Studies of Some Sugarcane (*Saccharumofficinarum*) Families for Resistance to Smut at Badge, Nigeria

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Abstract: *The need for continuous development and screening of sugarcane familiesfor smut resistant is paramount. Because substitution of susceptible varieties by resistant genotypes is one of the most successful and reliable methods to combat smut disease. A study was conducted to screensixty sugarcane bi parental progenies (from twelve families) under smut infestation at NCRI Badge. The hybrid clones were arranged on Randomized Complete Block Design (RCBD) with two replications at Badge and Edozhigi sugarcane field of NCRI. Analysis of variance reveals significant differences between the families for some traits. Average cane yield of 75.73 and 76.85 t/ha were recorded in Family 7 and Family 1(at Badge and Edozhigi).The best brixof 18.5% was recorded for family 2, 3, 10, 11at Badeggi and family 2 has the best brix mean value of 18.7% in Edozhigi.Combined smut index proved family 5 to be highly susceptible to smut infestation and only progenies of family 2 showed zero smut infestation. This study has demonstrated the potential of some sugarcane families and their progenies reaction to smut disease for subsequent evaluation in the national breeding program.*

Key Words: *Bi-parental, smut, progenies, resistant, susceptible*

1.0 Introduction

Sugarcane (*Saccharum*spp.) is one of the most important industrial crops cultivated in the tropics and subtropics (Ishaq*et al.* 2019).Sugarcane cultivation is impede by more than 200 pests and diseases caused by fungi, viruses, bacteria, phytoplasmas and nematodes, resulting in sugar losses worldwide (Allsopp*et al.*, 2000). Sugarcane whip smut (*S. scitaminea*) is a very destructive disease in all sugarcane growing areas of the world including Nigeria (Wada *et al.,* 2016). The disease was first observed in Nigeria in 1969 and it has continued to spread, which create significant impact on sugar estates and peasant farmers that practice cane cultivation (Nasiru I and Ifenkwe O.P. 2004).

Whip smut is a serious disease of sugarcane which causes significant quantitative and qualitative loses to cane farmers worldwide. Rajput *et al.* (2021) stated that smut disease can be checked through crop inspection; rouging and destruction of infected plants carried out regularly in order to maintain the disease below threshold levels. Rouging may not be practical for severe outbreaks involving commercial acreage.The best eco-friendly and most sustainable means to curtail the pathogen are through the use of resistant varieties (Sundravadana*et al.,* 2011).

However due to varietal degeneration and changes in smut races, it has become paramount for continuous hybridization activities to develops smut resistance genotypes that will replace any obsolete clone. Variety resistance is retained for few years, while a known resistant variety may succumb to a new physiological strain (race) of smut with changes in climatic conditions (Mansoor*et al.*, 2016). According to Sarmad*et al.* (2016) who screened some sugarcane varieties against whip smut in relation to epidemiological factors stated that resistance of a variety is sustained only for few years and further revealed that variety resistant previously to pertaining race may become susceptible to a new physiological race with changes in climatic conditions. Sundar*et al.* (2015) stated that the breakdown of disease resistance is attributed to the possible emergence of new virulent path types.

Kimbeng and Cox 2003 stated that Family evaluation and selection in sugarcane breeding entails the positive selection of a whole population of progenies from a cross based on data collected from family plots. However, the selection for superior individual genotypes is focused within elite families where a higher percentage of superior genotypes exist. Hogarth *et al.* (1990) had reported that family evaluation and selection increase the efficiency of breeding for quantitative traits.

The resistant to smut disease among crosses progenies of sugarcane willenhance assessment and development of resistant varieties through breeding program. Therefore, screening of sugarcane families against smut disease is a pre-requisite in the varietal development activities after hybridization and it will give clear view on the performance of the progenies resulting from different parental combinations.

2.0 Materials and Methods

2.1 Experimental Location

The experiment was carried out at the sugarcane research field of National Cereals Research Institute (NCRI) Badge and Edozhgi, Niger state. Hybridization crosses (bi-parental) was set up in the field between selected male sterile clones (maternal parents) and male fertile clones (paternal parents)

of promising high resistance clones with susceptible clones. At arrowing stage of the plants, selected female clone's arrows were enclosed in a suspended lantern to shield their flowers from undesired pollens. True sugarcane seeds (fuzz) were harvested from the female clones labeled and stored.
The stored fuzz was planted in the screen house for a period of three months before transplanting to the field. Emerged seedlings was transferred into poly pots and maintained for 2 months. Each individual seedling was transplanted to the field on a spacing of 1 x 1m and the generated clones. Sixty sugarcane progenies of twelve families (Bi parental crosses) were screened against smut diseases. The experiment was conducted in a randomized complete block design with two replications at Badeggi and Edozhigi (Edoz).

Table 1: Crosses combination (Bi parental using North Carolina II design with 4 females and 3 males)

Family	Parentage	Designation
1	KNB 9218 x N27	A
2	NCS 008 x N27	B
3	0535 x N27	C
4	NCS 007 x N27	D
5	KNB 9218 x NCS 009	E
6	NCS 008 x NCS 009	F
7	0535 x NCS 009	G
8	NCS 007 x NCS 009	H
9	KNB 9218 x B 1245/BO 197	I
10	NCS 008 x B 1245/BO 197	J
11	0535 x B 1245/BO 197	K
12	NCS 007 x B 1245/BO 197	L
13	NCS 009 (CHECK)	

2.2 Smut spore preparation

Fresh smut whips werecollected from smut affected plants grown at NCRI sugarcane field. The teliospores were gently scraped and thoroughly sieved, using 53 µm mesh. The sieved teliospores were sealed in cellophane bags and stored in the refrigerator at 10°C. Viability of inoculum was confirmed on potato agar and those that reveal viability of >70% were taken for preparation of inoculum suspension. Four grams of spores were added in 1 litre of distilled water. Finally, the inoculum density was adjusted to 4×10^6 spores/ml with the help of haemocytometer (Nasr, 1977).

2.3 Inoculation of planting material sand Planting

The stalks were cut into 3 budded setts and grown on a single row of 5m long with inter row spacing of one meter. The planting materials (setts) were completely immersed into the smut inoculum for an hour. The setts were then be removed and put into a sack under shade for 14 hours prior to planting. Ten inoculated setts were planted (lay end to end) per row at a depth of 6-7cm and covered with top soil. A known commercial variety B 47419 was used as check. The experiment covers a total area of 18m x 34m (612m^2).

2.4 Collection of Data and Analysis

Data was collected on sprout (%)count at 21, tiller count at 3 months after planting, plant height at 3 and 6 months after planting, stalk length, Milleable stalk per plot and cane yield ton/ha at maturity. Brix (sugar content) was measured with the aid of refractometer at 12th months after planting. Smut index was expressed by reaction types evaluated with a numerical rating scale of 1-9 where, 1=highly resistant and 9=highly susceptible as described by Satyavir and Beniwal (1978).

The data collected was use for analysis of variance (ANOVA) using Crop Stat package (version 7.2). Means were separated where significant differences occur among the genotypes.

2.0 Results

The analysis of variance had revealed the significant differences that exist among progenies and between families of sugarcane crosses evaluated for smut resistance at Badeggi and Edozhigi (Table 2). Seven traits (Germ %, Tiller, PLH3, PLH6, STK G, STUL/P & Brix) showed differences among the progenies at Badeggi and at Edozhigi there was no significant differences among the progenies for Germ, Tiller, Stul/P and Stk/P respectively. Most of the studied characters showed significant differences between the families at both location except for Germ, Tiller and Stul/P.

Table 2: Mean square of 60 hybrids (progenies) and within families at Badeggi and Edozhigi (2023-2024)

Source of Variation	Progenies (BDG)	Progenies (EDZ)	Within families (BDG)	Within families (EDZ)
DF	64	64	12	12
GERM	6.24**	3.24	5.43	4.1359
TILLER	70.39**	47.53	135.88**	80.677
PLH 3	1625.20**	950.27**	3789.00**	1853.7**
PLH6	1096.70*	1456.50*	2457.70**	2776.6**

STALK LT	-	1288.90*	-	3172.9**
STK GT	0.21**	0.32*	0.40**	0.55**
STUL/P	2.63*	2.80	3.68	6.31**
STK/STUL	3.54	-	7.18*	-
STK/PLOT	114.62	187.63	220.72**	573.40**
SSWT	0.02	0.06**	0.06**	0.17**
BRIX	3.01**	3.74**	7.59**	9.56**
YLD	1091.90	1182.70*	2587.80**	2219.10*

Note: BDG= Badge, EDZ= Edozhigi, Germ= germination, PLH= plant height, Stalk LT= stalk length, STK G= stalk girth, Stul/P= stool per plot, Stk/Stul= stalk per stul, STK/Plot= stalk per plot, SSWT= single stalk weight, YLD= yield

The result on table 3 exhibits that there were significant (P≤ 5%) differences between the families for the recorded characters. Family 3 had the highest germination mean among the families which were similar with the Germination recorded for NCS 009 and only four families (3,4,5 & 7) obtained germination mean above the grand germination mean at Badge. However at Edozhigi five of the families (2, 3, 4, 6, & 9) exhibit better germination above their grand mean. At Badge maximum number of tillers was recorded in family 1 and the least number of tillers was observed in family 6.

Plant height means at 6 months after planting (MAP) was highest in family 10 and family 6 recorded the shortest plants at 6 MAP in Badeggi. At Edozhigi the maximum plant height mean was noted on family 1 which was higher than the mean recorded for the check (NCS 009) and the grand mean.

Table 3: Mean values of growth performance for sugarcane families at NCRI Badeggi andEdozhigi (2023-2024)

Family	Germ bdg	Germ edz	Tiller bdg	Tiller edz	Plh 3 bdg	Plh3 edz	Plh6 bdg	Plh6 edz
1	3.40	4.20	16.80	10.90	139.86	122.07	182.59	191.67
2	3.60	5.80	5.70	6.90	115.85	104.83	161.72	156.56
3	5.20	5.00	6.80	8.80	107.37	108.71	141.15	176.30
4	3.90	5.90	6.60	12.90	138.70	155.02	169.19	184.20
5	3.90	4.30	5.50	9.70	109.71	110.16	152.63	171.04
6	2.60	5.70	4.00	9.50	90.05	126.15	128.69	140.82

7	4.20	4.10	10.10	10.30	137.51	133.19	168.65	164.23
8	3.60	4.80	6.80	8.80	117.92	125.83	148.92	148.56
9	3.50	5.70	8.60	7.40	118.54	112.70	150.71	165.63
10	3.40	4.50	6.40	17.10	130.46	132.62	183.38	148.48
11	3.80	4.80	8.00	8.00	140.75	134.64	161.68	182.65
12	3.70	4.70	5.10	12.30	78.88	130.58	149.30	189.08
13 (check)	5.38	4.50	14.13	13.30	129.03	119.96	150.73	156.65
LSD@ 5%	1.70	1.59	4.81	6.32	25.07	20.15	22.59	26.53
CV	51.00	37.00	78.20	70.30	27.40	20.40	18.20	19.30
G Mean	3.86	4.94	8.04	10.45	119.59	124.34	157.64	167.37

Note: BDG= Badge, EDZ= Edozhigi, Germ= germination, PLH= plant height, Stalk LT= stalk length, STK G= stalk girth, Stul/P= stool per plot, Stk/Stul= stalk per stul, STK/Plot= stalk per plot, SSWT= single stalk weight, YLD= yield

At Edozhigi family 7 and 9 showed similar stem girth which was lower than the average girth of the other tested families (table 4). Maximum stalk length was noted in family 5 at Edozhigi and the shortest stalk length was observed in NCS 009. Family 3 has more number of stools per plot and the lowest was observed in family 6 at Badge. However at Edozhigi six of the families recorded $\geq$ 4 number of stools per plot and were greater than the number of stools obtained at Badeggi. More milleable stalks was recorded in family 7 at Badeggi than other families and was lower than the milleable obtained by the check. NCS-007 has average of 43 milleable stalks per plot at Edozhigi and family 2 has fewer stalks than the other studied families.

Table 4: Mean values of some yield attributes for 12 sugarcane families at NCRI Badeggi andEdozhigi (2023-2024)

Fmly	Stk gt bdg	Stk gt edz	Stk lnt edz	Stul/p bdg	Stul/p edz	Stk/stul bdg	Stk/plot bdg	Stk/plot edz
1	2.00	2.11	270.25	2.80	4.00	5.60	17.30	20.80
2	2.65	2.73	283.03	2.90	4.50	3.80	10.80	13.60
3	2.16	2.23	256.58	4.40	3.80	4.20	17.60	15.40
4	2.00	2.41	282.66	3.50	4.50	5.30	17.30	19.90
5	2.21	2.39	294.69	3.40	3.90	5.90	20.30	24.50
6	2.36	2.43	285.23	2.60	4.10	4.90	14.10	19.00
7	2.43	1.90	263.69	4.00	3.10	6.30	25.60	17.50
8	2.13	2.30	255.00	3.30	4.20	5.20	19.30	23.30
9	1.87	2.16	255.46	3.40	4.20	4.10	14.50	17.80
10	2.22	1.95	255.84	3.20	3.80	6.00	20.30	23.20
11	2.18	2.43	237.62	2.70	3.10	5.40	15.60	13.60
12	2.11	2.02	248.79	2.80	3.70	5.70	14.00	17.20
13 (check)	2.21	2.40	242.50	4.38	6.30	6.50	27.63	43.00
LSD @ 5%	0.28	0.42	25.48	1.26	1.33	1.48	8.33	9.78
CV	16.3	22.6	12.3	43.6	38.7	32.5	55.4	62.1
G Mean	2.19	2.26	263.95	3.34	4.09	5.30	18.03	20.68

Note: STK LT= stalk length, STK G= stalk girth, Stul/P= stool per plot, Stk/Stul= stalk per stul, STK/Plot= stalk per plot, SSWT= single stalk weight, YLD= yield

Table 5 reveals significant variability that exists between the families for brix, single stalk weight and yield at Badge and Edozhigi. Six families (1, 2, 3, 10, 11 & 12) gave average brix % that was greater than the grand brix mean and least brix was obtained in family 5 at Badge. At Edozhigi family 2 gave an average brix mean of 18.73% which was significantly better than the brix mean value recorded for NCS 009 and six other families (1, 2, 3, 10, 11 & 12) has average brix mean above the grand brix mean. Single stalk weight was highly significant between the families at both locations as observed on table 4. Family 10 express the smallest girth at both locations during the evaluation. NCS-009significantly recorded the highest cane yield at both locations (Badeggi 108.10 t/ha and Edozhigi 96.10 t/ha). Family five gave average yield of 85.15 at Badeggi and family 12 gave the least yield. At Edozhigi only four families (4, 5, 7, 8) has average yield greater than the grand yield mean (54.82 t/ha).

Table 5: Mean values of brix and yield performance of 12 sugarcane families at NCRI Badeggi and Edozhigi (2023-2024)

Fmly	Brx bdg	Brx edz	Sswt bdg	Sswt edz	Yld bdg	Yld edz
1	18.09	18.16	0.45	0.41	76.85	44.65
2	18.49	18.73	0.67	0.58	65.05	35.81
3	18.51	18.49	0.38	0.37	58.50	47.95
4	17.32	17.01	0.50	0.42	85.15	58.07
5	16.29	16.20	0.37	0.37	72.00	60.33
6	17.02	16.67	0.48	0.37	71.15	44.65
7	16.77	16.23	0.42	0.41	63.00	75.73
8	16.65	16.28	0.38	0.39	62.70	60.32
9	17.08	17.14	0.47	0.43	58.00	43.90
10	18.48	18.59	0.36	0.31	64.68	51.99
11	18.50	18.37	0.37	0.46	70.35	49.12
12	17.90	17.85	0.37	0.40	47.60	43.97
13 (check)	18.90	16.67	0.80	0.59	108.10	96.10
LSD @ 5%	0.89	1.05	0.09	0.13	25.47	28.10
CV	7.30	8.50	30.70	40.80	57.60	48.30
G Mean	17.69	17.41	0.42	0.46	69.47	54.82

Note: SSWT= single stalk weight, YLD= yield

The smut incidence rating and reaction type of the studied progenies to smut inoculation is given on table 6. Resistance to smut disease caused by*S. scitamineum*varied among sugarcane families (parental combinations) at Badeggi and Edozhighi.All the progenies of family 2 (N27 x NCS 008) tend to be

highly resistant to smut infestation during the study at both locations. Three progenies of family (1, 3 & 9) were smutted and family 5 (KNB 9218 x NCS 009) has the highest number of smutted progenies. Progeny A4 and F30 had the highest smut % in this study. Out of the 60 progenies screened only 23 (13.8 %) were affected by the smut disease.

Table6: Smut index of Bi parental sugarcane progenies (12 families) screened at NCRI (Badeggiand Edozhigi)2023-2024

Entry	Progenies	Parentage	Smut% (bdg)	Smut% (edoz)	Average smut at the location
1	A1	N27 x KNB 9218	3.95	2.8	3.375
2	A3	N27 x KNB 9218	2.22	2	2.11
3	A4	N27 x KNB 9218	66.6	30	48.3
4	C11	N27 x NCS 0535	34.5	12	23.25
5	C12	N27 x NCS 0535	14.3	5	9.65
6	C14	N27 x NCS 0535	21.05	8	14.525
7	D18	N27 x NCS 007	12.5	4	8.25
8	E22	NCS 009 x KNB 9218	20	4	12
9	E23	NCS 009 x KNB 9218	37.5	13	25.25
10	E24	NCS 009 x KNB 9218	37.5	10	23.75
11	E25	NCS 009 x KNB 9218	41.8	11	26.4
12	F27	NCS 009 x NCS 008	18.75	4	11.375
13	F30	NCS 009 x NCS 008	67.86	22	44.93
14	G33	NCS 009 x NCS 0535	18.8	13	15.9
15	H39	NCS 009 x NCS 007	50.66	26	38.33
16	I40	B 1245/BO 197 x KNB 9218	14.26	7	10.63
17	I42	B 1245/BO 197 x KNB 9218	30.97	12	21.485
18	I43	B 1245/BO 197 x KNB 9218	20.36	8	14.18
19	J50	B 1245/BO 197 x NCS 008	4.34	2	3.17
20	K52	B 1245/BO 197	25	11	18
21	L57	B 1245/BO 197	50	22	36
22	L58	B 1245/BO 198	61.11	26	43.555
23	NCS 009	CHECK	0.3	0.1	0.2

2.1 Discussion

The Success of any hybridization relies on the combination of parents used, their ability to combine and pass on promising traits to their progenies. In this regard 12 cross combinations (4 females x 3 males) with a population size of 60 progenies were screened for growth and yield performance under smut infestation to identify a superior cross combination, which gives good number of resistant progenies based on the smut index percent. Reaction of progenies to disease and other agronomic attributes recorded plays an important role to determine the parent's to be used in subsequent breeding program. Result of this study had demonstrated significant differences within families and genotypes which can be used in selection at early progeny testing stage. Families with higher resistant progenies and better trait values can be selected, and then progenies within these selected families will be identified and advanced for further progeny testing series.

The result of our study affirms the report of Wijesuriya*et al.*, (2012) which indicated that there were significant differences among biparental sugarcane families for all characteristics studied and also among progenies within families for all characteristics except for plot weight. They further imply that significant differences existing between progenies within families indicated the possibility of undertaking individual selection within families targeting selection of elite progenies.

Mbuma (2019) stated that family selection focus on elite clones (individual clone selection) in the superior families, thereby increasing the chances of identifying better elite clones at advanced stages of testing within these families. He further highlighted that the added advantage of family selection in sugarcane is that family data can be used to address the breeding value of parents based on progeny performance.

Mohammed 2007 and Shanties *al.*, 2008 had also documented that selection of the best families based in their mean performance and further selection of individual clones within the best families in early stage of selection would increase the efficiency of selection.

4.0 Conclusion

Based on the result of this screening it is concluded that family selection can be used at early state of hybrid sugarcane progenies testing series to obtained better elite clones. Performance of progenies within a family also gives an insight for a breeder to identify better parental combinations for subsequent hybridization program based on specific objectives.

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