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Genetic divergence in sugarcane ratoon for productive traits and identification of better ratooner tolerant to water logging situation

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Abstract
Underground stubbles of sixteen genotypes after harvest of the plant crop (2012-13) left for evaluation of their ratoon during 2013-14 at RPCAU Pusa Farm, Samastipur, Bihar under low land area and grand growth phase coincides with water-stagnation depth 40-45 cm for 2 to 3 month to know the extent of genetic divergence for productive traits and identification of better ratooner. The traits *namely*, number of Shoots at 120 days, plant height at 150, 240 and 330 days (at harvest), Cane diameter at harvest, number of millable cane at harvest, single cane weight at harvest, Brix % at 9 & 11 month, Pol % in juice at 9 & 11 month, purity % at 9 & 11 month, CCS Per cent at harvest, cane yield at harvest and CCSt/ha were showed highly significant variation. Ratoon of all the sixteen genotypes differed significantly with regard to the traits studied and displayed marked divergence and grouped into five clusters following Tocher's method, Cluster I had seven genotypes *namely*, BO154, CoP092(CoP09437), CoP 02061(CoP 2061), CoP 091, CoP 111, BO155 and BO141 followed by Cluster II containing six *viz.* CoP 04181, BO146, BO91, CoSe 96436, CoP 081 & CoLk 94184 while Cluster III, IV and V were monogenotypic, comprising single genotype BO 147, BO 153 and CoX 07067, respectively. Maximum value for inter cluster distance was observed between cluster II and V (1050.77) followed by cluster III & V (817.02), cluster III & IV (623.84), cluster II & IV (567.85), cluster I & V (419.80) and between cluster I & II (319.39). The highest contribution towards genetic divergence was exhibited by pol % in juice at 9 month stage (45.0) followed by brix % at 11 month (15.0), CCS per cent at harvest (10.83), purity % at 11 month (8.33), single cane weight (7.50), pol % in juice at 11 month (5.0), plant height at 240 days (4.17), purity % at 11 month (2.50) and rest of the other traits had less than one. The genotype CoP 09437 had maximum value for cane yield (87.54 t/h) and CCSt/ha(10.0 t)/ha, as well as it performed top rank on the basis of percentage increase over both the checks (27.39% over BO91 and 17.85 % over BO147 for cane yield while for CCS t/ha 53.37% over BO91 and 31.41 % over BO147) followed by BO 154, CoX 07067 and CoP 2061, therefore these genotypes were Identified as better ratooner among the 16 genetically diverse genotypes under water-logging condition which would be cultivated in water-logging areas of Bihar to enhance the productivity and sugar recovery as well as it can be utilized as a water logging tolerant parent in sugarcane crossing programme.

Keywords: Cluster, D^2, genetic divergence, water-logging tolerant, identification, sugarcane ratoon

Introduction
Ratooning ability in sugarcane is one of the important economic considerations to decide the suitability of sugarcane varieties for commercial cultivation. Ratoon has an additional advantage in giving better juice quality and sugar recovery in comparison to the plant crop of the same variety under similar conditions. Sugarcane is considered as cash crop and cultivated in 0.3 million ha of land in Bihar here sugarcane cultivation and sugar industries have been facing several challenges due to various reasons, among them major is 35-40 per cent of sugarcane growing area is falls under water-logging condition resulted in low productivity, other reason is poor performance of ratoon crop which covered 50 percent area of sugarcane cultivation and another reason reflect present status of varieties that is most of the low yielder and low sugared, old/obsolete sugarcane varieties *namely*, BO 91, BO110 and BO 147 covered 30-40% cultivated area of Bihar(source Sugarcane Dett. Government of Bihar 2016-17) there is present need to replaced these poor performing varieties by better ratooner having high yield coupled with high sugar tolerant to water logging. As we know that presently all the cultivated varieties of sugarcane are hybrid complex of *Saccharum species* and its heterozygous nature resulted in generation of sufficient genetic diversity. Diversity analysis helps in assessing the nature of diversity in order to identified genetically diverse genotypes for their use in breeding programmes. A large difference in varietal response to water-logging in sugarcane has been observed as we know that varieties differ in degree of tolerance to water-logging based on certain inherent genetic traits, age of the crops and other growth parameters.

Water-logging affects the ratoon, their tillering and cane growth, which may result in crop failure. Generally in Bihar water-logging coincides with the grand growth phase and may extend up to maturity of the crop it depends upon nature and number of rainfall during monsoon, the fast growing cane suffers less. The genotype differences in response under water-logging and degree of tolerance. Mostly the genotypes of hybrid complexes (*Saccharum species)* were highly susceptible to water logging and did not survive under water logging conditions whereas the clones of *Saccharum barberi, Saccharum sinense, Saccharum sclerostachya* and *Saccharum erianthus* survived. Several clones of *Saccharum spontaneum, Saccharum robustum* and *Saccharum narenga* were water-logging tolerant and good ratooner. In the breeding of sugarcane, it has been a general practice to cross the different species with the noble cane, *S. officinarum*, to combine the high sugar yield of the *officinarum* clones with biotic and abiotic stress tolerance. Above said such clones and their ratoon with water-logging tolerant genes can do well under water-logging condition which requires systematic study on their comparative tolerance and knowledge of genetic divergence among them. Although the use of high yielding varieties coupled with moderate to high sucrose and also having water-logging tolerance capacity it can contribute substantially in sugarcane production and productivity but still there is need to evaluate ratoon of sugarcane varieties tolerant to water-logging condition for its better adaptability and to overcome the problem of low productivity of ratoon. Best performing ratoon crop under water-logging areas will enhance the productivity as well as recovery of this crop. Therefore, keeping in view the proposed investigation was carried out to estimate the Genetic Divergence among the ratoon of sugarcane genotypes and identification of better ratooner among them.

Material and Method

The material of this experiment were ratoon crop involving sixteen sugarcane genotypes *viz*, BO153, BO141, CoSe 96436, CoX 07067, CoP081, CoP091, CoP02061, CoP111, CoP04181, BO155, BO154, BO146, CoP092 (CoP 09437), CoLk 94184 including two checks (BO91 and BO147) during 2013-14.The plant crop for this ratoon trial were planted during 2012-2013 at Paddy Block, RPCAU Pusa Farm, Samastipur, Bihar under low land area where water stagnation (a minimum depth of 40-45 cm) maintained in the 2-3 months. All the underground stubbles of sixteen genotypes maintained after harvesting of plant crop of 2012-13 with 6 rows of 6 meters length, row to row distance 90 cm, in Randomized Block Design (RBD) with three replications follow all agronomical package and practices for ratoon management. The data of ratoon crop were recorded for various growth and cane yield parameters *viz*. number of shoots at 120 and 240 days (000/ha), plant height (cm) at 150,240 and 330 days (at harvest), number of millable canes 11 months (000/ha), cane diameter (cm) at harvest, single cane weight (kg) at harvest and cane yield (t/ha). Observations were record by selecting five random plants per genotype per replication for plant height, cane diameter and single cane weight. Cane length of five plants was marked from each genotype to measure cane length. The plant height was measured from base to the tip of cane at the 150, 240 and 330 days (at harvesting stage) as plant attained its growth at different stages. At harvest stage same five canes were used for measurement of cane diameter with help of Vernier Caliper. Single cane weight was recorded from the same set of five cane used for length and diameter. The mean data of five plants was used for statistical analysis. No. of shoots (000/ha) were recorded at 120 & 240 days old crop and same for number of millable clone (000/ha). For Juice quality traits Brix % is a measure of total soluble solids present in the juice. It was taken directly by using a Brix hygrometer. Taken 250 ml juice in measuring cylinder and hygrometer dip into the juice then reading was recorded from the juice level. These readings were corrected to the temperature at 20 ^{0}C using temperature correction chart as described by Spencer and Meade (1955). Pol % in juice refers to the sucrose per cent in juice estimated according to the method described by Spencer and Meade (1955) with the help of Polari scope. 100 ml juice was taken in conical flask and 4 gm Honey dry lead sub acetate was added and mixed well by shaking the flask. This solution was filtered twice through a dry Whatsman no. 1 filter paper after few minutes and the abstract was collected into a clean and dry beaker. The abstract poured into the Polari meter tube to record the Pol values in Polari scope this value called dial reading. Sucrose per cent in juice was obtained by referring the brix and dial reading to Schmitz's table. The CCS % and CCS (t/ha) were calculated as:

CCS (%) = 0.292 x Pol % juice ((0.035 x Purity %)-1) / Purity % X 100
CCS (t/ha) = CCS (%) x Cane yield (t/ha)

Statistical analysis

Genetic divergence among 16 varieties of sugarcane was estimated by analyzing the data of sixteen traits through D^2 statistics (Mahalanobis, 1936) [7] in Fig. 2. Ratoon of all the genotypes were evaluated and observed data were used for estimation of variances and co-variances.

Genotypic Variance (σ_g^2) = (vMSS – EMSS) x CF
Phenotypic variance (σ_p^2) = σ_g^2 + EMS

D^2 values were calculated by using the formula

$$D^2 = W_{ij} (\bar{X}_i^1 - \bar{X}_i^2) (\bar{X}_j^1 - \bar{X}_j^2)$$

Where

W_{ij} = Inverse of estimated variance, co-variance matrix.
$(\bar{X}_i^1 - X_i^2)$ and $(\bar{X}_j^1 - \bar{X}_j^2)$ = Differences in the mean of the two populations.

Contribution of individual character towards total divergence was checked out by taking the percentage of number of times each character ranked first on the basis of

$$d_i = Y_i^j - Y_i^k$$

Where

d_i = Mean deviation in population,
Y_i^j and Y_i^k = Values for characters in population

Rank 1 was given to the highest mean difference and 'p' to the lowest mean differences, where 'p' is the total number of characters. Using these ranks, a table was prepared to determine the percentage contribution of each character to the total divergence. Genotypes were grouped into various clusters by on the basis of Tocher's methods Rao, (1952) [12]. The population were arranged in ascending order on the basis of their relative distances (D^2 values) from each other. Two populations having small distance from each other were

considered first. Then second population having smallest D^2 from the first two populations was added to it. This step was continued until the average increase in D^2 value did not exceed the maximum D^2 value between any two populations in the first row of the table. Average inter and intra cluster distance was estimated by using the formula (Singh and Chaudhary, 1977) [13].

Average intra cluster distance

$$\sum D_i^2/n$$

Where

$\sum D_i^2$ = the sum of distance between all possible combinations (n) of the population included in a cluster.

Average inter cluster distance

$$\sum D\_i\text{^}2/(n\_1 \times n\_2)$$

Where

$\sum D_i^2$ = Sum of distance of all possible combinations of genotypes included in the two clusters considered

n_1 = Number of genotypes in first cluster

n_2 = Number of genotypes in second clusters

A cluster diagram was prepared showing the distances between clusters and genotypes on the basis of methods as explain above. Ratoon of all the sixteen genotypes based on statistical differences were used for genotypes classification in different clusters, results of inter and intra clusters D^2 values between clusters, as well as mean of intra-clusters D^2 values of different clusters are presented in table no. 1-5 and Fig 1-2.

Results and Discussion

Assessing the nature of diversity in order to identified genetically diverse genotypes for their use in breeding programmes is most important. In sugarcane breeding programme the diversity of parents must be emphasized for bi-parental/poly crossing. More diverse the parent within a reasonable range, better the chances of improving productive traits under consideration in the resulting offspring. In the present investigation clustering pattern in the ratoon of sixteen genotypes taken for genetic divergence analysis differed significantly with regard to the characters studied and displayed marked divergence and grouped into five clusters following Tocher's method (Table 1 and Fig.1). Mahalnobis's D^2 statistic is an unique tool for classifying genetically diverse parents based on quantitative traits (Fig.2) which could be appropriately utilized in hybridization programme. Ratoon of all the sixteen genotypes differed significantly with regard to the traits studied and displayed marked divergence and grouped into five clusters, Cluster I had seven clones *namely*, BO154, CoP092(CoP09437), CoP02061(CoP 2061), CoP 091, CoP 111, BO155 and BO141 followed by Cluster II containing six clones *viz.* CoP 04181, BO146, BO91, CoSe 96436, CoP 081 & CoLk 94184 while Cluster III, IV and V were monogenotypic, comprising single clone BO 147, BO 153 and CoX 07067, respectively. Similar studied based on D^2 statistic were also performed by Ahmed and Obeid (2010) [2], Bakshi and Hemaprabha (2005) [3], Gagan *et al*. (2005) [4], Hooda *et al*. (1989) [6], Kashif and Khan (2007) [9], Mali *et al*. (2009), Mishra *et al*. (2005) [8], Rao *et al*. (1985), Silva *et al*. (2011), Singh and Khan (1990) [17], Singh and Singh. (2002) [18], Singh *et al*. (1987) [14], Singh *et al*. (2001), Singh *et al*. (2004) [15], Agrawal and Kumar (2017) [1]. Cluster means of ratoon for different traits under water-logging condition has been presented in Table no. 2. A comparison of the mean values of sixteen traits for different clusters showed considerable differences among them. The highest mean values for brix percent at 9 & 11 month (20.10 & 19.95 %), pol percentage in juice at 9 &11 month (17.77 & 17.55%), purity at 9 &11 month stage (88.35 & 87.95 %) and CCS % (12.13) at harvest were observed in Cluster I. Cluster II had maximum mean value for number of shoots at 120 days (138680/ha), plant height at 150 days (159.55cm), plant height at 240 days (221.17 cm), plant height at 330 days (249.61), cane diameter(2.40 cm), single cane weight (0.79 Kg), Cane yield (85.10 t/ha) and CCS t/ha (9.72). Cluster IV having maximum mean value number of millable canes (116310/ha). No any maximum value was observed in Cluster III and V of ratoon it means BO 147 and CoX 07067 were showed relatively poor ratoon. The mean of intra and inter cluster distances (D^2) under water-logging condition of ratoon has been presented in Table no.3. The average distance of intra cluster ranged from 122.23 (cluster I) to 162.22 (cluster II). The highest inter cluster distance was recorded between cluster II and V (1050.77) followed by cluster III and V (817.02), cluster III and IV (623.84), cluster II and IV (567.85), cluster I and IV (419.80), cluster I and II (319.39) and cluster I and III (253.19). The ratooning of genotypes in cluster I bearing high mean value for juice quality traits while cluster II had high mean value for yield and its attribute traits between two cluster high degree of genetic diversity exhibited due to a value of 319.39 as inter cluster distance thus the genotypes of these cluster's may be utilized under inter varietal hybridization programme for getting high yield coupled with high pol % in juice as recombinants. These results of genetic diversity were in agreement with that of Gulzar *et al.* (2015) [5], Mishra *et al*. (2005) [8], Singh and Singh. (2002) [18], Singh *et al*. (2001) and Agrawal and Kumar (2017) [1]. The clustering pattern showed that varieties developed from same institution were noticed to have fallen into two different clusters. Further, it can also be seen from the cluster that the varieties in cluster II belong to different breeding stations and possible reason could be the narrow genetic base of clones used in the hybridization and limited traits explored for identification for the Bihar. Table no. 4 showed contribution percentage of each character towards total divergence under water-logging condition of ratoon. The highest contribution in the manifestation of genetic divergence was exhibited by pol % in juice at 9 month (45.00%) followed by brix % at 11 month (15.00%), CCS t/ha at harvest(10.83) purity % at 9 month (8.33%) and single cane weight(7.5%) and pol % in juice at 11 mont h(5.0 %). The contribution of remaining traits in manifestation of genetic divergence were less than 10% these traits were no. of shoot, cane diameter, plant height and cane yield. Different clusters comprises unique feature for different characters under investigation. The highest mean values for yield attributing traits *viz*, number of shoots at 120 days, plant height at 150 days, plant height at 240 days, plant height at 330 days, cane diameter, single cane weight and cane yield were observed in cluster II while Cluster I had maximum mean value for brix, pol, purity nd CCS per cent at harvest and these traits also contributed maximum percentage towards diversity reflect the importance of ratoon and their juicce quality potential. Selection of genotypes based on cluster mean for the better exploitation of genetic potential also reported by Ahmed and

Obeid (2010) [2], Mali *et al*. (2009), Mishra *et al*. (2005) [8], Singh and Khan (1990) [17], Singh *et al*. (2004) [15] and Agrawal and Kumar (2017) [1]. The highest intra cluster distance was observed in cluster II indicating differences in genotypes within cluster. Least intra cluster distance was found in cluster I indicating that close resemblance between the genotypes presented in this cluster. Table 5 reflect the percentage increase or decrease over checks (BO 91 & BO 147) under water-logging condition in ratoon crop of sixteen genotypes for identification of high yielding, coupled with high CCS t/ha bearing genotypes tolerant to water-logging condition. High CCS (t/ha) was observed for the genotype CoP09437 (10.00), followed by CoX07067 (9.89), BO154 (9.63) and CoP 02061 (9.52). Highest yielder genotype was CoP 09437 (87.54 t/ha), followed by CoP 02061 (84.28 t/ha) and BO154 (83.47 t/ha). Based on percentage increase over (BO 91 and BO 147) both checks the genotype CoP 09437 (27.39 & 17.85%, respectively) performed highest ranker for cane yield followed by CoP 2061(22.64 &13.46%) and BO 154 (21.46 & 12.37%) again for CCS t/ha, first rank was recorded for the CoP 09437 (53.37 & 31.41%) followed by CoX 07067(51.69 &29.96%), CoP 02061(46.01 &25.10%) over both the checks BO 91 and BO 147, respectively. On the basis of high *per se* performance and high percentage increase over (BO 91 and BO 147) both checks considering cane yield and CCS (t/ha) of ratoon under water-logging condition clones namely, CoP 09437, BO154 and CoP 02061 were identified as better ratooner. The ratoon of these genotypes, having high yielding ability coupled with high to moderate pol percent in juice even under water-logging condition would be utilized by the farmers to get more production and sugar factory will also get high sugar. In further sugarcane breeding programme CoP 09437, BO154 and CoP 02061 will be used as better ratooner and water logging tolerant parents in hybridization programme. Kumar *et al.* (2015) [11] reported CoP 2061- a released and notified midlate maturing sugarcane variety for Bihar, Eastern Uttar Pradesh, Assam and West Bengal and further during 2015 also reported CoP 09437 - an identified sugarcane variety and a better option for high yielding under North Central and North Eastern Zones of India Kumar *et al*. (2016) [10]. Parentage detail for most of the clones indicated that water logging tolerant ability transmitted through BO 91 as a parent either GC or bi-parental cross (Table 5) but it is not essential that it bears high cane and sugar yield due to highly heterozygous in nature and its uneven chromosomal distribution during gamete formation therefore selection and choice of parents mainly depends upon contribution of characters towards divergence.

Conclusion of the ratoon evaluation under low land area where its grand growth phase coincides water-stagnation depth 40-45 cm for three months reflect the potential of genotype tolerance against water logging. There were five clusters out of which Cluster I & II had high mean value and involve most of the genotypes. Crossing between the genotypes of these two clusters will be fretful to get high yielder coupled with high sugared clones tolerant to water logging ability. Performance of three identified genotypes *viz.* CoP092 (CoP 09437), BO154 and CoP02061 showed better ratooner and found superior for cane yield and CCS t/ha. Therefore in one hand these water-logging tolerant genotypes will be useful for sugarcane farmers to get high yield in water logging situation and other hand sugar mills to get more sugar recovery. These clones further utilize as a water-logging tolerant parent in crossing programme.

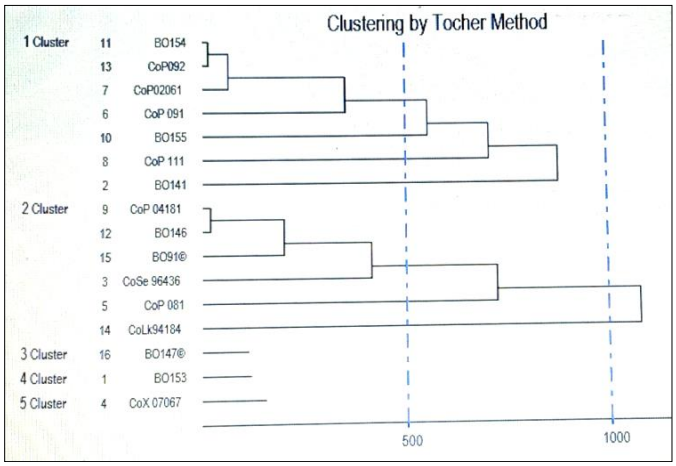

Fig 1: Clustering pattern of ratoon of 16 sugarcane clones on the basis of D^2statistic by Tocher method

Table 1: Clusters of 16 sugarcane ratoon under water-logging condition base on their productive traits followed D^2 statistic.

Cluster Number	No. of genotypes within cluster	Name of genotypes in cluster
I	7	BO154, CoP092, CoP 02061, CoP 111,BO155, BO141 & CoP 091
II	6	BO146, BO91, CoP 04181, CoLk 94184,CoSe 96436 & CoP 081
III	1	BO 147
IV	1	BO153
V	1	CoX 07067

Table 2: Cluster mean for productive traits in ratoon crop of sugarcane genotypes under water-logging condition.

		Plant Height			At 9 Month stage			At 11 Month stage			CCS		CD	SCW	NMC	Cane Yield t/ha
	S120	150 days	240days	330 days	B%	P%	PU%	B%11	P%11	PU%11	%	t/ha				
Cluster I	117.72	145.93	198.89	230.74	20.10	17.77	88.35	19.95	17.55	87.95	12.13	9.14	2.24	0.69	107.84	75.25
Cluster II	138.68	159.55	221.17	249.61	19.20	16.91	88.07	19.03	16.61	87.23	11.42	9.72	2.40	0.79	111.44	85.10
Cluster III	97.29	125.19	155.72	175.16	19.00	16.81	88.33	18.70	16.59	87.73	11.50	6.71	2.06	0.62	101.47	62.71
Cluster IV	120.46	131.97	199.62	217.06	18.47	15.93	86.67	18.13	15.65	87.13	10.70	8.43	2.16	0.66	116.31	78.70
Cluster V	102.76	138.32	169.17	197.19	18.35	16.10	87.88	16.93	14.71	86.75	10.09	5.39	2.17	0.59	90.48	53.04

Table 3: Mean intra and inter cluster distance (D^2) among five clusters in sugarcane genotypes under water-logging condition

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	122.23	319.39	253.19	220.14	419.80
Cluster II		162.22	230.54	567.85	1050.77
Cluster III			0.00	623.84	817.02
Cluster IV				0.00	196.47
Cluster V					0.00

Table 4: Contribution percentage of productive traits characters towards genetic divergence in sugarcane ratoon under water logging condition.

S. No.	Characters	Contribution % towards genetic divergence	Times Ranked 1st
1	No. of shoots at 120 days (000/ha)	0.01	0.001
2	Plant height at 150 days (cm)	0.01	0.001
3	Plant height at 240 days (cm)	4.17	5.000
4	Brix at 9 or 10 month stage (%)	0.01	0.001
5	Pol at 9 or 10 month stage (%)	45.00	54.000
6	Purity at 9 or 10 month stage (%)	8.33	10.000
7	Brix at 11 month stage (%)	15.00	18.000
8	Pol at 11 month stage (%)	5.00	6.000
9	Purity at 11 month stage (%)	2.50	3.000
10	CCS per cent at harvest (%)	0.01	0.001
11	CCS per t/ha at harvest	10.83	13.000
12	Plant height at harvest (cm)	0.01	0.001
13	Cane diameter at harvest (cm)	0.83	1.000
14	Single cane weight (kg)	7.50	9.000
15	No. of millable canes (000/ ha)	0.01	0.001
16	Cane yield (tonne/ ha)	0.83	1.000

Table 5: Ratoon of 16 sugarcane clones their performances for the yield and CCS t/ha its percentage increase or decrease over checks (BO 91 & BO 147) under water-logging condition.

S. No.	Genotypes	Parentage	Cane yield t/ha			CCS (t/ha)			Rank for best performance ratoon		
			Ratoon	% increase or decrease over		Ratoon	% increase or decrease over		Cane yield t/ha	CCS t/ha	Pooled
				BO 91	BO 147		BO91	BO147			
1.	BO153	BO131 self (BO 109 X BO 43)	69.81	01.60	-06.02	8.38	28.52	09.32	9	7	6
2.	BO141	BO89 FC (BO 47 self)	60.12	-12.51	-19.06	7.17	09.97	-6.14	12	10	7
3.	CoSe96436	BO 91 X Co62198	52.49	-23.62	-29.33	5.23	-24.67	-31.27	14	14	8
4.	CoX 07067	CoPant 90223 GC (BO 91 GC)	80.69	17.42	08.63	9.89	51.69	29.96	5	2	3
5.	CoP081	BO 99 GC (Co1207 X BO 43)	62.28	-09.37	-16.16	6.91	05.98	-09.20	11	11	7
6.	CoP091	BO 91 GC	70.12	02.04	-01.91	7.95	21.93	04.47	8	8	9
7.	CoP 02061	CoLk 8102 X HR 83/65	84.28	22.64	13.46	9.52	46.01	25.10	2	4	2
8.	CoP111	BO91 X Co62198	80.32	16.88	08.13	8.75	34.20	14.98	6	6	5
9.	CoP 04181	CoS 8408 GC(Co1148 GC)	50.48	-26.54	-32.04	5.60	-14.11	-26.41	15	13	8
10.	BO155	BO 122 F.C (CoP 2 X BO 99)	81.50	18.60	09.72	8.92	36.81	17.21	4	5	4
11.	BO154	CoSe 98235 X UP 9742(BO91)	83.47	21.46	12.37	9.63	26.54	47.70	3	3	2
12.	BO146	BO128 X BO121	40.46	-41.12	-45.53	4.21	-35.43	-44.67	16	16	10
13.	CoP092	BO 91 GC	87.54	27.39	17.85	10.00	53.37	31.41	1	1	1
14.	CoLk 94184	CoLk 8001 self	58.32	-15.13	-21.49	4.80	-26.38	-36.93	13	15	8
15.	BO 91 (C)	BO 55 X BO 43	68.72			6.52			10	12	7
16.	BO147 (C)	BO110 self	74.28			7.61			7	9	6

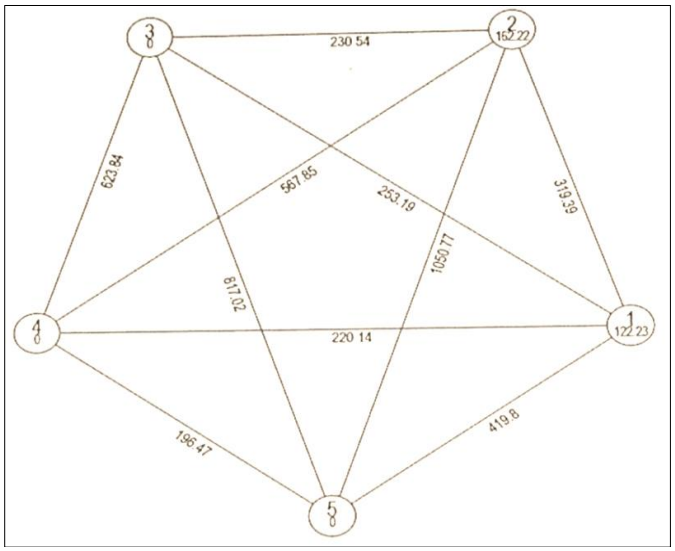

Fig 2: Mahalnobis Euclidean Disatnce (D^2) of 5 clusters involving ratoon of 16 sugarcane genotypes.

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