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Genetic Diversity in Grain Quality Traits of Rice Genotypes

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Abstract

Genetic diversity in grain quality among 92 rice cultivars was evaluated using Mahalanobis D2 statistic. Highly significant ($p < 0.01$) differences were observed among varieties for 14 quality characters namely hulling (%), milling (%), head rice recovery (%), kernel length and breadth (mm), length/breadth ratio, 1000 grain weight (g), kernel length after cooking (mm), kernel breadth after cooking (mm), kernel elongation ratio, volume expansion ratio and water uptake, amylose content (g%), gel consistency (mm) and alkali spreading value. Based on cluster analysis, the genotypes were grouped into 10 clusters of which clusters VII and IX are the largest clusters consisting of 16 genotypes each while cluster V was the smallest with only a single genotype. The maximum intra cluster distance (D = 14066.5) was found in cluster VI consisting of two traditional varieties AS 100 and Chittimutyalu. The most divergent clusters found were Clusters V and VI. Minimum inter cluster distance (D = 5144.43) was found between Clusters VIII and IX. Kernel breadth (0.01%), volume expansion ratio (0.39 %) and elongation ratio (0.30%) failed to contribute significantly towards genetic diversity. Amylose content (25.2%), gel consistency (20.4 %), 1000 grain weight (12.6 %) and head rice recovery (10.1%) were found to be the most contributing traits towards genetic diversity. Hence these traits could be focused for selection while improving grain quality.

Key words: Rice, Genetic diversity, Grain quality, cluster analysis, Mahalanobis D2

Introduction

Rice (*Oryza sativa*. L) is the most important cereal food crop in the world. Globally around three billion people depend on rice which provides 50 to 80 per cent of daily calories. Next to China, India is the second largest producer and consumer of rice. For meeting the dietary requirements of increasing population, genetic improvement of rice with higher yield, good grain quality, resistance to biotic and abiotic stresses is the most logical and promising approach. Genetic improvement mainly depends upon inclusion of genetically diverse parents having wider variability for different yield and quality characters in hybridization program. The more diverse the parents, the higher are the chances of obtaining more amounts of heterotic expression in F_1s and superior recombinants in the segregating generations. The present investigation aimed to assess the nature and magnitude of genetic divergence present in the 92 rice genotypes and to select suitable diverse genotypes as parents for further utilization in grain quality improvement programs.

Material and Methods

The experiment was conducted at DRR farm, ICRISAT campus, Patancheru during *kharif*, 2013. Ninety two rice varieties were transplanted randomly 20 cm apart between rows and 15 cm within row to each unit plot of 5 m^2 following randomized complete block design (RCBD) with three replications. Recommended crop management practices and need based plant protection measures were taken up. Observations were recorded on 14 grain quality traits: physical quality traits *viz.,* hulling (%), milling (%), head rice recovery (%), kernel length and breadth (mm), length/breadth ratio, 1000 grain weight (g) and cooking quality traits *viz.,* kernel length after cooking (mm), kernel breadth after cooking (mm), kernel elongation ratio, volume expansion ratio and water uptake; chemical quality attributes *viz.*, amylose content (%), gel consistency (mm), alkali spreading value. Genetic diversity analysis was done following D^2 statistics proposed by Mahalanobis (1936). The varieties were classified into a number of clusters by Toucher's method as described by Rao (1952).

Results and Discussion

The analysis of variance showed significant differences among genotypes for each character indicating the existence of variability among the genotypes (Table 1). The genotypes were grouped into 10 clusters based on D^2 value (Table 2, Fig1a &1b). Clusters VII and IX were the largest consisting of 16 genotypes followed by cluster VIII (15 genotypes), cluster I (13 genotypes), cluster X

(12 genotypes), cluster II & IV (6 genotypes), cluster III (5 genotypes) and cluster VI (2 genotypes). The smallest cluster (V) contained a single genotype. The genotypes of the biggest clusters VII and IX originated from different States like Andhra Pradesh, Telangana, Uttar Pradesh, Punjab, Chhattisgarh, Karnataka, West Bengal, Gujarat, Odisha, Assam, Punjab, Maharashtra, Tripura, Madhya Pradesh, Bihar and Haryana. It indicates that there was no relationship between clustering pattern and geographical distribution of genotypes.

Cluster II consisted of medium slender grain genotypes. There are six genotypes in this cluster and majority (66%) of them namely GR-103, Swarna, White Ponni and DL-184 possessed medium slender grains. In cluster IX, 10 of 16 genotypes possessed long slender grains. They are Manoharsali, NLR-33359 (Shravani), SGT-1, PR-116, Khitish, Kavya, Karjat-2, Amulya and Sahyadri. The clustering pattern of the hybrids appeared to be very distinct. All of them grouped into different clusters namely cluster 1, cluster 9 and cluster 10.

The genotypic distribution also indicated that the genotypes originated from similar geographic regions were distributed in different clusters. Therefore the kind of genetic diversity found among the genotypes belonging to same geographic origin might be due to differences in adaptation, selection criteria, selection pressure and environmental conditions. The genotypes having bold grain type were clustered together in cluster III. Among the five genotypes of cluster III, three genotypes Jalpriya, Jyothi and Madhukar possessed long bold grain type. The remaining two genotypes, Varsha and Kranti possessed short bold grains. Similarly cluster VI possessed genotypes, AS 100 and Chitti muthyalu with short bold grains. As expected all the aromatic varieties were found in same cluster grouped as cluster IV. They included Basmati-386, Taroari Basmati, Ranbir Basmati, Yamini, Type-3 and PR-115. However PR 115, a non aromatic variety is an exception in this cluster. Cluster IV had only one genotype Pusa Basmati 1 which is a most popular aromatic rice variety and being used as a quality check in basmati improvement programs. It was diverse and recorded high genetic distances from other clusters.

In general, the clustering pattern across locations showed that genotypes collected from the same geographic origin were found to be distributed in different clusters. Similar findings of non correspondence of genetic divergence with geographic diversity were reported earlier in rice by Murthy and Arunachalam, (1966), Sinha *et al*., (1991), Vivekananda and Subramanian, (1993), Manan *et al.,* (1993), Rahman *et al.,* (1997), Chaudhury *et al.,* (1999), Shanmugasundaram *et al.,* (2000), Masud *et al.,* (2003), Patil *et al.,*(2005), Raju *et al.,* (2004), Chandra *et al.,* (2007), Arun Sharma *et al.,* (2008) and Rajesh *et al.,* (2010). Murthy and Arunachalam, (1966) stated that genetic drift and selection in environment could cause greater diversity than geographic distances. Considering this, parents should be selected on the basis of genetic diversity rather than geographic diversity which are supported by the findings of Hasan *et al.,* (2000). Grouping of materials of similar origin into different clusters was an indication of broad genetic base of the genotypes belonging to that origin. So genotypes originating from same place may have different genetic architecture or *vice versa* (Shanmugam and Rangaswamy, 1982).

The intra cluster D^2 values ranged from zero (cluster V) to 14066.5 (cluster VI) followed by cluster II (6442.21); cluster IV (5662.09); cluster III (5422.41); cluster X (4764.55); cluster VII (4747.5); cluster I (4458.51); cluster IX (4245.36) and cluster VIII (3062). The highest intra cluster distance (14066.5) in cluster VI indicates wide genetic variation among the genotypes belonging to these clusters. The V^{th} cluster consisted of only one genotype (Pusa Basmati1) hence; it lacked intra-cluster distance (0.00).

The inter cluster D^2 was maximum between clusters V and VI (53342.32) indicating that genotypes in V were far diverse from those of VI. Choosing of genotypes belonging to distant clusters was expected to execute maximum heterosis in crossing and to be used in hybridization program for obtaining a wide spectrum of variation among the segregants. This was in conformity with Hossain *et al*., (2003). The least distance was observed between cluster VIII and IX (5144.43) which indicated genotypes included in them were closely related (Table 3).

The cluster wise mean values for fourteen quality characters were presented in Table 4. These are helpful to assess the superiority of clusters during the improvement of characters through hybridization programme. The cluster mean values showed a wide range of variation for majority of the characters undertaken in the present study. The diversity was also supported by the appreciable amount of variation among the cluster means for different characters. Cluster III exhibited highest kernel breadth (2.29 mm), amylose content (26.92%) and 1000 grain weight (28.69 g) while cluster IV contained genotypes with highest KLAC (12.63 mm) and elongation ratio (1.98). Cluster V recorded highest value of kernel length (6.82 mm), L/B ratio (4.15) and ASV (6.66). Cluster VII had highest value for hulling (79.73 %), milling (71.24 %), HRR (67.99 %), volume expansion ratio (5.95), water uptake (289 ml), gel

consistency (62.56 mm) and 1000 grain weight (28.69 g). Thus, these genotypes hold great promise as parents for obtaining promising elite lines through hybridization and to create further variability for these characters (Mishra and Pravin, 2004).

It is indicated from the study that hybridization between the genotypes of the clusters VI and VII (high HRR, medium and desirable AC, ASV, GC) with cluster V (high L/B ratio, high kernel length, high kernel length after cooking and low kernel breadth) forms a good cross combination producing superior recombinants. Likewise cluster V (high L/B ratio, low kernel breadth and medium and desirable AC) is suitable for hybridization with cluster VII (high VER) and cluster IV (high ER).

The genotypes from cluster VI *i.e.,* AS 100 and Chittimuthyalu having desired quality characters like high HRR, desirable medium ASV and AC, low kernel breadth; the genotypes from another cluster VII such as Kalanamak, NLR 33654 and WGL 14 possessing desirable quality characters namely high HRR, high L/B ratio indicating long slender grains, desirable medium AC and ASV; one genotype namely Pusa Basmati 1 from cluster V having preferred grain qualities like long slender grains with high l/b, desirable KLAC and medium desirable AC can be selected as ultimate parents for hybridization program. Ravindra Babu *et al*., (2006) and Subudhi *et al.,* (2009) also proposed to choose diverse parents for quality traits such as HRR, KLAC, GC, ER and AC from the most divergent clusters so that they produce larger variability and desirable segregants that would be productive in rice breeding program

Contribution of different quality characters to total divergence is presented in Table 4. At Andhra Pradesh the amylose content was having maximum contribution *ie.*, (25.2%) followed by gel consistency (20.4 %), 1000 grain weight (12.6%) and HRR (10.1 %). The lowest value is observed in kernel breadth (0.01 %). Hence amylose content and gel consistency were found to be potential contributors to genetic divergence in the genotypes. Subudhi *et al*., (2009) evaluated physico-chemical and cooking characters in rice to study the diversity pattern among the genotypes and reported that the characters amylose content, alkali spreading value, kernel length after cooking and kernel breadth together accounted for 83.78 per cent to the total divergence.

In our study 1000 grain weight was one of the main contributors to the total genetic diversity. Senapati and Sarkar, (2005), Ramesh Chandra *et al*., (2007) and Iftekharuddaula *et al.,* (2010) also found that 1000 grain weight to be the chief contributors towards genetic divergence and they suggested that this character must be given importance while selecting parents in crossing programme as well as selection of segregants in succeeding generations reported. Chand *et al*., (2005) conducted experiments to study genetic divergence in 57 genotypes of rice germplasm lines based on 14 agro morphological traits and found that 1000 grain weight character prominently contributed to total genetic divergence.

Ravindra Babu *et al*., (2006) reported genetic divergence using quality characters found that the characters gel consistency, water uptake, and head rice recovery per cent contributed maximum towards genetic divergence. However, Garg *et al*., (2011) observed the gel consistency contributed maximum towards genetic divergence. These observations corroborate well with those of earlier researchers (Sandhya Kishore *et al.,* 2007, Patil *et al.,* 2005). These traits should be given importance during hybridization and selection of segregating populations.

In the present experiment hybridization among the varieties AS 100 and Chittimutyalu from cluster VI for high HRR, soft gel consistency and intermediate amylose and ASV; Pusa Basmati 1 from cluster V for high L/B ratio, more kernel length and more KLAC would result in obtaining wide spectrum of variation and desirable heterotic recombinants in the segregating generations amenable for selection in improving grain quality.

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Table1. Analysis of variance of 14 characters for 92 genotypes

Characters	Source of variation (mean sum of squares)		
	Replication	Treatments	Error
Hulling (%)	0.235	12.535**	0.007
Milling (%)	0.137	40.935**	0.006
Head Rice recovery (%)	15.249	641.809**	10.038
Kernel Length (mm)	0.0002	1.298**	0.0006
Kernel Breadth (mm)	0.0006	0.133**	0.0003
L/B ratio	0.001	0.686**	0.0005
Kernel Length After Cooking	0.059	7.248**	0.007
Water Uptake (ml)	129.632	11856.66**	36.733
Volume Expansion Ratio	0.006	0.547**	0.005
Elongation Ratio	0.001	0.146**	0.0002
Alkali Spreading Value	1.981	3.354**	0.172
Gel Consistency (mm)	2.851	723.141**	0.785
Amylose Content (%)	0.008	17.279**	0.016
1000 grain weight (g)	0.204	50.607**	0.098

*Significant at 5% level, **Significant at 1% level

Table 2. Clustering pattern of 92 rice genotypes based on D2 analysis

Cluster No.	Number of genotypes	Name of genotypes
I	13	Aishwaraya, Kanchana, Harsha, Matta Triveni, KHP-2, BR-2655, Jalamagna, VRS-3, Shakthi, Nalini, Mandhya Vijaya, Pratap, Gouri
II	6	BPT-11711, GR-103, Swarna, White Ponni, DL-184, RAU 3043
III	5	Jalpriya, Jyothi, Madhukar, Kranti, Varsha
IV	6	Basmati-386, Taroari Basmati, Ranbir Basmati, Yamini, Type-3, PR-115
V	1	Pusa Basmati 1
VI	2	AS-100, Chittimutyalu
VII	16	Dharithri, WGL-14 (Warangal Sannalu), Pooja, Kalanamak, Nagari Dubraj, KMP-101, CN-1233-33-9-117, PantDhan-16, VRM-3, Dandi, VRM-31, VRS-25, High iron rice, Indravati, NLR-33654 (Apurva), Ranjeet
VIII	15	Bhuban, Jaya, MTU-3636(Prabhat), Sunandana, Birupa, Bhudeb, Suraksha, MTU-1001(Vijeta), MTU 1010 (Cottondora Sannalu), Gajapathi, Giri, Sashi, PR-113, PSD-1, Mahamaya
IX	16	CN-1039-9, MSS-5, NLR-145 (Swarnamukhi), Manoharsali, NLR-33359 (Shravani), SGT-1, Jagabndu, Prachi, MSE-9, PR-118, PR-116, Khitish, Kavya, Karjat-2, Amulya, Sahyadri
X	12	Barah Avarodhi, Sabita, PR-111, PR-114, Vasumati, Jalnidhi, Lalat, Konark, VRS-19, Sahyadri-2, Vikas, IR-64

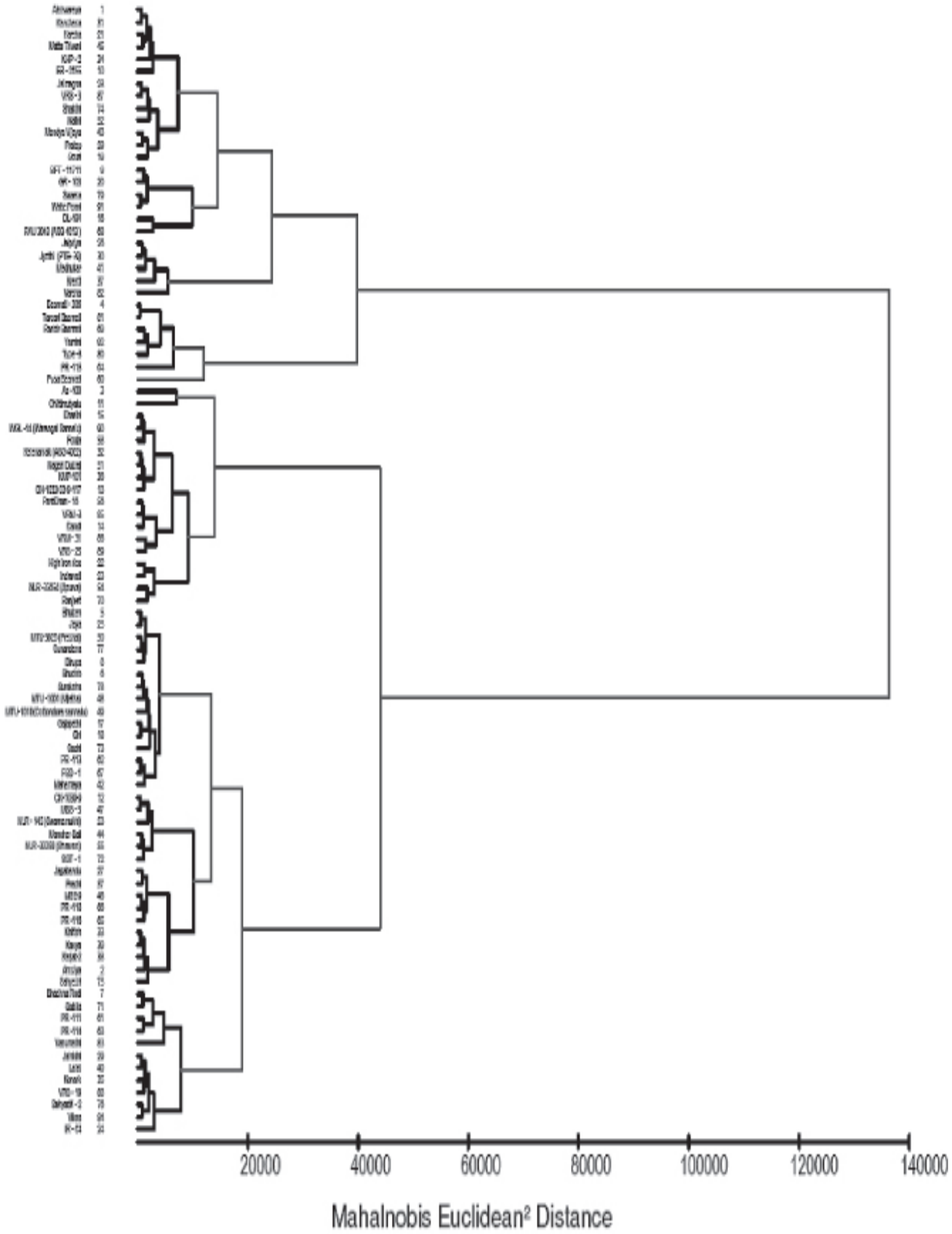

Fig. 1a. Dendrogram showing Clustering of rice genotypes by Tocher's method based on quality traits

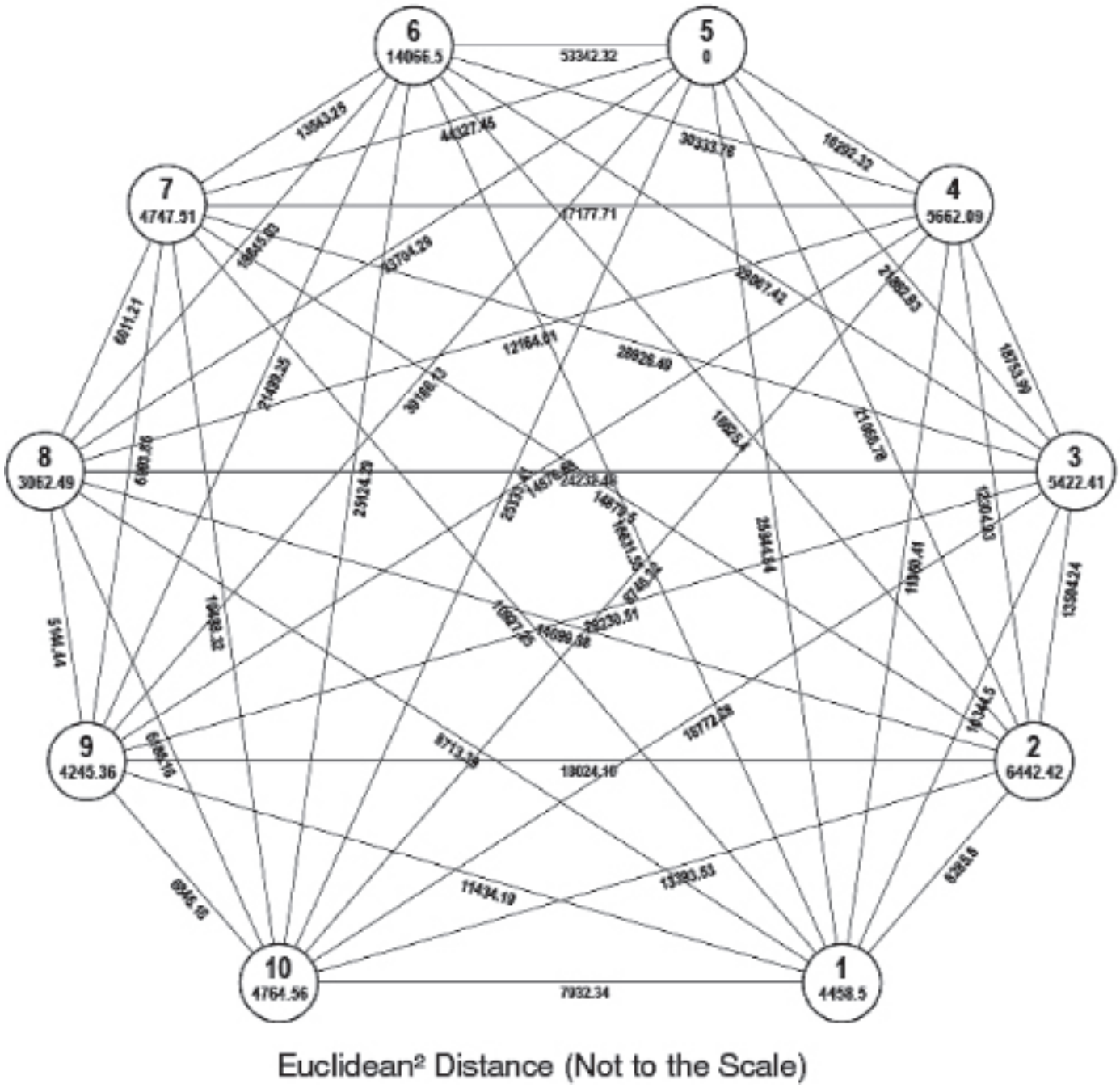

Fig. 1b. Ward Means

Table 3. Average intra (diagonal) and inter cluster distances for quality traits

Cluster	I cluster	II cluster	III cluster	IV cluster	V cluster	VI cluster	VII cluster	VIII cluster	IX cluster	X cluster
I cluster	4458.5	8285.60	10344.5	11960.41	25844.84	16631.55	10927.25	8713.39	11434.19	7932.339
II cluster		6442.41	13504.24	12304.93	21066.78	16625.4	14879.50	14099.38	18024.19	13393.53
III cluster			5422.41	18753.99	21862.93	29067.42	28926.49	24232.48	28230.51	18772.28
IV cluster				5662.09	16292.32	30333.76	17177.71	12164.01	14576.69	8748.324
V cluster					0	53342.32	44327.45	33704.29	39166.13	25333.41
VI cluster						14066.5	13543.25	19645.03	21499.25	25124.29
VII cluster							4747.51	6011.20	6993.85	10488.32
VIII cluster								3062.49	5144.43	6186.15
IX cluster									4245.36	6846.17
X cluster										4764.55

Table 4. Cluster means of quality traits and their contribution to total divergence

Clusters	Hulling (%)	Milling(%)	HRR (%)	KL mm)	KB (mm)	L/B	1000 grain wt (g)	VER	WU (ml)	KLAC (mm)	ER	ASV	AC (%)	GC(mm)
I	78.41	65.33	37.66	5.59	2.19	2.55	23.43	5.00	180.10	9.80	1.76	5.30	25.51	45.84
II	74.78	64.66	51.07	5.062	1.89	2.68	20.09	4.89	127.16	9.41	1.86	5.55	22.12	30.88
III	77.20	59.68	35.23	5.642	2.29	2.46	28.69	4.96	169.93	9.89	1.75	5.60	26.92	54.06
IV	77.01	64.88	40.87	6.374	1.76	3.63	22.96	4.90	156.88	12.63	1.98	5.38	19.53	37.00
V	69.50	58.93	40.76	6.82	1.64	4.15	21.79	4.73	286.00	12.13	1.77	6.66	23.77	27.33
VI	76.88	69.53	67.98	3.86	2.17	1.83	20.02	5.13	133.50	7.60	1.97	4.50	21.78	49.00
VII	79.73	71.24	67.99	5.34	2.13	2.52	28.69	5.95	289.69	9.63	1.81	4.89	22.39	62.56
VIII	79.30	69.86	49.07	6.18	2.16	2.88	24.74	5.05	208.17	10.29	1.66	5.11	24.26	28.62
IX	79.62	70.69	57.89	6.312	2.07	3.05	25.34	4.87	175.58	10.38	1.64	4.66	24.14	60.08
X	78.90	67.30	41.00	6.457	2.06	3.15	24.58	4.76	172.63	11.94	1.85	5.30	24.76	51.08
Mean	78.50	67.93	49.21	5.878	2.09	2.84	23.81	4.93	167.03	10.37	1.77	5.12	23.79	51.08
Contribution (%)	5.10	8.20	10.10	1.59	0.01	3.41	12.60	0.39	2.50	2.10	0.30	8.10	25.20	20.40