International Journal of Advanced Research in Biological Sciences
ISSN: 2348-8069
www.ijarbs.com
DOI: 10.22192/ijarbs Coden: IJARQG(USA) Volume 4, Issue 4 - 2017

Research Article

DOI: http://dx.doi.org/10.22192/ijarbs.2017.04.04.002

Observation Trail for Clones Generated from Fuzz at Beles Sugar Development Project

[1]Shitahun Alemu, and [2]Ashebir Gete
[1&2] Tana Beles Research and Development Center, Jawi, Ethiopia
Corresponding author – **Shitahun Alemu**
E-mail – *shitahunam@gmail.com*

Abstract

This study was done to screen best performing clones generated from true sugarcane seed based on basic agronomic traits and visual observations from large populations over the standard checks then to promote for next Sugar cane performance trial. The trial was laid out in an augmented randomized complete block design of which the three checks replicated but clones were not replicated during 2015 and 2016 growing season at Tana Beles Sugar Development Project. Data were collected for sprouting percent, number of tillers, millable stalk, plant height and visual observations were made for diseases, flowering, and over all performances. The results indicated that the clones had highly significant differences for stalk count and plant height indicating the availability of high genetic variability among the genotypes studied regarding these trait. Thus, based on the stalk count and cane height performances and by considering visual observation for flowering, diseases and etc. 46 genotypes were selected. These selected genotypes will be planted with three standard checks in three replications by using Lattice Square Design for to select best performing Sugarcane Genotypes through thoroughly selection procedures.

Keywords: Clones, Fuzz, Beles

1. Introduction

Sugarcane (*Saccharum officinarum* L.*)* is one of the six to thirty seven species (depending on taxonomic system) of the genus *Saccharum*, family poaceae and tribe Andropogoneae. Some of the sugarcane species are *S. munja, S. procerum, S. ravennae, S. robustum, S. sinense, S. spontaneum, S. arundinaceum, S. bengalense and S. edule*. *Saccharum officinarum* has chromosome number of 2n = 80 (Daniels and Roach, 1987). The present day sugarcane varieties (*S. officinarum*) have been the subject of many improvements. The original *S. spontaneum* and S. *robustum* were replaced by *S. barberi* and *S. sinense*, but were themselves ousted later by *S. officinarum* or noble cane (Richard, 2005).

Generally,sugarcane is a tall perennial crop that tillers at the base, grows three to four meters tall and about five cm in diameter (Singh, 2003). Sugarcane is grown in countries within latitudes 37^0 N and 32^0 S of the equator. It is an important cash crop as it is widely adapted to a wide range of tropical and semi tropical climate, soils and cultural conditions and to a long, warm growing season. The ideal climate for sugarcane is spelled as long warm growing season free from tropical storms and having adequate rainfall (or with irrigation), fairly dry and cool but frost free ripening and harvesting season (Singh, 2002). It is grown on soils varying in texture from light sands to heavy clays provided that it is supplied with the required elements.

It is also tolerant to wide variations in acidity and alkalinity (growing in soils with pH in the range of 5 to 8.5) (Blackburn, 1984). As a result of shortage of improved varieties for the diversified sugarcane production areas (particularly in saline soils, heavy and light soils, moisture stress and humid areas) and failure of varieties to give consistent yield over a long period of time, cane productivity was declining. Thus true sugarcane seed or fuzz was introduced to screen best genotypes that can tolerate biotic and a biotic stress condition of the sugar estates and projects with higher cane and sugar yield. Hence, releasing improved sugarcane genotypes increases productivity of sugar which has a paramount importance in enhancing the economic prosperity of the country. Therefore this study was initiated to screen best performing genotypes based on basic agronomic traits and visual observations over the standard checks then to promote for next Sugar cane performance trial.

2. Materials and Methods

1.1. Description of the Study Area

The experiment was conducted at Tana Beles Sugar Development Project. It is located in the Amhara Regional State of Ethiopia. It is located at about 650 km North of Addis Ababa, 11007'N and 36020'E latitude with an elevation of 1119 m asl. Tana Beles receives about 1490 mm annual average rainfall with mean maximum and mean minimum temperature of 32.5°C and 16.4°C, respectively.

1.2. Experimental Methods and Design

From a mixed variable population of around 10,000 clones, selection of around 1000 desirable clones by simple observation was done for simply inherited characters with high heritability at Wonji Sugar Estate of Ethiopia in 2015. Clones with obvious weaknesses were not selected. The number of clones is drastically reduced, and inferior clones were not selected. These clones were divided and distributed to the sugar estates and projects. Among these 130 clones with three standard checks were planted using two budded set on a single 4 m lengths furrow in five blocks in Augmented RCBD. The checks were replicated, while clones were planted without replication. This is done in view of the limited supply of propagating material for each clone and because of the large number of clones involved.

1.3. Data Collection

Data for the following quantitative traits were collected from a single four meter row.

1. **Sprouting** – sprouting was counted at 45th days after planting and determined by dividing the number of sprouts in a plot to the expected number of sprouts.
2. **Tillering** - number of tillers per plot were counted at 3 and 5 months after planting. The 5 month counts were used for statistical analysis.
3. **Millable stalks (MS)** - number of millable stalk per plot was counted at 7, 9, and 10 months. The counts at 10 month were used for statistical analysis.
4. **Plant height (cm)** – stalk length were measured from10 representative samples taken per plot at 10 months after planting using calibrated wooden meter. The average values were used for statistical analyses.

1.4. Data Analysis

The quantitative data recorded in this study was subjected to analysis of variance using statistical procedures described by Gomez and Gomez (1984) with the help of statistical analysis system software (SAS, 2002). Least significance difference (LSD) mean comparison method at 5% level of significance was used to separate the treatment means.

Results and Discussion

Analysis of variance for sprouting, tillers, and stalk count and plant height revealed significant differences between the genotypes at 5% level of significance. The differences among the 130 genotypes and three standard checks were very highly significant for stalk count and plant height indicating the availability of high genetic variability among the genotypes studied regarding these trait (Table 1).

Table 1 Analysis of variance for sprouting, number of tillers, millable stalks and plant height

Source of variation	DF	Sprouting MS	tillers	millable stalks MS	plant height MS
Treatment	133	40.104060	240.33830*	270.13233***	1467.5744***
Block	4	47.050000	213.25000	270.70000	1336.2976
CV		23.47918	13.31190	22.07400	11.22635
R-Square		0.936854	0.973730	0.935977	0.957192

Table 2 Best performing genotypes and standard checks based on the characters stalk count (Stc) and plant height (Pht) (cm)

#	Clones	Stc	Pht	#	Clones	Stc	Pht	#	Clones	Stc	Pht
1	NCO 334	64.2	197.80	**18**	787-14-188	88	248.00	**35**	787-14-285	92	210.83
2	N 14	76.6	228.67	**19**	787-14-93	82	265.83	**36**	787-14-280	68	285.00
3	B 52-298	70.4	245.67	**20**	787-14-271	82	262.17	**37**	787-14-217	71	269.17
4	787-14-70	121	289.17	**21**	787-14-362	67	320.00	**38**	787-14-229	70	271.00
5	787-14-275	93	285.83	**22**	787-14-195	77	276.50	**39**	787-14-233	70	270.50
6	787-14-221	95	274.50	**23**	787-14-191	89	235.83	**40**	787-14-406	70	270.33
7	787-14-270	86	287.67	**24**	787-14-318	68	307.50	**41**	787-14-226	89	209.83
8	787-14-409	91	270.50	**25**	787-14-332	88	236.50	**42**	787-14-111	88	210.83
9	787-14-110	99	245.67	**26**	787-14-348	84	246.67	**43**	787-14-311	69	267.50
10	787-14-321	102	237.00	**27**	787-14-355	84	243.67	**44**	787-14-294	62	293.83
11	787-14-313	78	305.00	**28**	787-14-224	74	275.33	**45**	787-14-304	74	246.00
12	787-14-206	89	262.67	**29**	787-14-73	73	277.67	**46**	787-14-405	66	274.83
13	787-14-178	89	260.83	**30**	787-14-286	72	280.50	**47**	787-14-288	66	272.83
14	787-14-256	79	284.17	**31**	787-14-393	93	216.17	**48**	787-14-400	74	241.83
15	787-14-413	72	309.83	**32**	787-14-198	71	282.83	**49**	787-14-220	61	292.67
16	787-14-29	91	243.67	**33**	787-14-407	86	230.83				
17	787-14-216	89	246.67	**34**	787-14-109	67	295.83				

Table 3 Diseases and insect pest free and non-flowering genotypes selected from 120 fuzz clones based on stalk number, height and observation at Beles sugar development project

#	Selected Clones	Observation report	#	Selected Clones	Observation report
1	787-14-70	High population, good stalk girth & height	24	787-14-301	High stalk population, girth & height
2	787-14-275	High stalk population, girth & height	25	787-14-344	High stalk population, girth & height
3	787-14-221	High stalk population, girth & height	26	787-14-79	Good stalk population, girth & height
4	787-14-321	High stalk population & height and good girth	27	787-14-303	High population and good stalk girth & height
5	787-14-206	High stalk population & height and good girth	28	787-14-279	High stalk population, girth & height
6	787-14-256	High stalk population, girth & height	29	787-14-398	High stalk population, girth & height
7	787-14-29	High stalk population, girth & height	30	787-14-352	Good population and girth & higher stalk height
8	787-14-195	High stalk population, girth & height	31	787-14-208	High stalk population, girth & height
9	787-14-332	High population, good stalk girth & height	32	787-14-294	High stalk population, girth & height
10	787-14-355	High stalk population & height and good girth	33	787-14-404	High stalk population, girth & height
11	787-14-286	High stalk population & height and good girth	34	787-14-394	Good population & higher girth and height
12	787-14-407	High population, good stalk girth & height	35	787-14-360	Good population and girth & higher stalk height
13	787-14-285	High stalk population & height and good girth	36	787-14-57	High stalk population, girth & height
14	787-14-233	High stalk population, girth & height	37	787-14-112	Good population and height & higher stalk girth
15	787-14-226	High stalk population & height and good girth	38	787-14-215	High stalk population, girth & height
16	787-14-111	High stalk population, good height and medium girth	39	787-14-218	High population and good stalk girth & height
17	787-14-294	High stalk population, girth & height	40	787-14-99	Good population and girth & higher stalk height
18	787-14-405	High stalk population, girth & height	41	787-14-293	High population & height and good stalk girth
19	787-14-288	High stalk population, girth & height	42	787-14-205	High population and good stalk girth & height
20	787-14-400	High stalk population, girth & height	43	787-14-411	Good population & higher girth and height
21	787-14-220	High stalk population, girth & height	44	787-14-209	High stalk population, girth & height
22	787-14-222	High stalk population, girth & height	45	787-14-235	High population and good stalk girth & height
23	787-14-246	High stalk population and good stalk girth & height	46	787-14-187	High population, good girth & medium height

All genotypes selected are free of diseases and insect pests and non flowering.

The phenotypic value of a plant or clone is due to the effects of its genotype (G), the environment (E) and the genotype X environment (G X E) interaction. Of these only the genotypic (G) effects are heritable and therefore stable. The environment and interaction effects are non- heritable and cannot be selected for. Therefore, selection for quantitative characters based on the observation on single plots in the earlier stage of clonal selection should be done by elimination of weak and undesirable plants or clones. Therefore as the genotypes evaluated were too many and planted on a single 4m row, more emphasis was done on basic quantitative characters of sugarcane. The best performing genotypes based on population and heights are presented in Table 2 and the selected genotypes based on population, height and visual observations are presented in Table 3 as the high variability was found for the trait stalk count and plant height and are of very important agronomic traits of sugarcane, the selection was done based on these traits with the consideration of visual observation report.

These 46 clones were selected based on stalk count, stalk girth and plant height collected quantitatively and visual observation on diseases and insect pests, side shoot, flowering and etc. (Table 3). From these selection, twelve clones namely; # 1, 2, 3, 5, 6, 8, 11, 14, 17, 18, 19 and 21had greatest plant heights (≥ 246cm) than the three standard checks and sixteen clones namely; 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 and 16 had greatest number of stalks (≥ 77/4m) than the three standard checks. Eight clones namely; 1, 2, 3, 5, 6, 8, 11and 14 had greatest both in number of stalks and plant height than the three standard checks.

4. Conclusion

Therefore based on the stalk count and cane height performances by considering visual observation for flowering, diseases and etc. 46 genotypes were selected. These selected genotypes will be planted with three standard checks in three replications by using Lattice Square Design for to select best performing Sugarcane Genotypes through thoroughly selection procedures. In this experiment phenotypic evaluation for important agronomic characters like sprouting, tillering, stalk count, cane height, stalk girth, single stalk weight, cane yield, brix, pol, fiber, sucrose percent, sugar yield, maturity time and biotic and a biotic stress tolerances will be done for plant cane, Ratoon I and II.

The ratoon I of 130 clones will be managed for present and future breeding purposes

References

Blackburn, F. 1984. Sugarcane. Longman Inc., New York. Pp 184.

Daniels J.S. and Roach D.F. 1987. Taxonomy and Evolution. Chapter 2. In:D.J. Heinz (ed). Sugarcane improvement through breeding. Elsevier publication, Amsterdom, Netherland, 11:7-84.

Gomez, K.A. and A.A. Gomez, 1984. Statistical procedure for agricultural research (2nd) ed. John Wiley and Sons Inc., New York.

Richard, A. 2005. Fuels from Sugar Crops: Systems Study for Sugar Cane, Sweet Sorghum and

Sugar Beets. US Dept. of Energy and University Press of the Pacific, Honolulu, Hawaii, 152p.

Singh, S.B. 2002. Tissue Culture Study of Sugarcane. An M.Sc. Thesis submitted to Thapar Institute of Engineering and Technology, Patiala, India.

Singh, S.B. 2003. Sugarcane Crop Management. Rainbow processors and printers, New Delhi, India.

Access this Article in Online

Website: www.ijarbs.com

Subject: Agricultural Sciences

Quick Response Code

DOI:10.22192/ijarbs.2017.04.04.002

How to cite this article:

Shitahun Alemu, and Ashebir Gete. (2017). Observation Trail for Clones Generated from Fuzz at Beles Sugar Development Project. Int. J. Adv. Res. Biol. Sci. 4(4): 6-10. DOI:http://dx.doi.org/10.22192/ijarbs.2017.04.04.002