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SUITABILITY OF 25 LOCALLY SELECTED SUGARCANE GENOTYPES (*SACCHARUM* SPP.) FOR USE AS DIFFERENTIALS IN SMUT [*USTILAGO SCITAMINEA* (SYD.)] RACE TYPING IN THE SUDAN

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ABSTRACT

Studies were conducted at Sugarcane Research Centre, Guneid, (Latitude 15^{o} N, longitude 33^{o} E) for three consecutive seasons namely, 2006/2007; 2007/2008 and 2008/2009. The objectives were to test 25 locally selected sugarcane genotypes for suitability and use as differentials in race typing of *Ustilago scitaminea* (Syd.) the causal agent of sugarcane smut disease. Six smut isolates from different sugarcane growing areas of Sudan namely, Guneid: (GN1), (GN2) and (GN3); Sennar: (SN); New Halfa: (NH) and AB from Abbasiya (Assalaya/ Kenana area) were tested. Test materials were inoculated by three methods of: pin-prick method (PPM); Dipping method (DM) and Natural spreader row infection methods (NIM), respectively. Results showed the presence of four races of *Ustilago scitaminea* (Syd.) in Sudanese sugarcane fields that have relatedness percentages of 60-80% to each other. Hence, there is no virulent race of *U. scitaminea* (Syd.) at this time in the country and, the occurrence of infections on the popular varieties is normal and does not signal any danger of an epiphytotic. Therefore, the study recommends the adoption of the 25 genotypes as suitable differentials for smut race typing, continuation of current agricultural practices and the re-examination of *U. scitaminea* (Syd.) race status within the next ten years.

Key words: *Saccharum* spp.; *Ustilago scitaminea*; smut; sugarcane; differentials; races;

1. NTRODUCTION

Sugarcane, hybrids of *Saccharum* spp. is a genus of about 37 species (depending on taxonomic interpretation) of tall perennial grasses (Poales: Poaceae), native to the tropical regions of the Old World. About 200 countries grow the crop to produce 1,324.6 million tons of cane; more than six times the amount of sugar beet produced and accounts for 60-70% of the world's sugar production of about 140-150 million metric tons (Francis, 2006). This figure is expected to grow as biofuels become more important on the global market. The world's largest producers of sugarcane are Brazil, India and China (Draycott, 2006). Uses of sugarcane include the production of sugar, molasses, rum, cachaça (the national spirit of Brazil), ethanol for automobile fuel, co-generation, paper, hard board production, animal feed supplements and other by-products.

Sugarcane smut disease induced by the fungus *Ustilago scitaminea* a disease first reported from South Africa in 1877 on Chinese cane (*Saccharum sinense*) which later spread out across Africa, and Asia, in the following decades (Antoine, 1961; Presley, 1978). Smut of sugarcane is a serious disease in most sugarcane producing countries and causes considerable yield losses and reduction in cane quality (Ferreira and Comstock, 1989). Croft *et al*. (2000) reported yield losses of 20-100% depending on the cane variety. Some workers put losses at between 60-70% (Raga *et al*., 1972; Solomon *et al*., 2000). Nasr and Ahmed (1974) indicated that smut of sugarcane was first recorded in the Sudan in early 1960's at Guneid with disease incidences of 100%. This led to the withdrawal from production of several excellent varieties of the time (i.e. NCO 310, CO 527 etc.). Currently it occurs in all sugar estates in the country and causes considerable losses in susceptible varieties. The most likely source of this initial infection was never determined, but it could have come with imported sugarcane materials or wind-blown spores from neighboring countries.

The use of resistant sugarcane varieties such as CO 997 and CO 6806 has maintained the disease under some good control. Nevertheless, of recent, occasional infections by *U. scitaminea* especially on CO 6806 the most popular cane variety has become common probably suggesting variety deterioration (resistance erosion) or variation in the pathogen population. Since successful disease management strategies and control require an understanding of the diversity in the pathogen population, information on the genetic variability of the smut pathogen present in Sudan became a concern in the face and the absence of the standard international sugarcane differentials. Hence, these studies were initiated to test the efficacy of locally selected sugarcane genotypes for suitability in race typing of *Ustilago scitaminea* (Sydow) isolates from different geographical locations in the Sudan and findings are hereby reported.

2. MATERIALS AND METHODS

2.1 Location of the study area

These studies were conducted at the Sugarcane Research Center, Guneid; located approximately at latitude 15^0N, longitude 33^0E; for three seasons, 2006/07; 2007/08 and 2008/09. The soils at the experimental site are typical heavy clay vertisols with about 64% clay, 0.09% N and 2- 8 ppm available P and alkaline in reaction with pH of 8.2. Mean annual rainfall is about 112 mm falling mainly in July and August.

2.2 Race typing of *U. scitaminea* isolates from different geographical locations by 25 local differential sugarcane genotypes

These experiments consisted of 12 trials namely, six smut isolates from different locations were tested separately inoculated each by the dip (DM) and pin-prick (PPM) methods.

2.3 Collection and maintenance of *U. scitaminea* Guneid isolates

Typical sugarcane smut whips or sori from location (1) Guneid were collected from sugarcane varieties NCO 376 coded as GN1; smut from CO 527 was coded as GN2; and finally that from CO 6806 was coded as GN3. (2) Smut isolates from Sennar was coded as SN; (3) isolates from New Halfa, with code NH and (4) finally isolates from Abbasiya with code AB. These six isolates were maintained separately each on either cane variety CO 527 or NCO 376 in the Pathology Museum in Guneid. Smut whips were then harvested periodically, sun dried for 48 hrs. Thereafter, smut teliospores were extracted by passing the materials through a 200 mm diameter (500, 250 and a final 106) mesh laboratory sieves mounted on an Endecotts (ELF 2000) sieve shaker. The teliospores were then maintained in sealed polythene bags in the laboratory prior to use in the inoculation trials.

2.4 Seedbed preparation and planting materials

For all field experiments, land was prepared according to the standard practice; by a disc plough then harrowed, leveled and ridged at a spacing of 1.5m between ridges. Plot size was 1 or 2 rows of 10 or 5 meter length.

2.5 Preparation of planting materials

About 20 to 25 three-node cuttings were prepared from 8-10 month old healthy field grown cane from each of twenty five (25) sugarcane differential genotypes; with known reactions types to smut from earlier trials namely, B 70531, B 79136, BJ 7451, BJ 7938, BJ 82105, BT 74209, COC 671, DB 75159, TUC 75-3, CO 527, CO 997$^{\alpha}$, CO 6806$^{\alpha}$, BJ 83125$^{\alpha}$, BJ 84111$^{\alpha}$, BT 83339$^{\alpha\alpha}$, BBZ

95681$^{\alpha\alpha}$, F 154$^{\alpha}$, B 97263$^{\alpha}$, ROC 10$^{\alpha\alpha}$, FR 9682$^{\alpha\alpha}$, KN 93-14$^{\alpha\alpha}$, N 52/219$^{\lambda}$, NCO 310$^{\lambda\lambda}$, NCO 376$^{\lambda\lambda}$, and R 570$^{\lambda}$. Genotypes marked ($^{\alpha}$) have highly resistant (HR) reaction types; ($^{\alpha\alpha}$) have susceptible or highly susceptible (S or HS) reaction types under Sudan conditions in earlier tests (Marchelo *et al*., 2008); and ($^{\lambda}$) have HR reaction types; ($^{\lambda\lambda}$) have MS (moderately susceptible), S or HS reaction types in China, Taiwan and South Africa. The planting materials were given a long hot water treatment (HWT) at 50^{0}C for 2 hrs. before being artificially inoculated by each of the six smut isolates GN1, GN2, GN3, SN, NH and AB as described below:-

2.6 Inoculation protocol and field design

All test materials were inoculated separately by each of two methods.

2.6.1 Dip method (DM)

The seed setts were inoculated by dipping into a smut spore suspension at a concentration of 1g smut teliospores/ L of water for 20 minutes. The inoculated setts were then kept under humid condition in polythene bags for 24 hr. prior to planting in the field. The plot size was 1 furrow of 10 m length, or 2 furrows of 5 m length; and furrows were spaced 1.5 m apart. About 20-25 cane setts were planted per plot and the plots were arranged in a randomized complete block design with three replications. Sixty buds were planted in each plot.

2.6.2 Taiwanese pin-prick method (TPPM)

About 2-3 pin pricks were administered at the base of each bud in each sett after being dipped into a freshly prepared spore paste at a concentration of 2-3 g spores/5 ml water for each isolate under test. The inoculated setts were also kept at room temperature under polythene bags for 24 hrs. before being planted in the field. The plot size was 1 furrow of 10 m or 2 furrows of 5 m length as above and rows were also spaced 1.5 m apart. Twenty cane setts were planted in each plot. The trial was also laid in a randomized complete block design with three replications as above.

2.7 Disease incidence and assessment of resistance

Disease incidence was determined from the proportion of diseased stools expressed as a percentage of the total number of the stools in the plot. Resistance as expressed by reaction types was evaluated with a numerical rating scale of 1-9 where, 1=highly resistant and 9=highly susceptible as described by Satya Vir Beniwal (1978). The cumulative number of whips as an infection index was also recorded. The final genotypic reaction types in all trials were determined at the age of 8 months for plant cane (PC); and at 6 months each for first ratoon (R1) and second ratoon (R2) crops, respectively.

2.7.1 Data collection

Data on (i) infection indexes like (a) smut incidence on stool basis (SI%) and (b) cumulative number of smut whips (CNOW) during the growing season was determined; and (ii) epidemiological parameters namely, (a) the latent infection period (= the time period from inoculation to disease symptom expression) in days (LIP/D); (b) sustained disease duration (=the

time from disease symptom expression or LIP/D to harvest in days (SDD/D); and (c) the area under the disease progress curve (AUDPC) was determined for each genotype; and subjected to a hierarchical cluster analysis by the complete linkage cluster algorithm. AUDPC was derived from the equation given by Xu *et al*. (2004) as follows:-

$$AUDPC = [\ SI_1 + SI_2 /2 \ x \ (t_2 - t_1)\ ],$$

Where: SI_1 and SI_2 are the percentages of infection on stool basis investigated at two points 1 and 2 in space/time; and t_1 and t_2 are the times of investigation in days or months.

2.7.2 Statistical analysis and race typing of the different *U. scitaminea* (Syd.) isolates

A hierarchical cluster analysis for the 25 differential sugarcane genotypes was performed for each of the six *U. scitaminea* isolates separately by the complete linkage cluster algorithm (CLINK) using the statistical software Genstat Discovery Edition 3 (2003). Thereafter, the resultant phylogenetic trees were interpreted accordingly.

2.7.3 Interpretation of phylogenetic tree patterns

The pattern and number of clusters imposed on the 25 differential genotypes by the six smut isolates were interpreted for similarity (= indicating none existence of genetic diversity in the *U. scitaminea* population or isolates) and dissimilarity (=indicate existence of diversity) for the tested isolates. Usually, isolates with similar genetic make-ups will be bracketed together and, isolates

that are not similar will be located in different sections of the dendrogram. The above procedures were followed for each of the six isolates which were inoculated by each of the two methods of DM and TPPM. Also, alternatively genetically similar smut isolates will tend to cluster the 25 differential varieties in a similar manner including the number of varieties placed in each cluster. Usually, the varieties that are being compared are listed on the left side of the tree, they are identified by the appropriate variety codes; there will be a bar or line extending to the right of each variety forming a 'pitchfork' appearance where it brackets with other varieties. Then, vertically align the bracket connecting the two genotypes with the scale below. The numerical value on the scale is the percentage relatedness or the percentage similarity of the two genotypes. Also, groups of varieties within the same dendrogram may be compared in the same manner, using the bracket that connects the two groups as per the methods of Romesburg (1984).

3. RESULTS AND DISCUSSION

3.1 Characterization of the genetic variability of six *U. scitaminea* isolates based on their pathogenic discrimination by the 25 local differential sugarcane genotypes.

Figures 1 to 4 show the phylogenetic trees derived from the complete linkage cluster analysis of infection and epidemiological data, used as cluster indexes for the six tested smut isolates. The differential sugarcane varieties were cluster discriminated in the dendrograms such that, materials, with the best resistance characters were located in clusters I and II, and, these characters decreased gradually in the higher clusters. For GN1 smut isolate 15 (60%) and 12 (48%) of the differential sugarcane genotypes were grouped in clusters I and II in DM and TPPM. Likewise for GN2 smut isolate 80% and 80%; for GN3, 80% and 72%; for SN, 76% and 84%; for AB, 88%; for NH, 84% and 84% of the differential sugarcane varieties were grouped in clusters I

and II accordingly for DM and TPPM, respectively. Meanwhile, the trees for the combined variables regardless of the method of inoculation, the percentages of the differential sugarcane varieties in clusters I and II were: GN1, 84%; GN2, 84%; GN3, 68%; SN, 76%; AB, 88% and NH, 80%, respectively. The resistance characters are usually stronger in cluster I and progressively decreasing toward the higher clusters. It is worth mentioning that, in all cases, the sugarcane differentials varieties showed greater resistance to all the tested smut isolates and were less aggressive in the trials inoculated by the dip method (DM) denoted by (A) compared to those inoculated by the Taiwanese pin-prick (TPPM) method denoted by (B) in Figs. 1 to 4. The reason for this behavior is apparent because in the DM of inoculation two mechanisms of resistance are in operation namely, internal/ physiological resistance and structural resistance. However, in the TPPM-inoculated trials only the internal/ physiological resistance is in operation as pin-pricking of buds completely destroyed and removed the structural resistance barriers. Therefore, TPPM inoculated materials usually gave the true level of physiological or internal resistance as opposed to DM. However, Whittle and Walker (1982) were of the opinion that results obtained from the TPPM used in screening trials should always be carefully interpreted as TPPM may tend to overestimate susceptibility. In the DM inoculation trials, all the resistance mechanisms e.g. structural, and physiological resistance mechanisms are actively in place and this explains the unusually low smut incidence in the DM-inoculated trials. In these race typing trials, we were, unable to biologically identify an aggressive strain or pathotype within the six tested Sudan isolates of *U. scitaminea*. This study tentatively identified four pathotypes that are rather genetically homogenous and have relatedness percentages of 65% to 80% to each other; therefore, they are more or less similar in pathogenicity and none was distinctly aggressive. On comparing the results of this study with the work of Abo and Okusanya (1996), Grisham (2001) and Toffano (1976) the

probable explanation is that the isolates used in this study represent the inbred-line or isolate which has been referred to as the most widespread and highly stable *U. scitaminea* pathotype reported by Shenck *et al*. (2005). This inbred-line is also known as the Hawaiian race A or Oahu isolate/ old race (Raboin *et al*., 2006b). Therefore, the high percentage of relatedness amongst the smut isolates tested in this study has tentatively validated this trend. Also, Nisha *et al.* (2005) working on isolates from South Africa, Hawaii, Guadeloupe, and Reunion using advanced techniques namely, RAPDs, rDNA sequence analysis, microscopy, germination and morphological studies reported that except for sequence data the other analyses yielded no differences between the isolates that could be used in a definite phylogenetic separation this again support our findings in this study. Raboin *et al.* (2006a; 2006b) used highly polymorphic, PCR-based, microsatellite markers in 142 single-spore isolates of *U. scitaminea* from different cultivars from 15 sugarcane-growing countries throughout the world for genetic diversity. They also found no differences between the isolates, but only recorded diversity within isolates from South East Asia. They further indicated that genetic diversity in America and Africa was found to be extremely low and all isolates belonged to a single inbred lineage, thus making it rather homogenous. All isolates except one were homozygous for all loci, indicating that selfing could be the highly preferential predominant reproductive mode of *Ustilago scitaminea*. In a separate study, Abo and Okusanya (1996) working on 9 isolates (=collected from different parts of Nigeria) reported two races 'X and Y' based on the morphology and colony characteristics on PDA and virulence/ pathogenicity reactions on some local sugarcane varieties. Schenck (2003) also reported two races: (a) race A or Oahu isolate (Old race) and (b) race B or Maui isolate (new race) from Hawaii.

However, Amire *et al*. (1982) and Wu *et al*. (1988) in detailed studies indicated that the second Hawaiian race B or Maui isolate (New race) is largely unstable and has otherwise

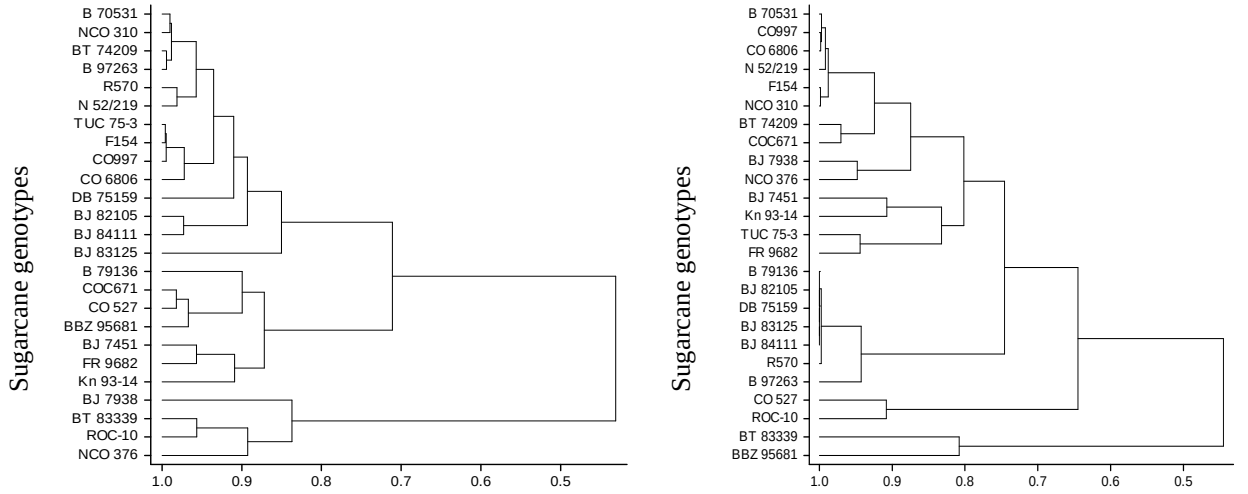
disappeared and could no longer be detected by conventional race typing methods and differentials including isozymes but, could only be detected and distinguished by neutron activation analysis. These findings led Presley (1978) to conclude that a single but widely adapted stable smut genotype, probably the Afro-American inbred line referred to by Raboin *et al*. (2006a; 2006b) as the only pathotype which is wide-spread, thus, explaining the lack of genetic variation in isolates collected from countries outside Asia. Whereby, this argument offers further proof for our inability in identifying a definite physiological race by biological characterization methods. Thus, implying that at present we only have a single but, relatively stable physiological race; which is the Afro-American inbred line or the Hawaiian race A. (Oahu isolate/ old race). The slight differences observed in the phylogenetic trees in Figures 1, 2 and 3 which were derived from cluster analyzing the combined variables of both the DM and PPM trials for each isolate, can therefore be attributed to only simple host-pathogen interactions enveloped and modified by the uncertain environmental components during the study.

This view is also clearly supported by the work of Peros and Baudin (1983) who compared isolates from Reunion, Guadeloupe, Ivory Coast, Mali, Upper Volta, and Kenya; and Grisham (2001) who co-ordinated a race typing study in nine countries and concluded that all the isolates from Africa and the Americas were generally homogenous in virulence and pathogenicity characteristics. The pathotypes X and Y reported by Abo and Okusanya (1996) from Nigeria could actually have been the physiological race A (the stable Oahu isolate/ old race) and the unstable Hawaiian race B. The slight differences in virulence/ pathogenicity characteristics might have been imposed by the interaction of the environment and the high instability components of race B as verified by Amire *et al*. (1982). In a separate study Grisham (2001) indicated that, real diversity and pathotypes were only found in the South-east Asia region. Ferreira and Comstock (1989) also

considered the true prevalence of races to be controversial; since many claims are based on the reaction of the same cultivar in different countries and environments. In our work, these relationships and phenomena of a generally homogenous virulence and pathogenicity characteristics attributed by Peros and Baudin (1983) can be seen and perceived in Figures 4. (A) and (B). Whereby, in the Euclidian distance of 1 the cluster discrimination showed that the six isolates treated as cases were separated and grouped into 4 and 5 clusters, respectively when the percentage smut infection/ number of whips were treated as variables or cluster indexes for the 25 differentials. However, under both circumstances GN1 with a similarity coefficient of 0.65 and GN2, GN3 with similarity coefficients of 0.85 were grouped in clusters I and II and SN, NH (similarity coefficient of 0.82) in cluster III and AB (similarity coefficient of 0.6) was grouped in cluster IV (Fig. 4. A). All the smut isolates from the different geographical locations exhibited relatedness percentages of 65% to 80% and the furthest related isolate AB has a relatedness percentage of 60%. Considering the mean number of whips/ fed. (Fig. 4. B), the smut isolate GN1 with similarity coefficient of 0.60 were grouped in cluster I, while GN2 and GN3 with similarity coefficient of 0.85 were grouped in clusters II. The other smut isolates AB, SN and NH with similarity coefficients of 0.72, .074 and 0.74, respectively were grouped in separate clusters of III, IV and V. However, all the isolates have a relatedness percentage of 70% to 85%. The furthest related isolate GN1 in this instant has a relatedness percentage of 60%. Table 1. Shows that the tested Sudanese isolates of *U. scitaminea* could be separated into four pathotypes or physiological races based on the percentage of smut infection on stool basis as the main infection index or criterion viz. (i) GN1 (ii) GN2, GN3 (iii) SN, NH and (iv) AB. According to the clustering protocols, isolate GN1 and NH were distinct and associated with some slight degree of virulence

(cane differentials showed more susceptibility), while GN2, GN3 and SN were difficult to separate.

However, isolate AB is also, probably distinct and associated with avirulence (differentials showed more resistance). Nevertheless, despite some of the obvious differences we consider that the Sudan populations of *U. scitaminea* are rather genetically homogenous with mild virulence rather than being heterogeneous and all the isolates are 60-85% related to each other. Therefore, we have no outstandingly aggressive *U. scitaminea* isolate at this time. This again can be perceived in Table 1. where the 25 sugarcane differentials are listed according to their reaction types to the six local *U. scitaminea* isolates. For isolate GN1 36%, 60% and 4% of the differentials were rated as HR, R and MS, respectively. For isolate GN2, 52% and 48% of the differentials were rated as HR and R. For isolate GN3, 28% and 62% of the differentials were rated as HR and R, respectively. For isolate SN, 32% and 68% of the differentials were rated as HR and R, respectively. For isolate AB, 92% and 8% of the differentials were rated as HR and R. Finally, for NH, 44%, 48% and 8% of the differentials were rated as HR, R and MS respectively.



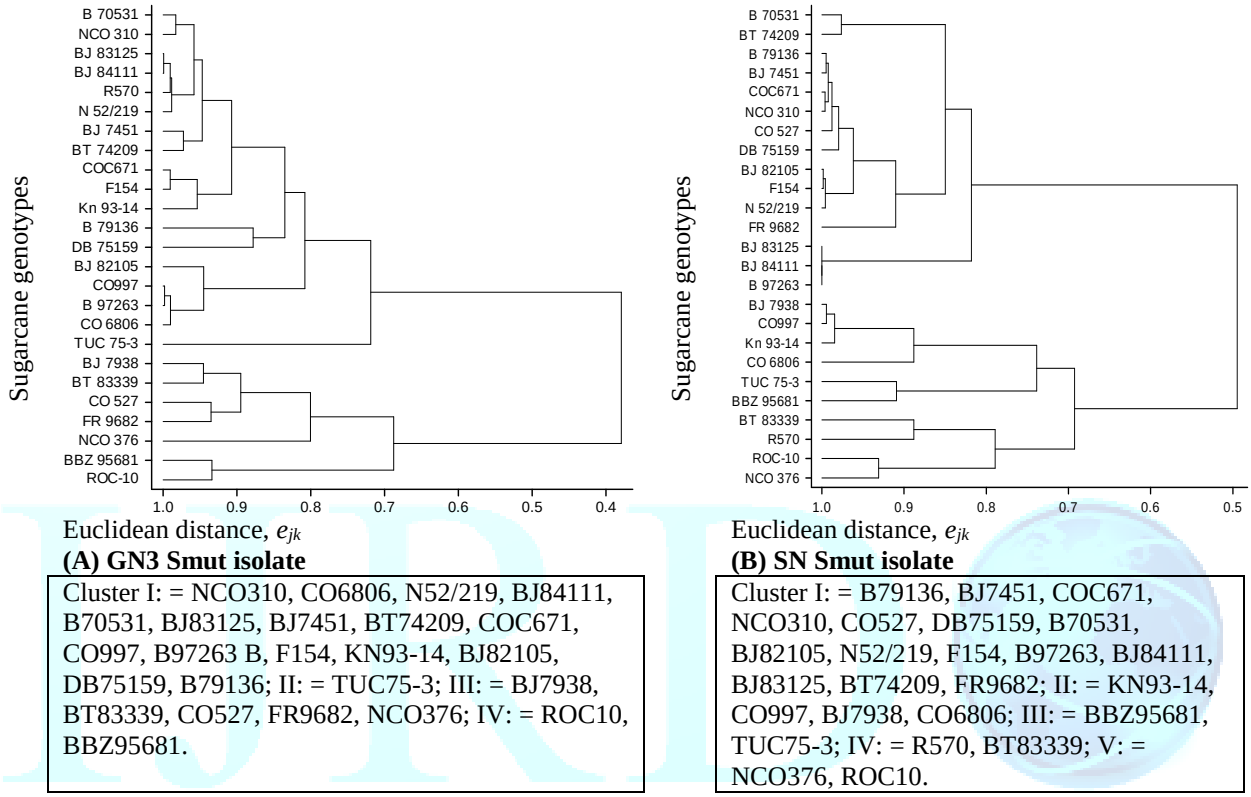
(A)

Cluster I: = B70531, B97263, BT74209, CO997, TUC75-3, R570, NCO310, F154, CO6806, N52/219, BJ84111, BJ82105, DB75159, BJ83125; **II**: = CO527, COC671, FR9682, BBZ95681, KN93-14, BJ7451, B79136; **III**: = ROC10, BT83339, NCO376, BJ7938.

(B)

Cluster I: = CO6806, CO997, NCO310, F154, BT74209, N52/219, BJ 7938, B70531, COC671, BJ7451, NCO376, KN93-14, TUC75-3, FR9682; **II**: = B79136, BJ84111, BJ83125, DB75159, BJ82105, R570, B97263; **III**: = ROC10, CO527; **IV**: = BBZ95681, BT83339.

Fig. 1. CLINK furthest neighbor dendrograms derived from combined parameters of DM and PPM inoculation methods, for (A) GN1 and (B) GN2 smut isolates for the 25 sugarcane differentials.



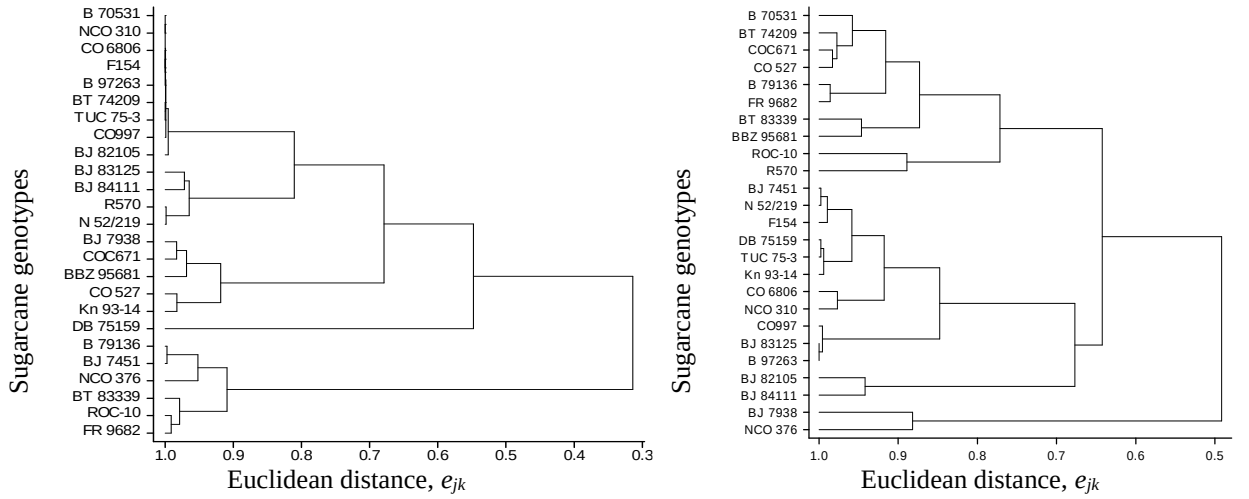
(A) GN3 Smut isolate

Cluster I: = NCO310, CO6806, N52/219, BJ84111, B70531, BJ83125, BJ7451, BT74209, COC671, CO997, B97263 B, F154, KN93-14, BJ82105, DB75159, B79136; II: = TUC75-3; III: = BJ7938, BT83339, CO527, FR9682, NCO376; IV: = ROC10, BBZ95681.

(B) SN Smut isolate

Cluster I: = B79136, BJ7451, COC671, NCO310, CO527, DB75159, B70531, BJ82105, N52/219, F154, B97263, BJ84111, BJ83125, BT74209, FR9682; II: = KN93-14, CO997, BJ7938, CO6806; III: = BBZ95681, TUC75-3; IV: = R570, BT83339; V: = NCO376, ROC10.

Fig. 2. CLINK furthest neighbor dendrograms derived from combined variables of DM and PPM inoculation methods, for (A) GN3 and (B) SN smut isolates.



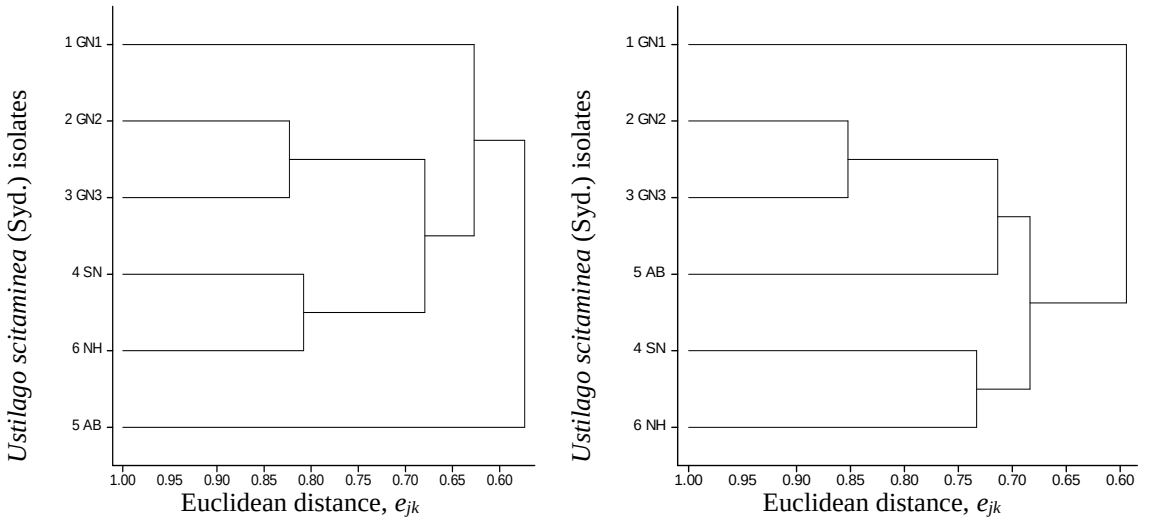
(A) AB (Abassiya) smut isolates

Cluster I: = CO527, BJ83125, TUC75-3, N52/219, KN93-14, FR9682, B97263, BJ84111, CO6806, CO997, DB75159, BT74209, BJ82105, B79136, B70531, BJ7938, R570, BJ7451, COC671, ROC10, BBZ 95681; II: = NCO310; III: = F154; IV: = BT83339; V: = NCO376.

(B) NH (New Halfa) smut isolates

Cluster I:= B70531, B79136, BT74209, COC671, CO527, BT83339, BBZ95681, FR9682 ; **II**:= ROC10, R570 ; **III:** = BJ7451, DB75159, TUC75-3, CO997, CO6806, BJ83125, F154, B97263, KN93-14, N52/219, NCO310 ; **IV**:= BJ82105, BJ84111 ; **V**:= NCO376, BJ7938.

Fig. 3. CLINK furthest neighbor dendrograms derived from the combined variables of DM and PPM inoculation methods, for (A) AB (Abassiya) and (B) NH (New Halfa) smut isolates for the 25 sugarcane differentials.



PSI

Cluster I: = GN1; II: = GN3, GN2; III: = SN, NH; IV: = AB.

CNOW

Cluster I: = GN1; II: = GN3, GN2; III: = AB; IV: = SN; V: = NH.

Fig. 4. CLINK furthest neighbor dendrograms for six smut isolates treated as cases and (A) percentage smut infection on stool bases, (PSI); (B) number of whips/F, (CNOW) for 25 sugarcane differentials (genotypes) treated as variables.

Table 1. Mean reaction types of the differential sugarcane varieties to the different smut (*U. scitaminea*) isolates regardless of method of inoculation.

Sugarcane differentials	*R*eaction types of the tested *U. scitaminea* isolates					
	GN1	GN2	GN3	SN	AB	NH
B 70531	(1) HR	(1) HR	(2) R	(4) R	(1) HR	(3) R
B 79136	(3) R	(1) HR	(2) R	(3) R	(1) HR	(1) HR
BJ 7451	(3) R	(2) R	(2) R	(3) R	(1) HR	(2) R
BJ 7938	(4) R	(2) R	(4) R	(2) R	(1) HR	(3) R
BJ 82105	(1) HR	(1) HR	(1) HR	(1) HR	(1) HR	(1) HR
BT 74209	(1) HR	(2) R	(2) R	(4) R	(1) HR	(2) R
COC 671	(2) R	(2) R	(2) R	(2) R	(1) HR	(4) R
DB 75159	(1) HR	(1) HR	(2) R	(2) R	(1) HR	(1) HR
TUC 75-3	(1) HR	(2) R	(3) R	(1) HR	(1) HR	(2) R
CO 527	(2) R	(2) R	(3) R	(2) R	(1) HR	(2) R
CO 997$^{\alpha}$	(1) HR	(1) HR	(1) HR	(2) R	(1) HR	(1) HR
CO 6806$^{\alpha}$	(1) HR	(1) HR	(1) HR	(1) HR	(1) HR	(1) HR
BJ 83125	(3) R	(1) HR	(1) HR	(1) HR	(1) HR	(1) HR
BJ 84111	(3) R	(1) HR	(1) HR	(1) HR	(1) HR	(1) HR
BT83339$^{\alpha\alpha}$	(4) R	(3) R	(4) R	(2) R	(1) HR	(3) R
BBZ95681$^{\alpha\alpha}$	(3) R	(3) R	(4) R	(2) R	(1) HR	(5) MS
F 154$^{\alpha}$	(1) HR	(1) HR	(3) R	(1) HR	(1) HR	(1) HR
B 97263$^{\alpha}$	(2) R	(1) HR	(1) HR	(1) HR	(1) HR	(1) HR
ROC 10$^{\alpha\alpha}$	(4) R	(3) R	(4) R	(4) R	(1) HR	(1) HR
R570$^{\lambda}$	(2) R	(1) HR	(2) R	(3) R	(1) HR	(1) HR
FR 9682$^{\alpha\alpha}$	(3) R	(2) R	(3) R	(2) R	(1) HR	(2) R
KN 93-14$^{\alpha\alpha}$	(2) R	(2) R	(2) R	(3) R	(1) HR	(2) R
N 52/219$^{\lambda}$	(2) R	(1) HR	(2) R	(2) R	(1) HR	(2) R
NCO 310$^{\lambda\lambda}$	(1) HR	(1) HR	(1) HR	(1) HR	(1) HR	(2) R
NCO 376$^{\lambda\lambda}$	(5) MS	(2) R	(4) R	(4) R	(4) R	(5) MS
Percentage of resistant/ susceptible genotypes						
HR	36%	52%	28%	32%	92%	44%
R	60%	48%	62%	68%	8%	48%
MS	4%	-	-	-	-	8%

Key: GN1 = Guneid NCO 376 isolate; GN2 = Guneid CO 527 isolate; GN3= Guneid CO 6806 isolate; SN = Sennar isolate; AB = Abbasiya isolate (Assalaya- Kenana); HF = New-Halfa isolate; $^{\alpha}$ = HR and $^{\alpha\alpha}$ = S or HS reaction types; $^{\lambda}$ = HR and $^{\lambda\lambda}$ = S to HS reaction types in China, Taiwan and South Africa; Figures in parenthesis are ratings from Satya Vir Beniwals' (1978) scale.

4. CONCLUSION

The findings in this study has shown that, the 25 locally selected sugarcane genotypes were effective in segregating the *U. scitaminea* pathotypes tested and they can therefore, be adapted for use in routine race typing studies for *U. scitamnea* (Syd.) in Sudan and the region. These studies should be repeated under Sudan conditions within the next 5 to 10 years to confirm and give a broader picture of the race dynamics in the face of global warming and changing climatic conditions in Sudan.

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