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Full Length Research Paper

Genetic diversity studies for quantitative traits of tomato (*Solanum lycopersicon* L.) genotypes in Western Tigray, Northern Ethiopia

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The objective of the study was to estimate genetic diversity among tomato genotypes. Thirty-six genotypes introduced from different countries were evaluated at Humera Agricultural Research Center, Northern Ethiopia, during 2010/2011 in 6 × 6 simple lattice design with two replications. Cluster analysis was made by average linkage method. Mahalanobis distance (D^2) was used to estimate the genetic distance between pair of clusters. Estimates of cluster analysis revealed that the thirty-six genotypes were grouped in to six distinct clusters. Genetic distance between any pair of clusters showed very highly significant difference. The maximum and minimum distances were recorded between clusters IV and V (1805.00) and cluster II and III (81.94) respectively. This indicated the existence of a possibility to improve genotypes through hybridization from any pair of clusters and subsequent selection can be made from the segregant generations. Principal component analysis showed that the first six principal components explained about 83.03% of the total variation. Generally, the study confirmed presence of adequate genetic diversity between any pair of clusters which could be exploited through hybridization.

Key words: Cluster analysis, Mahalanobis distance, principal component analysis, eigenvalue, eigenvector.

INTRODUCTION

Tomato (*Solanum lycopersicon* L.) belongs to the large and diverse *Solanaceae* family also called Nightshades which includes more than three thousand species. Among them, major crops arose from old world (Eggplant from Asia) and new world (pepper, potato, tobacco, tomato from South America) (Guillaume and Mathilde, 2012). All related wild species of tomato are native to the Andean region that includes parts of Chile, Ecuador, Bolivia and Peru (Sims, 1980). The most likely ancestor is the wild *Lycopersicon esculentum* var. *cerasiforme* (cherry tomato), which is indigenous throughout the tropical America. Tomatoes were domesticated in America;

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however, the original site of domestication and the early events of domestication are largely obscure (Peralta and Spooner, 2007). Although definite proof for the time and place of domestication is lacking, Mexico is presumed to be the most probable region of domestication, with Peru as the center of diversity for wild relatives (Larry and Joanne, 2007). It is a diploid species with 2n = 2x = 24 chromosomes.

Tomato is an important vegetable crop in the world. In Ethiopia the crop is cultivated by small scale farmers under irrigation and rain fed condition and large scale commercial vegetable growers. In Tigray region, were the study is conducted, the crop is cultivated mainly by small scale farmers and some investors in southern and western part of the region. The western low land of Tigray has vast plain arable land suitable for production of vegetables fruits and field crops both under rain fed and irrigation condition.

Tomato is one of the commercial vegetable grown by many farmers in Western Tigray. The crop is produced by 655 small holder farmers in the zone (CSA, 2009). However, cultivation of the crop is constrained by many factors in the whole country and the region. According to Lemma (2002) the major production constraints are shortage of varieties, unknown sources of seeds, disease and insect pests and high post-harvest loses. This showed that developing or introducing high yielding genotypes with desirable fruit characteristics should be primary task.

Information on the extent of genetic diversity among genotypes is very important in crosses between groups with maximum genetic divergence that would be more responsive for improvement since they are likely to produce desirable recombination and segregation in their progenies after hybridization (Norden, 1980; Reddy, 1988). To have this type of knowledge, research on genetic diversity is very essential. So far a number of research activities have been conducted by different research institutions and researchers in Ethiopia. Since 1969, about 300 tomato lines/cultivars of both short and tall set open-pollinated genotypes and hybrids have been introduced by Melkassa Agricultural Research Centre (MARC) from international seed companies, and from Asian Vegetable Research and Development Center (AVRDC). The lines have been tested at different research centers to identify lines having high fruit yield and good quality, resistance/ tolerance to diseases as well as insect pests (Lemma, 2002). It is because of the efforts a number of varieties released for different agro ecologies. Regarding diversity studies a number of authors' from different countries viz., Sekhar et al. (2008), Agong (2001), Naz et al. (2013) and Cebolla-Cornejo et al. (2013) studied genetic diversity in tomato genotypes. However, little information is available with respect to diversity study on tomato genotypes preserved under Ethiopian condition. Therefore, a study was conducted to estimate the genetic diversity among different tomato genotypes.

MATERIALS AND METHODS

Experimental site

The experiment was conducted at Humera Agricultural Research Center experimental site, Northern Ethioipia from July 2010 to February 2011 cropping season under irrigation condition. Humera is located 14° 06' N latitudes and 38° 31' E longitudes at an altitude of 604 m above sea level. It has chromic vertisol black in color characterized with very deep (>150 cm) clay textured. Agro-ecologically it is described as hot to warm semiarid plain sub agro-ecology (SA1-1). The maximum temperature varies from 42°C in April to 33°C in May while minimum temperature varies from 22.2°C in July to 17.5°C in August. The area receives an average rainfall of 400 to 650 mm per year (EARO, 2002).

Experimental material

The experimental materials comprise 36 tomato genotypes introduced from Asian Vegetable Research and Development (AVRDC), Israel, Italy, United States of America (USA), and France (Table 1). Seedlings of each genotype were raised in nursery in August and transplanted in the main field in September.

Experimental design and management

The trial was laid out in 6 x 6 simple lattice design in two replication. Seedlings of each genotype were raised in nursery in August 2010 and transplanted to the main field in September 2010. Each genotypes were planted in the main field in a plot size of 20.4 m^2 (4 rows, 5.1 m row length, 100 cm meter between rows and 30 cm between plants spacing). 200 kg ha^{-1} Di-ammonium Phosphate DAP and 100 kg ha^{-1} Urea were applied at time of planting and two weeks after transplanting as of recommended for the crop (Lemma, 2002). All agronomic practices were applied as per recommendation for the crop. The middle two rows were used for data collection leaving the two rows as borders.

Data collected

Ten plants were randomly sampled from the central two rows of each plot to measure growth parameters, fruit yield components and fruit characteristics data. At plant height (cm), primary and secondary branches, number of flowers per plant, average number of fruit clusters per plant, average number of fruits per cluster, average number of fruits per plant, fruit set percentage, weight of fruit per plant (kg $plant^{-1}$), single fruit weight (g), fruit polar diameter (mm), equatorial diameter (mm), fruit shape index, number of locules per fruit, pericarp thickness (mm), number of seeds per fruit and total soluble solids (TSS) (°Brix) were recorded from 10 plants selected. Measurements such as days to 50% flowering, days to 50% fruiting, days to maturity, number of pickings, marketable and unmarketable fruit yield (t ha^{-1}), average total yield per hectare (t ha^{-1}) were taken on plot basis.

Data analysis

Analysis of variance (ANOVA) was made using SAS version 9.2 (SAS Institute, 2008) after testing the ANOVA assumptions. Clustering of genotypes into different groups was carried out by

Table 1. List of experimental materials.

S/No.	Genotypes	Source	Growth habit
1	Fetan	Italy	Determinate
2	CLN-5915-206-D4-2-2-0	AVRDC	Indeterminate
3	Beaf steak	NA	Determinate
4	CLN-2037 H	AVRDC	Indeterminate
5	CLN-2366 C	AVRDC	Indeterminate
6	Chali	Italy	Determinate
7	CLN-2498 A	AVRDC	Determinate
8	CLN-2037 C	AVRDC	Indeterminate
9	Miya	Italy	Semi-determinate
10	Roma VF	France	Determinate
11	CLN-2037 A	AVRDC	Indeterminate
12	PT-4719 B	AVRDC	Determinate
13	Fire ball	Italy	Determinate
14	Supper Roma VF	NA	Determinate
15	CLN-2037 E	AVRDC	Indeterminate
16	Bishola	France	Determinate
17	CLN-2037 I	AVRDC	Indeterminate
18	Tomato1358/95	Hazera Seed Company	Indeterminate
19	CLN-1621 F	AVRDC	Determinate
20	Eshet	Italy	Determinate
21	Marglobe	USA	Determinate
22	CLN-5915-93-D4	AVRDC	Determinate
23	CLN-5915-206-D4-2-5-0	AVRDC	Indeterminate
24	Metadel	Guadaloupe	Semi-determinate
25	ARP-Tomato No.367-2	AVRDC	Determinate
26	Cathrine	Hazera Seed Company	Indeterminate
27	Tomato1365/95	Hazera Seed Company	Determinate
28	Electra	Hazera Seed Company	Indeterminate
29	CLN-1314 G	AVRDC	Determinate
30	H-1350	NA	Determinate
31	Cochoro	NA	Determinate
32	CLN-2366 A	AVRDC	Indeterminate
33	Melka-Salsa	Italy	Determinate
34	CLN-2366 B	AVRDC	Indeterminate
35	CLN-2070 A	AVRDC	Indeterminate
36	Melka-Shola	Italy	Semi-determinate

AVRDC: Asian Vegetable Research and Development, USA: United States of America, NA: information not available.

average linkage method and the appropriate numbers of clusters were determined from the values of pseudo F and pseudo t^2 statistics using the procedures of SAS (SAS Institute, 2008) computer software facilities so as to group sets of genotypes into homogeneous clusters. The distance between clusters were assessed by the so called Mahalanobis distance (D^2) such that the values calculated between pairs of clusters were considered as Chi-square values and tested for significance using P-1 degrees of freedom, where 'P' is the number of characters used in the study (Singh and Chaudhary, 1985).

Principal components analysis was performed using correlation matrix by employing PAST software of version 2.02 (Hammer et al., 2001) in order to evaluate the relationships among characters that are correlated among each other by converting into uncorrelated characters called principal components. The contribution of each character in Principal Component Analysis (PCA) is determined by eigenvector that is greater than half divided by the square root of the standard deviation of the eigenvalue of the respective PCA as suggested by Johnson and Wichern (1988). Principal components (PCs) with eigenvalue > 1.0 were used as criteria to determine the number of PCs (Kaiser, 1960).

RESULTS AND DISCUSSION

Mean square values of ANOVA of 24 quantitative characters for the thirty-six tomato genotypes showed

Table 2. Analysis of variance for 24 characters of tomato genotypes.

Source of variation	Mean square		R^2
	Treatments unadjusted	Treatments adjusted	
Degree of freedom	35	35	
Days to 50% flowering	79.95	74.63**	92.19
Days to 50% fruiting	702.73	647.23**	97.42
Days to maturity	1465.06	1402.28**	98.10
Plant height	961.75	823.84**	95.27
No of primary branches	3.29	3.19**	80.82
No of secondary branches	2.63	2.42**	97.04
No of flowers per plant	2343.49	1980.03**	95.59
No of fruit clusters per plant	44.30	43.59**	96.07
Number of fruits per fruit cluster	0.86	0.78**	92.75
No of matured fruits per plant	957.71	903.04**	99.28
Fruit set percentage (%)	835.02	787.75**	98.41
Weight of fruits per plant (kg)	0.46	0.42**	95.71
Single fruit weight per plant (g)	1248.07	1112.25**	96.14
No of pickings	2.02	1.97**	92.37
Fruit polar diameter (mm)	135.61	132.33**	96.65
Fruit equatorial diameter (mm)	89.69	86.23**	94.29
Shape index	0.14	0.14**	95.86
Number of seeds per fruit	1221.45	1032.03**	99.12
Number of locules per fruit	2.04	1.69**	97.87
Perricarp thickness (mm)	3.00	2.63**	91.70
Total soluble solids (^{0} Brix)	0.85	0.74**	98.56
Marketable yield (t ha^{-1})	243.17	223.08**	97.97
Un-marketable yield (t ha^{-1})	2.35	2.215**	99.43
Total yield (t ha^{-1})	281.38	258.55**	98.23

**, Significance at 1% probability level, R^2: coefficient of determination.

highly significant difference (*P< 0.01*) for all the characters studied (Table 2). This is in agreement with the findings of Mohanty (2003) who reported significant differences for all characters studied (plant height, number of branches per plant, days to first harvest, fruits per plant, average fruit weight and yield per hectare). Similarly Pradeepkumar et al. (2001) and Golani et al. (2007) obtained highly significant difference for all characters studied among the test tomato genotypes. All the traits had more than 80% estimate of coefficient of determination (R^2), showed adequacy of the model in explaining the variation.

Cluster analysis

The dendrogram obtained from the cluster analysis grouped the thirty-six tomato genotypes into six clusters (Figure 1) based on the value of pseudo F and pseudo t-square results obtained from SAS. Clusters II was the largest cluster (55.56%) containing 20 genotypes together followed by Cluster I (19.44%) containing seven genotypes, Cluster III (11.11%) comprises four genotypes, clusters IV and V (5.56%) each containing two genotypes and Cluster VI (2.78%) containing one genotype (Table 3). Genotypes in cluster III had the highest fruit yield per hectare than any other clusters. In line with this, Yashavantakumar et al. (2009) grouped 70 tomato genotypes in to seven clusters. Similarly, Shashikanth et al. (2010) clustered 30 tomato genotypes in to 10 clusters using Mahalanobis distance. Ghosh et al. (2009) also reported that 40 segregating hybrids of tomato were grouped in to 6 distant clusters. Nala et al. (2014) also employed Mahalanobis distance (D^2) to classify 27 tomato genotypes in to 9 clusters.

Cluster mean analysis

The mean value of the quantitative characters in each cluster is presented in Table 4. Cluster I consisted of seven genotypes having the characteristic of late flowering (46 days), fruiting (101 days) and maturity (151 days) than remaining clusters. It had relatively moderate

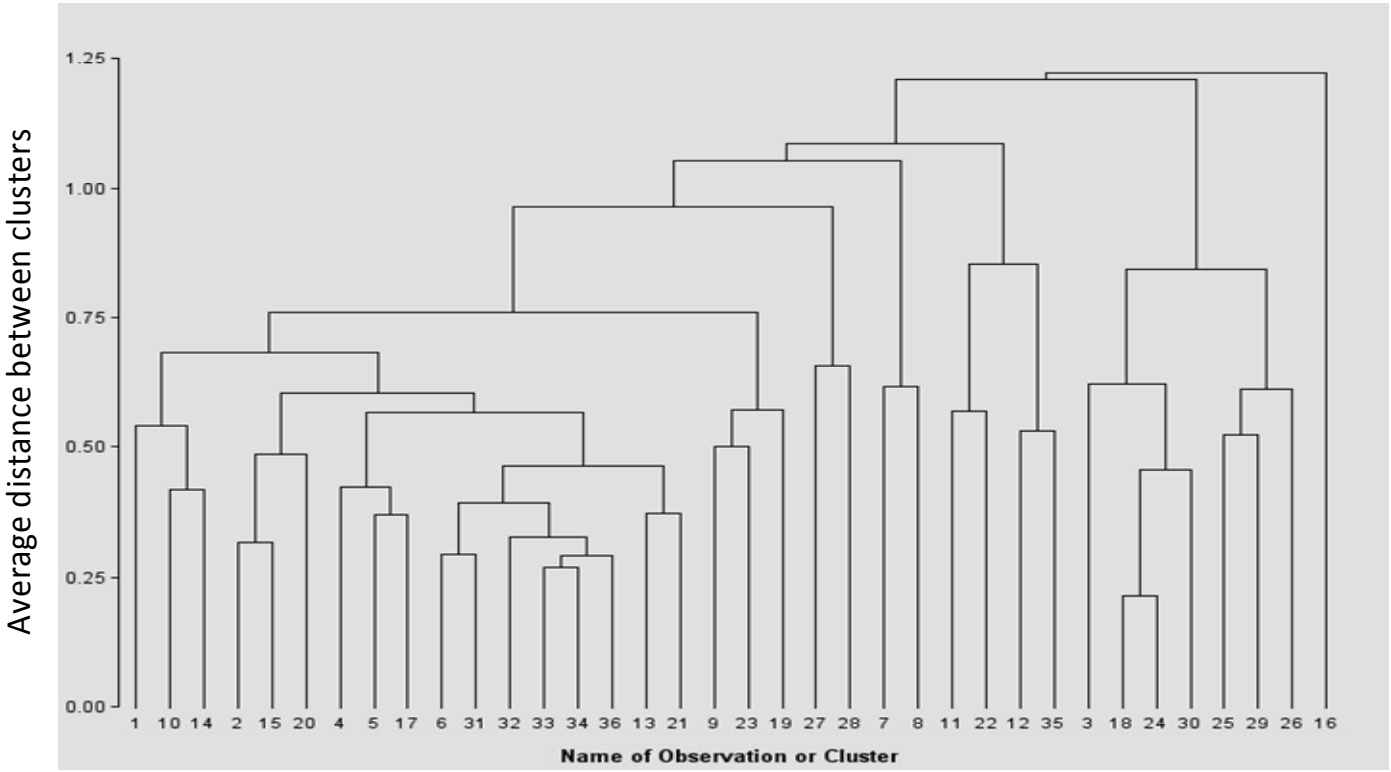

Figure 1. Dendrogram of 36 genotypes of tomato based on evaluation for 24 quantitative traits.

Table 3. Distribution of 36 tomato genotypes in to different cluster groups.

Cluster	No. of genotypes	Name of genotypes
Cluster I	7	Tomato 1358/95, Metadel, H-1350, ARP Tomato No 367-2, CLN-13114-G, Cathrine and Beaf steak
Cluster II	20	Melka-Salsa, CLN-2366-B, Melka-Shola, Chali, Cochora, 5915-206-d4-2-2-0, CLN-2037-E, CLN-2366-A, CLN-2366-C, CLN-2037-I, Fire ball, Marglobe, Roma-VF, Supper Roma-VF, CLN-2037-H, Eshet, Miya, 5915-206-d4-2-5-0, Fetan and CLN-1621-F
Cluster III	4	PT-4719B, CLN-2070-A, CLN-2037-A and CLN 5915-93-D4
Cluster IV	2	CLN-2498 and CLN-2037-C
Cluster V	2	Tomato 1365/95 and Electra
Cluster VI	1	Bishola

height (90.94 cm), number of primary and secondary branches per plant (6.3 and 3.4) and average single fruit weight (57.05 g). On the contrary cluster I had the least number of flowers per plant (61 flowers), number of fruit clusters per plant (2.4), number of matured fruits per plant (6.1), number of pickings (2.6) and average weight of fruits per plant (0.390 kg) as compared to the rest of clusters. As a result of less score from the yield contributing characters it had less total fruit yield per hectare (4.38 t ha^{-1}). Fruit characteristics data of cluster I showed moderate fruit length and width (40.8 and 38.9 mm) with shape index of (1.07) implies almost round shape. It had also thinner pericarp thickness (3.73 mm) than other clusters.

Cluster II consist majority of the test genotypes (55.65%) having the characteristic of moderate maturity period (94 days) as compared to cluster I and IV. Majority of the genotypes in this cluster showed moderate performance in most of the fruit yield and yield related traits as compared to Clusters I, IV and VI that is, moderate number of flowers per plant (108) with relatively moderate number of matured fruits per plant (28.1). It had relatively medium single fruit weight (50.58 g), moderate fruit weight per plant (0.920 kg), relatively many times of pickings (4.50) next to Cluster III, moderate total fruit yield per hectare (19.51 t ha^{-1}) as compared to Clusters I, IV and VI. It also showed relatively highest value of shape index (1.22) next to Cluster IV (1.27) implied the fruit was

Table 4. Cluster-wise mean values of characters in the studied tomato genotypes.

Character	Cluster					
	I	II	III	IV	V	VI
Days to 50 % flowering	46**	38	31*	38	36	42
Days to 50 % fruiting	101**	71	46*	84	65	93
Days to maturity	151**	94	76*	106	87	112
Plant height (cm)	90.94	87.66*	91.71	120.5**	89.44	101.82
Number of primary branches	6.33	6.21*	6.53	8.03**	6.42	6.70
Number of secondary branches	3.37*	3.53	4.22	4.23	3.47	6.30**
Number of flowers per plant	61*	108	116	185**	83	119
Number of fruit clusters per plant	2.44*	8.25	14.31**	3.72	13.92	4.86
Number of fruits per fruit cluster	1.34	1.62	2.80**	1.07*	1.26	1.89
Number of matured fruits per plant	6*	28	76**	19	20	10
Fruit set percentage (%)	11.33	28.33	65.66**	10.12	24.73	8.54*
Weight of fruits per plant (kg)	0.39*	0.92	1.52**	0.68	1.36	0.59
Single fruit weight per plant (g)	57.05	50.58	33.41*	51.65	90.98	146.5**
No of pickings	2.64*	4.50	5.25**	4.25	4.25	3.00
Fruit polar diameter (mm)	40.8	48.2	37.3*	49.7	51.1**	41.1
Fruit equatorial diameter (mm)	38.9	40.4	37.8*	40.4	53.2**	50.7
Shape index	1.07	1.22	0.99	1.27**	1.02	0.81*
Number of seeds per fruit	44.1	38.5*	74.5	48.6	102.0**	44.0
Number of locules per fruit	3.31	3.17	3.60	2.80*	5.65**	2.90
Perricarp thickness (mm)	3.73**	5.05	4.10	4.99	5.45**	4.81
Total soluble solids (^{0} Brix)	5.10	5.06	5.83**	5.08	5.55	4.93*
Marketable fruit yield (t ha^{-1})	3.89*	17.64	34.35**	10.93	20.25	5.58
Un-marketable fruit yield (t ha^{-1})	0.50*	1.86	2.01	1.22	3.07**	0.60
Total fruit yield (t ha^{-1})	4.38*	19.51	36.36**	12.14	23.32	6.19

* , ** indicate the smallest and highest mean value of the character.

cylinder or pear shaped. It also had relatively thick pericarp thickness (5.05 mm) next to Cluster V (5.45) and less TSS content (5.05 °Brix) next to Cluster VI (4.93 °Brix). This cluster consists of the third high yielding genotype, Miya.

Cluster III, which comprised the highest yield bearing genotypes, contained four genotypes characterized by the earliest genotypes in days to 50% flowering, 50% fruiting and maturity (31, 46 and 76 days respectively). Moreover, they had the highest number of fruit clusters per plant (14.3), number of fruits per fruit cluster (2.8), number of matured fruits per plant (76), fruit set percentage (65.66 %), average weight of fruits per plant (1.520 kg), number of pickings (5.3), total fruit yield per hectare (36.36 t ha^{-1}) and TSS (5.83 °Brix). On the contrary it had the least average single fruit weight per plant (33.41 g), fruit length and width (37.3 and 37.8 mm) with shape index of (0.99), plant height (87.96 cm). It had also high number of primary and secondary branches (6.5 and 4.2) next to cluster IV (8.0 and 4.2) and number of flowers per plant (116) next to Cluster IV (185).

Cluster IV comprises four genotypes having characteristics of moderate maturity period (106 days) as compared to cluster I (151 days). The genotypes in this cluster had the highest number of flowers per plant (185 days), longest plant height (120.5 cm), relatively few matured fruits per plant (19) as compared to Cluster III (76), least fruit set percentage (10.12%) next to Cluster (VI), low fruit yield per hectare (12.14 t ha^{-1}) next to Cluster IV and I, relatively long fruit length and moderate width (49.7 and 40.4 mm) with the highest fruit shape index (1.27) indicated the fruit had cylinder or pear shape. It also had least number of locules (2.90) among other clusters. Cluster V contained two genotypes having a property of early flowering, fruiting and maturity period (38, 64 and 87 days respectively) next to Cluster III. It showed high fruit yield per plant (1.26 kg) next to Cluster III, high average single fruit weight (90.98 g) next to Cluster VI, relatively moderate fruit yield per hectare (23.32 t ha^{-1}) as compared to Cluster II, IV,VI and I. Similarly it had the longest fruit length and width (51.1 and 53.2 mm) with shape index of (1.02) that is, almost round shape, highest seed per fruit (102) and relatively high TSS (5.55 °Brix) as compared to cluster III (5.83 °Brix).

Cluster VI which contained single genotypes had a characteristics of relatively late matured (112 days) as compared to Clusters II, III, IV and V. This genotype also

Table 5. Mahalanobis distance between groups of tomato genotypes.

Cluster	I	II	III	IV	V	VI
I	___	132.44***	269.91***	480.45***	1102.00***	806.10***
II		___	81.94***	323.76***	756.56***	505.87***
III			___	403.10***	808.72***	525.17***
IV				___	1805.00***	787.94***
V					___	684.56***
VI						___

χ^2=48.27 at 0.1% probability level; ***, indicate very highly significant at 0.1% probability level.

had highest single fruit weight (146.5 g), least number of harvesting (3 times) next to Cluster I, less total yield per hectare (6.19 t ha^{-1}) next to Cluster I, moderate fruit length and larger fruit width (41.1 and 50.6 mm) with the least fruit shape index (0.81) implied the fruit had flattened shape. It also had the least TSS content (4.93 ºBrix) as compared to the rest of clusters.

Estimation of inter cluster square distances (D^2)

The Chi-square (χ^2- test) for the six clusters indicated that there was a very highly significant difference among the clusters (Table 5). The highest inter-cluster distance were exhibited between cluster IV and V (D^2 = 1805.00), followed by Cluster I and V (D^2 = 1102), Cluster III and V (D^2 = 808.72) and Cluster I and IV (D^2 = 806.10) which implied these clusters were genetically more divergent from each other than any other pairs of cluster. Cluster II and III showed the least inter cluster distance (81.94) compared to other pair of clusters.

Increasing parental distance implies a great number of contrasting alleles at the desired loci, and then to the extent that these loci recombine in the F_2 and F_3 generation following a cross of distantly related parents, the greater will be the opportunities for the effective selection for yield factors (Ghaderi et al., 1984). Generally, divergence analysis showed presence of high genetic divergence among the tested tomato genotypes evaluated at Humera. Hence, hybridization of these genetically divergent parents could lead to the development of desirable recombinants and transgressive segregants, that in turn, may lead to the development of better performing varieties. Therefore, maximum recombination and segregation of the progenies is expected from crosses involving parents selected from Cluster IV, I or III with parents selected from genotypes in Cluster V as compared to others, however the breeder must specify his/her objectives in order to make best use of the characters where the traits are divergent.

Principal component analysis

The principal component analysis (Table 6) revealed that six principal components PC_1, PC_2, PC_3, PC_4, PC_5 and PC_6 with eigenvalues 8.915, 3.309, 3.104, 2.012, 1.430 and 1.330 respectively, have accounted for 83.03% of the total variation. The first two principal components PC_1 and PC_2 with a proportion of 37.14 and 13.79%, respectively, contributed more to the total variation. According to Chahal and Gosal (2002), characters with largest absolute values closer to unity with in the first principal component influence the clustering more than those with lower absolute values closer to zero. Therefore, in this study, differentiation of the genotypes into different cluster was because of a cumulative effect of a number of characters rather than the contribution of specific few characters. Characters having relatively higher value in the first principal component (PC_1) were total fruit yield ha^{-1}, marketable yield ha^{-1}, days to 50% fruiting, average weight of fruit per plant, number of matured fruits per plant, number of picking, days to maturity, number of fruit clusters per plant and fruit set percentage had more contribution to the total diversity and they were responsible for the differentiation of the six clusters. The second principal component, which accounted 13.79% of the total variation contributed from pericarp thickness, fruit polar diameter, number of primary branches per plant, number of secondary branches per plant, fruit equatorial diameter and single fruit weight per plant. Characters like fruit shape index, number of locules per fruit, fruit equatorial diameter and average single fruit weight were the characters which contributed to the third principal component (PC_3). Similarly number of seeds per fruit, number of flowers per plant, plant height, TSS and number of primary branches were the characters contributed to the fourth cluster (PC_4). Fifth Principal component (PC_5) contributed from characters number of seeds per fruit, number of flowers per plant and number of matured fruits per plant. The sixth principal component (PC_6) contributed from plant height, number of secondary branches, number of fruits per fruit cluster, number of locules per fruit and unmarketable yield per hectare. In line with the present finding, Agong (2001) employed PCA for detecting variation in 35 tomato germplasm in which the first three PCs were adequate in determining more than 70% of total variation. Similarly Ghosh et al. (2009) reported that the first two principal components accounted for 60% of the total variation among 22

Table 6. Eigenvectors and eigenvalues of the first six principal components (PCs).

Characters	Eigenvectors					
	PC_1	PC_2	PC_3	PC_4	PC_5	PC_6
Days to 50% flowering	-0.244	-0.084	0.123	-0.118	0.191	0.219
Days to 50% fruiting	-0.310	0.021	0.080	-0.046	0.134	0.052
Days to maturity	-0.285	-0.037	0.092	-0.074	0.129	-0.107
Plant height (cm)	-0.035	-0.049	0.166	0.385	0.093	0.507
Number of primary branches	-0.028	0.358	0.107	0.354	0.196	-0.128
Number of secondary branches	0.003	0.316	0.135	0.146	0.353	-0.422
Number of flowers per plant	0.090	0.249	-0.150	0.401	0.270	0.176
Number of fruit clusters per plant	0.281	0.008	0.003	0.005	-0.172	-0.104
Number of fruits per fruit cluster	0.219	-0.106	-0.030	0.016	0.065	-0.319
Number of matured fruits per plant	0.298	-0.128	-0.020	0.044	0.215	-0.105
Fruit set percentage (%)	0.277	-0.181	0.021	-0.112	0.124	-0.064
Weight of fruits per plant (Kg)	0.299	0.022	0.120	-0.062	0.057	0.083
Single fruit weight per plant (g)	-0.053	0.315	0.322	-0.191	-0.083	-0.090
Number of pickings	0.294	0.038	-0.097	0.009	-0.057	0.175
Fruit polar diameter (mm)	0.011	0.405	-0.284	-0.011	-0.177	0.196
Fruit equatorial diameter (mm)	0.063	0.295	0.398	-0.159	-0.168	0.029
Shape index	-0.034	0.141	-0.485	0.095	-0.056	0.142
Number of seeds per fruit	0.071	0.058	0.219	0.403	-0.277	-0.129
Number of locules per fruit	0.065	0.006	0.437	0.004	-0.113	0.284
Perricarp thickness (mm)	0.083	0.436	-0.134	-0.192	-0.069	-0.067
Total soluble solids (^{0} Brix)	0.074	-0.216	0.139	0.373	0.001	-0.053
Marketable fruit yield (t ha^{-1})	0.314	-0.019	0.021	-0.069	0.159	0.051
Un-marketable fruit yield (t ha^{-1})	0.241	0.138	0.088	-0.166	-0.049	0.281
Total fruit yield (t ha^{-1})	0.314	-0.005	0.028	-0.079	0.143	0.073
Eigenvalue	8.915	3.309	3.104	2.012	1.430	1.133
Proportion	37.143	13.786	12.932	8.385	5.959	4.721
Cumulative	37.143	50.929	63.961	72.346	78.305	83.026

characters describing 40 segregating populations of tomato hybrids. Merk et al. (2012) also found that the first three principal component explained 57.1% of the total variation for 143 processing tomato lines evaluated in North America.

Conclusion

The dendrogram obtained from the cluster analysis grouped the thirty-six tomato genotypes into six clusters. Chi-square (χ^2- test) demonstrated a very highly significant difference among the six clusters. This showed the possibility to improve genotypes through hybridization from any pair of clusters. Maximum recombination and segregation of progenies is expected from crosses involving parents selected from Cluster IV, I or III with parents selected from genotypes in Cluster V as compared to others, however the breeder must specify his/her objectives in order to make best use of the characters where the traits are divergent.

Conflict of Interest

The authors have not declared any conflict of interest.

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Full Length Research Paper

Efficient propagation of an endangered medicinal plant *Jurinea dolomiaea* Boiss in the North Western Himalaya using rhizome cuttings under *ex situ* conditions

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Jurinea dolomiaea **is an important medicinal and aromatic plant species of Kashmir Himalaya. Due to its tremendous overexploitation the species has been listed as endangered for Himalayan region. In this study we carried out the propagation of *J. dolomiaea* using rhizome cuttings. Propagation through rhizome cuttings is a means towards conserving the species and making available planting material of this species for cultivation. Bringing more species under large-scale cultivation helps reduce the pressure on the wild stocks. We investigated the sprouting ability and percentage survival of rhizome cuttings under *ex situ* conditions including soil textures, moisture contents and different concentrations of Indole acetic acid (IAA), Indole butyric acid (IBA) and Gibberellic acid (GA_3) treatments. A better rooting response ($p \leq 0.05$) was observed with GA_3 25 ppm treatment when compared to zero hormone soaked.**

Key words: Rhizome cuttings, field capacity, Indole acetic acid (IAA), Indole butyric acid (IBA) and Gibberellic acid (GA_3), vegetative propagation.

INTRODUCTION

Jurinea dolomiaea Boiss., commonly known in Kashmir as dhup, of family Asteraceae was selected for present study. It is endemic to Himalaya and is distributed from Pakistan to East Nepal between 3000 and 4300 m in open slopes (Chauhan, 1999). It is an important medicinal and aromatic herb of North Western Himalaya and is being exploited because of its medicinal values. A decoction of the roots is cordial. It is given in the treatment of colic and puerperal fever. The juice of the roots is used in the treatment of fevers, diarrhoea and stomachache. The crushed root is applied as a poultice to eruptions (Chopra et al., 1956). The root extract is used as incense (Manandhar, 2002). In India, *J. dolomiaea* has been used as aphrodisiac (Sekar and Srivastava, 2005). In Jammu and Kashmir, the plant is used for treatment of eye infection and it aromatic oil

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from roots is useful in gout and rheumatism (Kumar et al., 2009). Due to its tremendous overexploitation, the species has been listed as endangered for Himalayan region (IUCN, 2003; Pant and Pant, 2011; Siwach et al., 2013).

Vegetative propagation is one of the potential and useful means of propagating those species which are economically important and difficult to raise through seeds. Plant propagation through vegetative means multiplies these plants and preserves their essential genetic characters. This is an easy and effective technique for multiplication and conservation of plant species. Sexual reproduction is considered less important than vegetative propagation for arctic and alpine species (Bliss, 1971). Further, one of the most appropriate actions for safeguarding over exploited species is to improve propagation techniques and to encourage cultivation. The mode of regeneration of *J. dolomiaea* in nature is by seed as well as by rhizome. Any improvement in seed germination and vegetative multiplication can substantially help in propagation. The present study was carried out to develop an efficient method of propagation using rhizome cuttings so as to facilitate mass multiplication and conservation of species under *ex situ* conditions.

MATERIALS AND METHODS

Plant material

Rhizome section is the best planting material for cultivation other than seed because the planting material raised by the seeds takes more time for crop maturity as well as production (Nautiyal and Nautiyal, 2004; Anonymous, 2008). In this context, rhizomes were used for carrying out the mass propagation of *J. dolomiaea*. In the first week of June, rhizomes were collected from natural habitat Apharwat: an alpine zone (3378 m asl) located between 34°01'N Lat. and 74°21'E Long, in Kashmir Himalaya, India.

Effect of soil texture and field capacity on vegetative propagation

Before the collection of plant material the field capacity of different soil textures was determined using Buckner's funnel. Different planting trays were prepared by putting weighed amount of soil and sand in it as per the selected combination. Depending upon the size of parental rhizome, each rhizome was splitted longitudinally into a number of pieces but care was taken to ensure that each piece contains a portion of shoot apex. These cuttings were sown in the prepared plastic trays. In each case, three replicates with four cuttings each were used. Different moisture levels were ensured by adding the measured quantity of water as per the field capacity of each soil texture. The experiment was carried out under controlled conditions in green house of Kashmir University Botanical Garden (KUBG). Total sprouting was recorded at the culmination of the experiment in respect of all the treatments.

Effect of growth hormones on vegetative propagation

The rhizomes were washed thoroughly with running tap water so as to remove soil particles. Each rhizome was cut longitudinally, with a sterilized razor blade, into 2, 4, or 8 pieces, according to the size of the parental rhizome. The split rhizome cuttings were treated with different hormonal concentrations by placing them in sterilized petri-plates containing 25, 50, and 100 ppm concentrations of IAA, IBA and GA_3. One set in each case was treated with distilled water to treat as control. The hormone solutions were made using deionized water and analytical grade chemicals. In each treatment, three replicates with four cuttings each were used. After 48 h of treatment control and segments treated with the plant growth regulators (PGRs) were planted in earthen pots containing sandy loam soil in Kashmir University Botanical Garden (KUBG). The pots were irrigated and monitored regularly throughout the course of experiment. Days taken for first sprouting, percentage sprouting and rooting were recorded for each treatment.

Statistical analysis

The data was analysed statistically using MS-Excel 2007. Data was analysed for Mean and Standard Deviation. The analysis of variance (ANOVA) procedures were used to test for significant effect of treatments, followed by Duncan's Multiple Range Test (DMRT) for comparisons of different means of different treatments.

RESULTS

Effect of soil texture and field capacity on vegetative propagation

Sprouting percentage of rhizome cuttings of *J. dolomiaea* varied in different soil textures and moisture content of soil (Table 1). Maximum sprouting of 80.5±4.2% was recorded in soil texture having sand : soil in 1 : 1 ratio, followed by 63.8±4.8% sprouting in soil texture having sand : soil in 1 : 2 ratio (Figure 1). However, no sprouting occurred in pure sand. It was observed that irrespective of the soil texture, the rhizomes showed higher percentage of sprouting at ½ field capacity, followed by full field capacity and least when ¼ field capacity was used.

Effect of growth hormones on vegetative propagation

Effect of different hormonal treatments on the sprouting of rhizome cuttings of *J. dolomiaea* are shown in Table 2. The rhizome cuttings treated with GA_3 25 ppm took minimum days (8±1) for sprouting. Maximum shoot sprouting and percentage survival (rooting) was observed in GA_3 25 ppm (94.45±0.24% and 83.34±0.38% respectively), as compared to control treatments with 77.78±0.43% of sprouting and 44.45±0.51% of rooting. IAA 25 ppm, 50 ppm and 100 ppm treatments showed lesser percentage of sprouting and rooting than control. Among different treatments, GA_3 treatments proved to be most effective ($p \leq 0.05$) in increasing the sprouting and rooting percentage. However, IBA treatments were found to be ineffective as no shooting and rooting was observed in these treatments (Figure 2).

Table 1. Effect of soil texture and field capacity on sprouting percentage of rhizome cuttings of *J. dolomiaea*.

Soil texture	Field capacity-F.C (ml)	Percentage sprouting
Soil	Full F.C	27.7^{ae} ±9.6
	½ F.C	38.8^{ab} ±4.8
	¼ F.C	19.4^{a} ±4.8
Sand	Full F.C	0
	½ F.C	0
	¼ F.C	0
Sand : Soil 1 : 1	Full F.C	55.5^{bc} ±4.9
	½ F.C	**80.5^{d}** ±4.2
	¼ F.C	22.22^{ag} ±3.6
Sand : Soil 1 : 2	Full F.C	44.4^{beghi} ±4.8
	½ F.C	63.8^{cdfh} ±4.8
	¼ F.C	33.33^{ab} ±0
Sand : Soil 1 : 3	Full F.C	27.7^{ai} ±2.9
	½ F.C	38.8^{ab} ±4.6
	¼ F.C	0
Sand : Soil 2 : 1	Full F.C	33.33^{ab} ±5.4
	½ F.C	52.7^{bf} ±4.8
	¼ F.C	0
Sand : Soil 3 : 1	Full F.C	36.1^{ab} ±4.1
	½ F.C	0
	¼ F.C	0

*Mean values followed by the same letter are not significantly different by DMRT at $p < 0.05$. Each treatment consisted of twelve rhizome cuttings. Data was recorded after ninety days of setting the experiment.

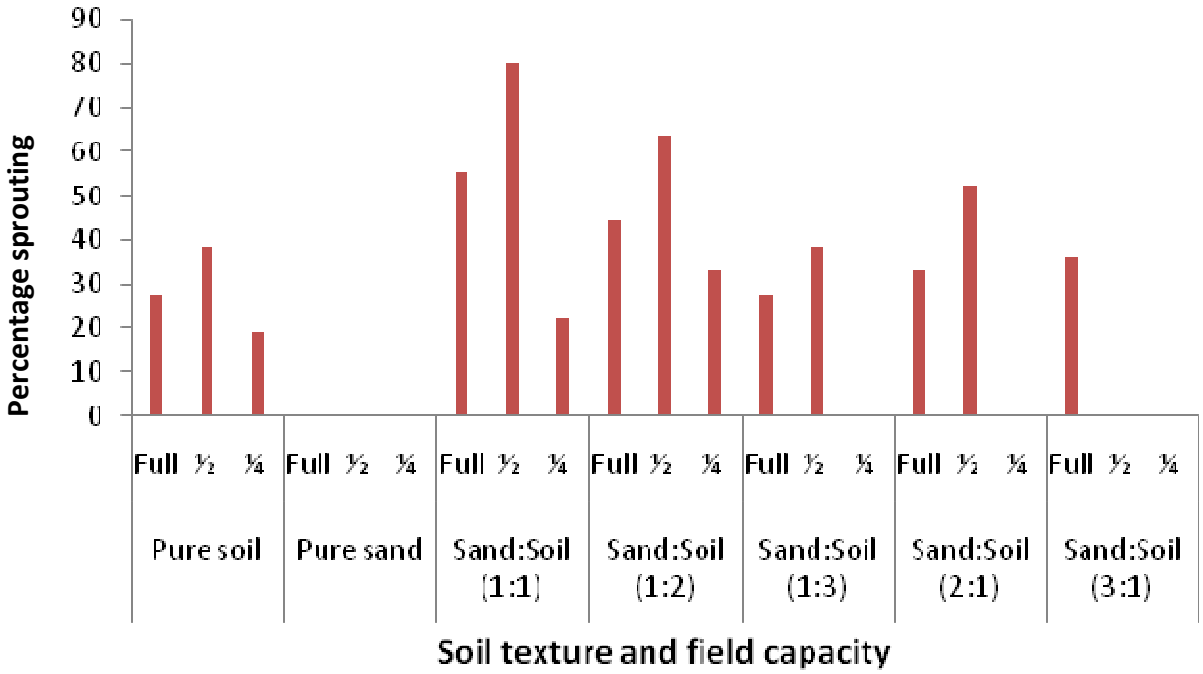

Figure 1. Effect of soil texture and moisture content on sprouting of rhizome cuttings of *J. dolomiaea*.

Table 2. Effect (Mean±S.D.) of different growth hormones on vegetative propagation of *J. dolomiaea* using rhizome segments.

S. No.	Treatments (ppm)	Days taken for first sprouting	Sprouting percentage	Rooting percentage
1	Control	10±1.73	77.78±0.43	44.45±0.51
2	IAA 25	14.6±1.15	44.45±0.51	27.78±0.46
3	IAA 50	11.3±1.52	55.56±0.51	38.89±0.50
4	IAA 100	9.6±0.57	66.67±0.49	50.00±0.51
5	IBA 25	-	-	-
6	IBA 50	-	-	-
7	IBA 100	-	-	-
8	GA_3 25	8±1	94.45±0.24	83.34±0.38
9	GA_3 50	10.6±0.57	83.34±0.38	72.73±0.46
10	GA_3 100	10.6±1.15	72.23±0.46	61.12±0.50
	p-value	0.03	0.02	0.01

*Each treatment consisted of twelve rhizome cuttings. Sprouting percentage was recorded after 30 days of planting the cuttings & rooting percentage after 100 days of setting the experiment.

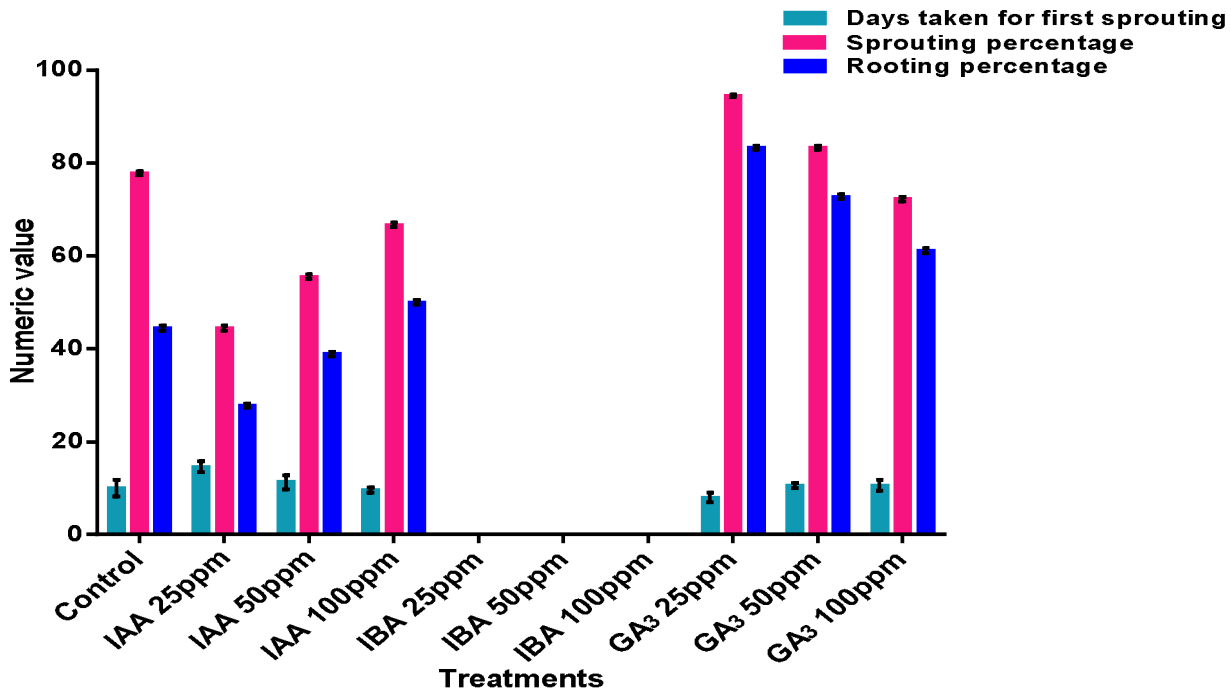

Figure 2. Effect of different growth hormones on vegetative propagation of *J. dolomiaea*.

DISCUSSION

Vegetative propagation can be used as an efficient tool for mass scale propagation of tuberous roots of medicinally important species as in case of *Aconitum atrox*, the species fails to establish through seeds under natural conditions in an alpine environment (Kuniyal, 1999). In *Picrorhiza kurrooa*, vegetative propagation using stolon segments was found successful for cultivation up to 1800 m altitude with high moisture regime and proper aeration (Nautiyal et al., 2001).

The results revealed that sprouting percentage decreased with the increase in sand content and no sprouting occurred in soil texture having only sand. Furthermore, it was evident that irrespective of the soil texture the rhizomes showed higher percentage of sprouting at ½ field capacity, followed by full field capacity and least when ¼ field capacity was used. This indicates that the species prefers less moisture for its better growth and survival. For successful cultivation of *Jurinea*, deep

sandy porous soil is best as the plant develops a thick rootstock (Chauhan, 1999).

Vegetative propagation through splitting of roots was found successful in *Nardostachys jatamansi* and observed as better for multiplication as well as higher production within a short period than cultivation through seedlings (Nautiyal and Nautiyal, 2004). Plant growth regulators and other chemicals have been widely used in vegetative propagation to improve rooting and subsequent growth of cuttings (Nadeem et al., 2000; Butola and Badola, 2007a). The results revealed that the rhizome cuttings treated with GA_3 25 ppm took minimum days (8±1) for sprouting. Maximum shoot sprouting of 94.45% and percentage survival of 83.34% was observed in GA_3 25 ppm, as compared to control with 77.78% of sprouting and 44.45% of rooting. The results contrast with those of Butola and Badola (2007b) who reported increased percentage of rooting after IAA and IBA treatments compared to control in *Angelica glauca* and *Heracleum candicans*. Further, the results were also contrary to Shabir et al. (2010) who reported that GA_3 concentrations are less effective particularly in the induction of adventitious root development in *Inula racemosa*. Chances of survival and growth performance of vegetatively propagated individuals were better implying that a reasonable number of plantlets could be raised from a single rhizome and their survival could be ensured by treating with GA_3 25 ppm.

Conclusion

Although *J. dolomiaea* has been considered as an endangered species, large scale removal (generally during the peak flowering) of its rhizomes still continues at an increasing rate. Therefore, special attention needs to be given for its propagation and conservation; systematic cultivation would go a long way in achieving its conservation. Propagation through rhizome cuttings is a convenient and cost effective method for large scale multiplication and conservation of species. We found that longitudinal cuttings treated with GA_3 25 ppm resulted in maximum sprouting and survival of species. Further, the species showing preference for habitats with less moisture, and thus maximum survival of seedlings resulted in soil texture of sand : soil (1 : 1) at half field capacity. Thus, splitting of rhizomes is a cheap and convenient way for ensuring large scale cultivation as well as conservation of species under *ex situ* conditions.

Conflict of Interests

The author(s) have not declared any conflict of interests.

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Full Length Research Paper

Effects of yield components on yield potential of some lowland rice (*Oyza sativa* L.) in coastal region of Southern Nigeria

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The coastal region of Nigeria has abundant water naturally good for rice production, which is untapped due to oil exploration. The study was conducted to access the relationship between grain yield (GY) and its components of twenty-six segregating lines for the coastal region of Southern Nigeria. The experiment was conducted at the University of Port Harcourt teaching and Research Institution of Faculty of Agriculture and replicated three times in a complete block design. Data was collected on yield components such as number of tillers per plant, leaf area index (LAI), total GY at maturity, and grain weight per panicle at maturity. About 8 lines had more tiller number than the general mean value (30) at maximum tillering stage of the rice crop, while lines with high effective tiller numbers were IRBW-180 (49) and IRBW-147 (48). GY significantly positively correlated with effective tiller number, grain weight per plant, number of grain per panicle and grain weight per panicle. The cluster analysis for genetic diversity revealed three major groupings (A, B and C). The genotypes in Group A posses the character of high grain weight and Group B posses characters for long panicle and high value of flag LAI (FLAI), which indicates broad leaf for light interception thus enhancing photosynthesis. In Group C, genotypes posses varying characters, however, high value of LAI and tall plant, which indicates tendency of good nutrient utilization. Soil in this region is saline and effect crop performance especially rice, these identified indexes will facility the breeding for this region.

Key words: *Oryza sativa* L., yield components, yield potential, segregating lines, cluster.

INTRODUCTION

Rice is an important annual crop in Nigeria. It is one of the major staples. The crop is commonly consumed even as a food crop for household food security. The average Nigerian consumes 24.8 kg of rice per year, representing 9% of annual calorie intake (IRRI, 2001). Thus, rice has, become a strategic commodity in the Nigerian economy. The three main production ecologies for rice in Nigeria are lowland rice, upland rice and irrigated rice. Among these, lowland rice has the highest priority being the ecology that represents the largest share of rice area and rice production.

Grain yield (GY) in cereals is one of the most important

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and complex traits in plant breeding experiments. Continue improvement of GY remains the top priority in most of the breeding programmes (Yan et al., 2002). In rice, GY depends on various growth and yield component traits such as the panicle number per plant, the filled grain number per panicle, and the weight per grain (Yoshida, 1983). Breeders have paid much attention to the concept of plant ideotypes and proposed several models for high-yielding rice, such as the 'heavy-panicle' and the 'multi-panicle' types. Thus, an increase in GY could be effectively achieved through yield component improvement since yield components have higher heritability than GY (Xiong, 1992). The agronomic value of a variety depends on many characteristics (Huang et al., 1991) and the most important characteristics are high yielding ability, resistance to diseases and pests, resistance to undesirable environmental factors and high quality of the products. But, the final aim is to increase the GY of rice (Swaminathan, 1999).

Rice GY is determined by several agronomic characters such as heading days, days to maturity, grain filling period, number of productive tiller, number of fertile grain per panicle, panicle length, 1000 grain weight and plant height (Halil and Necmi, 2005). Yield is a quantitative trait, greatly influenced by environmental fluctuations. Study on yield contributing characters assumes greater importance of fixing up characters that influence yield (Prasad et al., 2001; Kole and Hasib, 2008). A statistical analysis has been used to measure the mutual relationships between various characters and yield improvement. Genotypic evaluation of yield components could assist to identify their relationships with GY.

Tillering plays an important role in determining rice GY since it is closely related to panicle number per unit ground area. Too few tillers result in too few panicles, but excess tillers caused higher tiller mortality, small panicles, poor grain filling and consequent reduction in GY (Peng et al., 1994). In rice, the manipulation of tiller number is important for GY, but the physiological basis of the regulation of tiller growth remains unclear. In general, large tillers result in higher sink: source ratio, spikelet number, proportion of filled grains, leaf area (LA) per tiller and sink capacity (Choi and Kwon, 1985).

Leaf area index (LAI) is LA per unit ground area and is an important crop biophysical parameter. High leaf index was reported by Efisue et.al. (2009) which indicated that LAI is a good selection criteria for increasing GY of rice. Thus, varieties with higher value of LAI could yield better than varieties with low LAI. Plant height is the predominant factor determining the nitrogen response of rice plant. It determines the lodging behaviour thus deciding yield. Lodging disturbs leave display resulting in shading thus increasing the percentage of unfilled grain. High heritability coupled with high genetic advancement for these traits provide enough confidence for selection of desirable genotypes (Ali et al., 2002).

The number panicle with filled grains determines the ultimate yield of the crop. Thus, effective panicles should have high ripening percentage and high grain to straw ratio (harvest index). Panicles affect yield capacity, as yield capacity is determined by the number of grain per unit area and potential size of grains (Feil, 1992). Cultivars with larger grain size tend to have higher grain filling rate, resulting in higher assimilate accumulation and heavier grain weight (Jones et al., 1979; Jeng et al., 2003). Thus, the above information leads into this study in the coastal region of Nigeria.

The coastal region of Nigeria has abundant water naturally good for rice production, which is untapped due to oil exploration. Rice breeding for this region is timely and could curb youth restiveness. This could be done by examine yield components that will enhance rice production in the region. The study of this experiment is to examine the effects of some yield components of some lowland rice on yield that will enhance rice production.

MATERIALS AND METHODS

The experimental plot was located at the University of Port Harcourt, Faculty of Agriculture Teaching and Research Farm. Geographically, Rivers State is located in southern part of Niger Delta, Nigeria. It has an average temperature of 28 to 30°C and rainfall ranging from 2000 to 2680 mm per annum. Twenty-six segregating lines at F_3 generations were used for the experiment as indicated in Table 1.

Design and planting

It was a potted experiment in randomized complete block design in three replications. Four seeds were sown per pot and thinned to two seedlings after 15 days of emergence. Planting was done by seed dibbling at seeding rate of 60 kg/ha. Irrigation was applied as at when due to maintain soil capacity. Inorganic fertilizer (NPK 15:15:15) was applied in a basal application of 200 kg ha^{-1} (N_2, P_2O_5 and K_2O) and top dressed with 65 kg ha^{-1} urea at tillering and 35 kg ha^{-1} at booting.

Data collection

Data was collected at appropriate stage of the crop development. The agronomic characters were measured at weekly intervals. The 'Standard Evaluation System (SES) for Rice' reference manual (IRRI, 1996) was used for all trait measurements except where stated otherwise. The following data was collected at the appropriate crop phenology: Data was taken from five (5) plants of each line. Plant height was measured in cm from the plant base to the tip of the highest leaf. Effective tillers of each plant were counted to determine the total number of panicles in each plant. Panicle length of the central tiller of the each plant was measured using a meter rule. Two young fully expanded leaves from the main stem were randomly selected in each pot and LA was determined using a LA meter (li-3100, Lincoln, NE USA). LAI was calculated as described by Yoshida (1981) as follows:

LAI = (sum of the LA of all leaves / unit area where the leaves have been collected).

The number of filled grains (seeds) per panicle taken from the main tiller of each plant was counted at maturity stage separately after harvesting. Grain weight per panicle for each variety was measured

Table 1. Genetic material used, source and their peculiar agronomic traits.

Genotype	Sources	Peculiar traits
IRBW-125	AGRA germplasm of Uniport	Tall plant
IRBW-54	AGRA germplasm of Uniport	Tall plant
IRBW-26	AGRA germplasm of Uniport	Short plant
IRBW-144	AGRA germplasm of Uniport	Tall plant
IRBW-156	AGRA germplasm of Uniport	Short plant
IRBW-399	AGRA germplasm of Uniport	High tillering ability
IRBW-440	AGRA germplasm of Uniport	Tall plant
IRBW-255	AGRA germplasm of Uniport	Tall plant
IRBW-148	AGRA germplasm of Uniport	Short panicle
IRBW-295	AGRA germplasm of Uniport	Short plant
IRBW-275	AGRA germplasm of Uniport	Long panicle
IRBW-279	AGRA germplasm of Uniport	High tillering ability
IRBW-467	AGRA germplasm of Uniport	Tall plant
IRBW-274	AGRA germplasm of Uniport	Short plant
IRBW-263	AGRA germplasm of Uniport	Tall plant
IRBW-246	AGRA germplasm of Uniport	High tillering ability
IRBW-202	AGRA germplasm of Uniport	High yield
IRBW-103	AGRA germplasm of Uniport	Tall plant
IRBW-180	AGRA germplasm of Uniport	Tall plant
IRBW-307	AGRA germplasm of Uniport	High yield
IRBW-166	AGRA germplasm of Uniport	High tillering ability
IRBW-252	AGRA germplasm of Uniport	High grain weight
IRBW-123	AGRA germplasm of Uniport	Long panicle
IRBW-147	AGRA germplasm of Uniport	High yield
IRBW-105	AGRA germplasm of Uniport	High grain weight
IRBW-427	AGRA germplasm of Uniport	High yield

after harvesting. The plant yield was measured in grams after harvest for each variety.

Data analysis

All data were subjected to analysis of variance using GenStat discovery (4th Edition) for mean separation, correlation analysis and means of the traits. Pair-wise distance matrixes between genotypes were again derived using the numerical taxonomy and multivariate analysis system (NTSYS-PC), Version 2.1 (Rohlf, 2000) and the Jaccard coefficient of similarity (Jaccard, 1908). Genetic diversity dendogram for the genotypes was created by Unweighted pair group method with arithmetic mean (UPGMA) cluster analysis (Sneath and Sokal, 1973; Swofford and Olsen, 1990).

RESULTS

About eight genotypes performed better than the overall mean of the LAI (Table 2). The genotype with the highest LAI was IRBW-125 followed by IRBW-54 and the least was IRBW-279. The LAI showed highly significance difference among the tested genotypes. The flag LAI (FLAI) indicates a significant difference among the rice genotypes. IRBW-54 had the highest value of FLAI (1.10) and the least was IRBW-399(0.18). The genotypes with the highest panicle length is IRBW-123(20.64) and the least IRBW-148(13.87) showing a highly significance difference among the rice genotypes tested (Table 2).

Eight genotypes performed better than the overall mean of plant height and genotypes with highest plant height are IRBW-54(101.00), IRBW 103(101.00) and IRBW-125(101.00), while the least is IRBW-148(60.7). Plant height has significance difference among the genotypes tested. The result for the tiller number showed that about eight genotypes had more tiller number than the overall mean at maximum tillering stage of the rice crop (Table 3). The effective tillers which, is the number of tillers harvestable per plant, gave a mean value of 31.19 at maturity of the plant. The highest effective tiller rice genotypes are IRBW-180(49), IRBW-147(48), whilst the least is IRBW-440(7). Tilling ability of the genotypes also indicate a highly significance difference among the genotypes tested. About seven genotypes performed better than other genotypes for GY per plant with the highest been IRBW-180(224.42 g) and the least IRBW-54(34.00 g). The results indicate a significance difference among the genotypes tested (Table 3).

The genotype with the highest grain weight per panicle was IRBW- 166 (4.17 g) followed by IRBW-105(4.01 g)

Table 2. Agronomic performance of some lowland rice genotypes.

Genotype	LAI	FLAI	Panicle length (cm)
IRBW-125	3.38	0.94	20.54
IRBW-54	3.30	1.10	19.71
IRBW-26	2.89	0.95	20.15
IRBW-255	2.49	0.68	20.36
IRBW-467	2.43	1.00	20.17
IRBW-105	2.24	0.72	20.56
IRBW-252	2.23	0.78	20.36
IRBW-123	2.18	0.62	20.64
IRBW-147	2.14	0.57	20.45
IRBW-295	2.08	0.55	19.56
IRBW-180	2.07	0.40	20.63
IRBW-144	2.05	0.61	19.11
IRBW-202	1.93	0.92	19.82
IRBW-103	1.92	0.48	19.55
IRBW-427	1.74	0.61	20.42
IRBW-166	1.72	0.63	19.71
IRBW-263	1.70	0.45	17.65
IRBW-275	1.51	0.56	19.72
IRBW-399	1.49	0.18	19.47
IRBW-246	1.47	0.40	20.15
IRBW-274	1.41	0.39	20.45
IRBW-156	1.357	0.44	19.17
IRBW-307	1.28	0.53	18.42
IRBW-440	1.26	0.30	16.79
IRBW-148	1.21	0.38	13.87
IRBW-279	1.12	0.57	24.24
MEAN	1.92	0.63	19.53
LSD(0.05)	0.686***	0.326***	2.695***
CV(%)	21.80	31.80	8.40

LAI = Leaf area index, FLAI = Flag leaf area index, *** significant at 0.001 probability level, respectively

and the least IRBW-148(1.73 g). The grain weight showed highly significance difference among the genotypes tested. While genotype with the highest number of grain per panicle is IRBW-180 (131), followed by IRBW-166(122) and the least was IRBW-148(51) (Table 4).

FLAI significantly correlated with grain weight per panicle and number of grain per panicle at probability level of 0.05. While significance correlation at probability level of 0.001 was observed for LAI with FLAI (Table 5). Effective tiller number indicates a significant correlation with yield per plant, maximum tillering and number of grain per panicle. Grain weight per panicle indicates a significant correlation among some traits tested such as yield per plant, number of grain per panicle, and LAI (Table 5). LAI indicates a significant correlation with number of grain per panicle. Number of grain per panicle showed a significant correlation with yield per plant and maximum tillering (Table 5). At maximum, tillering indicates significant correlation with yield per plant in (Table 5). Yield per plant are highly and significantly correlated with effective tiller number, grain weight per panicle, number of grain per panicle and at maximum tilling stage of the crop at 0.001 probability level of significance.

Cluster analysis

Hierarchical cluster analysis of some agronomic traits and yield are presented in the Figure 1. Three main groups (A, B, and C) were identified at 0.02% coefficient of similarity index. The dendrogram revealed each group containing 11, 7 and 8 genotypes for A, B and C, respectively. At 0.04% of coefficient of similarity index, eight groups were identified and further down the similarity

Table 3. Agronomy performance of some lowland rice genotypes.

Genotype	Yield per plant (g)	plant height at maturity (cm)	Number of tillers at maximum tillering stage	Number of effective tillers at maturity
IRBW-180	224.42	90.40	53	49
IRBW-123	176.00	80.90	47	43
IRBW-427	162.00	80.70	26	28
IIRBW-252	147.00	90.40	50	45
IRBW-147	140.00	90.70	52	48
IRBW-166	129.00	80.90	33	31
IRBW-105	124.00	90.40	37	31
IRBW-274	91.30	100.00	26	28
IRBW-399	84.00	70.20	30	34
IRBW-467	77.50	90.70	24	24
IRBW-279	72.30	80.40	29	33
IRBW-125	68.50	101.00	22	21
IRBW 307	68.10	60.90	35	30
IRBW-275	66.20	70.60	23	26
IRBW-263	61.60	100.00	22	26
IRBW-144	60.00	100.00	29	25
IRBW-202	60.00	90.40	24	20
IRBW-103	56.70	101.00	27	27
IRBW-156	54.60	70.00	19	20
IRBW-440	54.00	90.90	25	7
IRBW-148	53.60	60.70	33	31
IRBW-26	51.20	70.60	18	17
IRBW-295	51.30	100.00	21	18
IRBW-255	46.80	100.00	16	20
IRBW-246	41.60	90.50	21	20
IRBW-54	34.00	101.00	17	20
Mean	86.70	86.67	31.2	88.2
S.E	2.530	2.281	2.439	3.246
CV(%)	14.90	38.70	39.90	47.65

index at 0.11% majority of the genotypes assumed individual identity.

The genotypes in Group A posses the character of high grain weight and Group B posses characters for long panicle and high value of FLAI, which indicates broad leaf for light interception for enhancing photosynthetic activities in plant. In Group C, genotypes posses varying characters, however, high value of LAI and tall plant, which indicates tendency of good nutrient utilization (Table 5).

DISCUSSION

Performance of some agronomic traits of lowland rice

One of the main objectives of any breeding program is to produce high yielding and better quality lines for release as cultivars to farmers. Detailed information on rice yield component that contributes to high yield is needed from which desired lines are to be selected for further manipulation to achieve the target. Introduction of new populations can be made from one region to the other easily and may be used for further manipulation to develop breeding lines. Various yield components are directly or indirectly responsible for rice yield potentials.

Grain weight per panicle is a varietal trait and of secondary importance in determining rice yield. Grain weight is determined by the source capacity (photosynthetic leaves) to supply assimilate during the ripening period, and by sink capacity (developing grain) to accumulate the imported assimilate (Ntanos and Koutroubas, 2002). Cultivars with larger grain weight value size tend to have higher grain filling rate, resulting in higher assimilate accumulation and heavier grain weight. Thus, genotype IRBW-166(4.17) has the highest grain weight per panicle value among the varieties

Table 4. Genotype performance based on number of grain and grain weight per panicle.

Genotype	No. of grains per panicle	Grain weight per panicle (g)
IRBW-54	62	2.11
IRBW-180	131	3.43
IRBW-467	94	3.23
IRBW-26	88	3.00
IRBW-125	95	3.26
IRBW-202	88	3.01
IRBW-252	95	3.25
IRBW-105	117	4.01
IRBW-255	68	2.34
IRBW-166	122	4.17
IRBW-123	119	3.67
IRBW-144	70	2.41
IRBW-427	101	3.45
IRBW-147	85	2.90
IRBW-279	64	2.20
IRBW-275	75	2.57
IRBW-295	83	2.85
IRBW-307	66	2.26
IRBW-103	61	2.08
IRBW-263	69	2.37
IRBW-156	80	2.73
IRBW-246	61	2.10
IRBW-274	95	3.26
IRBW-148	51	1.73
IRBW-440	60	2.05
IRBW-399	70	2.41
Mean	84	2.80
LSD (0.05)	35.9***	1.246**
CV(%)	26.2	27.1

, * significant at 0.01 and 0.001 probability level, respectively.

Table 5. Correlation coefficient between rice yield and its yield components.

EFF_till								
FLAI	0.1443^{ns}							
GWt_Pani	0.3650^{ns}	0.4052*						
LAI	0.1762^{ns}	0.7977***	0.3995*					
NG_Pani	0.4741*	0.4571*	0.9589***	0.4828*				
PANLT	0.3597^{ns}	0.3124^{ns}	0.2494^{ns}	0.2504^{ns}	0.2279^{ns}			
Plt_Ht	0.2385^{ns}	0.0616^{ns}	0.0365^{ns}	0.1036^{ns}	0.0723^{ns}	-0.1722^{ns}		
Tillmax	0.9043***	0.0948^{ns}	0.3762^{ns}	0.1652^{ns}	0.493*	0.0907^{ns}	0.2836^{ns}	
Yld_Plt	0.7986***	0.3543^{ns}	0.6900***	0.3208^{ns}	0.8070***	0.1717^{ns}	0.2149^{ns}	0.8201***
	Eff_till	FLAI	GWt_Pani	LAI	NG_Pani	PANLT	Plt_Ht	Tillmax

*, **, and *** significant at 0.05, 0.01 and 0.001 probability level respectively, ns = non significant. EFF_TILL= EFfective tillers, FLAI = Flag leaf area index. GWT_Pani = Grain weight per panicle, LAI = leaf area index, NG_Panicle =Number of grain per panicle, PANLT= Panicle length, PLT_Ht = Plant height, Tillmax = Maximum tillering, YLd_pLt = yYield per plan.

observed and may possess higher grain filling rate followed by genotype IRBW-105(4.01) and the least genotype IRBW-148(1.73). These results corroborate earlier reports (Jones et al., 1979; Jeng et al., 2003). The

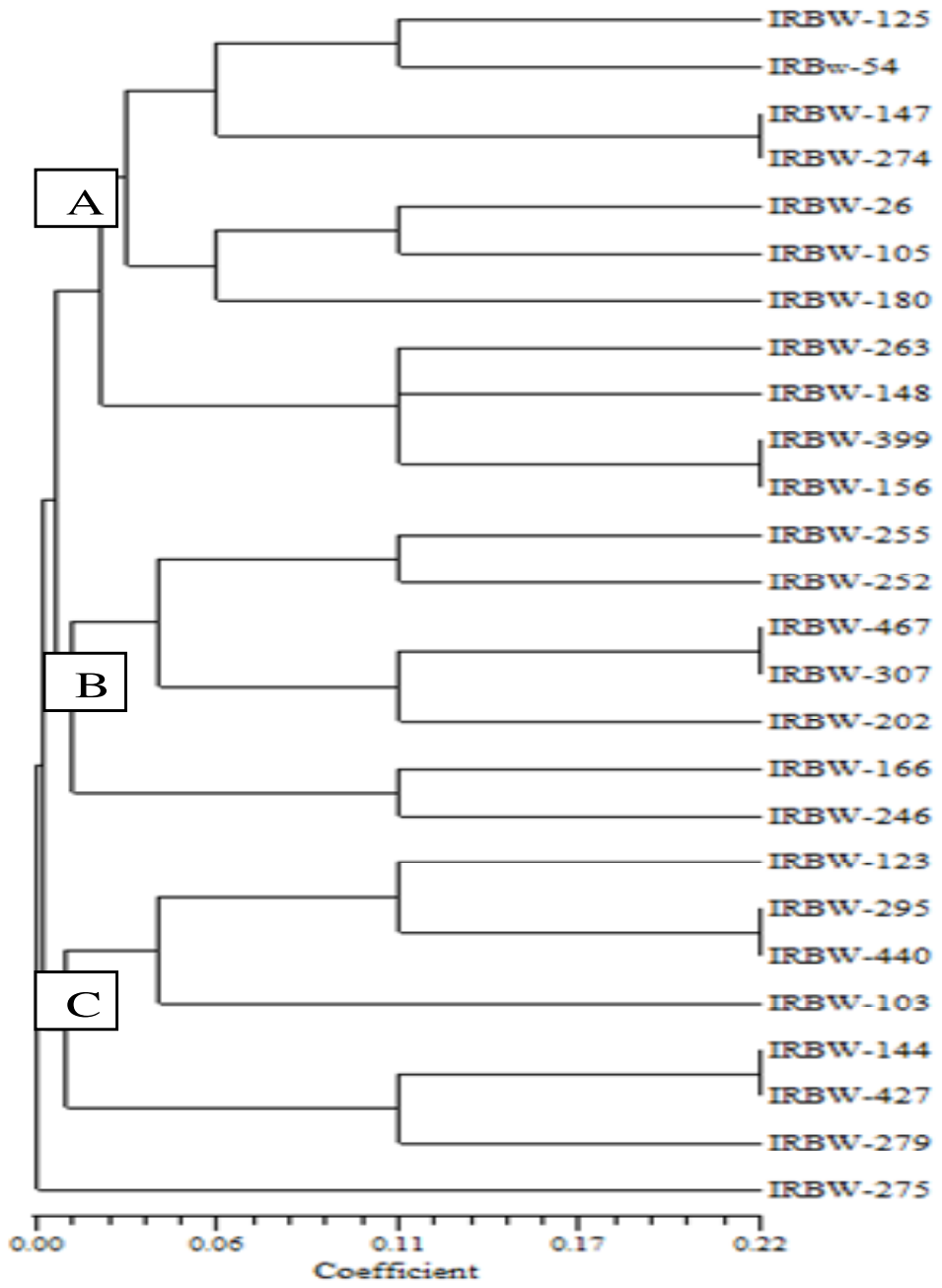

Figure 1. Dendogram showing genetic diversity of the entries.

number of grains per panicle is important yield-contributing characters. Feil (1992) reported that among the components of GY of a cereal crop, the number of spikelets per panicle appeared to be a predominant key character in the development of high-yielding cultivars. Thus genotype IRBW-180(131) and IRBW-166(122) of higher number of grains per panicle could be of high yielding.

LAI is the efficiency of photosynthetic process, contributing greatly to yield. High leaf index was reported by Efisue et al. (2009) which indicated that LAI is a good selection criterion for increasing GY of rice. Thus, genotypes with higher value of LAI could be higher yielding compared to low LAI genotypes, example, IRBW-125(3.383 of higher LAI and IRBW-279(1.103) lowest. FLAI played an important role in rice yield by increasing grain weight with high photosynthetic ability (Mohashami, 1998). Therefore, genotype IRBW-54 could be high yielding with FLAI (1.103).

The panicle determines the ultimate yield of the crop, as the length of a panicle determines the number of grain to be accommodated. This indicates that genotype with

long panicles will accommodate more grains than short panicles genotype. Thus, genotypes with long panicle could possess high yielding ability such as IRBW-123 (20.64) compared to IRBW-148 (13.87). Plant height is the predominant factor determining the nitrogen response of rice plant. It determines the lodging behaviour thus deciding yield. On the other hand, tall stature facilitates light penetration (Chandrasekaran et al., 2007), which may increase photosynthetic activities of plant. Aside from these good agronomic traits, tall plants easily lodge; this behaviour has negative effects on yield production. This suggest that there should be a balance where breeders develop varieties with strong culm (stem) that will resist lodging and fertilizer responsive that may translate to high yield such as IRBW-54(100.6) and IRBW-295(100.3) genotypes.

Tillering ability in rice is an important agronomy trait for grain production. Ibrahim et al. (1990) found out that effective tillers were most reliable character in selecting genotypes of rice for higher yield. Tillering plays an important role in determining rice GY since it is closely related to panicle number per unit ground area. Too few tillers result in too few panicles, but excess tillers caused hight tiller mortality, small panicles, poor grain filling and consequent reduction in GY (Peng et al., 1994). Higher tillers results in higher sink: source ratio, spikelet number, proportion of filled grain, LA per panicle and sink capacity (Choi and Kwon, 1985). Therefore, genotypes with high productive tillering ability could exhibit the aforementioned characters such as IRBW-180(49) and IRBW-147(48).

Rice GY is determined by several agronomic characters such as heading days, days to maturity, grain filling period, number of fertile tiller, number of fertile grain per panicle, panicle length, and plant height (Halil and Necmi, 2005). The result from the experiment showed that IRBW-180 (224.42 g) has the highest GY per plant among the genotypes tested, followed by IRBW-123 (176.00 g). The above genotypes could be deployed to farmers' field to enhance food production.

Relationship of some agronomic traits and yield

Data analysis regarding yield per plant indicates a highly significant association with maximum tillering, effective tiller number, grain weight per plant and number of grain per panicle. These relations mean that any increase in any one aforementioned yield components causes increase in GY. However, yield components have different effects on GY, depending on the contributing genes to GY. The number of grain per panicle showed a significant correlation with yield per plant, maximum tillering. This high and significant correlation indicates that number of grain per panicle is largely responsible for the determining GY in individual plants. Similarly, Mirza et al. (1992) found that number of grains panicle is positively correlated with panicle length, 1000-grains weight and GY. A significant variation was observed for grain per panicle amongst the genotypes examined, indicating broad genetic base of the genetic materials used in the study.

Effective tiller number indicated a significant correlation with yield per plant, maximum tillering and number of grain per panicle as expressed by genotypes IRBW-180 and IRBW-123. The FLAI results showed a significant correlation with grain weight per panicle, LAI and number of grain per panicle. This report is in conformity with Bharali et al. (1994) who found higher direct effect of FLAI on grain. LAI indicated a significant correlation with number of grain per panicle, grain weight per panicle and FLAI. LAI is a secondary trait for the selection of high yield of most crops and positively highly correlation was observed for the aforementioned traits. Thus indicates that large LAI value will result to increase in yield as equally observed by Ghosh and Singh (1998). Grain weight per panicle results indicate a significant positive correlation among some traits tested such as yield per plant, number of grain per panicle.

Conclusion

Plant breeders should focus more on the aforementioned traits that showed high association with GY, especially effective tiller number, grain weight per panicle and number of grains per panicle. Rice yield components are found to improve GY as observed from this experiment. Significant and positive correlation between tiller numbers and yield observed in study indicates that varieties with high tillering ability could yield more in response to increase in tiller numbers. Effective tillers results in higher grain as observed in genotype IRBW-180 and IRBW-123, breeders should therefore pay keen interest for higher effective tiller numbers in rice crop.

LAI and FLAI played an important role in rice GY production, because of their relationships with photosynthesis for the production of assimilates for the plant. Therefore, selection for these traits in the development of rice varieties will increase GY. This will inevitably increases the livelihood of our rice farmers. Also, in the development of a rice variety, selection for large grain size and fast grain filling rate through breeding program may be a feasible approach to increase the GY in rice. Thus, these varieties are recommended that IRBW-123 possess panicle length and high yield per plant, while IRBW-180 had the highest yield per plant and IRBW-166 had the highest grain weight per panicle, these genotypes could be deployed into farmers' field to increase rice production in Nigeria.

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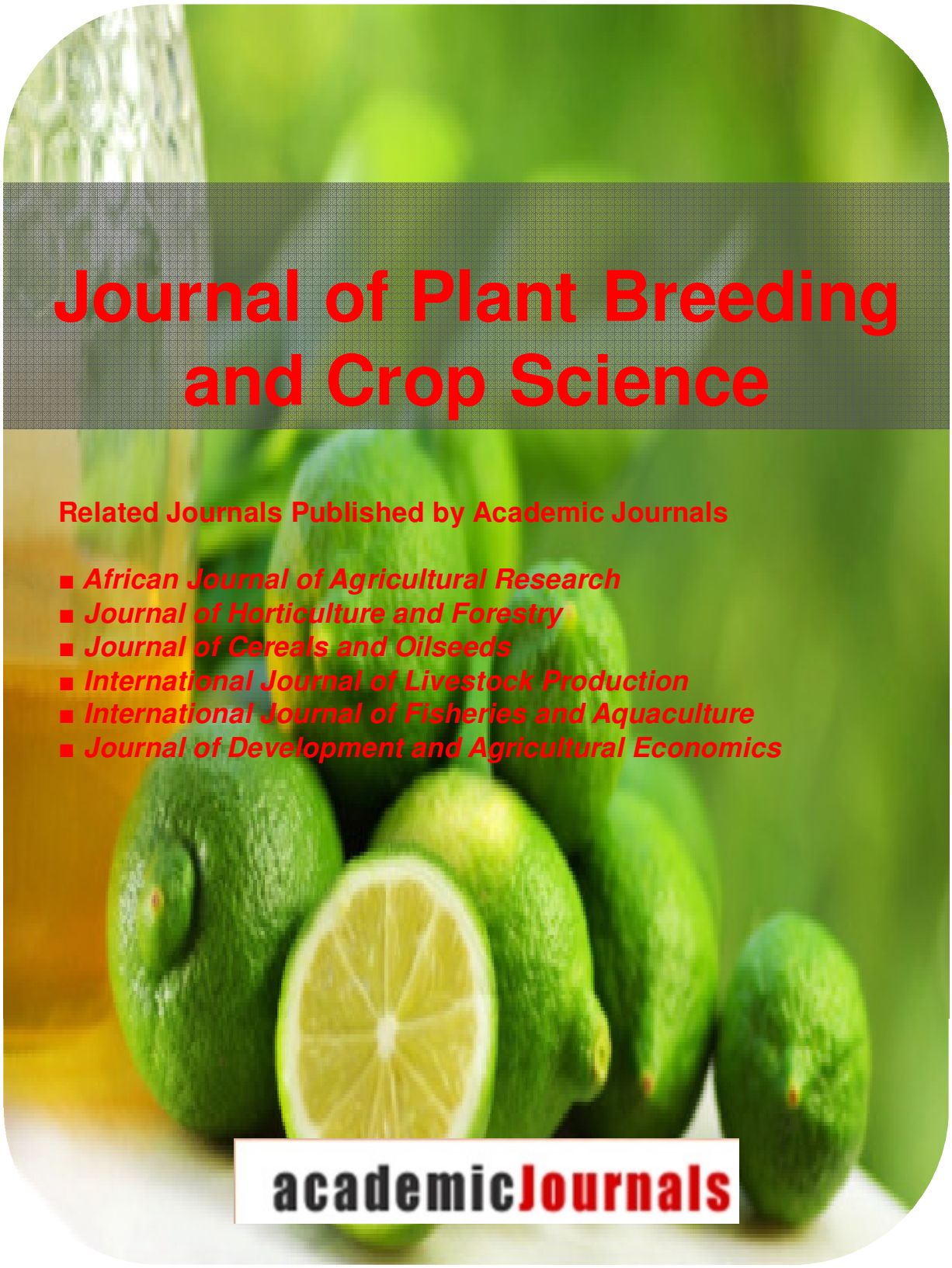

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