germination comparable to that of the susceptible sorghum control. Moderate levels of germination (>35.67%) were recorded by RSA(79)4a, ACSA(79)5f and TAMCOT-CAMD-E. SAMCOT-9 and RASA(78)11b recorded a low germination of 24.33 and 19.00%, respectively, with 19.00% being the least observed for the trial. At 2 weeks crop growth stage and *Striga* seeds preconditioned for a corresponding period, CK60B (susceptible sorghum control) out-performed all the cotton genotypes (Table 4 and Appendix III). ASA(78)17b, SAMCOT-10, TX-CABS-1-83 and TX-CDP37HH-1-83 were superior to all the other cotton genotypes except ACSA(70)5f. SAMCOT-9 and RASA(78)11b recorded a relatively low *Striga* seed germination of 21.67 and 22.33%, respectively.

Table 3: Germination of *S. hermonthica* seeds, induced by some cotton genotypes at 14 and 21 days growth stages.

	Mean (%) germination	
	Days after beginning of experiment**	
Genotypes*	14	21
G. barbadense		
Bar 14/25(81)16	30.00 a-g	30.67 d-i
Bar XL7(79)35	30.00 a-g	31.33 d-i
Bar XL7(79)36	26.33 c-j	39.33 b-e
Bar 14/25(81)1	22.67 c-k	25.00 h-k
Bar 14/25(87)14	28.00 b-i	33.33 c-h
Bar 14/25(81)14	31.33 a-f	34.00 c-h
Bar 14/25(81)24	20.00 d-k	37.33 b-g
G. hirsutum		
Commercial varieties		
SAMCOT-6	27.00 c-i	34.33 c-h
SAMCOT-8	29.33 a-h	32.67 d-h
SAMCOT-9	24.33 c-k	34.33 c-h
SAMCOT-10	25.00 c-k	49.33 a
Eastern Zone breeding lines		
ASA(78)17f	26.67 c-i	33.67 c-h
ACSA(79)8e	24.67 c-k	38.33 b-f
Y1422(79)19b	31.33 a-f	35.00 c-h
Y1422(70)19g	29.00 b-h	13.33 l
RSA(79)4a	29.33 a-h	34.33 c-h
ASA(78)17b	40.33 ab	29.67 e-k
ASA(75)13b	13.33 jk	40.00 bcd
Y1422(79)19g	21.33 d-k	20.00 kl
ACSA(79)5f	35.33 abc	45.00 ab
RASA(78)11a	15.33 ijk	30.00 d-j

Table 3 cont'd.

	Mean (%) germination	
	Days after beginning of experiment**	
Genotypes*	14	21
Northern Zone breeding lines		
ASA(74)80c	30.33 a-g	34.67 c-h
BJA 592(79)4f	27.00 c-l	25.67 h-k
Y1422(79)30c	32.67 a-d	31.00 d-i
ACSA(79)5c	26.33 c-j	25.67 h-k
ACSA(79)19e	19.67 d-k	29.67 e-k
ASA(78)17c	19.33 e-k	30.33 d-j
ASA(75)13c	16.67 i-k	27.67 h-k
Y1422(79)19h	25.00 c-k	29.00 f-k
ACSA(79)5g	18.67 f-k	33.67 c-h
RASA(78)11b	18.67 f-k	20.67 jkl
Exotic breeding lines		
TX-CABS-1-83	27.00 c-i	50.00 a
TX-CABCHUS-1-84	23.00 c-k	39.33 b-e
TX-LEBOCAS-3-1-85	19.67 d-k	34.00 c-h
TX-CABUC-2-1-83	18.00 g-k	36.00 b-g
TX-CABCUS-2-1-84	19.33 e-k	32.00 d-i
TAMCOT-CAMD-E	21.33 d-k	40.00 bcd
TXCDP37HH-1-83	41.67 a	43.00 abc
TAMCOT SP 21S	32.00 a-e	35.00 c-h
TAMCOT SP 37	26.00 c-j	28.67 f-k
Control (Sorghum Varieties)		
SAR 35	23.00 c-k	22.00 i-l
IS1260	13.00 k	14.67 l

*Means followed by the same letter(s) are not significantly different at 0.01 level of probability (DMRT).

**An experiment is started with the planting of crop seed/preconditioning of *S. hermonthica* seeds.

Table 4: Germination of *S. hermonthica* seeds, induced by some cotton genotypes at 14 and 21 days (confirmatory trial).

	Mean (%) germination	
	Days after beginning of experiment**	
Genotypes*	14	21
Bar XL7(79)36	29.00 cd	29.67 d
ACSA(79)8c	28.67 cd	46.00 a
RSA(79)4a	25.67 de	37.00 bc
ACSA(79)5f	33.00 bc	37.67 bc
ASA(78)17b	36.67 b	42.00 ab
RASA(78)11b	22.33 de	19.00 f
SAMCOT-9	21.67 e	24.33 e
SAMCOT-10	35.67 b	46.00 a
TX-CABS-1-83	37.00 b	46.00 a
TX-CABCHUS-1-84	28.67 cd	35.67 c
TAMCOT-CAMD-E	26.00 de	37.00 bc
TX-CDP37HH-1-83	37.33 b	37.33 bc
CK60B (Sorghum control)	46.00 a	47.33 a

*Means followed by the same letter(s) are not significantly different at 0.01 level of probability (DMRT).

**An experiment is started with the planting of crop seed/preconditioning of *S. hermonthica* seeds.

4.2 Generation Means

The mean performance of RASA(78)11b (P_1), SAMCOT-10 (P_2), TX-CABS-1-83 (P3), F_1 and F_2 generations resulting from the crosses P_1 x P_2, P_1 x P_3 (low x high) are presented in Tables 5, 6, 7 and 8; and Figs. 5 and 6. The mean of the F_1s resulting from the cross, P_1 x P_2 is very close to that of the high *Striga* germination stimulating parent, while that resulting from the cross, P_1 x P_3 is almost exactly equal to that of the high germination stimulating parent. The F_2 mean for each of the crosses is lower than that of the high germination stimulating parent, but higher than that of the low *Striga* seed germination stimulating parent. While the parentals and F_1s showed no significant differences, the differences among the F_2 genotypes were highly significant (Table 7 and Appendix III). The difference between low and high parents was highly significant. The F_2 mean for each of the crosses was about equal to the mid-parent value in each case (Table 8). The F_1 and F_2 means relative to those of the parents for each cross are shown in Figs. 5 and 6.

4.3 Segregation Pattern

The distribution of F_2 segregating population for the two crosses, RASA(78)11b x SAMCOT-10 and RASA(78)11b x TX-CABS-1-83, are presented in Table 9, Figs. 5 and 6. The F_2 distribution fall into two distinct phenotypic classes of high and low *Striga* seed germination stimulation (Fig. 4 and Table 7). Although none of the F_2 plants exceeded the high *Striga* germination stimulating parents, at least 64.00% of the plants were high stimulant producers in each of the

crosses, while 36.00% were low stimulant producers, with 14 and 10 plants being lower than the low parent in the cross: RASA(78)11b x SAMCOT-10 and RASA(78)11b x TX-CABS-1-83 (Tables 7 and 8), respectively. However, these differences in the number of plants within the segregating population were not significantly different for both crosses. The rest of the plants falling within the low germination stimulating groups were either equal to, or slightly higher than the low stimulant producing parent (Table 9). The Chi-square (X^2) test for goodness of fit to classical phenotypic ratio under the hypothesis of 3:1, indicated that the pattern of segregation in the F_2 fits a ratio of 3 high: 1 low *Striga* germination stimulating plants for each of the crosses (Table 9). In both crosses, RASA(78)11b x SAMCOT-10 and RASA(78)11b x TX-CABS-1-83, all the F_1s were high *Striga* seed germination stimulating plants (Tables 5, 6, 8 and 9).

4.4 Heritability Estimates and Gene Numbers

Broadsense heritability estimates in crosses involving low and high *Striga* germination stimulating plants were greater than 70% for each of the crosses. Broadsense heritability estimate using genetic components from the analysis of variance were 74.58 and 78.51% for the cross, RASA(78)11b x SAMCOT-10 and RASA(78)11b x TX-CABS-1-83, respectively (Table 8). The estimate obtained using Weber and Moorthy (1952) formula were relatively lower, with a broadsense heritability estimates of 71.80 and 72.20% for the cross, RASA(78)11b x SAMCOT-10 and RASA(78)11b x TX-CABS-1-83, respectively (Table 8).

Estimates of the minimum number of genes controlling *Striga* germination stimulation in the cross, RASA(78)11b x SAMCOT-10 and RASA(78)11b x TX-

CABS-1-83 gave values of less than 1, using Wright's (1921) and Wright and Castle (1921) formulae. Using Wright's (1921) formula, values of 0.72 and 0.67 gene number were obtained for the cross, RASA(78)11b x SAMCOT-10 and RASA(78)11b x TX-CABS-1-83, respectively. The estimates using Wright and Castle (1921) was slightly lower for the cross RASA(78)11b x SAMCOT-10 (0.68 gene), but gave a similar value (0.67 gene) for the cross RASA(78)11b x TX-CABS-1-83 (Table 8).

Table 5: Germination of *S. hermonthica* seeds induced by some cotton genotypes: Parents and F_1s for the cross, RASA(78)11b x SAMCOT-10

	Mean (%) germination		
	Days after beginning of experiment**		
	21		
Genotypes*	RASA(78)11b	SAMCOT-10	F_1s
1	21.33 b	41.33 a	40.67 a
2	23.33 b	46.67 a	43.33 a
3	19.67 b	42.33 a	42.67 a
4	20.33 b	47.67 a	40.00 a
5	25.33 b	43.67 a	40.33 a
6	21.00 b	44.67 a	38.67 a
7	18.33 b	48.00 a	42.33 a
8	22.67 b	47.00 a	41.67 a
9	18.67 b	49.00 a	41.67 a
10	20.33 b	45.67 a	42.67 a
11	19.33 b	45.67 a	42.67 a
12	21.67 b	46.33 a	40.67 a
CK60B (Sorghum control)	45.33 a	48.00 a	44.00 a

*Means followed by the same letter are not significantly different at 0.01 level of probability (DMRT).

**An experiment is started with the planting of crop seed/preconditioning of *S. hermonthica* seeds.

Table 6: Germination of *S. hermonthica* seeds induced by some cotton genotypes: Parents and F_1s for the cross, RASA(78)11b x TX-CABS-1-83.

	Mean (%) germination		
	Days after beginning of experiment**		
	21		
Genotypes*	RASA(78)11b	TX-CABS-1-83	F_1s
1	21.33 b	40.67 a	44.67 a
2	23.33 b	48.67 a	41.33 a
3	19.67 b	48.00 a	48.00 a
4	20.33 b	45.67 a	44.00 a
5	25.33 b	46.67 a	43.00 a
6	21.00 b	45.67 a	45.33 a
7	18.33 b	49.00 a	49.00 a
8	22.67 b	46.33 a	48.33 a
9	18.67 b	48.00 a	46.33 a
10	20.33 b	46.00 a	47.67 a
11	19.33 b	47.00 a	48.00 a
12	21.67 b	48.33 a	45.67 a
CK60B (Sorghum control)	45.33 a	40.33 a	48.33 a

*Means followed by the same letter are not significantly different at 0.01 level of probability (DMRT).

**An experiment is started with the planting of crop seed/preconditioning of *S. hermonthica* seeds.

Table 7: Germination of *S. hermonthica* seeds induced by F_2 cotton genotypes from the cross RASA(78)11b x SAMCOT (P_1 x P_2) and RASA(78)11b x TX-CABS-1-83 (P_1 x P_3).

	Mean (%) germination	
	Days after beginning of experiment**	
	21	
Genotypes*	P_1 x P_2(F_2)	P_1 x P_3(F_2)
1	41.33 a	42.00 a
2	21.33 b	41.33 a
3	39.00 a	41.33 a
4	42.00 a	19.67 b
5	20.67 b	43.33 a
6	45.33 a	18.00 b
7	40.33 a	42.67 a
8	20.33 b	42.67 a
9	39.67 a	17.67 b
10	39.33 a	38.33 a
11	18.33 b	38.33 a
12	40.33 a	33.67 a
13	40.00 a	18.67 b
14	19.00 b	38.67 a
15	39.67 a	39.33 a
16	40.00 a	21.00 b
17	40.00 a	18.33 b
18	19.33 b	43.33 a
19	19.00 b	40.33 a
20	40.33 a	21.00 b
21	41.67 a	40.00 a
22	20.67 b	41.00 a
23	42.00 a	20.67 b
24	38.67 a	19.00 b
25	42.33 a	41.67 a
26	19.33 b	19.00 b
27	42.33 a	45.67 a
28	20.33 b	40.67 a
29	40.67 a	43.33 a
30	40.33 a	38.67 a
31	18.67 b	41.00 a
32	39.00 a	18.00 b
33	30.67 a	39.33 a
34	23.00 b	40.33 a

Table 7 continued.

	Mean (%) germination	
	Days after beginning of experiment**	
	21	
Genotypes*	$P_1 \times P_2(F_2)$	$P_1 \times P_3(F_2)$
35	38.33 a	41.67 a
36	40.67 a	20.00 b
37	39.00 a	41.00 a
38	20.33 b	16.00 b
39	16.00 b	40.67 a
40	40.33 a	39.33 b
41	18.33 b	43.33 a
42	40.33 a	22.33 b
43	18.00 b	40.67 a
44	21.00 b	39.00 a
45	41.00 a	40.00 a
46	40.33 a	18.67 b
47	20.33 b	40.33 a
48	39.33 a	44.00 a
49	39.67 a	20.33 b
50	19.33 b	41.33 a
CK60B (Sorghum control)	42.67 a	41.33 a

*Means followed by the same letter are not significantly different at 0.01 level of probability (DMRT).

**An experiment is started with the planting of crop seed/preconditioning of *S. hermonthica* seeds.

Table 8: Heritability, frequency distribution, means, gene number, genotypic and phenotypic coefficients of variability for *Striga* seed germination stimulation.

Generation/ cross	Number of plants	Mean (%) germination	Broadsense* heritability (%)		Coefficient of variability (%)		Gene number**	
			I	II	Genotypic	Phenotypic	I	II
P_1 (low)	12	21.00						
P_2 (high)	12	46.00						
P_3 (high)	12	46.67						
$\frac{P_1 \times P_2}{F_1}$	12	41.00					**0.72**	**0.68**
F_2	50	33.00	74.58	71.80	**28.86**	**33.42**		
Mid-parent		33.50						
$\frac{P_1 \times P_3}{F_1}$	12	46.00					**0.67**	**0.67**
F_2	50	34.22	**78.51**	**72.20**	29.39	33.17		
Mid-parent		33.84						

*I = Estimated from genetic components.
II = Weber and Morthy (1952) formula.

**I = Wright (1921) formula
II = Castle and Wright (1921) formula.

Table 9: Segregation for *Striga* seed germination stimulation in the cross; RASA(78)11b x SAMCOT-10 (P_1 x P_2) and RASA(78)11b x TX-CABS-1-83 (P_1 x P_3) in the F_1 and F_2 generations.

Generation/ cross	Hypothesis	Number of plants	Segregation (high:low)		X^2 value	
			Expected	Observed	Calc	Tab.05
P_1 x P_2						
F_1		12	12:0	12:0		
F_2	3:1	50	37.5:12.5	32:18	3.23	3.84
P_1 x P_3						
F_1		12	12:0	12:0		
F_2	3:1	50	37.5:12.5	34:16	1.31	3.84

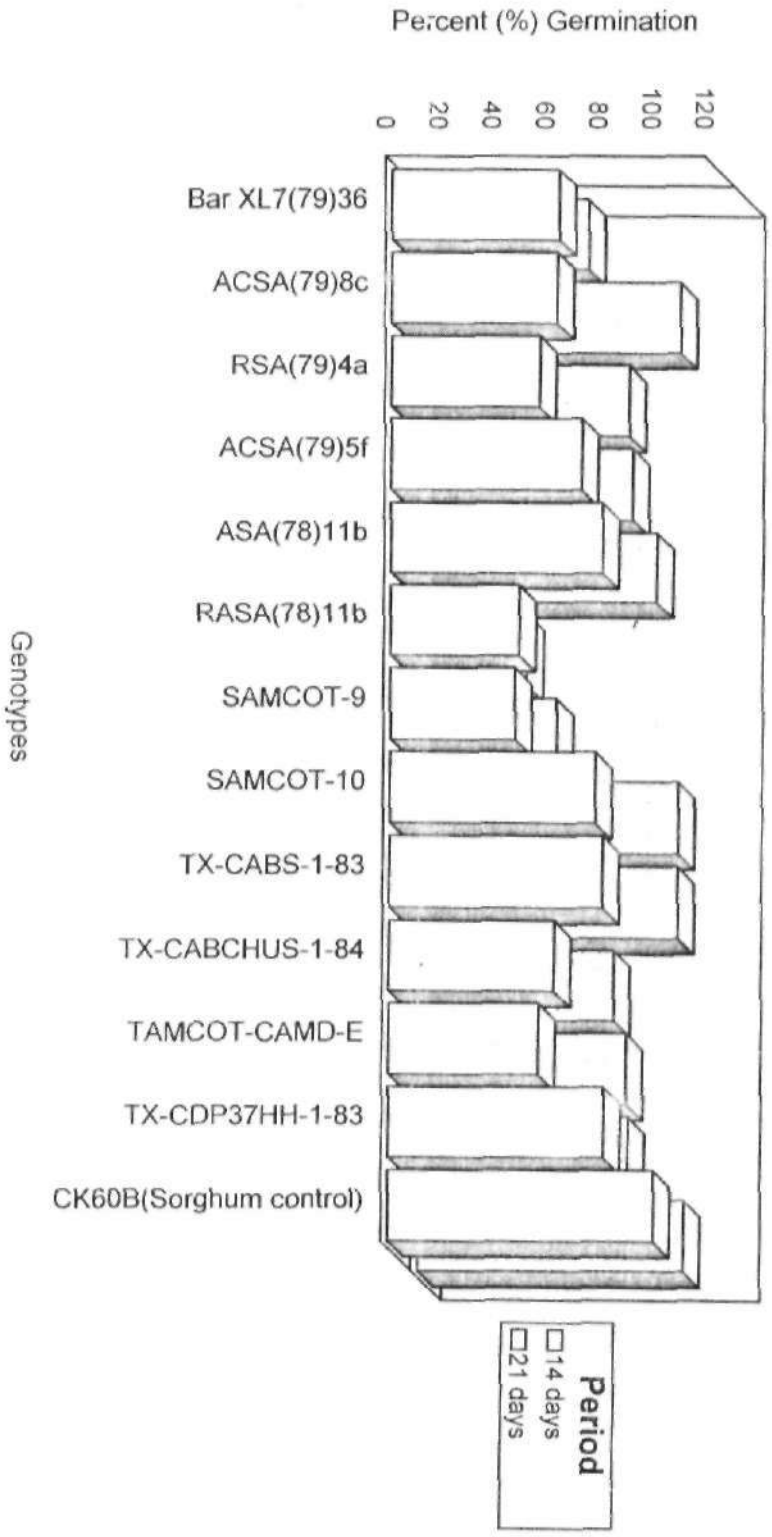

Fig. 3: Germination of *S. hermonthica*, induced by some cotton genotypes at 14 and 21 days as percent of control (Confirmatory Trial).

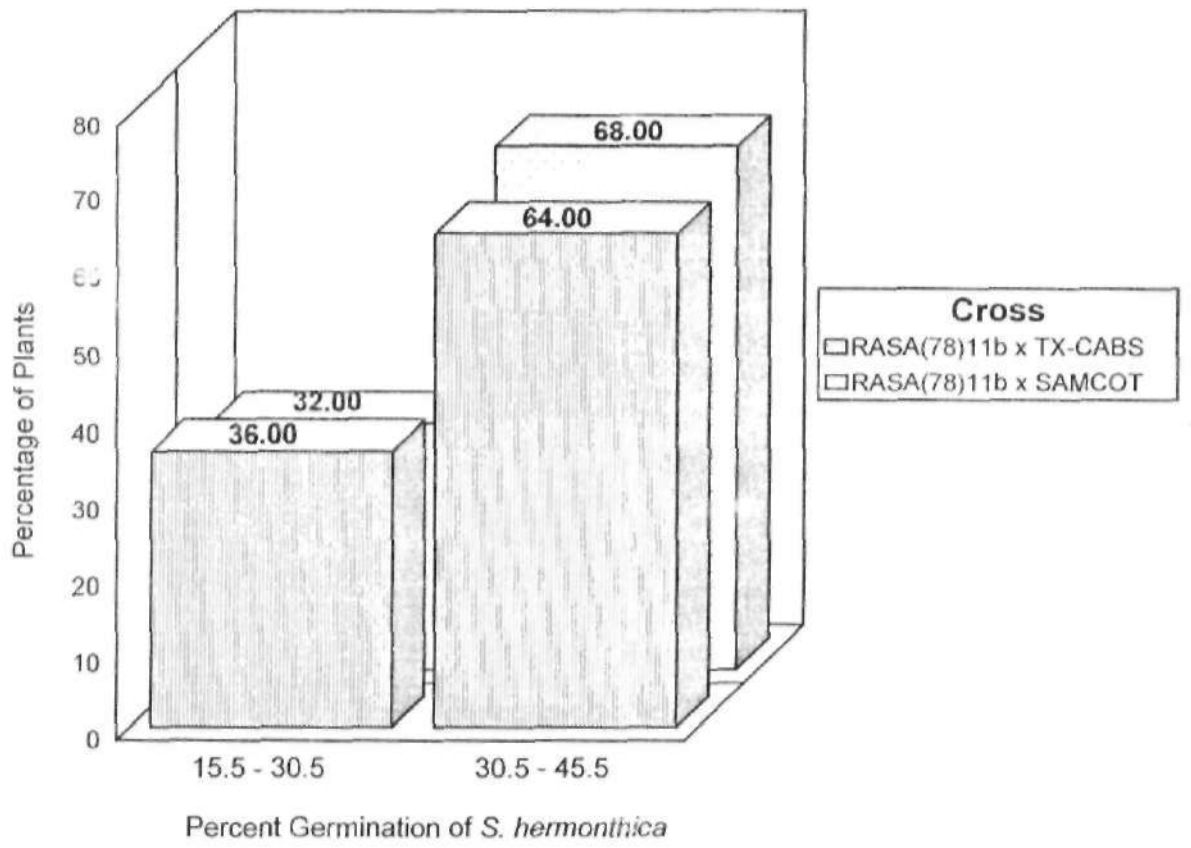

Fig. 4: Frequency of segregation in the F_2 generation for *S. hermonthica* germination from the cross; RASA(78)11b x SAMCOT-10 & RASA(78)11b x TX-CABS-1-83.

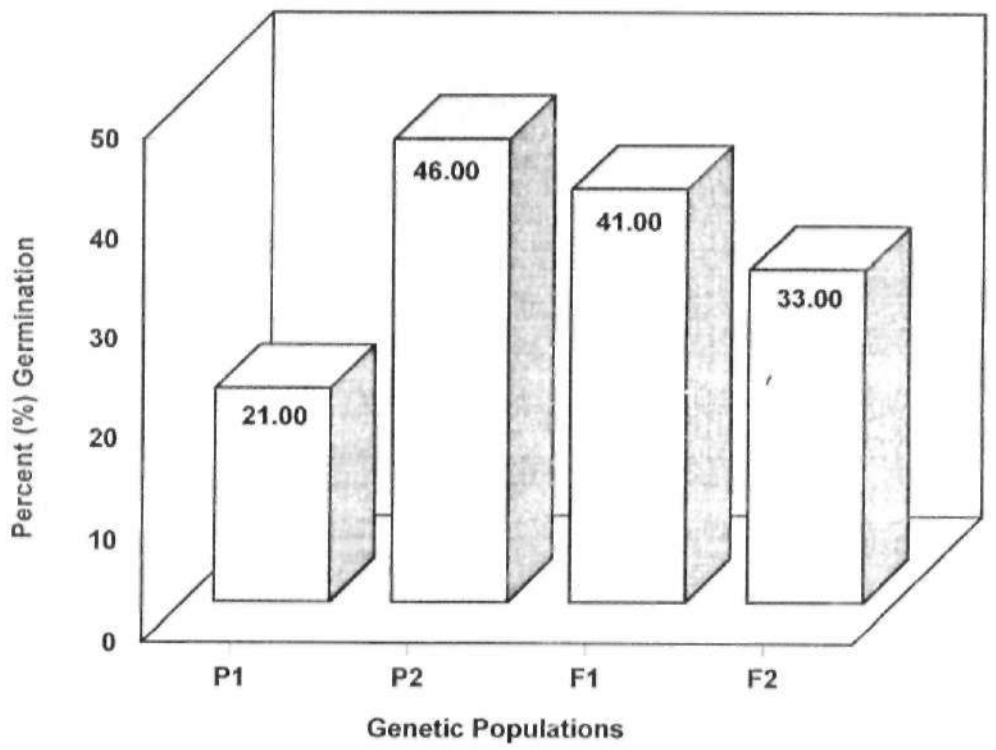

Fig. 5: Mean performance of genetic populations in the stimulation of *S. hermonthica* germination for the cross; RASA(78)11b x SAMCOT-10 (P1 x P2).

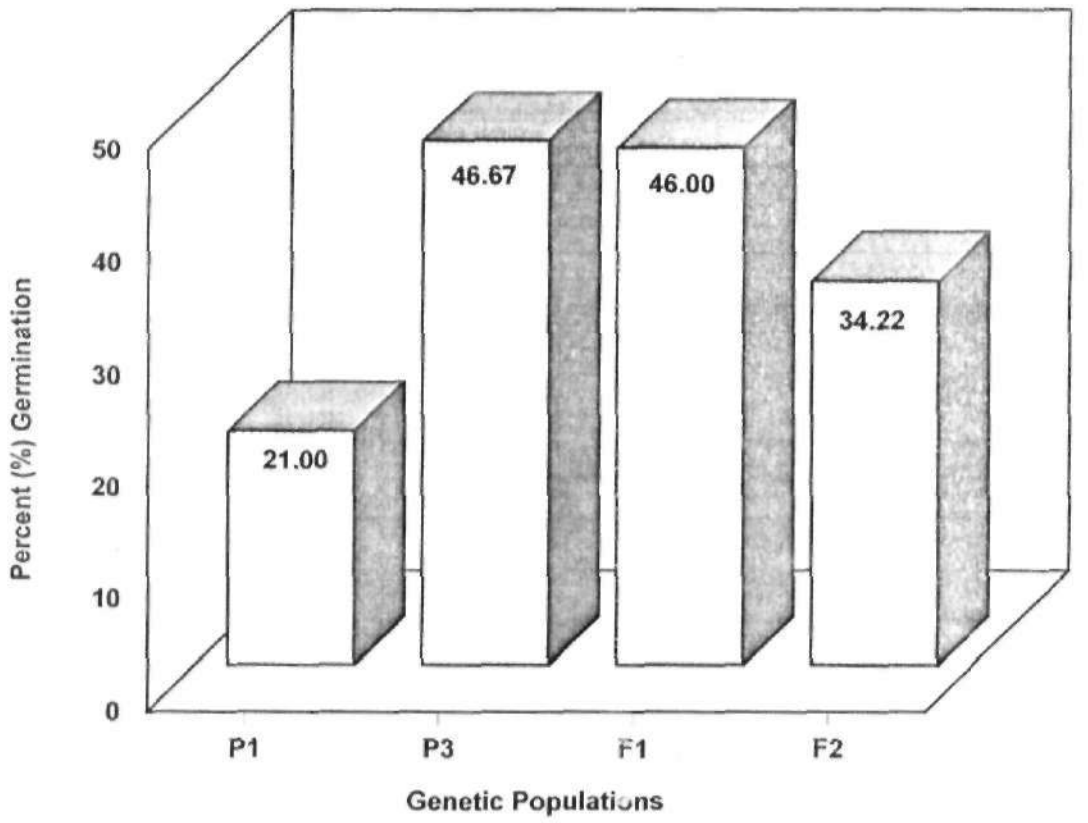

Fig. 6: Mean performance of genetic populations in the stimulation of *S. hermonthica* germination for the cross; RASA(78)11b x TX-CABS-1-83 (P1 x P3).

CHAPTER FIVE

DISCUSSION

5.1 *Striga* Seed Germination Stimulation and Variability among Cotton Genotypes

The results indicated a wide variability among cotton genotypes for their ability to stimulate *S. hermonthica* germination (Tables 3 and 4). Butler (1995) observed that sorghum genotypes showed wide differences in their capacity to produce germination stimulant compared to a relatively little variability in their capacity to produce haustorial initiation factor, and that the inheritance of these traits were completely independent. The mean percent *Striga* germination at 3 weeks crop growth stage (32.47%) was higher than that at 2 weeks (25.21%) in the preliminary trial. A similar trend of 36.23 and 31.36% was recorded for 3 and 2 weeks crop growth stages, respectively in the confirmatory trial (Tables 3 and 4, Fig.3), an indication that *Striga* germination increased with a combined increase in the stage of crop growth and the length of preconditioning period. This result is consistent with reports of increased sensitivity of *Striga* seeds to germination stimulants with length of preconditioning period (Worsham, 1987; Babiker *et al.*, 1993). Babiker *et al.* (1993) observed that a major step in preconditioning process is the release of a restriction on ethylene biosynthesis from the precusor 1-aminocyclopropane-1-carboxylic acid (ACC).

The two sorghum varieties, SAR 35 and IS1260, gave relatively very poor results at 2 and 3 weeks (Table 3). This result tend to suggest that these two varieties only promote the germination and subsequent emergence of *S. hermonthica* at an advanced stage under field conditions. This probably explains

the tolerance of IS1260 to *S. hermonthica* (Lagoke, personal comm., 1996). These varieties were selected for use as control based on their support of high emergence of *S. hermonthica* in the field, usually at 9 to 12 WAS. A susceptible variety CK60B, however stimulated a high level of germination in the laboratory when used later as the control. It was therefore a more suitable control in the confirmatory trial. The wide variability observed among cotton genotypes (Tables 3 and 4) with respect to their ability to stimulate *S. hermonthica* seed germination is an indication of enormous potential of improving the crop for the trait. Dejongh *et al.* (1993) reported variabilities in *Striga* seed germination stimulation among crop cultivars and types including cotton (*Gossypium* spp.). It is therefore, possible to select and breed for cotton genotypes that cause high *Striga* seed germination against an acceptable agronomic background. The phenotypic expression of variability is most likely due to inherent genetic differences among the genotypes for the trait in question.

5.2 Dominance of *Striga* Seed Germination Trait in Cotton Genotypes

Considering the tedious and laborious procedures involved in the evaluation for the trait, genetic populations (P_1, P_2, F_1 and F_2) were evaluated in separate experiments involving batches of twelve (12) genotypes in each trial. The closeness of F_1 means from the crosses RASA(78)11b x SAMCOT-10 and RASA(78)11b x TX-CABS-1-83 to the high *Striga* seed germination stimulating parents indicates that high *Striga* germination stimulation is dominant over low *Striga* germination stimulation. Also, all the F_1s for each of the two crosses caused high *Striga* seed germination (Table 8). The dominance of high *Striga* germination

stimulation over low *Striga* germination stimulation production was also reflected in the means of the F_2 generation for both crosses, which are very close (P_1 x P_2) to the mid-parent value or slightly above the mid-parent value ($_{P1}$ x P_3) (Table 8). Although F_2 means are lower than those of the high parent, they are, however, higher than those of the low *Striga* seed germination stimulating parents.

5.3 F_2 Segregation

Chi-square values were calculated with the assumption that high *Striga* germination stimulation was determined by a single or a few dominant gene(s). Thus, the F_2 segregating populations were tested for goodness of fit to classical phenotypic ratio under the hypothesis of 3:1. Chi-square test gave values of 3.23 and 1.31 for the cross, RASA(78)11b x SAMCOT-10, and RASA(78)11b x TX-CABS-1-83, respectively. With 1 degree of freedom, these values are less than the threshold (P=0.05), indicating that the difference between the observed and the expected ratios was not significant. Consequently, the segregation in the F_2 fits a 3 high *Striga* germination stimulation: 1 low *Striga* seed germination stimulation (Table 9). The fitness for the cross, RASA(78)11b x TX-CABS-1-83 was closer than that for the cross, RASA(78)11b x SAMCOT-10. This difference may be attributed to inherent genetic differences between the two high *Striga* germination stimulating parents, as they differ in their genetic background. In preliminary studies, Butler (1995) observed that germination stimulant production was inherited independently of haustorial initiation factor in sorghum.

The fitness to a 3:1 phenotypic ratio indicates that high *Striga* germination stimulant production in cotton is controlled by a dominant gene. Hess and Ejeta

(1992) have earlier reported the dominance of high stimulant production in sorghum.

5.4 Heritability Estimates and Gene Numbers

Broadsense heritability estimates for both crosses involving low and high *Striga* germination stimulating parents were high (Table 8), indicating that the trait (*Striga* seed germination stimulation) is under genetic control. Comparing the two methods used in estimating broadsense heritability, estimates from genetic components gave relatively higher values than estimates using the non-segregating populations variance as an estimate of environmental variance. For the former, estimates of 74.58% and 78.51%, and the latter, 71.80% and 72.20% were obtained (Tables 8). This is attributed to the larger error variance obtained in the estimates using the non-segregating population variance relative to that of the genetic components. Narrowsense heritability was not estimated as backcross populations were not available. Difficulties in obtaining backcross data is attributed to the tedious and labourious procedures involved in evaluation for the trait.

Estimates of minimum number of genes gave values of less than 1 for both crosses, using Wright (1921), and Castle and Wright (1921) formulae, indicating that *Striga* germination stimulation is monogenically controlled, and that it is a qualitative trait. This fact is also reflected in the F_2 populations, where two distinct classes of segregates were obtained (Tables 5, 6 and 8; Figs. 4). The same values (0.67) were obtained for the cross RASA(78)11b x TX-CABS-1-83 using Wright (1921), and Castle and Wright (1921). However for the cross, RASA(78)11b x SAMCOT-10 slightly different values of 0.72 and 0.68 were

obtained using Wright (1921), and Castle and Wright (1921) formulae respectively. It is worth noting here that the materials used in this study did not meet the assumptions that go with these formulae in totality. The estimates obtained using Wright (1921) formula are more acceptable since the materials used in the study appear relatively close to meeting the assumptions that go with the formula.

Although this study was not set out to investigate the mechanism of suicidal germination, it was observed that cotton genotypes have the ability to induce haustoria formation in *S. hermonthica* seeds. It would appear therefore that cotton produces the second chemical required for haustoria initiation. Thus, the failure of this crop to support the growth of *S. hermonthica* is likely not a result of the absence of the haustoria initiation chemical. Consequently, there is need to investigate the mechanism of suicidal germination in the cotton plant.

The crosses used in this study did not involve any reciprocals, largely due to the large number of genotypes to be handled. Again, maternal effects has not been reported in other agronomic traits in cotton (Alabi; Echekwu, Personal Comm., 1996). Consequently the possibility of maternal effects or cytoplasmic inheritance on the control of this trait (*Striga* seed germination stimulation) can not be ruled out in totality.

CHAPTER SIX

SUMMARY AND CONCLUSION

Forty genotypes of cotton (*Gossypium* spp.) from the Fibre Research Programme of the Institute for Agricultural Research, Zaria (Nigeria) were screened in the laboratory for *Striga* seed germination stimulation ability using the cut root technique. The aim of the investigation was to study the variability among these genotypes with respect to their ability to stimulate germination of *S. hermonthica*, and identifying parental materials for use in a genetic study. Three parents (one low *Striga* germination stimulating and two high *Striga* germination stimulating) were selected and crosses made in the combination of low x high *striga* germination stimulation, with the high germination stimulating parents as pollinators. RASA(78)11b was the low parent, while SAMCOT-10 and TX-CABS-1-83 were the high *Striga* germination stimulating parents. The F_1s obtained from both crosses were advanced to the F_2 generation through controlled selfing. The resulting genetic populations (parents F_1s and F_2s) were evaluated in separate experiments.

With higher percentage of *Striga* seed germination repeatedly recorded with combination of roots obtained from 3 weeks old plant and *Striga* seeds preconditioned for the same period in the laboratory experiment, 3 weeks appear to be ideal for the effective screening of potential "trap" crop genotypes for *S. hermonthica*. With such a wide variability observed among the cotton genotypes used in this study with respect to their ability to stimulate *S. hermonthica*

germination, it is therefore possible to improve the crop for this trait while incorporating other excellent agronomic attributes.

The genetics of suicidal germination of *S. hermonthica* was the same for the two crosses used in the study. However, the cross, RASA(78)11b x TX-CABS-1-83 was superior to RASA(78)11b x SAMCOT-10, as reflected in the relatively closer fitting of the F_2 segregating population to classical phenotypic ratio under the hypothesis of 3:1, and the higher broadsense heritability estimate. Nevertheless, these differences were small in magnitude.

The high broadsense heritability estimates of over 70% observed in the population used for the genetic study suggest high genetic control for *Striga* germination stimulant production in cotton. In addition, gene number estimates also revealed that the character is monogenic. Thus, the cotton gene controlling *Striga* germination stimulation is simply inherited, with high stimulation dominant over low stimulant production. With the segregating populations (F_2) falling in discrete classes, *Striga* germination stimulation in cotton is a qualitative trait.

The genetic populations developed in this study can form the basis for improving the crop for this trait and for mapping the gene on the cotton genome. Also there is need to ascertain the mechanism of suicidal germination in cotton. However, in the interim, SAMCOT-10 is recommended for use by farmers, either in rotation or as an intercrop with susceptible host crops in *S. hermonthica* endemic areas where cotton can be grown.

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APPENDICES

Appendix I

Sources of variation, degrees of freedom, sum of squares and mean square values in the analysis of variance for *S. hermonthica* seed germination induced by some cotton genotypes at 2 and 3 weeks growth stages.

		SS		MS	
Source	Df	14*	21*	14*	21*
Genotypes	41	5175.88	7478.71	126.24**	182.41**
Error	84	3513.33	2176.67	41.83	25.91
Corrected total	125	8689.21	9655.37		

* Days after the beginning of experiment

** Significant at 0.01 probability level (DMRT).

Appendix II

Sources of variation, degrees of freedom, sum of squares and mean square values for the analysis of variance for *S. hermonthica* seed germination induced by some cotton genotypes at 2 and 3 weeks growth stages.

		SS		MS	
Source	Df	14*	21*	14*	21*
Genotypes	12	1763.64	2555.97	146.97**	212.91**
Error	26	329.33	244.00	12.67	9.38
Corrected total	38	2092.97	2798.92		

* Days after the beginning of experiment

** Significant at 0.01 probability level (DMRT).

Appendix III

Sources of variation, degrees of freedom, mean squares and expected mean square values for the analysis of variance for *S. hermonthica* seed germination for the cross; RASA(78)11b x SAMCOT-10 (P_1 x P_2) and RASA(78)11b x TX-CABS-1-83(P_1 x P_3).

		MS		EMS	
Source	Df	P_1 x P_2	P_1 x P_3	P_1 x P_2	P_1 x P_3
Genotypes	49	303.06**	331.23**	940.10	1021.39
Error	100	30.92	27.69	30.92	27.69
Corrected total	149				

** Significant at 0.01 probability level (DMRT).

Appendix IV

BIOGRAPHY

Name : Christopher Jomia BOTANGA

Date & Place of Birth : 19th December, 1969 at
Bali Nyonga (Cameroon)

Business Address : c/o Dr. J.G. Kling
International Institute of Tropical Agriculture (IITA)
PMB 5320, Oyo Road
Ibadan, Nigeria
E-mail: j.kling@cgnet.com.

Home Address : Presbyterian Church Njenka
P.O. Box 80, Bali Nyonga
Bamenda-North West Province
Cameroon

Institutions Attended	From	To	Certificate/Diploma/Degree
Presbyterian School Njenka, Bali Nyonga Cameroon	1974	1981	First School Leaving Certificate (F.S.L.C.)
Government High School Wum, Cameroon	1982	1987	General Certificate of Education, Ordinary Level (G.C.E. O/L)
Cameroon College of Arts, Science and Technology, Bambili, Cameroon	1987	1989	General Certificate of Education, Advanced Level (G.C.E. A/L)
Ahmadu Bello University, Zaria, Nigeria	1990	1995	Bachelor of Agriculture (B.Agric.)

Post(s) Held Since Award of First Degree: Nil

Year of Admission for Graduate Studies: 1996

Admission Number: M.Sc/Agric/08631/95-96.