Original Article

Genetic diversity, genetic variability, and path analysis for yield and its components in indigenous upland rice (*Oryza sativa* L. var. glutinosa)

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Abstract

Genetic diversity, genetic variability, and relationships of yield and its components are very important data for plant breeders that affect the design of a breeding program. Twenty-two upland rice genotypes were evaluated. The genotypes indicated significant variations in nine traits. High phenotypic and genetic coefficients of variation were observed for yield per plant, number of panicles per plant, and number of spikelets per panicle. High broad-sense heritability and genetic adaptations were found for yield per plant. Positive significant correlations were recorded between flag leaf length, number of panicles per plant, and number of spikelets per panicle. The highest direct effects on yield were attributed to the number of spikelets per panicle and the number of panicles per plant. Cluster analysis grouped the 22 genotypes into groups I, II, and III, and the out-groups consisting of nine, five, six, and two genotypes. These results may facilitate upland rice breeding programs to improve yield.

Keywords: correlation, genetic diversity, genetic variability, path analysis, upland rice

1. Introduction

Rice (*Oryza sativa* L.) is a staple food in many Asian countries and also constitutes a major part of the diet elsewhere, for example in Nigeria. *Oryza sativa* has Indica and Japonica subspecies, and the diverse ecosystems for its cultivation include irrigated, rain fed lowland, deep water, and upland ecosystems (Bridhikitti & Overcamp, 2011). Genetic diversity is the basis of plant breeding. The segregation for selective breeding by yield in each generation (or by yield component traits) presumes genetic diversity in the parent generation. Thus, estimating the genetic diversity in yield traits (a population statistic characterizing its genotypes) is important for the policies to select parents in crossing pro-

grams (Khare *et al*., 2014). The plant breeders tend to assess genetic diversity from morphological characters because this is inexpensive, rapid, and simple to score. In their vegetative traits, the rice plants have great morphological variation, with plant height and number of tillers as examples. Rice breeders or geneticists can classify rice genotypes based on the morphological traits (Kajonphol *et al*., 2012; Sohrabi *et al*., 2012; Thanh *et al*., 1999; Tuhina-Khatun *et al*., 2012).

Rice breeders are interested in improving new high yield varieties with other desirable agronomic traits. Estimates of the genetic variances of these traits can assist the design of breeding programs for new varieties. Broad-sense heritability (H^2) is the fraction of genetic variance in the total phenotypic variance (Bernardo, 2002). Heritability determines the responses to selection. The yield component traits have been demonstrated to be most effective in improving grain yield when these traits have high heritability and are positively correlated with each other (Surek & Beser, 2003). The

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correlation coefficient shows the relationship between two traits stemming from linkage or pleiotropy. The correlation represents effects of genes that control these two traits. It indicates the direct and indirect effects of the causal components on the effect component. The direct effect is very significant for plant breeders for selecting exactly by the traits directly related to the targeted trait. These effects can be calculated using path analysis (Dabholkar, 1992). Path analysis has been used to assess the relationships of yield and its components across several crops such as baby corn (Koauychai *et al.*, 2001), oil palm (Krualee *et al.*, 2013), and soybean (Sarutayophat, 2011).

Therefore the aims of this study were: i) to evaluate the level of genetic diversity of upland rice genotypes; ii) to estimate the broad-sense heritability and the genetic advance among 11 select agro-morphological traits; and iii) to calculate the correlation coefficients, direct effects and indirect effects of the agronomic traits on yields of the upland rice with 22 genotypes. The results can facilitate selecting desirable genotypes in future breeding programs of rice cultivars.

2. Materials and Methods

2.1 Plant material and experimental design

Twenty-two upland rice genotypes were collected from farm fields in Nan Province (Table 1). They were grown in pots (27×24 cm) in the greenhouse of Faculty of Natural Resources, Prince of Songkla University. Each pot was filled with a 1:1 mix of top soil and coconut soil mixes. The experimental design was a randomized complete block design with two replications and five pots per experimental unit and with three plants per pot. Agronomic procedures, such as weed control, were in general done manually, and insect control was through the application of 20 ml per 1 L cypermethrin 10% w/v EC. and 50 ml per 1 L benfuracarb 20% w/v EC. NPK fertilizer (15-15-15) was applied at the rate of 20 g/pot before planting. Urea (46-0-0) was applied at 30 days after planting at the rate of 10 g/pot.

Table 1. Location and local name of the indigenous upland rice accessions in Nan Province, Thailand.

S.N.	Accession	Collection site (District)	Local name
1	NR002	Chaloem Phra Kiat	Mai Kan Noi
2	NR005	Chaloem Phra Kiat	Khaoʹ Hawn Khao
3	NR007	Chaloem Phra Kiat	Khaoʹ Aew
4	NR008	Chaloem Phra Kiat	Khaoʹ Daeng
5	NR012	Chaloem Phra Kiat	Khaoʹ Lai
6	NR013	Tha Wang Pha	Niaw Muang
7	NR022	Tha Wang Pha	Khaoʹ Tew
8	NR025	Chaloem Phra Kiat	Khaoʹ Jao Houng
9	NR026	Chaloem Phra Kiat	Khaoʹ Peek
10	NR027	Chaloem Phra Kiat	Khaoʹ Leuang
11	NR029	Chaloem Phra Kiat	Khaoʹ kaab saung
12	NR030	Chaloem Phra Kiat	Khaoʹ Nam-ngern
13	NR031	Chaloem Phra Kiat	Khaoʹ Hoan Kam
14	NR035	Tha Wang Pha	E-daeng
15	NR037	Mueang	Pra-rat-cha-tan
16	NR038	Tha Wang Pha	Niaw Khao
17	NR042	Tha Wang Pha	Khaoʹ Gam Doi
18	NR044	Mueang	Sew Phan
19	NR048	Chaloem Phra Kiat	Khaoʹ Gam Pleuak Khao
20	NR051	Chaloem Phra Kiat	Gam Med San
21	NR052	Chaloem Phra Kiat	Gam Med Yao
22	NR057	Tha Wang Pha	Sew Khon Jum

2.2 Data collection

Eleven agro-morphological characters were recorded on an individual plant basis using fifteen plants per genotype in each replicate, i.e., plant height (cm), days to flowering (day), days to maturity (day), flag leaf length (cm), flag leaf width (cm), number of tillers per hill (no.), weight of one thousand grains (g), yield per plant (g), number of panicles per plant (no.), panicle length (cm), and number of spikelets per panicle (no.).

2.3 Statistical and genetic analysis

The agro-morphological characters were subjected to analysis of variance (ANOVA) using the R program (Mendiburu & Simon, 2007). The 22 genotypes were clustered on the basis of correlation coefficients among ten agronomic variables, using the average linkage algorithm (Johnson & Wichern, 2007). The broad-sense heritability (H^2) and estimates of genetic variance were obtained following Bernardo (2002). The following equations were used to estimate the genetic parameters:

$$\text{Genotypic variance } (V_g) = \frac{(\text{MS}_{\text{Genotypes}} - \text{MS}_{\text{Error}})}{r}$$

$\text{MS}_{\text{Genotypes}}$ = mean square of genotypes
MS_{Error} = mean square of error
r = number of replications
Error variance $(V_e) = \text{MS}_{\text{Error}}$
Phenotypic variance $(V_p) = V_g + V_e$

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sqrt{V_g}}{\overline{X}} \times 100$$

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sqrt{V_p}}{\overline{X}} \times 100$$

$$\text{Broad-sense heritability } (H^2) = \frac{V_g}{V_p}$$

$\overline{X}$ = mean of the trait
Expected genetic advance (GA) was estimated using the formula of Allard (1960).

$$\text{Expected genetic advance} = k \times \frac{\sqrt{V_p}}{\overline{X}} \times H^2 \times 100$$

Here k is the selection intensity. It was assigned the value k=5%, which gave the result 2.06.

The Pearson correlation coefficients were calculated for all pairs of characters, and the path analysis followed Dabholkar (1992). The correlation coefficients were analyzed on individual plant basis.

3. Results and Discussion

3.1 Analysis of variance and genetic parameters

Plant height, days to flowering, flag leaf length, flag leaf width, number of tillers per hill, yield per plant, number of panicles per plant, panicle length, and number of spikelets per panicle showed highly significant variations, while the days to maturity and the weight of one thousand grains did not (Table 2). The observed large variation in significant traits

between the genotypes indicated that genetic improvements by way of crossing and selection could be practiced. Similar results were reported by Vange (2009). In contrast, Sohrabi *et al.* (2012) reported that the weight of one thousand grains had highly significant variation among 50 genotypes of upland rice in Malaysia. Sew Phan variety had the highest 127.91 g/plant yield (Table 3), and it also had the highest flag leaf length (61.25 cm), the largest number of panicles per plant (5.10), and the largest number of spikelets per panicle (102.97).

Table 2.   Mean squares from analysis of variance concerning 11 agronomic traits of upland rice varieties.

Source	df	Plant height	Days to flowering	Days to maturity	Flag leaf length	Flag leaf width	No tillers per hill	1000 grain weight	Yield per plant	No panicles per plant	Panicle length	No Spikelet per panicle
Block	1	99.60	6.05	152.82	31.15	0.0002	0.77	6.41	42.20	0.17	20.42	9.60
Genotypes	21	274.10**	57.26**	70.61^{ns}	58.04**	0.08**	1.80**	71.49^{ns}	1561.20**	2.42**	26.81**	849.50**
Error	21	21.67	3.99	43.72	4.45	0.06	0.41	8.26	136.40	0.34	14.83	170.60

** = significant at 0.01 level
ns = not significant

Table 3.   Means of 11 agronomic traits by upland rice variety.

Accession name	Plant height (cm)	Days to flowering	Days to maturity	Flag leaf length (cm)	Flag leaf width (cm)	No tillers per hill	1000 grain weight (g)	Yield per plant (g)	No panicles per plant	Panicle length (cm)	No Spikelet per panicle
Mai Kan Noi	161.80	82.20	122.00	45.15	2.38	4.62	40.05	20.25	2.71	27.41	44.38
Khao/ Hawn Khao	139.20	75.70	108.00	44.19	2.28	4.17	40.85	52.50	3.05	26.37	57.73
Khao/ Aew	151.00	87.00	113.00	46.08	2.63	4.32	29.80	23.87	2.38	27.71	40.60
Khao/ Daeng	144.70	82.60	134.00	53.89	2.41	4.24	29.93	52.47	2.73	27.76	77.84
Khao/ Lai Niaw	163.40	85.50	113.00	54.49	2.35	5.23	35.48	42.98	3.27	33.90	73.30
Muang	150.60	82.00	109.00	50.32	2.53	5.08	26.99	57.79	4.37	31.97	65.13
Khao/ Tew	143.00	65.50	112.00	53.03	1.64	6.17	22.43	57.44	5.38	21.59	60.70
Khao/ Jao Houng	161.30	74.80	113.00	52.38	2.40	4.92	32.45	56.68	3.41	31.68	56.67
Khao/ Peek	163.70	74.20	113.00	47.63	2.29	4.35	33.28	33.21	2.33	30.66	47.60
Khao/ Leuang	174.30	80.10	113.00	52.73	2.42	4.99	28.54	28.93	3.36	30.21	38.93
Khao/ Kaab Saung	168.20	80.10	113.00	55.70	2.50	4.93	30.12	18.20	2.43	27.06	32.73
Khao/ Nam-ngern	183.00	82.60	109.00	63.54	2.47	7.02	38.10	58.81	5.27	34.32	52.47
Khao/ Hoan Kam	155.28	88.58	109.00	50.03	2.35	5.26	39.35	18.77	3.65	27.63	37.91
E-daeng	180.50	81.00	109.00	58.99	2.46	6.18	32.39	38.86	4.00	33.10	75.42
Pra-rat-cha-tan	170.30	84.18	109.00	55.27	2.33	7.03	35.65	10.96	5.93	32.76	31.00
Niaw Khao	170.40	78.50	112.00	60.36	2.38	5.03	32.19	55.04	3.29	33.97	73.33
Khao/ Gam Doi	161.20	78.20	108.00	58.00	2.09	5.53	26.78	74.80	4.64	30.09	64.60
Sew Pan	168.10	77.10	108.00	61.25	2.02	4.93	24.68	127.91	5.10	28.43	102.97
Khao/ Gam Pleuak Khao	172.20	77.50	112.00	57.45	2.36	4.83	30.89	91.72	3.80	35.44	95.10
Gam Med San	167.60	84.40	112.00	54.37	2.61	4.10	23.24	24.92	3.65	28.08	39.30
Gam Med Yao	156.63	88.00	122.00	46.25	2.35	3.13	41.55	11.82	1.78	24.99	32.39
Sew Khon Jum	152.90	76.00	113.00	55.21	1.93	4.08	22.01	40.02	3.46	23.91	80.03
Mean	161.79	80.26	113.00	53.47	2.33	5.01	31.67	45.36	3.64	29.50	58.19
LSD$_{.01}$	13.18	2.83	-	5.97	0.24	1.81	-	33.07	1.64	5.08	36.98
CV (%)	2.88	2.49	5.85	3.94	3.58	12.76	9.08	25.75	15.98	4.24	22.44

The largest phenotypic coefficient of variation was observed for the yield per plant (64.23%), followed by the number of spikelets per panicle (38.81%) and the number of panicles per plant (32.27%). The maximum among genetic coefficients of variation was observed for the yield per plant (58.84%), followed by the number of spikelets per panicle (31.66%) and the number of panicles per plant (28.02%). The phenotypic coefficient of variation was greater than the genotypic coefficient of variation, showing large environmental effects on the expression of the traits. The broad-sense heritability of plant height, days to flowering, flag leaf length, and yield per plant ranged from 83.93% to 86.97%. Number of tillers per hill, one thousand grains weight, number of panicles per plant, and number of spikelets per panicle also showed over 60% broad-sense heritability. This indicates that the genetic variations of these traits are comparatively large in relation to their environmental variations, so selective breeding could be highly effective (Poehlman, 1979).

In general, the heritability estimate based on one environment, i.e., one location or one year, is less accurate than estimates from several-environment-based programs (Allard, 1960). Because genotypic variance measurements of quantitative traits are biased upwards by genotype x environment variance, thus the estimate of broad-sense heritability is higher when expressed on a single environment than on multiple environments. Sohrabi *et al.* (2012) reported high broad sense heritabilities (80.28-99.76%) among 50 upland rice varieties in the one thousand grains weight, the flag leaf length-to-width ratio, the plant height, the spikelets per panicle, and the days to maturity. Jambhulkar and Bose (2014) reported that the heritabilities of days to flowering and of plant height exceeded 98%. On the other hand, Akinwale *et al.* (2011) reported low broad-sense heritability for the number of tillers per hill and for the one thousand grains weight.

Yield per plant showed the highest value of genetic advance (111.05%) among the observed traits in the current study. The number of panicles per plant and the number of spikelets per panicle showed more than 50% genetic advance. These results showed that the yield per plant, number of panicles per plant, and number of spikelets per panicle were controlled by additive gene effects because there was both high broad-sense heritability and high genetic advance. Vange (2009) reported similar results in upland rice genotypes of Nigeria.

3.2 Correlation and path analysis

The pairwise correlation coefficients of the 11 agronomic traits are shown in Table 5, whereas the path analysis results are shown in Table 6. Flag leaf length (r = 0.52[*]), number of panicles per plant (r = 0.43[*]), and number of spikelets per panicle (r = 0.85[*]) had significant positive phenotypic coefficients affecting yield per plant, while day to flowering (r = -0.47*) had a significant negative phenotypic coefficient. Similar to the current study, Mehetre *et al.* (1994) reported that grain yield was positively correlated with spikelets per panicle and negatively correlated with days to flowering. Seyoum *et al.* (2012) stated that grain yield was positively correlated with spikelets per panicle. Sravan *et al.* (2012) reported that grain yield was positively correlated with flag leaf length and spikelets per panicle. The correlation coefficients were used in the path analysis, to estimate the correlation between yield on one hand and various traits on the other (direct and indirect effects). It reveals that the number of spikelets per panicle had the highest direct effect (0.67) on yield, followed by the number of panicles per plant (0.62), the flag leaf width (0.30), the flag leaf length (0.24), and the weight of one thousand grains (0.24). On the other hand, the number of tillers per hill and the days to flowering had negative path coefficients (-0.53 and -0.35, respectively) on targeting yield. In addition, the flag leaf length had a positive indirect effect on the yield, via the number of panicles per plant (0.37) and the number of spikelets per panicle (0.33). The number of tillers per hill had a positive indirect effect on yield, via the number of panicles per plant (0.50). This suggests that these traits can be beneficially used in breeding for high yield. As in this study, Osman *et al.* (2012) and Khare *et al.* (2014) reported that the spikelets per panicle had the largest direct contribution to grain yield.

Table 4.   Genetic parameter estimates for 11 agronomic traits of upland rice varieties.

Trait	V_g	V_p	PCV(%)	GCV(%)	H^2(%)	GA(%)
Plant height	126.22	147.89	7.52	6.94	85.35	13.21
Days to flowering	26.64	30.63	6.90	6.43	86.97	12.35
Days to maturity	13.45	57.17	6.69	3.24	23.52	3.24
Flag leaf length	26.80	31.25	10.45	9.68	85.76	18.47
Flag leaf width	0.01	0.07	11.36	4.29	14.29	3.34
No tillers per hill	0.70	1.11	20.98	16.64	62.90	27.19
1000 grains weight	31.62	39.88	19.94	17.75	79.29	32.57
Yield per plant	712.40	848.80	64.23	58.84	83.93	111.05
No Panicles per plant	1.04	1.38	32.27	28.02	75.36	50.10
Panicle length	5.99	20.82	15.47	8.30	28.77	9.17
No spikelets per panicle	339.45	510.05	38.81	31.66	66.55	53.21

V_g: genotypic variance, V_p: phenotypic variance, PCV: phenotypic coefficient of variation.
GCV: genotypic coefficient of variation, H^2: board sense heritability, and GA: genetic advance.

Table 5.   Phenotypic pairwise correlations of the 11 agronomic traits across a sample of upland rice varieties.

	PH	DF	DM	FL	FW	NT/H	1000GW	Y/P	NP/P	PL
PH										
DF	0.19									
DM	-0.30	0.20								
FL	0.64**	-0.14	-0.29							
FW	0.33	0.70**	0.13	-0.14						
NT/H	0.45*	-0.13	-0.47**	0.57**	-0.13					
1000GW	0.07	0.45*	0.14	-0.37	0.36	0.00				
Y/P	0.06	-0.47*	-0.24	0.52*	-0.39	0.12	-0.38			
NP/P	0.68**	-0.27	-0.54**	0.59**	-0.40	0.81**	-0.30	0.43*		
PL	0.68**	0.22	-0.28	0.47*	0.49*	0.43*	0.22	0.22	0.23	
NS/P	0.01	-0.39	0.05	0.50*	-0.38	0.02	-0.39	0.85**	0.26	0.23

*, ** = significant at 0.05 and 0.01 level, respectively
PH = Plant height, DF = Days to flowering, DM = Days to maturity, FL = Flag leaf length, FW = Flag leaf width, NT/H = No of tillers per hill, 1000GW = one thousand grains weight, Y/P = Yield per plant, NP/P = No of panicles per plant, PL = Panicle length, NS/P = No of spikelets per panicle

Table 6.   Phenotypic path analysis of agronomic trait effects on yield of upland rice varieties.

Trait	Direct and indirect effects										Correlation coefficient with Y/P
	PH	DF	DM	FL	FW	NT/H	1000GW	NP/P	PL	NS/P	
PH	-0.04	-0.07	0.03	0.16	0.10	-0.24	0.02	0.15	-0.066	0.01	0.06
DF	-0.01	-0.35	-0.02	-0.03	0.21	0.07	0.11	-0.17	-0.02	-0.26	-0.47*
DM	0.02	-0.07	-0.10	-0.07	0.04	0.25	0.04	-0.33	0.02	0.03	-0.24
FL	-0.03	0.05	0.03	0.24	-0.04	-0.30	-0.09	0.37	-0.04	0.33	0.52**
FW	-0.02	-0.25	-0.01	-0.03	0.30	0.07	0.09	-0.25	-0.04	-0.25	-0.39
NT/H	-0.02	0.05	0.04	0.14	-0.04	-0.53	0.00	0.50	-0.03	0.01	0.12
1000GW	0.00	-0.16	-0.01	-0.09	0.11	0.00	0.24	-0.19	-0.02	-0.26	-0.38
NP/P	-0.01	0.10	0.05	0.14	-0.12	-0.43	-0.07	0.62	-0.02	0.17	0.43*
PL	-0.03	-0.08	0.03	0.12	0.15	-0.23	0.05	0.14	-0.09	0.15	0.22
NS/P	0.00	0.14	0.00	0.12	-0.12	-0.01	-0.09	0.16	-0.02	0.67	0.85**

The underlined numbers on diagonal show direct effects, the rest stand for indirect effects. Residual effect $(1-R^2) = 14.70$ %
PH = Plant height, DF = Days to flowering, DM = Days to maturity, FL = Flag leaf length, FW = Flag leaf width, NT/H = No of tillers per hill, 1000GW = one thousand grain weight, Y/P = Yield per plant, NP/P = No of panicles per plant, PL = Panicle length, NS/P = No of spikelets per panicle

3.3 Cluster analysis

When the average distance between clusters was 0.75, the genetic diversity based on the agronomic data grouped the 22 upland rice varieties into three clusters (Figure 1 and Table 7). Group I consisted of nine varieties (Mai Kan Noi, Khao′ Aew, Khao′ Peek, Khao′ Leuang, Khao′ Kaab Saung, Khao′ Hoan Kam, Pra-rat-cha-tan, Gam Med San, and Gam Med Yao); Group II consisted of five varieties (Khao′ Daeng, Khao′ Lai, E-daeng, Niaw Khao, and Sew Khon Jum); and Group III contained six varieties (Khao′ Hawn Khao, Niaw Muang, Khao′ Tew, Khao′ Jao Houng, Khao′ Nam-ngern, and Khao′ Gam Doi). Each group was comprised of upland rice varieties from several districts or collection sites, indicating effectiveness of the clustering method. Sew Phan and Khao′ Gam Pleuak Khao varieties were not assigned to any of the main clusters, so they had little similarity to the other 20 genotypes.

Group I had the highest mean values of agronomic traits, such as plant height (163.20 cm), days to flowering (83.20 days), flag leaf width (2.43 cm), and one thousand grains weight (33.51 g). Group II showed the highest mean values in the days to maturity (116.20 days), flag leaf length (56.59 cm), panicle length (30.53 cm), and number of panicles per plant (75.98). Group III showed the highest mean values in the number tillers per hill (5.48), yield per plant (59.67 g), and number of panicles per plant (4.35). In addition, Sew Phan variety (outside the main groups) had higher flag leaf length (61.25 cm), yield per plant (127.91 g), number of panicles per plant (5.1), and number of spikelets per plant (102.97) than the varieties assigned to the main groups (Table 2). The genotypes of Gam Med Yao (Group I), Niaw Khao (Group II), and Khao′ Tew (Group III) had the best key agronomic traits: one thousand grains weight, flag leaf length or days to flowering. Thus, these genotypes appear particularly good choices for breeding programs.
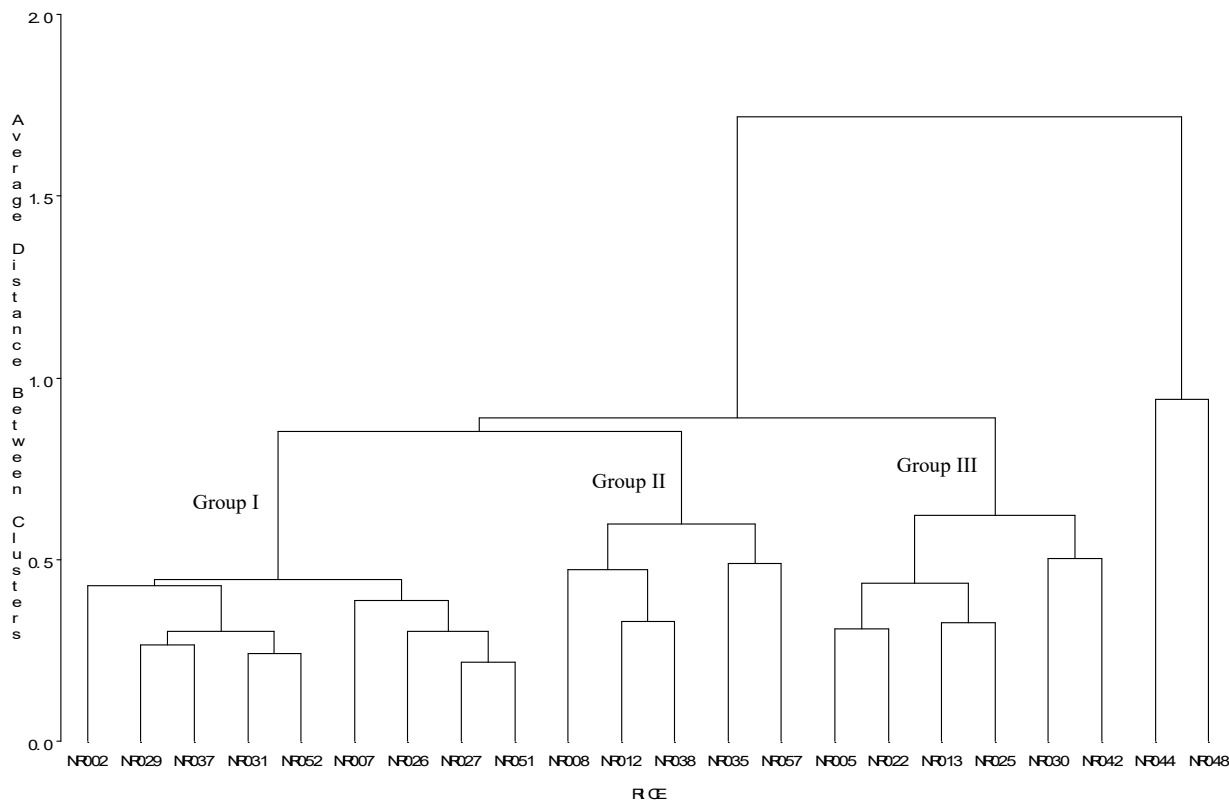
Figure 1.   Average linkage dendrogram of rice varieties, hierarchically clustered based on similarity of 11 agronomic variables. The labels NR002-NR057 represent rice germplasm accessions as described in Table 1.

Table 7.   Groups of upland rice varieties identified by cluster analysis of genotypes.

Groups	Genotypes
Group I	Mai Kan Noi, Khao′ Aew, Khao′ Peek, Khao′ Leuang, Khao′ Kaab Saung, Khao′ Hoan Kam, Pra-rat-cha-tan, Gam Med San, Gam Med Yao
Group II	Khao′ Daeng, Khao′ Lai, E-daeng, Niaw Khao, Sew Khon Jum
Group III	Khao′ Hawn Khao, Niaw Muang, Khao′ Tew, Khao′ Jao Houng, Khao′ Nam-ngern, Khao′ Gam Doi
Out group	Sew Pan, Khao′ Gam Pleuak Khao

Khare *et al*. (2012) clustered 60 genotypes of upland rice in India based on 10 agronomic traits. The genotypes formed 7 clusters. Their cluster 3 had the most genotypes (14), followed by cluster 1 (11 genotypes) and clusters 6, 7, 5, 4, and 2 (9, 8, 7, 6, and 5 genotypes, respectively). Sohrabi *et al*. (2012) clustered 50 genotypes of upland rice in Malaysia by 12 agronomic traits, and they fell into 6 clusters. The third one was the largest with 27 members. Group VI was the smallest cluster with only one genotype. Groups I, II, IV, and V consisted of 6, 10, 2, and 4 members, respectively. Ahmad *et al*. (2015) clustered 42 genotypes of colored upland rice by 15 agronomic traits into 4 clusters. The first group was the largest with 17 members, consisting of red rice genotypes of various origins. Group 4 was the smallest with only 3 genotypes.

Groups 2 and 3 had 6 and 16 members, respectively. These patterns of clustering indicated the genetic diversity of the sampled genotypes. The genotypes within one cluster were more similar to each other than to others outside this cluster. So, the rice breeder can use these results to select diverse parents for future breeding programs. The more diverse parents may be crossed to potentially obtain superior segregates (Poehlman, 1979). Similar results were also re-ported by Patel *et al*. (2008) and Seetharam *et al*. (2008).

4. Conclusions

The results of genetic analysis from this study indicated that genotypes of a sampling of rice varieties had adequate genetic variability in yield, number of spikelets per panicle, and number of panicles per plant. These traits had high genetic advance and broad-sense heritability. The traits flag leaf length, number of panicles per plant, and number of spikelets per panicle were significantly positively phenol-typically correlated with yield, while day to flowering was significantly negatively phenotypically correlated with yield. Day to flowering, number of spikelets per panicle, number of panicles per plant, and flag leaf width had strong direct effects on yield. The indirect effect of flag leaf length was positive on yield, via the number of panicles per plant and the number of spikelets per panicle. The indirect effect of number of tillers per hill was positive on yield, via the number of panicles per plant. Thus, on selective breeding to increase yield, day to

flowering, flag leaf length and width, number of tillers per hill, number of panicles per plant, and number of spikelets per panicle are genotypic traits that should be assessed for the upland rice varieties. Based on agronomic information and clustering results, the high-potential genotypes that should be selected for an advance breeding program included Gam Med Yao (Group I), Niaw Khao (Group II), Khao$^/$ Tew (Group III), and Sew Phan. These genotypes also had the best days to flowering, flag leaf length, one thousand grains weight, yield per plant, number of panicles per plant, and number of spikelets per plant.

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