



GENETIC VARIABILITY AND SMUT RESISTANCE OF SUGARCANE (*SACCHARUM OFFICINARUM* L.) GENOTYPES FOR BREEDING IMPROVEMENT

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ABSTRACT

This study evaluated the agronomic performance, genetic variability and smut resistance of sugarcane (*Saccharum officinarum* L.) genotypes under field conditions. Thirty-five genotypes were evaluated using a Randomized Complete Block Design (RCBD) with three replications. Phenotypic and genotypic variances were estimated from analysis of variance, while cluster analysis, principal component analysis and correlation analysis were employed to assess genetic diversity and trait relationships. Seven selected genotypes, comprising five resistant and two susceptible parents were crossed using the North Carolina II mating design to estimate additive and dominance genetic variances, dominance ratio and heritability. Significant ($P < 0.05$) differences were observed among the genotypes for several agronomic and quality traits. The highest cane yields in the plant crop were recorded for NCS-009 (112.80 t ha⁻¹), NCS-003 (111.10 t ha⁻¹) and NCS-002 (104.43 t ha⁻¹), whereas NCS-002 produced the highest ratoon yield (74.43 t ha⁻¹). CP72-2086-1 recorded the highest plant crop brix (23.00%), while BR971007 (23.87%) and CP72-2086-1 (23.70%) maintained superior brix values in the ratoon crop. Genotypes NCS-002, NCS-007, KNB9218, NCS-003, DB75159, BR971007 and B245/B0197 exhibited high resistance to smut. High genotypic and phenotypic coefficients of variation for millable stalk and cane yield indicated a substantial genetic variability. The evaluated genotypes and progenies displayed variable responses to smut infestation across environments and crop cycles. Notably, the cross N27 × NCS-008 produced progenies with complete resistance to smut, highlighting its potential for developing resistant sugarcane cultivars.

Keywords: Evaluation, Sugarcane, Genotypes, Yield

INTRODUCTION

Sugarcane (*Saccharum* spp.) is one of the world's most economically important industrial crops, cultivated extensively across tropical and subtropical regions where it serves as the principal source of sugar and renewable biomass (Bhuiyan *et al.*, 2021). Sugarcane contributes approximately 80% of global sugar production, with the remainder derived from sugar beet, while also providing essential feedstock for numerous bio-based industries (Ahmad and Ming, 2024). Beyond its traditional role in sugar production, the crop has become a strategic crop within the global bioeconomy system as a result of its versatility in the production of high-value products, such as biohydrogen, biodegradable plastics, bioethanol, bioelectricity, biogas, bio-based chemicals and other renewable biomaterials (Sukphun *et al.*, 2023). These products have contributed significantly to the sustainable development in industrial and climate change mitigation thereby reducing dependency on fossil fuels and also lowering greenhouse gas emissions (Ahmad and Ming, 2024). In Nigeria, sugarcane is an important agricultural crop that supports household consumption and supplies raw materials to manufacturing industries, such as pharmaceuticals, food processing, confectionery, beverage production and emerging bioenergy enterprises (Voora *et al.*, 202). The growing demand for domestic sugar production and renewable energy has further increased the importance of improving sugarcane productivity and resilience against biotic stresses. Despite its economic importance, sugarcane production is constrained by numerous diseases caused by viruses, phytoplasmas fungi, bacteria and other pathogens (Olahan *et al.*, 2020). Among these, sugarcane smut, caused by *Sporisorium scitamineum*, is one of the most destructive and widely distributed diseases affecting commercial sugarcane production worldwide (Bhuiyan *et al.*, 2021). The pathogen is capable of infecting susceptible cultivars throughout their growth cycle and can



always spread rapidly through airborne teliospores that remain viable under adverse environmental conditions for extended periods of time (Rajput *et al.*, 2021). Sugarcane smut was reported in virtually all major sugar-producing regions and continues to pose a serious threat to sustainable sugar production in the world due to its detrimental effects on cane growth, tillering, sucrose accumulation, stalk development and overall cane quality. Disease severity varies depending on the cultivar susceptibility, environmental conditions, pathogen race and crop management practices, with yield reductions from 20% to over 70% under severe epidemics (Bhuiyan *et al.*, 2021). In addition to reducing cane yield, smut infection greatly decreases sugar recovery and juice quality, thereby causing substantial economic losses throughout the sugar value chain system (Gillani *et al.*, 2024). In Nigeria, field surveys have similarly revealed considerable variation in smut incidence across sugarcane-growing locations, indicating differences in varietal susceptibility, disease pressure and environmental conditions (Olahan *et al.*, 2020). The continuous emergence of new pathogen races and the influence of climate variability further threaten the durability of resistance in previously resistant cultivars, making periodic evaluation of breeding materials essential for sustainable disease management (Msomba *et al.*, 2024). Host plant resistance remains the most effective, environmentally sustainable, and economically viable strategy for managing sugarcane smut. Consequently, identifying resistant germplasm and incorporating durable resistance into elite breeding populations have become major priorities in modern sugarcane improvement programmes. The success of such programmes depends largely on understanding the genetic diversity and inheritance of resistance within available germplasm, enabling breeders to select genetically diverse parents capable of producing superior segregating populations with enhanced disease resistance and agronomic performance (Ahmad and Ming, 2024). Although numerous sugarcane clones have been introduced, evaluated, and maintained in breeding programmes, the effectiveness of resistance genes often declines over time because of pathogen evolution and changing environmental conditions (Msomba *et al.*, 2024). Consequently, continuous hybridization, genetic evaluation, and screening of new breeding populations are required to replace obsolete cultivars with improved genotypes possessing durable resistance, high cane yield, and superior sugar quality (Bhuiyan *et al.*, 2021). Therefore, the objective of this study was to investigate the genetic basis of smut resistance in selected sugarcane genotypes to facilitate the development of improved cultivars with durable resistance and enhanced agronomic performance for sustainable sugarcane production.

MATERIALS AND METHODS

The field experiment was conducted at the Sugarcane Research Field of the National Cereals Research Institute (NCRI), Badeggi, Niger State, Nigeria (9°03'N, 6°09'E; 70.5 m above sea level). The experimental site is located within the Southern Guinea Savannah agroecological zone of Nigeria. Thirty-five sugarcane genotypes were obtained from the National Sugarcane Germplasm Collection maintained at NCRI, Badeggi. Smut spores (*Sporisorium scitamineum*) were collected from naturally infected sugarcane plants within the NCRI sugarcane research field. The pathogen was multiplied using 0.2% Yeast Extract Sucrose Broth (YESB) prepared by dissolving 20 g sucrose and 2 g yeast extract in 1 L of distilled water. The medium was sterilized by autoclaving at 121°C and 15 kPa for 20 min before inoculation with a one-week-old pure culture of *S. scitamineum*. The culture was incubated at room temperature for 10 days to obtain sufficient inoculum. The spore suspension was adjusted to a concentration of 4×10^6 spores mL⁻¹ using a haemocytometer. Three-budded sugarcane setts were immersed in the spore suspension for 1 h and subsequently incubated under shade for 14 h prior to planting. The experimental field was manually cleared, tilled, and furrows were prepared using hand hoes. The experiment was established in a randomized complete block design (RCBD) with three replications. Each experimental unit consisted of a single 5-m row planted with ten inoculated three-budded setts arranged end-to-end at a planting depth of 6–7 cm and an inter-row spacing of 1.0 m. Fertilizer was applied at the rate of 200:60:60 kg ha⁻¹ NPK in two equal splits: the first at 42 days after planting and the second at six months after planting. Weed control was carried out manually at 4, 8, 12, and 16 weeks after planting. Earthing-up was performed four months after planting to improve root anchorage and minimize lodging. At physiological maturity, sugarcane stalks were harvested manually by cutting at the base, bundled according to treatment plots, and the field was cleaned to facilitate ratoon



establishment. Data were collected on millable stalks per plot, stalk length (cm), brix (%), and cane yield ($t\ ha^{-1}$). Juice extracted from representative stalks using a hand-operated cane press was used to determine brix percentage with a hand refractometer according to standard procedures. The data were subjected to analysis of variance (ANOVA) using the Statistical Tool for Agricultural Research (STAR) software. Treatment means were separated using the Least Significant Difference (LSD) test at the 5% probability level whenever significant differences were detected. Cluster analysis, principal component analysis, and correlation analysis were performed to evaluate genetic diversity, trait associations, and relationships among the evaluated genotypes. Genotypic variance, phenotypic variance, environmental variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability, and genetic advance were estimated from the analysis of variance following the procedures of Burton and DeVane (1953), with interpretation based on contemporary quantitative genetic principles described by Bernardo (2020) and recent reviews on genetic parameter estimation in plant breeding.

Genotypic variance (σ^2_g) = $(MS_g - MS_e)/r$

Environmental variance (σ^2_e) = MS_e

Phenotypic variance (σ^2_p) = $\sigma^2_g + \sigma^2_e$

Where MS_g and MS_e are mean sum of squares for genotypes and error in the analysis of variance, respectively, and r the number of replicates.

Genotypic and phenotypic coefficients of variation (GCV, PCV) were computed as follows (Singh R. K. and Chaundary B. D., 1977)

GCV = $\sigma_g \times 100 / \text{grand mean}$

PCV = $\sigma_p \times 100 / \text{grand mean}$

RESULTS

The result as presented in Table 1 revealed a significant difference among some sugarcane accessions under smut infestation for yield parameters. The NCS-003 had more average millable stalks than all the evaluated entries followed by NCS-002, NCS-007, KNB9218, N27, RB86-3129, NCS-009 and B 245/B0197 in that order. The millable stalks of ratooned crop was higher in NCS 002 which did not significantly differs with number of millable stalks recorded for NCS-007, NCS-003, B-2 NCS-003 and B 245/B0197. A very high reduction in number of millable stalks of ratoon crop was noticed in B85266, Boo 270, B881602, B 96399 and B 93220. Some of the screened genotypes (NCS-002, B-2, SP71-618, NCS-006, NCS-009 and NCS-008) had more millable stalks in the ratoon crop above their plant crop. RB86-3129, NCS-006 and NCS-009 had longer stalks (236.7, 233.3 and 230.30 cm) in the plant crop result which were similar with stalk length of KNB9218, B881602, NCS-001, B96399, SP81-3250, N27, NCS-005, B93220, BBZ 921101, NCS-008, 0535, BBZ92653 and B 245/B0197. B9054 had the shortest stalk length (149.23cm) during the plant crop. The ratoon result revealed that, NCS-009 and B 245/B0197 perform better in stalk length (186.10 & 186.0cm), while the shortest stalks were observed in B85266, B51410 and Cp72-2086-1 (107.23, 106.90 & 109.0 cm). There was a general reduction in stalk length of the ratooned crop as against what was observed for plant crop. High brix of 23.00 % was recorded for Cp72-2086-1 which was similar with the brix mean values of B51410, NCS-003, BR00001, RB94-2291, SP71-618, B93220 and BR971007. Many of the studied genotypes show increase in brix of their ratooned crop. BR 971007 and Cp72-2086-1 has the best brix mean value of 23.87 and 23.70 %. NCS-006 had lower brix value (17.13 %) in the ratooned crop. The thirty-five sugarcane genotypes studied showed highly significant differences in their cane yield per hectare. Three genotypes such as NCS-009, NCS-003 and NCS-002 yielded higher (112.80, 111.10 and 104.43 t/ha) and were better in cane yield than other entries. The lowest cane yield of the plant crop was recorded in B881602 (22.57 t/ha). High cane yield mean value for the ratooned crop was observed in NCS-002 (74.43 t/h) which was significantly heavier than the yield observed for many of the studied genotypes followed by NCS-003, DB75159, NCS-001, B-2, NCS-009 and B 245/B0197.



Table 1: Yield Performance of Sugarcane Genotypes Screened for Smut Resistant

GENOTYPES	MILEABLE/PLOT		STLK LNT (cm)		BRIX %		YIELD ton/ha	
	PC	RC	PC	RC	PC	RC	PC	RC
NCS-002	40.33	42.67	169.67	148.10	19.07	21.13	104.43	74.43
NCS-007	38.00	36.33	163.67	118.10	18.10	21.23	64.43	43.30
B 85266	30.00	5.00	161.23	107.23	18.90	21.17	56.67	36.67
B 9054	21.00	11.00	149.23	134.10	17.43	19.43	32.23	37.77
KNB 9218	41.33	22.33	195.67	159.00	19.20	22.17	74.43	40.00
B 51410	23.67	23.00	179.23	106.90	21.50	20.67	39.00	39.97
NCS-003	44.33	38.00	175.67	158.03	20.93	21.30	111.10	72.03
BR 00001	29.00	24.67	190.37	183.47	20.90	22.40	70.00	48.30
BOO 270	19.33	6.33	178.90	117.20	17.53	21.67	33.77	25.53
B 881602	13.33	5.33	197.13	130.80	20.13	20.57	22.57	27.77
DB 75159	17.33	17.00	195.00	158.53	20.03	19.77	48.90	54.43
NCS-001	23.33	20.67	202.87	154.80	17.30	20.67	62.97	51.10
B-2	30.67	38.00	183.67	168.43	18.00	20.57	78.90	52.20
B 96399	19.00	9.33	208.87	153.80	19.97	21.20	38.90	18.90
BBZ 951034	21.33	10.00	191.23	128.90	15.87	18.00	58.90	39.97
SP81-3250	23.33	22.00	206.67	159.10	19.57	20.70	62.23	38.87
D 8687	21.00	17.33	211.43	156.37	18.87	21.30	76.67	49.97
N 27	34.67	23.33	204.20	165.87	19.00	19.60	76.67	47.80
RB 94-2291	24.67	13.33	185.00	137.10	21.70	19.20	71.67	25.57
NCS-005	20.67	13.33	199.67	139.10	17.43	19.03	52.23	34.43
SP71-618	24.67	27.00	190.57	143.00	20.67	19.80	66.67	40.00
RB 86-3129	32.33	14.67	236.67	152.10	18.70	21.50	80.00	48.90
NCS-006	21.67	22.67	233.33	153.57	15.67	17.13	80.00	48.90
NCS-009	37.67	46.00	230.30	186.10	18.80	21.23	112.80	62.23
CP 72-2086-1	27.33	14.67	156.33	109.00	23.00	23.70	87.77	31.10
B 93220	22.67	8.67	195.87	138.57	20.77	22.57	46.30	34.47
RB 86-7512	23.67	14.00	187.00	154.10	18.67	22.10	63.33	37.80
BR 971007	26.33	20.33	179.67	137.97	21.63	23.87	66.67	33.37
BBZ 921101	17.67	14.67	196.33	153.20	18.43	22.63	50.47	31.13
B 47419	21.33	21.67	191.67	118.10	15.67	20.03	88.33	37.77
NCS 008	23.33	26.67	201.67	171.43	18.30	21.53	85.57	46.67
RB 82-5211	17.00	19.33	178.90	148.97	18.17	20.63	64.43	38.90
O535	21.33	21.67	209.43	170.57	18.43	21.50	54.00	36.67
BBZ 92653	28.67	25.67	205.67	147.33	18.63	22.03	82.67	45.57
B 245/B 0197	37.33	34.67	210.33	186.00	17.67	22.23	78.87	62.20
CV %	30.1	30.3	13.2	12.7	7.6	5.0	37.2	34.7
LSD @ 5 %	12.87	10.32	41.53	30.49	2.53	1.70	40.65	24.12

Note: STLK LNT= Stalk length, PC= plant crop, RC= ratooned crop
Means were separated using LSD at $P \leq 5\%$

Total cane yield and other yield attributes (sprout, tillering, stool/line, millable and internode length) had negative loadings on PC1 (figure 1). On the contrary, smut incidence made significant positive impact on the same PC1. In the second PC (PC 2), girth, stalk length and plant height had positive effects on the vectors while tillering made the most negative impact on the PC.

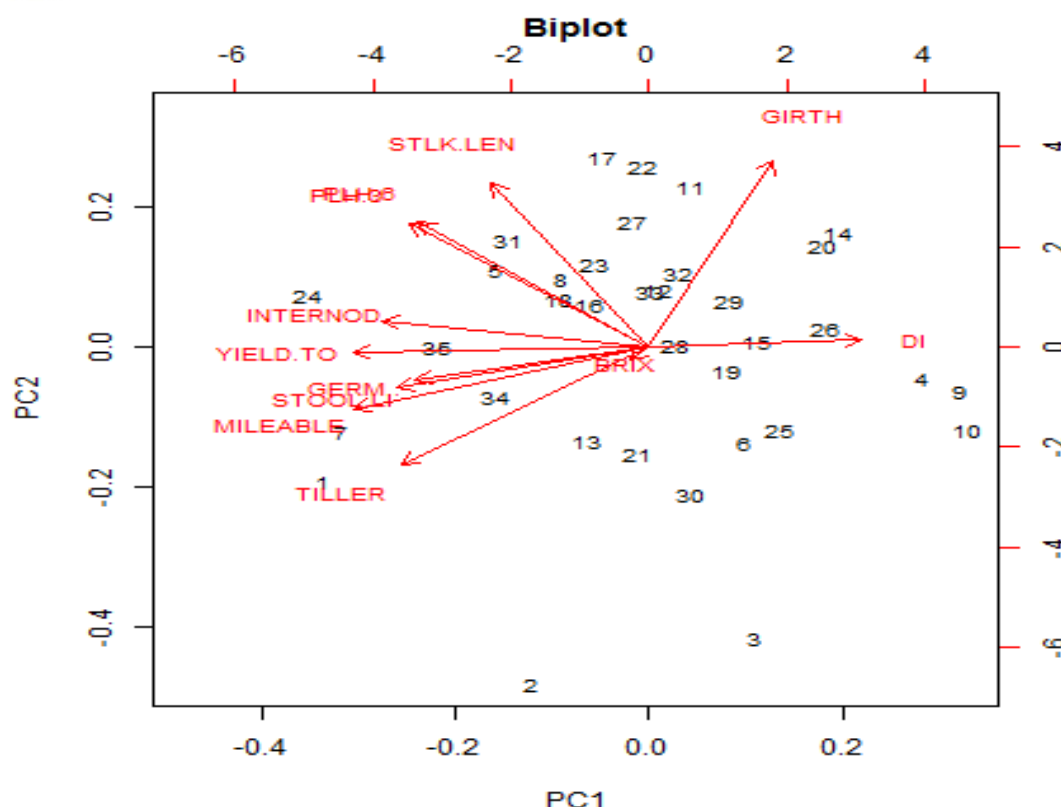


Figure 1: Scatter Plot Showing the Clustering and Loading Plot of Agronomic Traits of 35 Sugarcane Genotypes

Note: PLH: plant height, DI= diseases index, STLK LEN= stalk length, 1=NCS-002, 2=NCS-007, 3=B 85266, 4=B 9054, 5=KNB 9218, 6=B 51410, 7=NCS-003, 8=BR 00001, 9=BOO 270, 10=B 881602, 11=DB 75159, 12=NCS-001, 13=B-2, 14=B 96399, 15=BBZ 951034, 16=SP81-3250, 17=D 8687, 8=N 27, 19=RB 94-2291, 20=NCS-005, 21=SP71-618, 22=RB 86-3129, 23=NCS-006, 24=NCS-009, 25=CP 72-2086-1, 26=B 93220, 27=RB 86-7512, 28=BR 971007, 29=BBZ 921101, 30=B 47419, 31=NCS 008, 32=RB 82-5211, 33=O535 (IAA-873396), 34=BBZ 92653, 35=B 245/B 0197.

For combined plant and ratooned crop (Table 2), the mild differential values between GCV and PCV showed a reduced or minimal environmental influenced on the studied characters. Higher GCV and PCV values were recorded for sprout count (30.7/43.8), Tillering (42.3/54.8), Millable stalk (47.52/56.39) and yield (33.9/50.5). Most other traits showed moderate values except for the low GCV recorded for Brix. The heritability estimates of these traits revealed moderate values for most traits, although, millable stalk and internode length recorded highest heritability values of 71 % and 67 % respectively. Only millable stalk (82.5 %) was distinguished in terms of genetic advance of mean, while brix (15.1 %) and plant height at 6 months were relatively low.

Table 2: Estimates of Genotypic Variance, Phenotypic Variance, Environmental Variance, Broad Sense Heritability, Genotypic Coefficient of Variability, Phenotypic Coefficient of Variation and Genetic Advance for Sugarcane Genotypes

Traits	Means	GV	PV	EV	G x L V	BSH (h ²)	GCV	PCV	G x L CV	GAM
GERM	41.10	159.57	324.04	164.47	242.99	0.49	30.74	43.80	37.93	44.44
Tiller	27.21	132.13	221.81	89.69	203.25	0.60	42.25	54.75	52.40	67.18
PLH3	149.90	389.95	706.66	316.71	312.25	0.55	13.17	17.73	11.79	20.16
PLH6	208.21	411.12	914.10	502.97	611.18	0.45	9.74	14.52	11.87	13.45
STL/Li	5.80	1.40	2.84	1.44	2.72	0.49	20.40	29.03	28.42	29.54
Mileable	23.58	125.58	176.83	51.25	83.88	0.71	47.52	56.39	38.84	82.50
Internode	10.41	2.79	4.15	1.36	1.72	0.67	16.05	19.56	12.61	27.12
Girth	1.90	0.06	0.11	0.05	0.07	0.53	12.54	17.19	14.21	18.86
Stk lent	170.11	510.66	1032.47	521.81	530.91	0.49	13.28	18.89	13.55	19.25
Brix	19.98	3.21	4.82	1.61	3.82	0.67	8.97	10.99	9.78	15.08
Yield	54.85	347.02	767.23	420.21	351.24	0.45	33.97	50.50	34.17	47.06

Note: GV=genotypic variance, PV=phenotypic variance, EV=Environmental Variance, GxLV= genotype x location variance, BSH= broad sense heritability, GCV=genotypic coefficient of variation, PCV=phenotypic coefficient of variation, ECV=Environmental coefficient of variation, GxLCV= genotype x location coefficient of variation, GAM= genetic advance of mean

DISCUSSION

The evaluated sugarcane genotypes exhibited a considerable variation in their responses to artificial smut inoculation, demonstrating differences in their levels of resistance and susceptibility to *Sporisorium scitamineum*. These findings are consistent with those of Aslam *et al.* (2024), who reported reduced sprouting and increased tillering in smut-susceptible sugarcane clones following pathogen infection. Smut disease is known to adversely affect vegetative growth by reducing the production of millable stalks through its detrimental effects on tillers and stalk development. The reduction in cane yield and its associated components observed in the present study can therefore be attributed to increased smut incidence. Similarly, Bhuiyan *et al.* (2021) reported that smut infection significantly reduces cane yield through decreases in millable stalk number and stalk girth in susceptible sugarcane clones. Comparable reductions in sugarcane productivity resulting from the negative effects of smut on growth and yield components have also been documented by Aslam *et al.* (2024). The substantial genotypic and phenotypic variability observed among the evaluated genotypes indicates the presence of considerable genetic diversity for the traits studied. High genotypic and phenotypic variances recorded for stalk length, plant height, and cane yield suggest that the evaluated genotypes originated from genetically diverse backgrounds, thereby providing substantial opportunities for genetic improvement through selection and hybridization. However, environmental variance exceeded the corresponding genotypic variance for traits such as stalk length and cane yield, indicating that environmental conditions exerted a greater influence on the expression of these traits than genetic factors under the conditions of this study. This finding contrasts with the observations of Kumaraswamy and Huang (2026), who reported higher genotypic than environmental variance for cane yield, stalk length, and millable cane number. Likewise, Yali *et al.* (2026) reported greater genetic than environmental contributions to the expression of internode number, millable cane, and stalk weight. The consistently higher phenotypic coefficients of variation (PCV) relative to their corresponding genotypic coefficients of variation (GCV) observed in this study indicate that environmental factors contributed to the expression of all measured traits. This observation corroborates the findings of Ogunniyan (2020) and Barajehfard *et al.* (2026), who similarly reported higher PCV than GCV across evaluated traits, suggesting that phenotypic variation results from the combined effects of genetic and environmental influences. Nevertheless, the relatively high GCV and PCV values recorded for sprouting, tillering, stool number, and cane yield indicate the existence of substantial inherent genetic variability for these traits, implying that their phenotypic performance can serve as reliable indicators of genetic potential and that considerable genetic gain can be achieved through selection. In contrast,



plant height and brix recorded low genotypic coefficients of variation (<10%), indicating relatively limited genetic variability and a stronger influence of environmental factors on their expression. Similar observations were reported by Tolera *et al.* (2023), who found that PCV values generally exceeded GCV values for all evaluated traits, thereby highlighting the influence of non-genetic factors on phenotypic expression. The low PCV and GCV values observed for brix are also consistent with the findings of Tolera *et al.* (2023) and Belwal and Ahmad (2020), suggesting limited genetic variability for sugar content among the evaluated genotypes. Consequently, broadening the genetic base through the introduction of diverse germplasm may be necessary to enhance this economically important quality trait. Furthermore, the relatively narrow differences observed between GCV and PCV for plant height, internode length, stem girth, stalk length, and brix suggest that these traits were comparatively stable and less influenced by environmental fluctuations. The magnitude of the difference between GCV and PCV provides an indication of the extent to which environmental factors influence trait expression. As noted by Regmi *et al.* (2021), wider differences between these parameters indicate greater environmental influence, whereas smaller differences suggest that phenotypic performance more accurately reflects the underlying genetic constitution. The present findings demonstrate the existence of substantial genetic variability among the evaluated sugarcane genotypes and indicate that yield-related traits, particularly tillering, millable stalk number, and cane yield, offer considerable potential for effective selection in breeding programmes aimed at developing high-yielding and smut-resistant sugarcane cultivars.

CONCLUSION AND RECOMMENDATION

The study demonstrated a substantial genetic variation among the evaluated sugarcane genotypes and hybrid progenies in their responses to *Sporisorium scitamineum* infection, indicating that smut resistance is influenced by both genetic constitution and environmental conditions across crop cycles. The observed variability in agronomic performance, genetic parameters, and disease response provides valuable opportunities for the identification and selection of superior parental lines for sugarcane improvement. The significant effects of smut infection on growth and yield components further emphasize the importance of incorporating durable disease resistance into breeding programmes. The study also revealed that the reaction of parental genotypes to smut does not necessarily predict the performance of their progenies, as resistant parents may produce susceptible offspring, while susceptible parents may generate resistant progenies. Among the evaluated crosses, N27 × NCS-008 was the most promising, with all progenies exhibiting complete resistance to smut, indicating its potential as an effective parental combination for developing resistant cultivars. The findings highlighted the importance of integrating smut resistance with desirable agronomic traits during parental selection. Simultaneous consideration of disease resistance, yield potential, and other key agronomic characteristics will enhance the development of high-yielding, smut-resistant sugarcane cultivars adapted to the target production environments.

REFERENCES

- Ahmad, K., & Ming, R. (2024). Harnessing genetic tools for sustainable bioenergy: A review of sugarcane biotechnology in biofuel production. *Agriculture*, **14**(8): 131-142.
- Aslam, M. R, Iqbal, O., Naz Syed, R., Elsalahy H., Nasir, A. R., Sagheer, A., Rizwan K. (2024). Screening of sugarcane germplasm against *Sporisorium scitamineum* and its effects on setts germination and tillering. *Scientific Reports*, **14**:14653
- Barajehfard, M., Ahmadi, A., & Sabouri, A. (2026). Selection for high-yielding sugarcane ideotypes and multi-trait selection indices for synchronized high sugar content and yield stability. *Frontiers in Plant Science*
- Belwal, V., and Ahmad, S. (2020). Estimation of variability parameters in sugarcane under water logging conditions. *International Journal of Agriculture Sciences*, **12**: 9451–9453.
- Bhuiyan S.A, Robert C.M., Meredith D.M. & Aitken S.K. (2021). Sugarcane Smut, Caused by *Sporisorium scitamineum*, a Major Disease of Sugarcane: A Contemporary Review. *Phytopathology*, **111**(11):1905-1917



- Burton G. W. & Devane E. H. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal materials. *Agronomy Journal*, **45**:487-88.
- Gillani, S. W., Teng, L., Khan, A., Xu, Y., Powell, C. A., & Zhang, M. (2024). Fungal diversity and gibberellin hormones associated with long whips of smut-infected sugarcane. *International Journal of Molecular Sciences*, **25**(16): 9129.
- Kumaraswamy, S., & Huang, Y. (2026). Plant resistance: Scientific basis and latest research progress. *Frontiers in Plant Science*, **17**: 1789793
- Msomba, B. H., Ndaki, P. M., & Joseph, C. O. (2024). Sugarcane sustainability in a changing climate: A systematic review on pests, diseases, and adaptive strategies. *Frontiers in Agronomy*, **6**: 1423233.
- Ogunniyan D. J., Olakojo O. O., Olowolafe and Ogunruku B. O (2020). Estimation of genetic parameters in agronomic characters and maturity index of sugarcane (*Saccharum* spp). *Journal of Tropical Agriculture* **58**(2): 147-157
- Olahan, G. S., Fatoba, P. O. and Balogun, O. S. (2020). Incidence of Smut and Red Rot diseases of sugarcane in Southern part of Niger State, North Central Nigeria. *Science World Journal*, **15**(2): 72-75
- Olahan, G. S., Wada, A. C., & Bassey, E. E. (2020). Incidence and distribution of sugarcane smut disease in selected sugarcane-growing areas of Nigeria. *Nigerian Journal of Plant Protection*, **34**(1): 63–73.
- Rajput, M. A., Rajput NA, Syed RN, Lodhi AM. and Que Y. (2021). Sugarcane Smut: Current Knowledge and the Way Forward for Management. *Journal of Fungi (Basel)*. **7**(12):1095
- Regmi, S., Poudel, B., Ojha, B. R., Kharel, R., Joshi, P., Khanal, S., and Kandel, B. P. (2021). Estimation of Genetic Parameters of Different Wheat Genotype Traits in Chitwan, Nepal. *International Journal of Agronomy*, **20**: 6651325
- Sharma, S. (2021). A review on sugarcane smut caused by *Sporisorium citamineum* and its ecofriendly Management. *Pantnagar Journal of Research*, **19**(2): 245-255
- Sukphun, P., Reungsang, A., Sittijunda, S., O-Thong, S., & Rongsayamanont, C. (2023). Two-stage biohydrogen and methane production from sugarcane-based sugar and ethanol industrial wastes: A comprehensive review. *Renewable and Sustainable Energy Reviews*, **181**: 113357.
- Tolera B, Gedebo A. & Tena E., (2023) Variability, heritability and genetic advance in sugarcane (*Saccharum* spp. hybrid) genotypes, *Cogent Food & Agriculture*, **9**(1): 1-15
- Voora, V., Larrea, C., & Bermudez, S. (2023). Global market report: Sugar cane prices and sustainability. International Institute for Sustainable Development.
- Yali, W., Li, J., Zhang, H., Liu, Y., & Wang, X. (2026). Assessment of genetic variation, heritability, and genetic advance for enhancing cane yield and quality traits in sugarcane (*Saccharum* spp.). *Journal of Integrative Agriculture*