JOURNAL OF FOREST PRODUCTS & INDUSTRIES, 2015, 4(2), 21-32 ISSN:2325–4513(PRINT) ISSN 2325 - 453X (ONLINE)

Research Publisher
Discovery that Matters

Genetic Variability in Rice Genotypes (*Oryza Sativa* L.) in Yield and Yield Component under Semi-Arid Zone (Sudan)

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(**Received:** November 17, 2014; **Accepted:** January 31, 2015)

***ABSTRACT*- The field experiment was conducted at Sudan University of Science and Technology (Shambat) in July of 2011 and 2013, to investigate genetic variability of rice in yield and yield component under semi-arid zone, Sudan. A randomized complete block design with three replications was used at each season. In general phenotypic coefficients of variation (PCV) estimates were higher than genotypic coefficients of variation (GCV) estimates for all the studied characters in all genotypes displaying the influence of environment effect on the studied characters. Highly significant differences observed in both seasons for plant height (cm), days to 50% flowering, days to 50 % maturity, number of filled grain/panicle and grain yield (t/ha), high significant for number of panicle/m^2, panicle length (cm), number of grain/panicle, percentage of unfiled grain/ panicle (%), and 100-seed weight (gm) in season 2011. Stem diameter (cm) and number of tillers/plant in season 2013. Significant differences in both seasons for leaf area (cm^2), Number of leaves in season 2011, and number of panicle/m^2, number of grain/panicle and 100-seed weight (gm) in season 2013. Handao221, WAB19, Yunlu33 and Nerica5 were highly yielding genotypes gave (4.03, 3.70, 2.43, 2.167 t/ha) respectively. Handao221 and WAB19 were classified as high yielding and stable genotypes .There could be used in the breeding program and/or may be released to farmers for cultivation. The study revealed that there was highly genetic variability among the tested genotypes, indicating that it could be used for further improvement in rice breeding.**

Index term: Rice genotypes; growth; yield; variability; heritability; genetic advance.

I. INTRODUCTION

Rice (*Oryza sativa* L.) is one of the world's most important cereal crops, **[1, 2, 3]** with about 154 million ha harvested in 2010 **[4]**. In 2002, nearly 50% of the world's population depended on rice for a substantial amount of its calories (>800 kcal person-1 day-1) **[5]**. Population increases and climatic change have made it difficult to meet demand for rice **[5, 6, 7, 8]** However, yields in some areas have increased due to advances in plant breeding and crop management. A number of cultivars now offer increased yield potential **[9]**. Elite hybrid rice has increased yields 10-30% compared to elite inbred lines **[10, 11]**. Raising the yield potential may be possible through higher yielding varieties and reducing the yield gap in farmer's fields **[8]**

Exploring new regions for rice production could help meet world demand. Rice has been raised from latitudes 53ºN to 40ºS, though 75% of global rice production in 2004 was in tropical regions **[5]**. Rice grown outside of the temperate region is grown in the Tropics of Cancer and Capricorn. However, temperate rice generally has greater yields **[10]** Most U.S. rice production is temperate rice (25ºN to 45ºN), or rice grown in latitudes north or south of 23º27' **[12]** The world population is expected to reach 8 billion by 2030 and rice production must increase by 50 percent in order to meet the growing demand **[13]**. Genetic variability for agronomic traits is the key component of breeding programmes for broadening the gene pool of both rice and other crops. However, the genetic variability for many traits is limited in cultivated germplasm

In Sudan rice has been grown since 1905, but limited acreage and information about methods of reproduction is lacking **[14]**. Rice in Sudan is grown on 7.60 thousand hectares producing 30 thousand tons. However, Sudan produce an average of 3947 kg/ha **[15]**. Swamp and upland varieties were first tried as the Gezira research farm in 1951. Later extensive rice trials were carried out at Malakal and several varieties were selected at the Gezira Research Station although rice cultivation in the Sudan was known for something especially in south Sudan and White Nile area. Large scale production starts only in the years 1950 in the Upper Nile Province (Malakal) and in 1960 in Aweel. But for security reasons production was abandoned. Rice production was stated once again a bang the White Nile at Gassaba **[16]**. Its promising and potential cereal crop in White Nile areas. Its production and average yield exhibits fluctuation mainly due to cultivation of low yielding and environment sensitive genotypes. Identification of genotypes that show minimum interaction with the

JOURNAL OF FOREST PRODUCTS & INDUSTRIES, 2015, 4(2), 21-32 ISSN:2325–4513(PRINT) ISSN 2325 - 453X (ONLINE)

environment or possess greater yield stability is an important consideration in areas where environmental fluctuations are considerable [17].

The specific objective of the study is to investigate genetic variability and characters association among different traits and constructing selection criteria on the basis of these traits for high yielding genotypes under semi-arid zone (Sudan).

II. MATERIALS AND METHODS

The field experiments were conducted at Sudan at College of Agricultural Studies, Sudan University of Science and Technology (Shambat) in growing season of (2011 and 2013) located at longitude 32˚-35˚E, latitude 15˚-40˚N, and latitude 280m above sea level. The climate of the locality is semi-arid, with low relative humidity, the temperature varies between 45˚C maximum and 21˚C in summer **[18].** In July to November of 2013, the soil of the experimental site (Shambat) is described as loam clay. It's characterized by a deep cracking moderately alkaline with low permeability low nitrogen content and ph of 7.5-8 and a high exchange able sodium percentage (ESP) is subsoil **[19]**. The plant material used in this study, includes 18 rice genotypes; 7 NERICA genotypes from WARDA (West African Rice Development Association, Benin) Named as (N_4, N_2, N_{15}, N_5, N_{17}, N_{14}, N_{12}), 5YUNLU genotypes from China and named as (Y_{22}, Y_{33}, Y_{30}, Y_{24}, Y_{26}) and 6 genotypes (HANDAO 221, HANDAO 502 and ZHONGHAN 3) named as (H_{221}, H_{502} and $_{Z3}$)from IRRI (International Rice Research Institute, Philippines), The material was provided by the Agricultural Research Corporation (ARC), Sudan. Soil was deep ploughed, harrowed tow times and leveled to prepare the experimental area, then it divided to 54 plots for three replications, the plot size was 2×3 meters, Seeds were sown manually by hands in 8th July 2013, each hole was consisted of 3-4 seeds in depth of 3-4 cm, then thinned to 2 plants per hole after two weeks from sowing. The phosphorous was applied in form of triple super phosphate (P_2O_5) as a basal dose in rate of 50kg/fed at the same day of sowing, the Nitrogen in form of Urea (46% N) was applied in two equal split doses, in rate of 80kg/fed, the first one 40kg/fed after one month from sowing date, the second one after two months from sowing in the same rate. The land was irrigated tow times a week to avoid stress, especially in the case of upland Rice that needs a lot of water. Weeds were controlled manually every two weeks to avoid competition.

Five plants were selected randomly from each plot, Plant height (cm), Number of leaves/plant., Leaf area (cm^2), Stem diameter (cm), Number of Tillers/plant, Days to 50% flowering, Days to 50% maturity, Number of panicles/ m^2 , Panicle length (cm), Number of grains/ panicle, Number of filled grains/panicle (12- Percentage of unfilled grains/panicle , 100-grains weight (g), Grain yield (t/ha). The collected data for growth and yield was subjected to analysis of variances for a randomized complete block design (RCBD), for each season separately to test for significant differences among genotypes. Using computer program Statistical Analysis System **[20]**.

The estimates of phenotypic (σ^2ph) and genotypic (σ^2g) variances were worked out according to the method suggested by **[21]** using mean square values from the individual and combined ANOVA tables as the following formula:

$$\sigma^2 g = (M2 - M1) / r$$

$$\sigma^2 ph = \sigma^2 g + \sigma^2 e$$

Where:
r = number of replications.
σ^2e = error mean squares.
M1, M2 = error and genotype mean squares.

Phenotypic (PCV) and genotypic (GCV) coefficients of variation were calculated based on the method advocated by **[22]** as the following formula:

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sqrt{\sigma^2 Ph} \times 100}{\text{Grand mean}}$$

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sqrt{\sigma^2 g} \text{ x } 100\%}{\text{Grand mean}}$$

Heritability percentage in broad sense h2 (bs) and Genetic advance (GA) were estimated according to the method suggested by **[21]** as the following formulas:

$$h^2 = \sigma^2 g / \sigma^2 ph$$

Where:
σ^2g, σ^2ph = genotypic and phenotypic variances.

$$\text{(GA) from individual analysis of variance} = K \frac{\sigma^2 g}{\sqrt{\sigma^2 Ph}}$$

σ^2g = is the estimated genetic variance
σ^2e = is the pooled error variance
r = number of replications
K= selection differential and it was 2.06 as defined by **[23]** at selection intensity of 5%.

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III. RESULTS AND DISCUSSION

Genotypic coefficient of variation (GCV) measures the range of variability in crop and also enables to compare the amount of variability present in different characters. The phenotypic coefficients of variation (PCV) estimates were higher than genotypic coefficients of variation (GCV) for all the characters studied among the eighteen rice genotypes, indicated that the substantial influence of environment in the expression of these characters. Similar findings were observed in pearl millet by [24], in 2013 High GCV was observed for stem diameter high PCV was observed for grain yield, Heritability gives the information on the magnitude of inheritance of characters, while genetic advance is helpful in formulating suitable selection procedures. The information on heritability alone may not help in pointing characters for enforcing selection. Nevertheless, the heritability estimates in conjunction with predicted genetic advance will be more reliable. The estimates of heritability in broad sense and genetic advance for the studied characters were fluctuating at the two seasons. The differences in the magnitude of heritability would be attributed to the effect of the environment. [25] attributed the change in heritability estimates in maize (*Zea mays* L.) to differential response of genotypes to the environment.

Growth parameter

Individual analysis of variance (ANOVA) indicated highly statistical significant differences among tested genotypes in plant height in both seasons (2011-2013) Table (1, 2). In season 2011 showed that Y_{26} and Y_{33} were the longest plant (80.70, 79.89 cm) respectively, followed by Y_{30}, Y_{24}, N_{12} and N_{15} (75. 06, 74. 85, 73.36, 71.83 cm) respectively, while N_5 and Z_3 were the shortest genotypes (52.43, 50.95 cm) respectively, Table (3). Y_{26} and Y_{30} were the longest genotypes in season 2013 (80.97 and 78.13 cm) followed by Z_3 (74.68 cm), N_5 (74.56 cm), Y_{22} (71.99 cm), W_{19} (71.99 cm) and N_{15} (71.70 cm), while N_{12} was the shortest one (47.05 cm), Table (3). A study by [26] in low land rice indicated that the application of Nitrogen fertilizer gave more vigorous, less injurious and taller rice plant. In this study the application of Nitrogen is 80 kg/fd. The genotype N_{12} and N_5 might not respond to the Nitrogen as it's up land rice. [27] studied genetic variability, coefficient of selection and correlation for various yield and yield contributing parameters and found significant correlation between grain yield and plant height. [28] reported that water and soil condition, planting and sowing method affect plant height in rice. [29] studied 14 genotypes of basmati rice and observe high heritability coupled with high genetic advance for plant height and 1000-grain weight. He also reported that plant height has negative correlation with yield. In addition he observed the positive relationship of plant height with grain quality. A significant difference was noticed season 2011 for number of leaves and non significant difference in season 2013 Table (1,2).The least significant different test (LSD) at 5% level showed that, in season 2011, H_{221} gave the highest number of leaves/plant (4.13), followed by N_{14} (3.73), while N_{17} and W_{19} gave the lowest number of leaves/plant (2.90 - 2.87) respectively, Table (3) In season 2013 the genotypes Y_{26} and N_{14} had the highest number of leaves (3.80- 3.73) respectively. The lowest number of leaves/plant were given by the genotypes H_{221} and Y_{30} (2.93), W_{12} and N_5 (2.87) and Y_{22} (2.80). Table(3) A significant different showed in leaf area at both seasons (2011 and 2013) by individual analysis of variance (ANOVA), Table(3) .analysis of season 2011showed that N_{12} and W_{12} had the best measuring in leaf area (30.20 , 28.96 cm^2) followed by Z_3 (26.10 cm^2). N_{14} and H_{502} gave the lowest measuring (16.01, 14.53 cm^2) respectively, Table (3). In season 2013, Z_3 followed by W_{19} gave the highest leaf area (35.13, 34.95 cm^2), while H_{502}, Y_{22} and W_8 gave the lowest (19.96, 19.67 and 17.63 cm^2) respectively, Table (3). A study by [30] in crossing between japonica and indica japonica, indicated that Generally the increase in flag leaf area of Japonica /indica japonica was higher than japonica/japonica, this was mainly due to hybrid vigor resulted from the crosses between japonica and indica japonica (there are genetic diversity among them), while no significant difference between japonica/ indica japonica and indica japonica/indica japonica. Individual analysis of stem diameter revealed There were no statistical significant different among tested genotypes in seasons 2011 and there were high significant different in season 2013 (table 1, 2). Y_{33} gave the highest diameter in separate analysis of 2011 (4.92 cm) then N_{12} (4.34 cm), while Y_{24}, Y_{22}, N_2 and H_{502} gave the lowest diameter (3.32. 3.26, 3.09 and 3.08 cm) respectively, Table (3). In 2013, N_4 gave the best measure of stem diameter (2.55 cm), while N_{14} gave the lowest measure (1.58 cm), Table (3). There is no statistical significant difference in number of tillers/plant in season 2011. While a highly significant difference was notice in season 2013 that's recorded by individual analysis of variance, Table (1, 2). In season 2011 the genotype N_{15} gave the highest number of tillers/plant (10.73) followed by N_{14} (10.67) respectively. Y_{26} and Z_3 gave the lowest number of tillers/plant (6.96, 6.80) respectively, Table (3). In season 2013 the highest number of tillers/plant was given by the genotype Y_{22} (11.50) followed by H_{221} (10.40). N_2 gave the lowest number of tillers/plant (5.13), Table (3). A result by [29] in twelve genotypes of coarse rice to check their yield performance in Kallar tract and reported highly significant variation for different traits including the number of productive tillers plant, an important yield component in the rice. A highly significant difference noticed in Days to 50 % flowering among genotypes over both seasons (2011-2013), Table (1, 2). Individual analysis In season 2011showed that N_{14} flowered in 67.00 days followed by W_8 (67.33 days) and Y_{26} (69.33 days) which were the earliest genotypes to flowering, Table (3). The latest genotypes to get flowers were W_{19} (83.67 days), Y_{22} (84.33 days), N_{12} (85.67 days) and H_{221} (90.00 days), Table (3). In season 2013, W_8 was the earliest genotype to flowering (66.67 days), while H_{221} and Y_{22}were the latest genotypes to flowering (90.0 and 83.33 days), Table (3). [31] reported that the N_2 was the least affected by water deficit because it took the least number of days to attain 50% flowering in the plants watered after every 2, 4 and 6 days. In this research the H_{221} took the least number of days to flowering more than N_2, in season 2013. The number of days to reach maturity plays a significant role in the cropping system. Early maturing genotypes evacuate the land early for the next crop and escape from insects and pests attack and timely handled. Individual Analysis of variance (ANOVA) for number of Days to physiological maturity revealed highly significant difference among the evaluated genotypes at both seasons (2011- 2013) table (1, 2), season 2011 indicated N_5 and N_{12} were the earliest genotypes to get mature (95.00, 89.33 days) (Table 3), while Y_{30} and H_{221}were the latest genotypes to get mature (123.0, 128.0 days) respectively, Table (3). In 2013, N_{14} had the least number of days to get mature (111.00 days), while $H_{221}$and W_{19} is the latest genotype to get mature (122.00 days). Table (3). [32] studied 41 aromatic rice genotypes for variability and genetic parameter analysis and found highly significant mean sum of square due to genotypes for days to maturity. He reported that variation for days to maturity was attributed by genetic constituent rather than environment. Short duration lines can be a good source for breeder to use parents.

Table (1) summary of ANOVA table for growth parameter, season 2011

Source	D.F	F. Value 2011						
		Plant height (cm)	Number of leaves /plant	Leaf Area (cm^2)	Stem diameter (cm)	Number of tillers/ plant	Days to 50% flowering	Days to 50% maturity
Replication	2	7.0909	3.2639	12.2052	0.1903	1.7355	0.0350	1.8956
Variety	17	2.8065**	2.3337*	2.3997*	1.531NS	6.3643**	3.0037**	11.620**
Error	34	-	_	_	_	_	_	_
Total	53	-	_	_	_	_	_	_
EMS	_	102.646	0.116	21.055	0.422	0.457	40.231	27.784
C.V%	_	15.82	10.36	20.48	17.71	7.15	8.34	4.82
SE±	_	2.3880	0.0803	1.0815	0.1531	0.1593	1.4950	1.2424

**=high significant, *= significant, NS =not significant

Table 2: Summary ANOVA table for growth parameter, season 2013

Source	D.F	F. Value 2013						
		Plant height (cm)	Number of leaves /plant	Leaf Area (cm^2)	Stem diameter (cm)	Number of tillers/ plant	Days to 50% flowering	Days to 50% maturity
Replication	2	2.4276	5.4699	0.9199	0.4496	2.1799	3.7355	0.0531
Variety	17	3.8004**	1.3982ns	1.9363*	1.4016ns	1.4240ns	43.8959**	10.6982**
Error	34	_	_	_	_	_	_	_
Total	53	_	_	_	_	_	_	_
EMS	_	60.550	0.176	37.02	0.093	1.034	9.404	2.443
C.V%	_	11.66	13.16	22.72	14.89	12.69	3.92	1.32
SE±	_	1.8341	0.0988	1.4330	0.0720	0.5126	0.7228	0.3684

**=high significant, *= significant, NS =not significant

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Table 3: Mean of different growth parameter for season (2011-2013)

Geno types	Plant height(cm)		Number of leaves/ plant		Leaf Area(cm^2)		Stem diameter(cm)		Number of tillers /plant		Days to 50% flowering		Days to 50% maturity	
	2011	2013	2011	2013	2011	2013	2011	2013	2011	2013	2011	2013	2011	2013
W12	56.933FG	52.49H	2.867BC	2.867BC	28.96DEF	29.95DEF	3.77DE	2.01DEF	9.500EF	7.30GH	75.67DE	78.67DE	116.33D	120.33G
N2	56.767FG	61.91F	3.333FG	3.333FG	21.55AB	28.83EF	3.08CD	2.02CD	9.333FG	5.13FG	76.33CD	76.3D	98.66I	116.33D
Y26	80.700A	80.98A	3.800BCD	3.800BCD	24.96J	34.95I	3.95D	1.95FGH	7.633J	9.70L	69.33I	74.33L	112.33E	120.00G
W19	63.953CD	71.99B	3.333H	3.333H	20.13FG	25.89C	3.38H	2.07J	10.133CD	6.13K	83.67CD	79.67EF	120.33C	122.00I
Z3	50.953H	74.68B	3.400BC	3.400BC	26.10ABC	35.13A	3.68G	1.97CDE	7.800J	6.27CD	73.33GH	75.00HI	109.66F	120.00G
H221	67.560C	68.45C	2.933A	2.933A	22.12G	23.69EF	4.10BC	1.80EFG	10.400B	10.40J	90.00B	90.00C	128.0A	122.33I
N15	71.833B	71.70B	3.000BC	3.000BC	25.12A	28.28A	3.80EF	2.31CDE	10.733A	6.80J	71.33EF	74.67GH	109.66F	116.33D
Y22	61.767DE	74.16B	2.800B	2.800B	22.57EF	19.67FG	3.26D	1.83DEF	9.133G	11.50B	84.33A	83.33A	101.66H	116.0D
H502	54.650FGH	62.63EF	3.333FG	3.333FG	14.53ABC	19.96CD	3.08B	1.81H	9.667E	8.23I	75.33FG	75.00GH	100.0HI	114.33B
Y33	79.887A	65.07DE	3.400EF	3.400EF	23.55DEF	31.39H	4.92CD	1.95B	9.567EF	8.40A	73.67B	75.67B	112.66E	116.67D
W8	63.700CD	58.29G	3.200G	3.200G	24.07I	17.63H	3.67FG	1.58GH	9.667E	7.67FG	67.33DE	66.67GH	117.33D	120.00G
N17	53.267GH	64.4EF	3.133BC	3.133BC	21.30CDE	22.67B	3.36G	2.16GH	10.300BC	8.13F	78.67EF	78.33FG	112.33E	119.00F
N5	52.433H	74.56B	2.867B	2.867B	16.32BCD	25.75H	3.40A	2.08EFG	9.967D	10.07H	71.67H	74.67K	95.00J	118.67E
N14	57.067FG	67.94CD	3.733CD	3.733CD	16.01FG	25.520G	3.69D	2.10I	10.667A	7.10FG	67.00C	68.00D	107.00G	111.00A
Y30	75.060B	78.13A	2.933DE	2.933DE	22.70H	27.13EF	3.38EF	2.55C	7.833I	9.50BC	75.67FG	79.67GH	123.00B	121.67H
Y24	74.853B	62.30EF	3.133FG	3.133FG	22.56HI	27.90EF	3.32EF	2.09CDE	10.207BCD	9.00I	75.67H	73.33J	116.66D	115.67C
N12	73.363B	47.05I	3.000A	3.000A	30.20DEF	26.18CDE	4.34D	1.61CD	9.433EF	6.93D	85.67DE	80.67C	89.33K	118.33E
N4	57.893EF	64.21EF	3.133FG	3.133FG	20.51DEF	31.12CDE	3.85EF	2.11A	8.200H	6.00E	73.67DE	73.33I	99.00I	116.67D
C.V%	1161.639	11.66	13.16	13.16	20.48	22.74	17.71	18.39	7.15	12.69	8.34	3.88	4.82	1.32
L.S.D	3.962	3.043	0.1641	0.1641	1.795	2.380	0.2541	0.1437	0.2644	0.3977	2.481	1.161	2.062	0.61133

Means with the same letter for each parameter are not significant at 5% level (LSD)

Yield Parameters

Analysis of variance (ANOVA) for number of panicles/m^2 indicated highly significant difference in season 2011, and there was a significant difference in season 2013, Table (4, 5). In season 2011 indicated Y_{22} gave the highest number of panicles/m^2 (591.70), followed by W_{19}, Y_{24}, H_{221} (586.70, 576.70, and 573.30) respectively, while N_2 was the lowest number of panicle/m^2 (387.00) respectively, Table (6). In season 2013, N_{17}, H_{502} and Y_{26} gave the highest number of panicle/m^2 (449.70, 426.70 and 426.30) respectively, while N_4 gave the lowest number of panicle/m^2 (209.30), Table (4). This result is the same with result by [33] who studied sixteen genotypes x location in Alduim and Kosti he reported that N_{17} was gave the highest number of Panicles/m^2 (461.6, 447.5) at Kosti in 2008. Analysis of variance for panicle length (cm) revealed a highly significant difference in season 2011and no significant difference in season 2013, Table (4,5).In season 2011, H_{221} had the longest panicle (17.58 cm) followed by Z_3 (17.39 cm), while H_{502}, Y_{33}, and N_5 (13.10, 13.03, and 12.68 cm) gave the shortest length of panicle, Table (6). In season 2013, H_{221} had the longest number of panicle (22.02 cm), followed by Y_{26} (20.78 cm) and Z_3

JOURNAL OF FOREST PRODUCTS & INDUSTRIES, 2015, 4(2), 21-32 ISSN:2325–4513(PRINT) ISSN 2325 - 453X (ONLINE)

(20.67 cm) while H_{502} gave the shortest length of panicle (16.33 cm) Table (6). This result is in contrast with the result by **[33]** that Y_{26} is the shortest panicle (13 cm). **[34]** studied genetic variability for different characters in ten rice genotypes variability for various traits. He found that these traits are under the genetic control and could be used in the selection of the desirable traits. **[31]** indicated that there was no significant difference (P≤0.05) in panicle length among the varieties. Plant watered daily had longer panicles than plants watered every 2, 4 and 6 days. Nerica 2 was the least affected by water deficit and it had the longest panicle in plants watered after 4 and 6 days. Nerica 4 had the most pronounced reduction in panicle length and the highest water deficit compared to the control. Thats mean watering days affected directly panicle length. In this research plant irrigated 2 times a week influenced the panicle length of H_{221} and H_{502}. Highly statistic significant different number of grain/panicle in season 2011while there was a significant different in seasons 2013, Table (4, 5). W_8 had the highest number of grain/panicle (73.72) in season 2011 followed by H_{221} (71.07) .H_{502} had the lowest number of grain/panicle (35.62) then W_{12} (38.06), Table (6). In season 2013 the highest number of grain/panicle was given by H_{221} (67.77) followed by N_5 (65.17). H_{502} gave the lowest number of grain/panicle (39.12), Table (6). H_{221} had the highest length of panicle and fewest days to get flowering which might be the reason behind the Number of grain/panicles. **[35]** who studied 25 early maturing genotypes for interrelation ship and found that number of Grain panicles is positively correlated with panicle length, 1000-grain weight and grain yield. **[27]** also reported highly genetic heritability for the number of grain/panicle. This contrasted with **[34]** who reported highly significant variation for the grain/panicle for different genotypes. Other factors i.e. soil fertility, plant nutrient and weather condition might also responsible. There was highly statistical significant differences in number of filled grain/panicle in season 2013 and2011 among evaluated genotypes, table (4,5) In season 2011 the highest number of filled grain/panicle was given by W_8 (55.28) followed by Y_{33} (53.69), the lowest number of filled grain/panicle (21.43) was given by Z_3 and W_{19} (22.94), Table (6). In 2013, the lowest number of filled grain/panicle was given by W_8 and H_{502} (23.38 and 23.34) respectively, while H_{221} gave the highest number of filled grain/panicle (51.59) followed by N_5 and Y30 (46.21 and 45.41) respectively. Table (6). H_{502} had the lowest length of panicle and number of grain/panicle that highly affected the number of filled grain/panicle. This is matching with the result of **[36]** who noted that grains number in panicle is affected by factors such as panicle growth conditions and the formation of its component including primary and secondary branches and florets before emergence and also panicle fertility rate and photosynthetic products supply during the maturity period. Thus, it seems that due to thermal conditions, lower weight and more panicles infertility and further competition for absorbing photosynthetic products were among the causes of reduction in the number of filled grains per panicle. The result is in agreement with result by **[37,38]** There was a significant difference between cultivars in terms of the number of filled grains. This arises from the genetic difference and different cultivars' responses to environmental conditions. **[39]** attributed that to the contribution of climatic conditions to the number of filled grains during meiosis division time, the heading stage and maturity period. There were highly significant differences in percentage of unfilled grin/panicle (%) among evaluated genotypes in individual analysis of variance in seasons 2011 and there were no significant different in season 2013, table (4,5) W_{19} had the highest percentage of unfilled grin/panicle in season 2011 (53.93%), followed by Z_3 (53.61%). N_4 (9.52 %) and Y33 (11.81%) were the lowest percentage of unfilled grin/panicle, Table (6). In season 2013, W_8 gave the highest percentage of unfilled grin/panicle (48.25%) followed by N_{12} (44.99%), while N_4, Y_{26}, and H_{221} gave the lowest percentage of unfilled grin/panicle (28.15, 24.80, and 24.40%) respectively, Table (6). A result is in contrast with a result by **[40]** who showed that N_{14} was the lowest percent of unfilled grain/ panicle of (0.000). Highly statistical significant difference in 100-seed weight (g) among tested genotypes in season 2011, while a significant different in season 2013 table (4, 5). N_{15} gave the highest weight of 100-seed in season 2011 (3.300 gm), then Z_3 (3.00 gm) and Y_{24} (2.900 gm). Y_{30} (2.100 gm) and N_{14} (2.00 gm) gave the lowest weight of 100-seed, Table (6). In season 2013, Y_{33} (2.733 gm) and N_5 (2.53 gm) were the best weight of 100-seed, W_8 (1.70 gm), W_{19} (1.67 gm) and N_{15} (0.140 gm) were the lowest weight of 100-seed, Table (6). Grain weight is determined by the supply of assimilates during the ripening period and the capacity of the developing grain to accumulate the translocated assimilates **[41]**. In addition, grain weight is variable proportion of spikelet's sterility regulation by moisture, therefore the reason which may be behind grain yield loss with moisture of decrease in the number of filled grain/ panicle and 100 seed weight. Highly statistical significant difference for this trait among evaluated genotypes in grain yield (t/ha) season 2011 and 2013 table (4.5).In season 2011, H_{221} gave the highest grain yield (4.03 t/ha) followed by W_{19} (3.70 t/ha), while the lowest yield was given by Y_{33}, N_{17} (1.10 t/ha), N_4, and N_2 (1.06 t/ha), Table (6). Y_{33} and N_5 had the highest yield in season 2013 (2.43 and 2.17 t/ha), N_{12} gave the lowest yield (0.86 t/ha), Table (6). In season 2011, H_{221} had the highest number of leaves, earliest genotype to get flower and mature, highest number of

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panicles/m^2, longest panicle and highest number of grain/ panicle among the tested genotypes, also in season 2013, Y_{33} had and N_5 had the best weight of 100 seed (gm), N5 was the longest plant and highest number of grain/panicle that means there was a positive effect between these traits and grain yield, which might refer to a physiological reason. The same result was achieved by [29] who studied twelve genotypes of coars rise to check their yield performance in Kallar tract and reported highly significant variation in the grains yield which might be due to the environment [42] or the correlation of grain yield/plant with various yield contributing characteristic like fertility of soil, flag leaf area, grain/panicle and gain weight and correlation these traits. Similarly [35] reported positive correlation among number of panicle/plant, panicle length, number of grain /panicle and 1000-seed weight and grain yield /plant. [43, 44] suggested a determining role for temperature and day duration on panicle emergence and their impact on physiological, growth and maturity process and finally on the highest grain yield. Their results were in agreement with the finding of this result. Planting methods and growing environment are therefore among factors influencing yield of the crop. Proper spacing is said to ensure good water management [45] and photosynthetic activities and assimilate partitioning [46], thereby resulting in good yield in well-spaced rice fields. [47, 27, 48] studied the affect of environment, temperature genotypes and found significant heritability for yield contributing traits. C.V in 2011 was high that's because it contributed with other traits and it affected by the different of replication, that the replication 3 was higher than replication1 and 2, the water flow rabidly to replication 1 and 2.

Table 4: Summary ANOVA table for yield parameters, season 2011

Source	D.F	F. Value 2011						
		Number of Panicles / plant	Panicle length (cm)	Number of grain / panicle	Number of filled grain/ panicle	Percent-age of unfilled grain/ panicle	100-seed weight (gm)	Grain yield (t/ha)
Replication	2	1.3962	2.3905	0.9631	0.4371	0.7399	0.4016	0.3514
Variety	17	2.6732**	2.7124^{ns}	3.1770**	3.7856**	10.3985**	4.4595**	5.1293
Error	34	-	_	-	-	-	_	_
Total	53	-	_	-	-	-	_	_
EMS	_	6132.898	2.489	94.942	64.899	57.251	0.079	0.462
C.V%	_	14.51	10.34	18.56	21.90	25.48	11.46	35.97
SE±	_	18.4585	0.3719	2.2966	1.8988	1.7834	0.0664	0.1601

Table 5: Summary ANOVA table for yield parameter, season 2013

Source	D.F	F. Value 2013						
		Number of Panicles / plant	Panicle length (cm)	Number of grain/ panicle	Number of filled grain/ panicle	Percentage of unfilled grain/ panicle	100-seed weight (gm)	Grain yield (t/ha)
Replication	2	2.5875	0.8272	23.4829	22.2816	2.7420	0.3418	4.1191
Variety	17	0.9564^{ns}	1.6019^{ns}	1.0249^{ns}	1.5499^{ns}	1.3253^{ns}	1.8785*	4.9169**
Error	34	_	_	–	–	–	–	–
Total	53	_	_	–	–	–	–	–
EMS	_	7716.35	3.763	173.859	114.257	102.125	0.105	0.176
C.V%	_	25.22	10.10	24.34	29.34	29.29	15.67	29.27
SE±	_	25.3395	0.4572	3.1079	2.5194	2.3819	0.0762	0.0990

**=high significant, *= significant, NS =not significant

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Table 6: Mean of different yield parameter for season (2011-2013)

Genotypes	Number of Panicles/plant		Panicle length (cm)		Number of grain/ panicle		Number of filled grain/ panicle		Percentage of unfilled grain/ panicle		100-seed weight (gm)		Grain yield (t/ha)	
	2011	2013	2011	2013	2011	2013	2011	2013	2011	2013	2011	2013	2011	2013
W12	563.333 GH	423.67F	14.45 DEF	19.73EF	38.060 L	55.68 A	25.327 G	55.68 A	33.780E F	31.08HI	2.43C D	2.03CD EF	2.13E	1.03F G
N2	387.000 J	263.33C D	14.51 GH	18.45EF	42.560 K	55.16 F	37.367C D	55.16 F	12.190I JK	31.34D EF	2.57D E	2.07CD E	1.06J	1.03F G
Y26	495.000 FG	426.33C	15.45 K	20.78J	57.61B CD	57.08 F	35.613 DE	57.08 F	38.250C D	24.8DE F	2.4DE	2.07DE FG	2.40D	1.30D E
W19	619.000 AB	306.67I	16.33 H	19.51F G	50.34F GH	51.11 H	22.943 GH	51.11 H	53.933 A	37.7K	2.13J	1.67I	3.70B	1.03F G
Z3	455.000 H	274.33 H	17.39 FG	20.67B	47.02HI J	51.54 CD	21.430 H	51.54 CD	53.607 A	33.8GH I	3.0C	2.1CDE F	3.06C	1.10F
H221	573.667 AB	416.00 A	17.58 D	22.02D E	71.07 A	67.77 C	40.303C	67.77 C	47.573B	24.4J	2.37D E	2.1CDE F	4.03A	0.90G H
N15	576.667 EF	373.00F G	15.70 AB	20.38B	53.93D EF	56.82 DE	40.000C	56.82 DE	25.857 GH	36.0CD E	3.30H	2.0H	1.40H I	1.03F G
Y22	625.000 A	329.00 GH	16.09A	18.92A	43.69JK	57.43 DE	33.860E F	57.43 DE	23.120 H	30.9FG H	2.5B	2.1CDE F	1.40H I	1.16E F
H502	634.333 ABC	426.67 AB	13.10 EF	16.33B C	35.617L	39.12 AB	30.883F	39.12 AB	13.537I J	42.5J	2.40E F	1.93CD E	1.70F G	2.00C
Y33	446.667 HI	308.33C	13.03D E	19.89EF	60.810B	47.06 C	53.687 A	47.06 C	11.810J K	39.5DE F	2.60A	2.73EF G	1.10J	2.43A
W8	547.333 DEF	313.0D EF	16.95IJ	18.37I	73.717 A	44.84 C	55.250 A	44.84 C	25.047 GH	48.2GH I	2.267 CD	1.70CD	1.76F	0.90G H
N17	475.000 GH	449.67 A	13.42IJ	17.65C D	54.39D E	47.03 G	38.453C D	47.03 G	27.270 G	33.1B	2.167 DE	1.97G	1.10J	1.33D
N5	541.000 CD	350.00F G	12.68B C	19.8FG H	55.34C D	65.17 EF	33.340E F	65.17 EF	40.093C	29.1BC D	2.20C	2.53A	1.66F G	2.16B
N14	480.000 DEF	319.33F	16.52 I	19.40H	51.03EF G	47.76 F	43.663B	47.76 F	14.900I	41.09A	2.00F G	2.17H	1.20IJ	2.10B C
Y30	487.000 I	383.67 A	14.76 J	18.23C D	55.53C D	59.96 EF	35.500 DE	59.96 EF	36.420 DE	34.0FG H	2.10G H	2.03FG	1.90E F	2.06B C
Y24	643.333 AB	390.67C DE	16.00C D	17.95D E	46.27IJ K	47.39 B	32.873E F	47.39 B	30.843F	30.0I	2.90G H	1.93B	1.83F	2.10B C
N12	606.667 CDE	306.67E F	15.66H	17.32F GH	58.807B C	61.76 EF	37.230C D	61.76 EF	36.850 D	44.9BC	2.70I	1.80C	1.46G H	0.86H
N4	558.333 BC	209.33B C	15.1 DEF	20.12G H	49.19G HI	62.13 C	44.530B	62.13 C	9.520K	28.1EF G	2.20H I	2.20DE FG	1.06J	1.26D E
C.V%	14.51	25.22	10.34	10.10	18.26	24.34	21.90	24.34	25.48	29.29	11.46	15.67	35.97	29.27
L.S.D	30.63	34.36	0.6170	0.7587	3.811	5.155	3.151	5.155	2.959	3.952	0.1099	0.1267	0.2658	0.1641

Means with the same letter for each parameter are not significant at 5% level (LSD)

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Table (7) Estimates of genotypic (σ^2g), phenotypic (σ^2ph) variances, heritability (h2) of different characters of rice at (Shambat) during seasons 2011 and 2013for seasons (2011-2013)

traits	genotypic		Phenotypic		Heritability	
	2011	2013	2011	2013	2011	2013
Plant height(cm)	61.808	56.522	164.454	117.072	0.3758	0.4827
Number of Leaves/plant	0.05166	0.0233	0.21766	0.1993	0.2373	0.11690
Number of Tillers/plant	0.817	2.6756	1.274	3.7096	0.641	0.7212
Leaf Area(cm2)	9.823	31.542	30.878	68.558	0.3181	0.4600
Stem diameter(cm)	0.07466	0.012	0.4966	1.105	0.15032	0.114
Days to 50% flowering	26.870	25.302	67.101	34.111	0.400	0.7417
Days to 50 % maturity	98.363	7.8986	126.147	10.3416	0.779	0.7637
Number of Panicle/m2	3420.56	1895.627	9553.454	9611.97	0.358	0.1972
Panicle length(cm)	1.4206	0.755	3.9096	4.518	0.3633	0.1673
Number of Grain/panicle	68.897	1.391	163.839	75.145	0.4205	0.0185
Number of filled grain/panicle	60.260	20.9443	125.159	135.2013	0.4814	0.1549
Percentage of unfilled	179.35	11.0733	236.60	113.1983	0.758	0.0978
100seed weight(gm)	0.0916	0.0303	0.170	0.1353	0.5388	0.2239
Grain yield(t/ha)	0.635	0.230	1.097	0.406	0.57	0.566

Table (8) Estimates of Phenotypic coefficients of variation (PCV%) Genotypic coefficients of variation (GCV%) and Genetic advance (GA) of different characters of rice at (Shambat) during seasons 2011 and 2013

traits	PCV%		GCV%		GA	
	2011	2013	2011	2013	2011	2013
Plant height(cm)	20.026	16.216	12.277	11.267	9.928	10.7611
Number of Leaves/plant	14.193	14.016	6.9147	4.7925	0.2281	0.1076
Number of Tillers/plant	0.1193	24.030	0.095	20.408	0.188	2.8617
Leaf Area(cm2)	24.80	30.942	13.989	20.988	3.6415	7.847
Stem diameter(cm)	19.202	18.9171	7.4452	4.474	0.218	0.0435
Days to 50% flowering	10.775	7.6326	6.8188	6.5736	6.757	8.9243
Days to 50 % maturity	1.0738	2.7235	0.9482	2.3802	18.04	5.0596
Number of Panicle/m2	4.20736	28.1471	0.1083	12.4998	72.091	39.830
Panicle length(cm)	12.955	48.590	7.809	19.83	1.4800	0.7317
Number of Grain/panicle	0.2438	117.793	0.1581	16.0264	11.088	0.3305
Number of filled grain/panicle	0.3040	31.9132	0.210	12.560	11.095	3.7105
Percentage of unfilled	0.517	30.83.63	0.450	9.644	24.019	2.1439
100seed weight(gm)	16.781	17.829	12.318	8.437	0.457	0.1696
Grain yield(t/ha)	55.44	44.40	42.18	33.42	1.248	0.743

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IV. CONCLUSION

The M-state-c program for analysis and the least significant difference (LSD) showed that Handao221 was the best genotype that it was earliest genotype to get flower and rich 50 % maturity, longest panicle, and highest number of grain/panicle in both seasons. Highest number of leaves/plant and highly grain yield (t/ha) in season2011, highly number of tillers/plant in season 2013 among testing genotypes. Followed by WAB 19 which was earliest genotype to get flower , highest number of panicle/m^2, percentage of unfilled grain/ panicle (%), minimum number of filled grain/panicle that in season 2011. In season 2013 it had the best plant height (cm), highest measuring of leaf area (cm), and earliest genotype to rich 50 % maturity. These two genotypes can also be of a great benefit in selection for high yield rice genotypes and/ or hybridization between them or with any other high yield rice genotypes.

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