



# Variability, Heritability and Genetic Advance of Introduced Upland Rice Genotypes at Fogera in North Western Ethiopia

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**Abstract:** Variability, heritability and genetic advance are basic in order to provide information for plant breeding programs. Forty nine upland rice genotypes were tested in 7\*7 simple lattice design at Fogera in Wereta station of Adet Agricultural Research Center in 2012/13. The objectives of the study were to estimate the genetic variability, heritability and genetic advance of the genotypes tested. Analysis of variance revealed that there was highly significant difference among the 49 genotypes for all the characters studied. Accessions IR 78937-B-3-B-B-1 and IR 78937-B-3-B-B-2 had the highest yield with a score of 5374.5 kg/ha and 5305.6 kg/ha respectively. The high yielding genotype IR 78937-B-3-B-B-1 had a yield advantage of 57% and 22.2%, respectively, as compared to standard checks Nerica-4 and Hidasie. Phenotypic coefficient of variation (PCV) values ranged from 2.5% for panicle length to 49.98% for number of spikelet per panicle. While the genotypic coefficient of variation (GCV) ranged from 2.4% for panicle length to 47.6% for number of spikelet per panicle. Number of tiller per plant (22.47%), number spikelet per panicle (49.98%), thousand seed weight (25.56%) and yield (23.93%) had higher PCV values. The PCV values for flag leaf length (14.79%), flag leaf width (16.12%), and culm length (16.42%) and number of panicle per plant (16.32%) were medium. Flowering cycle (7.81%), maturation cycle (2.9%), and panicle length (2.5%) had lower PCV values. GCV values were low for flowering cycle (7.21%), maturation cycle (1.82%) and panicle length (2.4%); medium for flag leaf length (14.26%), flag leaf width (15.39%), culm length (15.19%) and number of panicle per plant (15.72%); high for number of tillers per plant (22.18%), yield (23.07%), thousand seed weight (25.18%) and number of spikelet per panicle (47.60%). The high GCV values of these characters suggest that genetic impact is higher and environmental influence is lower. This study generally had indicated that there was significant genetic variability or divergence among the genotypes. Thus, the improvement program of the upland rice genotypes through direct selection rather than a lengthy crossing program is recommended.

**Keywords:** Variability, Heritability, Morphological Traits

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## 1. Introduction

Rice belongs to the genus *Oryzae*, and is one of the leading food crops in the world. As such, it is a staple food of over a half of the world's population, mostly in Asia. It is the second most cultivated cereal after wheat. It is the world's most important food crop, which occupies 11% of the world's total arable land; it supplies 2,808 calories/person/day, which represents 21% of the total calorie supply. It is source of income for more than 100 million householders around the world and is one of the crops responsible for the so-called

green revolution that happened in the 1960s and 1970s. Upland rice is one of the main staple crop or staple food in inter-tropical highland areas. It is grown in rainfed, naturally well-drained soils without surface water accumulation, usually without water logging. Land slopes vary from 0 to more than 30% [5].

Rice cultivation and its utilization as a food crop in Ethiopia is a very recent phenomenon. The cultivation of the crop has begun at Fogera, Amhara Region and Gambella plains in the early 1970's. Currently, Fogera, Gambella, Metema, and Pawe are major rice producing areas in Ethiopia. The occurrence of

wild rice *Oryza longistaminata* in the swampy and water logged areas of Fogera locally known as Zurha and Gambella plains is believed to have prompted the cultivation of the crop at these locations. Subsequently, rice adaptation and screening experiments were initiated and conducted at Fogera, Gambella, Werer, Debre Zeit, and Arba Minch since its introduction in the 1970's [8].

Knowledge on the extent and pattern of genetic variability present in a population is absolutely essential for further improvement of the crop. Besides, knowledge of the naturally occurring diversity in a population helps to identify diverse groups of genotypes that can be useful for the breeding program. Such information is scarce in upland rice production system of Ethiopia. Hence, the present study is initiated with the following objectives:

### 1.1. Objective

To assess the magnitude of variability, heritability and genetic advance for traits as well as to estimate the genetic divergence among tested genotypes.

### 1.2. Materials Used and Experimental Design

Forty-nine upland genotypes/lines which are comprised from different preliminary variety trials and variety adaptation trial accessions were evaluated together with two standard check varieties. The experiment was conducted in a simple lattice design with two replications. The experimental plots were prepared by tractor ploughing and harrowing. Clean seeds of each genotype were selected and planted on well prepared plots. The plot size was 2.5 m long and 0.4 m wide, consisting of two rows per plot with 20 cm spacing between them and 0.3 m spacing between plots as well as 1 m spacing between blocks. Sowing was done by hand drilling at a seed rate of 60 kg/ha. Nitrogen was applied in the form of urea at the rate of 100 kg/ha, in three splits, i.e., one-third at planting, tillering and panicle initiation. Phosphorus was applied in the form of Di-Amonium phpsphate (DAP) at the rate of 100 kg/ha at planting. All other management practices were uniformly applied to all plots using recommended practices. Data on plot and plant basis was collected. Data on plant basis were recorded by randomly taking six plants from each experimental plot.

**Table 1.** Forty nine upland genotypes/accessions used in the study.

Entry.No	Genotypes	Seed source
1	IR 28635-B-B-23-1	AARC
2	IR 83399-B-B-52-1	"
3	IR 82310-B-B-67-2	"
4	IR 82639-B-B-115-1	"
5	IR 79915-B-83-4-3	"
6	IR 78937-B-4-B-B-B	"
7	IR 82319-B-B-103-2	"
8	IR 78913-B-10-B-B-B	"
9	IR 78877-048-B-B-3	"
10	IR 78948-B-1-B-B-B	"
11	UPLR1-7	"
12	IR 78937-B-3-B-B-2	"
13	IR 82039-B-B-103-4	"

Entry.No	Genotypes	Seed source
14	IR 82635-B-B-32-4	"
15	IR 82638-B-B-147-1	"
16	IR 82639-B-B-118-3	"
17	IR 82589-B-B-114-3	"
18	IR 82635-B-B-58-1	"
19	IR 82635-B-B-88-2	"
20	IR 82639-B-B-140-1	"
21	IR 82635-B-B-4 7-1	"
22	IR 82635-B-B-72-2	"
23	IR 82589-B-B-7-2	"
24	IR 78937-B-3-B-B-1	"
25	IR 78940-B-22-B-B-5B1	"
26	IR 77298-14-1-2-10	"
27	KMP34	"
28	IR 60080-46A	"
29	ACCU16 bar 9-16-17-3-B-1	"
30	ACCU 16 bar 5-6-22-2B-1	"
31	ACCU 16 bar 12-13-14-B-1	"
32	ACCU 16 bar 12-12-33-2B-1	"
33	ACCU 16 bar 15-3-22-2-B-B	"
34	ACCU 16 bar 12-14-19-3-B-B	"
35	ACCU 16 bar 9-4-16-3-B-1	"
36	ACCU 16 bar 13-13-2-2-B-B	"
37	ACCU 16 bar 9-7-20-4-B-B	"
38	ACCU 16 bar 4-8-17-2-8-8	"
39	NERICA 11	"
40	FOFIFA 3730	"
41	FOFIFA 3737	"

**Table 1.** Forty nine upland genotypes/accessions used in the study (Continued).

Entry No	Genotypes	Seed source
42	NERICA 14	AARC
43	NERICA 15	"
44	NERICA 8	"
45	NERICA 9	"
46	NERICA 15	"
47	FOFIFA 4129	"
48	NERICA 4 (Check)	"
49	HIDASIE (Check)	"

Source: AARC (Adet Agricultural Research Center).

## 2. Methods of Data Collection

Quantitative descriptors were used to collect data. The data for the following characters were recorded from six randomly taken plants from each experimental plot and the average was used to in subsequent data manipulation.

- 1) Culm length (cm): measures from the base of the plant to the base of the panicle.
- 2) Flag leaf length (cm): measures length of the flag leaf, from the ligule to the tip of the blade.
- 3) Flag leaf width (cm): measures width at the widest portion of the flag leaf.
- 4) Number of tillers per plant: recorded as the total number of grain-bearing and non bearing tillers.
- 5) Number of panicles per plant: number of primary panicle branches attached to the basal whorl of the panicle.
- 6) Panicle length (cm): Length of main axis of panicle measured from the panicle base to the tip.
- 7) Number of spikelets per panicle: total counted spikelets within a single panicle.

- 8) Flowering cycle: Number of days until 50% flowering starting from germination.
- 9) Maturation Cycle: Number of days until 50% of the panicles matured.
- 10) 1000-grain weight (gm): Random sample of 1000 well-developed, whole grains and dried to 13% moisture content weigh on a precision balance.
- 11) Grain yield (kg): estimated from the harvestable rows of the plot.

### 3. Data Analysis

Analysis of variance

Analysis of variance (ANOVA) was conducted using SAS computer software program following SAS (Version 9.1) statement for simple lattice design.

Estimation of genetic parameters

Estimation of variance components

The phenotypic and genotypic coefficients of variation were estimated according to the method suggested by Burton and Devane (1953) as follows: [3]

Environmental variance ( $\sigma^2_e$ ) =  $MS_e$

$$\text{Genotypic variance } (\sigma^2_g) = \left[ \frac{MS_g - MS_e}{r} \right]$$

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_e$$

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sigma_p}{\bar{x}} \times 100$$

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sigma_g}{\bar{x}} \times 100,$$

Where,  $\bar{x}$  = grand mean of character. Generally, quantitative

characters or traits could be highly influenced by environment which could be estimated through the combination genotypic (GCV), phenotypic (PCV) and environmental (ECV) coefficient of variations. According to Deshmukh *et al* (1986), PCV and GCV values >20% are regarded as high, values <10% are considered to be low and values between 10% and 20% to be medium [4].

*Estimation of Heritability in Broad Sense*

Broad sense heritability ( $h^2$ ) expressed as the percentage of the ratio of the genotypic variance ( $\sigma^2_g$ ) to the phenotypic variance ( $\sigma^2_p$ ) and was estimated on genotype mean basis as described by Allard (1960) as: [2]

$$h^2 = \left[ \frac{\sigma_g^2}{\sigma_p^2} \right] \times 100$$

### 4. Results and Discussion

The result of analysis of variance (ANOVA) of 11 quantitative characters for the 49 upland rice genotypes is presented in Table 2. There was highly significant difference ( $P < 0.01$ ) among the tested genotypes indicating variation in measured traits. Veasey *et al* (2008) also found significant differences and high variability for traits of *Oryza glumaepatula* mainly for the characters number of tillers, plant height at flowering, leaf length and width, culm length, days to heading, panicle number, panicle height, flag leaf length, spikelet length and awn length. Simple lattice was more efficient over RCBD in detecting variation of most characters except flag leaf width (98.41%), number of panicle per plant (94.34%), and number of spikelet per panicle (90.43%) [11].

**Table 2.** Analysis of variance for 11 quantitative characters of 49 upland rice genotypes evaluated at Fogera 2012/13.

Source of variation	Mean squares											
	DF	FLL	FLW	CL	NTPP	FC	MC	NPP	NSPP	PL	TSW	YLD
Replication	1	8.75	0.11	3.94	3.21	2.15	0.26	4.88	3.63	3.81	5.87	94178
Treatment Undj.	48	27.68 **	0.13**	235.38**	7.03**	109.86**	21.5**	3.77**	168.83**	6.46**	77.73**	1676924**
Blocks with in reps (Adj)	12	0.17	0.003	0.77	0.16	14.62	11.46	0.11	0.27	0.24	1.23	81753
Error												
Intrablock	36	0.12	0.004	0.43	0.09	8.80	9.38	0.14	0.4350	0.23	1.17	53500
RCBD	48	0.13	0.004	0.51	0.11	10.25	9.90	0.13	0.3934	0.23	1.18	60564
Relative Efficiency to RCBD (%)		101.99	98.41	107.81	107.43	105.99	100.96	94.34	90.43	100.06	100.06	104.2
Coefficient of variation (%)		2.12	4.54	1.067	4.83	3.23	2.30	5.43	0.92	2.84	4.61	6.35

\*\* indicates significant at 1% probability level DF: Days to Flowering, FLL: Flag leaf length (cm), FLW: Flag leaf width (cm), CL: Culm length (cm), NTPP: Number of tiller per plant, FC: Flowering cycle, MC: Maturation cycle, NPP: Number of panicle per plant, NSPP: Number of spikelet per panicle, PL: Panicle length (cm), TSW: Thousand seed weight (gm), YLD: Yield (Kg/ha).

#### 4.1. Mean, Range and Estimates of Genetic Parameters

##### 4.1.1. Mean and Range

There was wide variation from seed yield which ranged from 1556.5 kg/ha to 5374.5 kg/ha with a mean of 3883.7 kg/ha, Which indicates that the genotypes tested have divergence base which will have importance for future breeding and selection. Accessions IR 78937-B-3-B-B-1 and IR 78937-B-3-B-B-2 had the highest yield with a score of 5374.5 kg/ha and 5305.6 kg/ha respectively. The high

yielding genotype IR 78937-B-3-B-B-1 had a yield advantage of 57% and 22.2%, respectively, as compared to standard checks Nerica-4 and Hidasie.

In the study of genetic variability for yield and related attributes of upland rice genotypes in semi arid zone, the high yielding genotypes were found to be WAB891 SG14, WAB981 SG33 and Yunlu No. 30 with grain yields of 3,600 kg, 3,500 kg and 3,400 kg respectively [7]. This actually is very far result as compared to the finding of this study.

**Table 3.** Mean performance of 49 upland rice accessions for eleven quantitative characters tested at Fogera 2012/13.

Genotypes	FLL	FLW	CL	NTPP	FC	MC	NPP	NSPP	PL	TSW	YLD
IR 28635-B-B-23-1	28.7	1.8	68.5	10.6	103.3	139.5	9.7	85.4	20.5	16	4230
IR 83399-B-B-52-1	24.9	1.5	71.5	9.7	93.2	135.5	10.1	68.8	19.8	22	4059
IR 82310-B-B-67-2	24.9	1.3	72.4	9.4	100.1	135.0	8.5	60.8	22.9	24	5107
IR 82639-B-B-115-1	25.4	1.4	66.9	9.7	103.4	134.0	8.6	71.0	20.9	22	5038
IR 79915-B-83-4-3	21.7	1.3	69.8	7.6	96.1	131.0	9.9	68.6	19.7	20	4321
IR 78937-B-4-B-B-B	26.7	1.6	59.6	10.8	106.7	140.0	7.0	62.0	19	20	4401
IR 82319-B-B-103-2	28.5	1.9	68.4	8.7	96.0	134.5	8.8	67.3	18.9	25	4764
IR 78913-B-10-B-B-B	25.9	1.9	61.1	6.0	107.1	131.5	12.5	75.8	18	25	4129
IR 78877-048-B-B-3	21.7	1.3	61	10.9	109.1	138.5	7.9	70.5	15.5	17	1557
IR 78948-B-1-B-B-B	21.5	1.5	68.6	7.0	97.0	133.0	6.4	65.8	20.9	22	3074
UPLR1-7	32.8	2	52.7	6.9	109.2	136.5	6.3	58.5	18.7	20	3068
IR 78937-B-3-B-B-2	31.8	1.8	62.7	9.7	112.5	141.5	9.5	65.0	19.8	21	5306
IR 82039-B-B-103-4	29.7	1.7	82.8	9.8	97.1	135.5	10.6	74.3	18.3	23	3536
IR 82635-B-B-32-4	30	1.9	72.8	7.1	100.9	138.0	7.9	78.5	21.8	22	5186
IR 82638-B-B-147-1	32.7	1.7	63.9	9.9	105.7	135.0	9.5	92.5	18.5	20	5154
IR 82639-B-B-118-3	25.8	1.5	63.2	8.8	108.1	135.0	11.8	86.1	23.1	22	3876
IR 82589-B-B-114-3	25.6	1.6	62.3	11.6	107.5	137.5	10.5	82.8	22.1	16	4041
IR 82635-B-B-58-1	21	1.5	69.1	9.0	103.2	135.0	8.5	88.2	21	20	4432
IR 82635-B-B-88-2	26.5	1.5	66	8.5	100.0	135.0	9.1	76.3	20	20	4851
IR 82639-B-B-140-1	31.5	1.5	72	7.5	99.6	133.0	9.8	70.7	20.8	24	4367
IR 82635-B-B-4 7-1	26.3	1.7	66	6.8	99.4	133.0	9.5	77.5	17.6	27	2322
IR 82635-B-B-72-2	24.5	1.5	56.9	7.6	103.6	133.5	7.7	72.7	15.8	19	3602
IR 82589-B-B-7-2	25.3	1.7	54.2	6.4	108.5	138.5	7.8	72.8	18.5	16	2842
IR 78937-B-3-B-B-1	21.7	1.7	78.8	8.5	99.4	132.0	8.4	92.3	19.5	26	5375
IR 78940-B-22-B-B-5B1	28.8	1.7	56.6	7.9	102.7	136.0	9.6	76.8	20.5	20	5234
IR 77298-14-1-2-10	31.5	1.9	74.9	7.4	103.4	135.0	8.5	82.8	19.8	24	4946

**Table 3.** Continued.

KMP34	19.8	1.1	51.6	11.5	100.0	139.0	6.8	52.7	18.5	20	3117
IR 60080-46A	19.7	1.1	43.7	9.9	101.8	141.0	6.5	69.8	15	18	4939
ACCU16 bar 9-16-17-3-B-1	27.8	2.2	77.8	7.6	103.8	140.0	9.6	70.1	21.5	23	2683
ACCU 16 bar 5-6-22-2B-1	26.3	2.1	84.5	8.6	78.8	136.0	9.5	69.5	20.5	17	3914
ACCU 16 bar 12-13-14-B-1	29.9	2	94.8	5.7	87.7	138.0	9.8	84.0	19.8	26	3200
ACCU 16 bar 12-12-33-2B-1	25.8	1.8	84.1	7.5	88.9	135.0	9.0	69.7	21	26	3114
ACCU 16 bar 15-3-22-2-B-B	29.5	1.5	76.6	6.9	97.2	137.0	9.5	70.5	21.1	25	4041
ACCU 16 bar 12-14-19-3-B-B	22.5	1.5	79.9	6.3	84.7	134.5	7.5	65.5	18.5	22	3803
ACCU 16 bar 9-4-16-3-B-1	22	1.3	83.3	7.1	91.8	133.5	7.5	56.2	17.6	26	2180
ACCU 16 bar 13-13-2-2-B-B	34.2	1.7	74.9	6.6	100.8	120.0	8.9	78.1	18.2	26	3000
ACCU 16 bar 9-7-20-4-B-B	22.7	1.5	81.8	6.9	105.7	135.5	9.8	75.2	17	26	3202
ACCU 16 bar 4-8-17-2-8-8	23.1	2	81.5	7.5	89.6	135.0	7.7	71.0	18.9	24	2865
NERICA 11	28.5	1.7	88.7	11.5	101.4	133.0	8.8	79.7	19	20	3408
FOFIFA 3730	29	1.9	80.4	7.5	92.1	138.0	7.1	71.3	18.5	25	4347
FOFIFA 3737	25.5	1.8	85.9	10.6	95.2	135.0	10.8	74.8	18.1	22	4434
NERICA 14	30.8	1.9	89.5	7.7	91.5	136.5	9.2	79.0	18.8	20	4539
NERICA 15	22.8	1.8	73.9	11.0	92.4	134.5	6.9	74.8	22.8	23	2610
NERICA 8	31.7	2	77.5	11.8	88.3	136.0	7.5	70.5	21.2	24	3503
NERICA 9	23.5	1.9	69.8	8.5	89.2	135.5	8.9	61.8	20	26	3517
NERICA 15	24.7	2	77.7	7.9	88.5	135.5	10.5	90.7	18.2	23	3404
FOFIFA 4129	23.5	1.5	74.4	7.4	97.2	135.5	8.5	86.8	20.7	25	4364
NERICA 4 (Check)	23.7	1.5	73.7	11.5	87.3	133.0	8.5	62.8	17.8	29	3419
HIDASIE (Check)	27.5	1.5	77.8	9.9	93.1	135.0	7.5	70.7	19.5	22	4471
Mean	26.3	1.7	71.56	8.58	98.36	135.39	8.79	73.45	19.5	22	3895
SE	0.002	0.0057	0.058	0.17	10.08	9.70	0.23	0.46	0.03	0.013	61.3
LSD (1%)	9.2	0.16	1.88	0.64	6.31	6.16	0.75	1.33	1.28	2.9	620.4
CV (%)	2.12	4.54	1.067	4.83	3.23	2.30	5.43	0.92	2.84	4.61	6.35

CV (%): Coefficient of variation, LSD (5%): Least Significance difference, FLL (cm): Flag leaf length, FLW (cm): Flag leaf width (cm), CL (cm): Culm length, NTPP: Number of tiller per plant, FC: Flowering cycle, MC: Maturation cycle, NPP: Number of panicle per plant, NSPP: Number of spikelet per panicle, PL (cm): Panicle length, TSW (gm): Thousand seed weight, YLD (kg/ha): Yield.

#### 4.1.2. Estimates of Genetic Parameters

Number of tillers per plant (22.47%), number spikelet per panicle (49.98%), thousand seed weight (25.56%) and yield

(23.93%) had higher PCV values. The PCV values for flag leaf length (14.79%), flag leaf width (16.12%), and culm length (16.42%) and number of panicle per plant (16.32%) were

medium. Flowering cycle (7.81%), maturation cycle (2.9%), and panicle length (2.5%) had lower PCV values (Table 4).

GCV values were low for flowering cycle (7.21%), maturation cycle (1.82%) and panicle length (2.4%); medium for flag leaf length (14.26%), flag leaf width (15.39%), culm length (15.19%) and number of panicle per plant (15.72%); high for number of tillers per plant (22.18%), yield (23.07%), thousand seed weight (25.18%) and number of spikelet per panicle (47.60%). The high GCV values of these characters suggest that genetic impact is higher and lower environmental influences.

Abdusaleem (2009) in his study of estimation of genetic variability and correlation for grain yield components in rice

found GCV ranged from 0.19% (grain yield per plant) to 8.32% (number of grain per plant) and PCV ranged from 0.29% (grain yield per plant) 8.59% (Number of grain per plant) which implies lower genetic impact in contrary to this finding [1].

The difference between PCV and GCV values was high for number of spikelet per panicle (2.38%), maturation cycle (1.08%) and culm length (1.23%) which indicated how much the environment influenced these characters. However, this difference was very low for panicle length (0.1%), flag leaf length (0.53%) and number of tiller per plant (0.29%) suggesting minimal influence of environment on the expression of these characters which could be easier to improve these characters through phenotypic selection.

**Table 4.** Estimate of range, mean, phenotypic (PV) and genotypic (GV) component of variances, broad sense heritability, and genetic advance of parameters.

Character	Min	Max	Mean	PV	GV	PCV (%)	GCV (%)	h <sup>2</sup> (%)	GA
FLL	19.33	34	26.02	13.9	13.78	14.79	14.26	99.13	7.59
FLW	1	2.1	1.63	0.067	0.063	16.12	15.39	95.52	0.5
CL	43.33	94	71.36	117.9	117.48	16.42	15.19	99.64	22.24
NTPP	5.66	13	8.398	3.56	3.47	22.47	22.18	97.47	3.78
FC	85	112	98.51	59.2	50.5	7.81	7.21	85.3	13.49
MC	132	141	135.35	15.44	6.06	2.9	1.82	39.25	3.17
NPP	6.33	12	8.57	1.96	1.815	16.32	15.72	92.84	2.67
PL	52.33	93	73.26	3.34	3.115	2.5	2.4	93.12	3.50
NSPP	14	23.33	19.28	84.63	84.20	49.98	47.60	99.49	18.82
TSW	7.2	37.3	24.57	39.45	38.28	25.56	25.18	97.03	12.56
YLD	1556.5	5374.5	3895.5	869086.6	807837	23.93	23.07	92.95	45.88

PV: Phenotypic variance, GV: Genotypic variance, PCV (%): Phenotypic coefficient of variation, GCV (%): Genotypic coefficient of variation, h<sup>2</sup> (%): Broad sense heritability, GA (%): Genetic advance, FLL: Flag leaf length (cm), FLW: Flag leaf width (cm), CL: Culm length (cm), NTPP: Number of tiller per plant, FC: Flowering cycle, MC: Maturation cycle, NPP: Number of panicle per plant, PL: Panicle length (cm), NSPP: Number of spikelet per panicle, TSW: Thousand seed weight (gm), YLD: Yield, Min: Minimum, Max: Maximum.

#### 4.2. Estimation of Broad-Sense Heritability and Genetic Advance

Estimates of heritability in broad sense ranged from 39.25% for maturation cycle to 99.6% for culm length (Table 4). According to Singh (2001), if heritability of a character is very high, say 80% or more, selection for such characters could be fairly easy. This is because there would be a close correspondence between the genotype and the phenotype due to the relative small contribution of the environment to the phenotype. But, for characters with low heritability, say 40% or less, selection may be considerably difficult or virtually impractical due to the masking effect of the environment. Considering this benchmark, heritability estimate was high (>80%) for all traits except for maturation cycle (39.25%). Abdusaleem (2009) also in his study of estimation of genetic variability and correlation for grain yield components in rice found heritability value of lower than 78% for all characters studied which is in contrary lower than the findings of this study [1].

Genetic advance under selection (GA) refers the improvement of characters in genotypic value for the new population compared with the base population under one cycle of selection at a given selection intensity [10]. Estimates of GA for seed yield was 45.88 kg/ha indicating that selection of the best 5% high yielding genotypes as parents, mean seed yield of progenies could be improved

by 45.88 kg/ha for the first cycle i.e., mean genotypic value of the new population for seed yield will be improved from 3895.5 kg/ha to 3941.38 kg/ha. Emphasis should be placed on those characters which had high heritability and genetic advance for formulating reliable selection indices for the development of high yielding upland rice genotypes.

According to Johnson *et al* (1955) high heritability estimates along with the high genetic advance is usually more helpful in predicting gain under selection than heritability estimates alone [6]. High heritability (99.64%), (99.49%) and (92.95%) coupled with high genetic advance (22.24%), (18.82%) and (45.88%) respectively were observed for culm length, number of spikelets per panicle and grain yield which indicates that these characters could be improved easily than the other characters. Some of the characters had shown high heritability and very low genetic advance i.e., improvement of such traits of the genotypes is difficult.

Parikh *et al* (2012) in his study of agro-morphological characterization and assessment of variability in aromatic rice germplasm found that the highest genetic advance was recorded for hundred seed weight (58.15) followed by fertile spikelets per panicle (49.98), spikelet density (44.88), and grain yield per plant (39.73) and high heritability coupled with high genetic advance recorded for fertile spikelets per panicle, spikelet sterility percentage, spikelet density, and grain yield per plant, suggesting preponderance of additive

gene action in the expression of these characters which is more or less has similar finding with this study [9].

## 5. Conclusion and Recommendation

This study generally had indicated that there was significant genetic variability or divergence among the genotypes. Culm length, number of spikelet per panicle and yield were more heritable parameters than others. Thus, there is an enormous opportunity in the improvement program of the upland rice genotypes through direct selection rather than a lengthy crossing program and hybridization which involves technical expertise crossing of the genotypes from different clusters that would produce viable and a potential segregate population. Regarding this, I recommend further study on accessions IR 78937-B-3-B-B-1 for further selection procedures which had the highest yield with a score of 5374.5 kg/ha and a yield advantage of 57% and 22.2%, respectively, as compared to standard checks Nerica-4 and Hidasie.

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