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Agro-morphological Variability of Upland Rice Hill Landraces Evaluated at Central Terai Region of Nepal

Dev Nidhi Tiwari[1*], Bishwas Raj Bastola[2], Bikash Ghimire[3]

[1]National Rice Research Program, Hardinath, Dhanusha, Nepal

[2]Agricultural Research Station

Belachapi, Dhanusha

[3]Agricultural Research Station

Kimugaon, Dailekh

Nepal

ABSTRACT

Landraces are the major sources for creating variation in crops which offer enormous opportunity to plant breeders for development of new cultivars through selection. Fifteen upland rice landraces were considered in this study to determine the genetic variation based on phenotypic evaluation of traits. The study was carried out in two wet season during 2015 and 2016 in randomized complete block design with three replications. The genotypes were evaluated for phenotypic characters such as days to heading, days to maturity, plant height, panicle length, number of filled grains, tillers/m^2, thousand grain weight and grain yield. The statistical analysis revealed highly significant difference ($P<0.001$) for all the traits except panicle length, filled grains and grain yield. Similarly, year effect was highly significant ($P\leq0.001$) for majority of traits except for plant height and panicle length. The genotype x year interaction was found significant ($P<0.01$) for days to heading and plant height ($P<0.05$). The result demonstrated that the genotype UR D010 found earliest in heading (64 days) and maturity (94 days). Although statistically non-significant, two genotypes UR D010 (5.23 t ha^{-1}) and UR D002 (5.21 t ha^{-1}) were at par with check variety Ghaiya-1(5.36 t ha^{-1}) in grain yield respectively. The genotypes UR D009 and UR D006 possessed fine grain (17.3 g) and (17.8 g) respectively according to 1000 grain weight basis. The genotype UR D005 has the longest panicle (25.8 cm) followed by UR D008 with panicle length (25.5cm). It is obvious from the study that the genotypes were greatly differed among each other for various morphological traits. The findings of this study suggested us to further investigation of genotypes to identify best suited genotype to utilize for varietal improvement programs.

***Keywords:** Evolutionary, Himalaya, Ghaiya-1, Maturity pattern, Mid and far western.*

1. INTRODUCTION

Rice (*Oryza sativa* L., 2n=2x=24) is the number one staple food crop in Nepal and contributed significantly to livelihood of majority of people and also to national economy. Nepal has diverse agro-ecosystem in which its altitude varies from 60m above sea level (asl) in the southern plains to above 8800m asl in the northern Himalaya. The geographical distribution of the country is categorized into lowlands, foothills including valleys, midhills, high hills and mountains [1]. Nepal has abundant agro biodiversity including wild relatives of rice and it reported that around 2000 rice landraces known to exist in Nepal that are grown from 60 to 3050 m altitude due to presence of wide range of agro-ecological and socioeconomic variations present [1-3]. The agricultural diversity is largely shaped by human interference and evolutionary phenomenon and different levels of diversity is present in our farming community [4]. Agro-morphological characterization of germplasm is prerequisite tool and use of agro-

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morphological markers in the characterizing and evaluation of rice has become widespread to assess the genetic diversity. One hundred and forty six upland rice accessions were analyzed for morphological variation [5]. About 147 germplasm collections from high altitude Jumla from Nepal were investigated for genetic relationship with the use of morphological markers [6]. Similarly, agro-morphological genetic diversity was assessed for upland rice in Jaypore tract of India has also been reported [7]. Genetic variability present in landraces provides opportunity to researchers for breeding and selection of desirable materials based on the correlation among the traits [8]. The morphological diversity analysis assists in making good decision for formulating appropriate conservation and utilization strategy for successful breeding programs [9]. Rice landraces have the reservoir of genetic potential and contain several resistant genes for biotic and abiotic stress where the modern varieties are devoid of such quality. Upland landraces are one of these useful of resources that are at risk of extinction and mostly grown by minority groups residing in mountain areas from ancient times. These people prepare fields are maintained by the slash and burn farming system especially in the sloppy lands without bunds and mainly grown depending upon monsoon rains. With the invent of newly developed varieties over local area have replaced local landraces and now the environmental condition around the landrace are becoming vulnerable [10]. Traditional rice varieties utilized and grown by farmers in upland ecosystems are valuable genetic resources for development of new cultivars. These local varieties are well adapted in the wide range of abiotic and biotic stresses that reflect great genetic variability within them which are rarely found in the improved varieties. Characterization is the foremost step for germplasm to utilize in rice breeding and provides valued information on developing new rice cultivars. These traditional rice varieties play vital role to the increased productivity in the remote and mountainous regions that contributed to reduce hunger [11, 12]. Farmers in the hills and plains have limited access to new improved varieties and thus cultivating their traditional varieties that are found most adapted to their locality despite of poor yield and prone to biotic and abiotic stress. There are very few upland rice varieties suited for different domains and new variety has not been developed for several years for upland ecosystem. It necessitates urgent need to development of high yielding and quality upland rice variety otherwise the farmers will be shifted towards other crops and diversity of upland rice will be lost from the agro-ecosystem.The objective of the present study is to identify the genetic variability in the landrace of upland rice evaluated and use of information derived from this study for future breeding programs for the development of new cultivar.

2. MATERIALS AND METHODS

Coordinated Varietal Trial (CVT) on upland rice landraces collections obtained from Agricultural Research Station (ARS), Kimugaun, Dailekh each year was conducted at National Rice Research Program (NRRP), Hardinath, Dhanusha of Nepal. Altogether fifteen genotypes were evaluated in the study including standard check variety Ghaiya-1. The experiment was carried out during two consecutive wet seasons of 2015 and 2016 with randomized complete block design (RCBD) in three replications. The plot size was maintained at $6m^2$ with spacing of 25cm x continuous line sowing. Direct seeding operation was done during last week of June in both years. Fertilizer and farmyard manure (FYM) was applied at the rate of 60:30:30 $NP_2O_5K_2O$ kg ha^{-1} and 10 t ha^{-1} respectively as per the recommendation. Full dose of P_2O_5 and K_2O and half dose of Nwere applied as basal dose and remaining 50% nitrogenous fertilizer was further split into two parts. First half dose at tillering stage and second half at the booting stage. The genotypes were evaluated based on measurement of morphological traits such as days to heading, days to maturity, plant height, panicle length, tillering per square meter, number of filled grains from five panicles, thousand grain weight and grain yield. The statistical analysis was carried out using GenStat 15th Edition with Two Way ANOVA in randomized block design.

3.RESULTS AND DISCUSSION

3.1 Heading and Maturity days

The statistical result indicated that both genotypes and year were observed highly significant ($P<0.001$) for both heading and maturity days. However, genotype by year interaction was found significant for days to heading ($P<0.01$) and non significant for days to maturity (Table 1). The result illustrated that the genotype UR D010 was found early in heading and maturity days at 64 and 94 days respectively. On the other hand, genotypes UR D006 and UR D009 were both observed delayed in heading at 72 days and consequently delayed maturity at 101 days as compared to other tested genotypes including standard check Ghaiya-1 (Table 1). We found that there is clear difference in the flowering and maturity pattern within the landraces in two years result. The flowering and maturity days has a slight shift between two years, it means same genotype was flowering or maturing few days before in the first year or few days after in the next year. This variation in flowering ranges from 6 days in 2015 and 10 days in 2016 also similar pattern is observed in maturity days in both years. The genotype UR D010 and UR D007 has taken equal (64 and 68) days for heading. Likewise same genotype UR D010 has matured approximately at same number of days i.e. 95 days (Table1). The difference in heading and maturity days of same genotypes in different year is attributed to environmental effect

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which includes difference in the weather variability or soil moisture characteristics between these years. According to [13], there is significant genotype by year effect for the flowering and maturity days which is in consistent with the findings in our study (Table 1). Year to year variation was found "as reported by [1]" for the genotypes evaluated in different environments which is in agreement with the result in this study. The consistency in flowering and maturity days of the genotype UR D010 (Table 1) in different years is due to fact that phenotype is directly governed by genotype and could be due to additive gene action. The result from the study reflected that 50% flowering (herein heading days) and maturity explained high heritability coupled with high genetic advance and suggested additive gene action as well as high expected gain from selection for such trait "as illustrated by [8]" in his earlier study.

Table 1. Evaluation of upland rice genotypes for heading and maturity days at NRRP, Hardinath during wet season 2015 and 2016

Entry	**Designation**	**Heading days**			**Maturity days**		
		2015	**2016**	**Mean**	**2015**	**2016**	**Mean**
1	UR D001	67	70	69	97	101	99
2	UR D002	64	66	65	94	98	96
3	UR D003	69	71	70	98	102	100
4	UR D004	67	70	68	96	102	99
5	UR D005	69	73	71	98	103	100
6	UR D006	70	74	72	98	104	101
7	UR D007	68	68	68	96	102	99
8	UR D008	68	72	70	97	103	100
9	UR D009	70	74	72	99	103	101
10	UR D010	64	64	64	94	95	94
11	UR D011	68	71	70	97	102	100
12	UR D012	66	68	67	96	99	97
13	UR D013	64	66	65	95	97	96
14	UR D014	68	67	67	96	99	98
15	Ghaiya-1	67	69	68	96	101	99
GM		67	70	68	96	101	99
P-value	Ent	***	***	***	***	***	***
	Year			***			***
	Ent*Year			**			ns
$LSD_{0.05}$	Ent	1.51	1.9	1.365	1.58	3	1.789
	Year			0.498			0.653
	Ent*Year			1.93			2.529
CV%		1.3	1.6	1.7	1	1.8	1.6

[†]P<0.001indicated as ***, P0.001 and P<0.01 denoted by **, P<0.05 symbolized as *, ns= non-significant

3.2 Plant height and Tillers

The highly significant difference (P<0.001) among genotypes was observed for plant height and varied significantly (P<0.05) in case of tillers m^{-2} as well as mean difference was highly significant (P<0.001) for tillers m^{-2}. However, genotype by year interaction was observed significant for plant height (P<0.05) and non significant for tillers m^{-2} (Table 2). The result demonstrated that highest plant height of 136.5 cm was obtained in genotype UR D011 whereas lowest plant height of 112.5 cm was recorded in genotype UR D002 among test genotypes. In case of tillering capacity of genotypes, standard check variety Ghaiya-1 produced maximum tillers (224.7 m^{-2}) followed by the genotype UR D010 (204.7 m^{-2}), UR D002 (193.3 m^{-2}) and UR D013(193 m^{-2}) (Table 2). Although correlation analysis was not performed in this work, the result demonstrated that the genotypes with more plant height produced reduced tillers and vice versa (Table 2). It indicated that the plant height and tiller numbers have indirect association with each other

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[†] P-values at 0.1%, 1% and 5% level of significance

Table 2. Evaluation of upland rice genotypes for plant height and tillers per square meter at NRRP, Hardinath during wet season 2015 and 2016

Entry	Designation	Plant height (cm)			Tiller/m^2		
		2015	2016	Mean	2015	2016	Mean
1	UR D001	135	134	134.5	146.3	155	150.7
2	UR D002	116	109	112.5	163.3	223.3	193.3
3	UR D003	125.7	139	132.3	154.3	200	177.2
4	UR D004	125.3	133.3	129.3	150.7	197.7	174.2
5	UR D005	110.3	142.7	126.5	169	172	170.5
6	UR D006	130.3	124.7	127.5	153.7	196.7	175.2
7	UR D007	128.3	131.3	129.8	171.3	187	179.2
8	UR D008	129.7	130.7	130.2	147	183.3	165.2
9	UR D009	124.3	124.7	124.5	146	218.3	182.2
10	UR D010	120.7	116.7	118.7	165.3	244	204.7
11	UR D011	129	144	136.5	168	138.3	153.2
12	UR D012	114.7	118	116.3	157.7	168.3	163
13	UR D013	120	110.7	115.3	178.3	207.7	193
14	UR D014	121	126	123.5	190.3	177.7	184
15	Ghaiya-1	96.7	95.7	96.2	201	248.3	224.7
GM		121.8	125.4	123.6	164.2	194.5	179.3
P-value	Ent	*	***	***	ns	**	*
	Year			ns			***
	Ent*Year			*			ns
$LSD_{0.05}$	Ent	18.6	13.6	11.18	48	51.2	36.11
	Year			4.08			13.18
	Ent*Year			15.81			51.06
CV%		9.1	6.5	7.8	17.5	15.7	17.4

‡ $P<0.001$indicated as ***, P0.001 and $P<0.01$ denoted by **, $P<0.05$ symbolized as *, ns= non-significant

3.3 Panicle length and Filled grains

The statistical analysis revealed that there was non-significant difference among the genotype and year as well as their interaction for panicle length and filled grain numbers. However, effect of year was distinctly different ($P<0.001$) in case of number of filled grains (Table 3). Despite of non-significant difference among the genotypes, longest panicle of length 25.83 cm was observed in the genotype UR D005 followed by UR D008 with panicle size of 25.5 cm. The panicle size of the all tested genotypes was higher than the standard check variety Ghaiya-1 (22.5 cm). In case of filled grain number, the genotype UR D004 produced the maximum filled grains of 580 from five panicles followed by the genotype UR D006 that possessed 544 filled grains and lowest number of grains (384) was observed in UR D005. From the results it is obvious that all the genotypes under investigation produced higher number of grains compared to check variety Ghaiya-1 that having 327 grains in five panicles (Table 3). On the other hand tillers numbers (Table 2) and grain yield (Table 4) were directly correlated. It clearly described that increased grain yield is attributed to the presence of effective tillers. From our study no specific pattern of association was visible among the filled grains (Table 3), 1000 grain weight (Table 4) and grain yield (Table 4). It contradicted with the previous finding described by [14] where high significant association of grain yield with panicle weight (here referred to as filled grains) and 1000 grain weight was reported.

Table 3. Evaluation of upland rice genotypes for panicle length and filled grains at NRRP, Hardinath during wet season 2015 and 2016

Entry	Designation	Panicle length (cm)			Filled grains/5 panicle)		
		2015	2016	Mean	2015	2016	Mean
1	UR D001	23	24.33	23.67	533	412	472

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‡ P-values at 0.1%, 1% and 5% level of significance

2	UR D002	24.33	23	23.67	483	390	436
3	UR D003	24	24.33	24.17	578	446	512
4	UR D004	25	23	24	627	533	580
5	UR D005	25.67	26	25.83	397	371	384
6	UR D006	25.67	23.67	24.67	601	488	544
7	UR D007	24	24	24	448	338	393
8	UR D008	26.67	24.33	25.5	528	374	451
9	UR D009	22.33	22.67	22.5	580	354	467
10	UR D010	25	23	24	537	459	498
11	UR D011	23.67	23.33	23.5	520	399	460
12	UR D012	23.33	25	24.17	588	428	508
13	UR D013	26.33	23	24.67	410	450	430
14	UR D014	25	24.33	24.67	527	380	453
15	Ghaiya-1	23	22	22.5	372	282	327
GM		24.47	23.73	24.1	515	407	461
P-value	Ent	ns	ns	ns	ns	ns	ns
	Year			ns			***
	Ent*Year			ns			ns
$LSD_{0.05}$	Ent	3.86	3.3	2.569	240	199	151.1
	Year			0.938			55.2
	Ent*Year			3.633			213.7
CV%		9.4	8.3	9.2	27.8	29.2	28.4

[§] *P<0.001indicated as ***, P0.001 and P<0.01 denoted by **, P<0.05 symbolized as *, ns= non-significant*

3.4 1000 grain weight and Grain yield

Based on the mean of thousand grain weight, genotypes were found highly significant (P<0.001) and however genotypes were differed for grain yield. Furthermore, effect of year on both 1000 grain weight and grain yield was significantly different (P<0.01) while the interaction of genotype by year was non-significant for both the traits (Table 4). The genotype UR D009 possessed finest grain of size 17.3 g based on 1000 grain weight followed by the genotype UR D006 with 1000 grain size of 17.8 g. The genotypes UR D001 and UR D011 contained the bold grain of size 25.3 g and 26.32 g respectively according to 1000 grain weight criteria. All the tested genotypes were inferior in terms of grain yield compared to standard check variety Ghaiya-1 with grain yield of 5.26 t ha^{-1}. Despite of non-significant interaction among the genotypes, UR D010 followed by UR D002 and UR D013 produced highest yield of 5.23 t ha^{-1}, 5.21 t ha^{-1} and 5.11 t ha^{-1} at par with check variety Ghaiya-1 (Table 4). However, mean grain yield of all the tested genotypes was higher than the nation average of 3.34 t ha^{-1}under the research field with standard crop management practices followed. Interestingly, in our study the genotypes which had short flowering and maturity days (Table 1) produced higher grain yield (Table 4) is in agreement with [14]. According to them, 50% flowering had negative correlation with grain yield and 1000 grain weight.

[§] *P-values at 0.1%, 1% and 5% level of significance*

Table 4. Evaluation of upland rice genotypes for 1000 grain weight and grain yield ton per hectare at NRRP, Hardinath during wet season 2015 and 2016

Entry	**Designation**	**1000 g.wt (g)**			**Grain yield t/ha**		
		2015	**2016**	**Mean**	**2015**	**2016**	**Mean**
1	UR D001	25.6	25	25.3	4.87	4.72	4.8
2	UR D002	19.17	18.07	18.6	4.4	6.03	5.21
3	UR D003	20.1	21.28	20.7	4.06	4.72	4.39
4	UR D004	19.93	20.07	20	4.05	4.66	4.35
5	UR D005	22.49	17.56	20.03	3.79	4.46	4.13
6	UR D006	20.04	15.64	17.8	4.9	5.04	4.97
7	UR D007	22.28	21.86	22.07	4.57	4.94	4.75
8	UR D008	22.38	18.44	20.41	4.37	4.73	4.55
9	UR D009	16.95	17.65	17.3	4.48	5.05	4.76
10	UR D010	19.77	18.81	19.3	4.48	5.97	5.23
11	UR D011	28.77	23.87	26.32	4.07	5.29	4.68
12	UR D012	21.71	19.53	20.62	3.37	5.28	4.32
13	UR D013	22.76	17.99	20.38	4.84	5.38	5.11
14	UR D014	23.89	21.89	22.89	3.86	4.33	4.09
15	Ghaiya-1	19.3	18.27	18.79	5.06	5.67	5.36
GM		21.7	19.7	20.7	4.34	5.08	4.71
P-value	Ent	***	ns	***	ns	ns	ns
	Year			**			**
	Ent*Year			ns			ns
LSD$_{0.05}$	Ent	3.31	6.67	3.616	1.14	1.79	1.113
	Year			1.32			0.406
	Ent*Year			5.114			1.573
CV%		9.1	20.2	15.1	15.6	21	20.4

** *P<0.001indicated as ***, P 0.001 and P<0.01 denoted by **, P<0.05 symbolized as *, ns= non-significant*

4. CONCLUSION

This study assessed the variability of upland rice landraces at Central Terai region at NRRP, Hardinath, Dhanusha, Nepal which represents sub-tropical climate. The landraces were of hilly origin and collected from the mid and far western part of the country. The upland has played significant role in the livelihood and food security of people basically in the hills and mountainous region of the country. The results obtained from the study reflected that there exists wide genetic diversity within and between the genotypes i.e. landraces. The genotypes exhibited variability for major traits which is indicated by its differences in earliness, plant height, tillering ability as well as their grain size variations. The above result showed that the genotypes UR D002, UR D006 and UR D010 were highly outstanding in performance in terms of grain yield, maturity, plant height, panicle length and 1000 grain weight. We concluded that the evaluated genotypes had wide genetic variability on the traits measured. The variability among the genotypes could be utilized for the further screening for future breeding programs. This will enrich the genetic diversity of hill landraces and ultimately contribute to the conservation and utilization of upland rice genetic resources and farmers will benefit from the cultivation and utilization of most adaptable variety to enhance the production and productivity. It will serve for fulfilling the farmers' requirement for high yielding improved variety which was lacking for several years. The genotypes should be further screened in multi-environments representing various ecological domains to identify and select for the most stable and adaptable genotypes over a wide range of environment. Based on the present study we could recommend genotypes UR D002, UR D006 and UR D010 for promotion and large scale verification as well as dissemination for faster varietal development process.

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** *P-values at 0.1%, 1% and 5% level of significance*

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