



Performance of lowland Green Super Rice Genotypes for the lowland rice Ecosystem in North-West Ethiopia

Abebaw Dessie*

Fogera National rice research and Training Center/Ethiopian Institute of Agricultural Research Center, Ethiopia

Abstract

The experiment was conducted in Pawe and Assosa from 2016-2018 main cropping seasons with the major objectives of high yielding and disease resistance in the lowland production system. A total of 20 genotypes including two checks were used for the study. The trial was laid out in randomized complete block design with three replications with plot size of 7.5 m². The combined analysis revealed that no genotype significant difference than the standard check on grain yield. This revealed that the tested genotypes failed to give high grain yield than the standard check (KOMBOKA) and there is no genotype for wider adaptability. The mean grain yield ranged from 2730.30kg/ha-1(G7) to 3683.40 kg ha⁻¹ (G13). Even though all tested genotypes failed on combined analysis for both locations, the separate location combined analysis revealed that there is a significant difference on grain yield and other agronomic characteristics than the standard check. The separate location combined analysis revealed that there is a significant difference on grain yield and other agronomic characteristics than the standard check. In Assosa, one genotype (G13) and in Pawe two genotypes (G14 and G1) revealed significant different than the standard check and gave grain yield advantage of 26.7%, 21.7% and 20.6%, respectively than the check.

Keywords: GSR, Stability, GGE bi-plot, Rice

Corresponding author: Abebaw Dessie

Fogera National rice research and Training Center/Ethiopian Institute of Agricultural Research Center, Ethiopia

Email: dessieabebaw7@gmail.com

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Introduction

Rice (*Oryza sativa* L.) which was originated from the tropics and subtropics is widely cultivated in diverse environments. The tremendous growth of human population worldwide has increased the demand for rice production [1], requiring an improvement of 50% by the year 2025 [2]. Due to its origin in tropical and subtropical regions, rice is more sensitive to cold stress than other cereals crop such as Wheat and Barley. Therefore, the production of rice is severely limited by cold stress in temperate areas [3]. Cold stress is the major factor affecting rice growth, productivity, its distribution worldwide [4]. Production of rice is affected primary due to its vulnerability to cold stress at seedling stage, as well as reproductive stage leading to spikelet sterility.

In Africa, rice also constantly increasing as staple food and there has been increasing demand in Africa in the past three decades from 1999-2018 [5]; however, these demands have not been commensurate with the total production and most of African countries are net importer of milled rice, which costs 6.4 billion USD annually [5]. Although rice has recently introduced to Ethiopia, recognizing its importance as a food security crop and a source of income and employment opportunity [6]. The production, productivity and consumption of rice in Ethiopia is constantly increasing in the country [7]. Ethiopia's geography is noticeable by immense depressions and mountains. Consequently vast arable lands are located at high altitudes more than 2000 meter above sea level. Rice can grow in wide agro climatic zones; however, low temperature stresses are serious challenges for rice farmers at high elevations in the tropics. Lack of cold tolerant rice varieties in the high lands of Ethiopia is the main constraints for the promotion of rice. Therefore, the main objectives of these studies were to evaluate the performance and stability of introduced lowland greed super rice gen-

otypes for their wider or specific recommendation in the North-West Ethiopia and similar agro ecologies.

Materials and Methods

Two sets of low land Green Super Rice (GSR) experiment were conducted. For the first experiment, a total of 16 genotypes (Table 1) were introduced from China/CAAS in 2014 with major objectives of cold tolerance and high grain yield whereas 40 GSR genotypes (Table 2) were introduced from IRRI in 2014 for the second experiment with major objective of high grain yield. Laboratory and field quarantine/observation for both sets of experiment were conducted in Holeta agricultural research center and Andasa, respectively in 2014 main cropping season. Both sets of preliminary variety trials were conducted in 2015 in woreda on station. For the second experiment, 36 genotypes including one check were planted again as preliminary variety trial in a place where temperature and humidity are high (Pawe). The plot size and type of design for observation and preliminary variety trial are not standard and vary based on the amount of seed and experimental area.

The experiment was conducted in Pawe and Assosa from 2016-2018. The locations are where the trials conducted differ in soil type, annual rain fall, altitude and annual temperature based on the experiments nature (Table 1). A total of 20 genotypes including one check were used (Table 2). The trial was laid out in randomized complete block design with three replications for both sets of experiments in all locations. Each plot had a size of 7.5 m² (Six rows with 5 m long with 0.25 m row spacing). Seed rate of 60 kg/ha was used and direct seeding methods in a row was applied. Fertilizer (UREA and DAP) were applied based on each location recommendation. All DAP was applied at the time of sowing. For UREA, split application was applied; 1/3 at sowing, 1/3 at active tillering and the remaining 1/3 during panicle initiations. Other agronomic practices were applied according to each location recommendations. The data were subjected to the GLM procedure for analysis of variance using SAS software V.9.0. And Genotype x environment and stability analysis were done by using Genstat 18th edition software.

Location	Altitude (m)	Latitude	Longitude	Annual rain fall (mm)	Temperature °C (Mean)	
					Max	Min
Pawe	1050	1109' N	3603' E	1457	32.8	17.2
Assosa	1590	10003'N	34059'E	1120	28.0	14.5

Table 1: Description of study environment for Lowland GSR experiment

No	Genotype	Seed Source	No	Genotype	Seed Source
1	GSR IR1-17-Y16-Y3-Y2	IRRI	11	GSR IR1-5-Y3-S2-SU1	IRRI
2	GSR IR1-15-D4-D1-Y1	IRRI	12	GSR IR1-11-Y10-D3-Y3	IRRI
3	GSR IR1-5-D1-D1	IRRI	13	GSR IR1-12-D10-S1-D1	IRRI
4	GSR IR1-12-Y4-Y1-D1	IRRI	14	GSR IR1-12-Y4-D1-Y2	IRRI
5	GSR IR1-8-S9-D2-Y2	IRRI	15	GSR IR1-12-S8-Y1-Y2	IRRI
6	GSR IR1-12-S2-Y3-Y2	IRRI	16	GSR IR1-5-S10-D1-D1	IRRI
7	GSR IR1-5-D20-D2-D1	IRRI	17	GSR IR1-8-S6-S3-S1	IRRI
8	GSR IR1-5-S10-D3-Y2	IRRI	18	GSR IR1-5-S12-D3-Y2	IRRI
9	GSR IR1-12-S8-Y1-S1	IRRI	19	GSR IR1-5-S8-D2-S1	IRRI
10	GSR IR1-8-S14-S1-SU1	IRRI	20	KOMBOKA (Check)-	Fogera/NRTTC

Table 2: List of genotypes used for national variety trial

Result and Discussion

Combined analysis of variance

The combined analysis of variance for grain yield, days to maturity, days to heading, plant height and thousand grains weight showed significant difference ($P \leq 0.01$); panicle length revealed significant different ($P \leq 0.05$). There was no significant difference observed among tested genotypes on filled grain per panicle. The analysis of environment effect also revealed significant difference ($P \leq 0.01$) for grain yield and other agronomic characters. Except panicle length and filled grain per panicle, the three way interaction of genotypes x environment x years were showed significant variation ($P \leq 0.01$) for yield and other agronomic characters (table 8).

The significant interaction difference of the three way interaction of

genotype x environment x years revealed that the possibility of getting genotypes which can be adapted widely/or specifically. As indicated (table 8), the mean grain yield of the 20 lowland green super rice genotypes ranged from 2730.30 kg/ha⁻¹ (G7) to 3683.40 kg/ha⁻¹ (G13) with the mean grain yield of 3310.04 kg/ha⁻¹. Compared to the standard check (G20), seven genotypes (G13, G14, G1, G12, G15, G4, G8,) were statistically high yielder than the check. However there is no genotype showed significant difference than the standard check on grain yield. This revealed that the tested genotypes failed to give high grain yield than the standard check (KOMBOKA) and there is no genotype for wider adaptability. Even though all tested genotypes failed on combined analysis for both locations, the separate location combined analysis revealed that there is a significant difference on grain yield and other agronomic characteristics than the standard check.

Genotype	Genotype code	DTH	DTM	PL	PH	FTP	FGP	Gykg/ha
GSR IR1-17-Y16-Y3-Y2	1	104.11	139.22	19.62	77.75	6.40	87.71	3653.70
GSR IR1-15-D4-D1-Y1	2	104.89	140.22	19.93	78.21	6.08	96.84	2929.70
GSR IR1-5-D1-D1	3	105.61	142.72	20.53	78.36	6.57	96.01	3347.10
GSR IR1-12-Y4-Y1-D1	4	105.56	140.17	19.81	78.48	6.37	91.57	3436.40
GSR IR1-8-S9-D2-Y2	5	107.94	142.17	20.41	79.26	6.40	90.35	3307.00
GSR IR1-12-S2-Y3-Y2	6	106.50	142.50	21.23	79.39	5.91	91.98	3351.80
GSR IR1-5-D20-D2-D1	7	107.11	142.00	19.47	79.43	6.71	95.68	2730.30
GSR IR1-5-S10-D3-Y2	8	110.78	144.78	19.95	80.51	5.98	93.27	3409.20
GSR IR1-12-S8-Y1-S1	9	104.17	137.72	20.02	80.87	6.47	86.69	3089.50
GSR IR1-8-S14-S1-SU1	10	104.56	140.00	21.70	81.31	5.68	100.6	3113.80
GSR IR1-5-Y3-S2-SU1	11	106.28	141.67	21.51	81.43	5.92	89.61	3136.40
GSR IR1-11-Y10-D3-Y3	12	103.78	138.61	20.48	81.72	6.12	91.29	3603.30
GSR IR1-12-D10-S1-D1	13	108.44	142.22	19.89	81.91	5.72	90.73	3683.40
GSR IR1-12-Y4-D1-Y2	14	105.72	139.61	19.59	82.22	6.41	91.97	3644.50
GSR IR1-12-S8-Y1-Y2	15	106.89	142.33	19.79	83.28	5.71	92.67	3578.90
GSR IR1-5-S10-D1-D1	16	108.17	142.50	20.06	83.44	5.78	100.8	3211.20
GSR IR1-8-S6-S3-S1	17	105.44	141.00	19.38	83.57	6.19	87.48	3113.90
GSR IR1-5-S12-D3-Y2	18	105.39	141.06	19.69	83.89	6.99	101.9	3284.80
GSR IR1-5-S8-D2-S1	19	104.22	140.28	19.82	85.62	5.42	98.91	3205.00
KOMBOKA (Check)	20	103.89	139.00	20.90	86.09	5.97	97.80	3371.00
	Mean	106.00	140.99	20.19	81.34	6.14	93.70	3310.04
	CV (%)	3.30	2.50	10.70	7.10	25.60	14.60	18.90
	LSD (5%)	2.32	2.36	1.42	3.81	1.03	8.99	411.09
	Genotype (G)	***	***	*	***	NS	***	***
	Environment (E)	***	***	***	***	***	***	***
	Year (Y)	***	***	NS	***	***	***	***
	G*Y	***	***	**	***	NS	*	***
	G*E*Y	***	***	NS	***	***	NS	***

Table 3: Mean grain yield and other yield related parameters of 20 lowland green super rice genotypes at Assosa and Pawe over three years (2016-2018)

Note: *, **, and *** refers to significant at 5%, 1% and 0.1% level, NS=non-significant, CV= coefficient of variation, LSD= list significance different, G*E= genotype by environment, G*E*Y= genotype by environment by year, DH= days to 50% heading, DM= days to 85% maturity, FGP= filled grains/panicle, PH= plant height (cm), PL= panicle length (cm) and Gykg/ha= grain yield (kg/ha)

In Assosa, the three years combined grain yield ranged from 1872.5 kg/ha-1 to 3809.7 kg/ha-1 and mean grain yield of 2836.23 kg/ha-1. Seven genotypes (G13, G12, G6, G4, G3, G15 and G8) showed statistically high-

er grain yield than the standard check (table 9). Only one genotype (G13) showed significant different than the check and gave grain yield advantage of 26.7% than the check.

Genotype	Genotype code	DTH	DTM	PL	PH	FTP	FGP	TGW	GY
GSR IR1-17-Y16-Y3-Y2	1	115.89	153.00	19.61	83.94	4.16	74.22	22.48	2804.20
GSR IR1-15-D4-D1-Y1	2	115.11	152.56	19.90	85.91	4.44	86.07	23.82	2194.50
GSR IR1-5-D1-D1	3	114.67	155.67	20.98	91.96	4.73	84.20	24.42	3265.70
GSR IR1-12-Y4-Y1-D1	4	116.78	153.56	20.02	89.81	5.00	82.56	23.74	3239.60
GSR IR1-8-S9-D2-Y2	5	115.22	153.11	22.09	91.27	4.56	82.87	24.82	2802.70
GSR IR1-12-S2-Y3-Y2	6	115.67	153.22	23.50	85.39	4.78	81.13	23.37	3287.00
GSR IR1-5-D20-D2-D1	7	119.11	155.56	20.70	90.46	4.44	85.29	52.21	1872.50
GSR IR1-5-S10-D3-Y2	8	119.56	156.22	20.83	93.56	4.38	81.91	52.00	3143.20
GSR IR1-12-S8-Y1-S1	9	108.22	143.67	22.20	93.49	5.16	72.20	26.53	2775.00
GSR IR1-8-S14-S1-SU1	10	113.11	150.33	23.56	100.67	4.91	94.71	27.38	2697.90
GSR IR1-5-Y3-S2-SU1	11	116.22	154.78	22.32	93.67	4.02	76.29	25.03	2574.60
GSR IR1-11-Y10-D3-Y3	12	118.00	154.00	20.42	100.32	4.18	83.73	22.93	3440.40
GSR IR1-12-D10-S1-D1	13	119.89	154.78	21.02	91.03	4.51	82.09	25.41	3809.70
GSR IR1-12-Y4-D1-Y2	14	114.00	150.33	19.58	87.72	4.82	76.04	23.50	2743.20
GSR IR1-12-S8-Y1-Y2	15	118.11	155.56	20.80	91.23	4.22	88.36	23.86	3170.80
GSR IR1-5-S10-D1-D1	16	120.00	156.00	20.61	91.96	4.60	95.33	24.02	2449.00
GSR IR1-8-S6-S3-S1	17	114.56	152.22	20.69	97.84	4.40	68.40	25.19	2402.80
GSR IR1-5-S12-D3-Y2	18	115.11	152.89	20.78	94.83	4.62	103.0	24.47	2569.00
GSR IR1-5-S8-D2-S1	19	113.56	151.56	21.04	97.16	4.20	87.33	25.77	2475.10
KOMBOKA (Check)	20	111.44	148.56	21.62	96.29	4.33	85.60	22.58	3007.80
	Mean	115.71	152.88	21.11	92.43	4.52	83.57	27.18	2836.23
	CV (%)	2.8	2.3	12.9	7.5	18.5	18.5	93.8	20.8
	LSD (5 %)	3.05	3.21	2.54	6.44	0.78	14.42	23.79	551.95
	Genotype (G)	***	***	NS	***	NS	***	NS	***
	Year (Y)	NS	***	NS	NS	NS	NS	NS	***
	G*Y	NS	NS	NS	NS	NS	NS	NS	

Table 4: Mean grain yield and other yield related parameters of 20 lowland green super rice genotypes at Assosa over three years (2016-2018)

Note: *, **, and *** refers to significant at 5%, 1% and 0.1% level, NS=non -significant, CV= coefficient of variation, LSD= list significance different, G*E= genotype by environment, DH= days to 50% heading, DM= days to 85% maturity, FGP= filled grains/panicle, PH= plant height (cm), PL= panicle length (cm), TGW=thousand grain weight and Gykg/ha= grain yield (kg/ha)

In Pawe, The combined analysis of variance (table 10) for grain yield, days to maturity, days to heading and plant height showed significant difference ($P \leq 0.01$); thousand grain weights revealed significant different ($P \leq 0.05$). There was no significant difference observed among tested genotypes on fertile tillers per plant and fertile grain per pani-

cle. Except plant height ($P \leq 0.01$) and grain yield ($P \leq 0.05$), there is no genotype by year interaction significant difference. The mean grain yield ranges from 3416.7 kg/ha-1 to 4545.8 kg/ha-1. Two genotypes (G14 and G1) showed significant different than the check and gave yield advantage of 21.7% and 20.6%, respectively (table 10).

Genotype	Genotype code	DTH	DTM	PL	PH	FTP	FGP	TGW	Gykgaha
GSR IR1-17-Y16-Y3-Y2	1	92	125	19.62	77.07	8.64	101.20	21.17	4503.20
GSR IR1-15-D4-D1-Y1	2	95	128	19.96	72.60	7.71	107.62	25.94	3664.80
GSR IR1-5-D1-D1	3	97	130	20.09	74.93	8.40	107.82	21.50	3428.40
GSR IR1-12-Y4-Y1-D1	4	94	127	19.60	73.04	7.73	100.58	22.38	3633.10
GSR IR1-8-S9-D2-Y2	5	101	131	18.73	67.51	8.24	97.83	20.06	3811.30
GSR IR1-12-S2-Y3-Y2	6	97	132	18.96	70.11	7.04	102.82	20.89	3416.70
GSR IR1-5-D20-D2-D1	7	95	128	18.24	66.27	8.98	106.07	20.06	3588.20
GSR IR1-5-S10-D3-Y2	8	102	133	19.07	69.89	7.58	104.62	20.22	3675.20
GSR IR1-12-S8-Y1-S1	9	100	132	17.84	70.33	7.78	101.18	19.23	3403.90
GSR IR1-8-S14-S1-SU1	10	96	130	19.84	71.51	6.44	106.64	21.17	3529.70
GSR IR1-5-Y3-S2-SU1	11	96	129	20.69	70.78	7.82	102.93	22.89	3698.20
GSR IR1-11-Y10-D3-Y3	12	90	123	20.53	70.91	8.07	98.84	21.73	3766.10
GSR IR1-12-D10-S1-D1	13	97	130	18.76	65.38	6.93	99.38	19.94	3557.10
GSR IR1-12-Y4-D1-Y2	14	97	129	19.60	69.24	8.00	107.89	21.96	4545.80
GSR IR1-12-S8-Y1-Y2	15	96	129	18.78	67.62	7.20	96.98	20.73	3987.00
GSR IR1-5-S10-D1-D1	16	96	129	19.51	69.78	6.96	106.36	21.28	3973.30
GSR IR1-8-S6-S3-S1	17	96	130	18.07	69.93	7.98	106.56	20.22	3825.00
GSR IR1-5-S12-D3-Y2	18	96	129	18.60	72.31	9.36	100.87	20.56	4000.60
GSR IR1-5-S8-D2-S1	19	95	129	18.60	65.47	6.64	110.49	20.06	3934.90
KOMBOKA (Check)	20	96	129	20.18	70.27	7.60	110.00	19.83	3734.20
	Mean	96	129	19.26	70.25	7.76	103.83	21.09	3783.84
	CV (%)	3.9	2.9	7.1	6.3	26.7	10.8	14.9	17.2
	LSD (5%)	3.46	3.48	1.28	4.16	1.94	10.51	2.94	608.89
	Genotype (G)	***	***	***	***	NS	NS	*	***
	Year (Y)	***	***	***	***	***	***	***	***
	G*Y	NS	NS	NS	***	NS	NS	NS	*

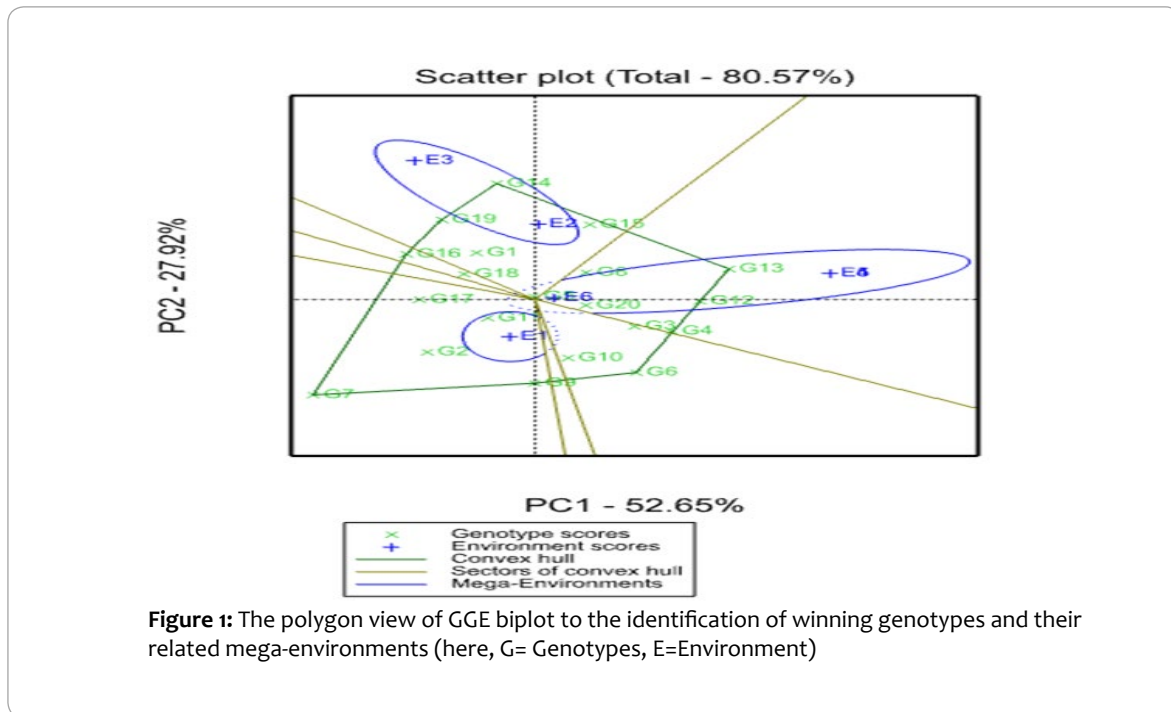
Table 5: Mean grain yield and other yield related parameters of 20 lowland green super rice genotypes at Pawe over three years (2016-2018)

Note: *, **, and *** refers to significant at 5%, 1% and 0.1% level, NS=non-significant, CV= coefficient of variation, LSD= list significance different, G*E= genotype by environment, DH= days to 50% heading, DM= days to 85% maturity, FGP= filled grains/panicle, PH= plant height (cm), PL= panicle length (cm), TGW=thousand grain weight and Gykgaha= grain yield (kg/ha)

Polygon view of GGE biplot analysis

The polygon view of GGE biplot (Fig1) is the best way for the identification which-won-where by visualizing the interaction patterns between genotypes and environments [8][9]. In this GGE biplot, the vertex genotypes were G13, G14, G19, G16, G7 and G6 having the largest distance from the origin. In the present study, seven rays in Fig.1, the biplot was divided into seven sectors and the environments only into three

of them. The rest four sectors in the polygon had no test environment. The vertex genotypes (G13 and G14) were the highest yielding genotypes in E5 and E3, respectively. G6, G10, G9 and G18 were not adapted to any of the tested environments. Both discriminating ability and representativeness view of the GGE biplot are the most important measures of testing environment, which provide not only valuable but also unbiased information about the testing genotypes [10].



Conclusion and Recommendations

The present study revealed that there are no genotypes higher than the standard check for grain yield and related agronomic traits. However in Pawe two genotypes, G14 (GSR IR1-12-Y4-D1-Y2 and G1 (GSR IR1-17-Y16-Y3-Y2) gave higher grain yield with yield advantage of 21.7% and 20.6%, respectively than the check. And in Assosa G13 (GSR IR1-12-D10-S1-D1) gave grain yield advantage of 26.7% than the check. Therefore further investigation of regional variety trial is necessary for Pawe and Assosa areas to recommend for their specific locations.

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