



Selection Index for Yield and Yield Contributing Traits in Improved Rice Genotypes

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Abstract To select improved rice lines according to a selection index, a field experiment was conducted using fifty improved rice genotypes, during the dry season of 2017 at the Department of Plant Breeding, Physiology and Ecology, Yezin Agricultural University, Myanmar. The examination used a Randomized Complete Block Design with three replications. Days to 50% flowering, plant height, number of effective tillers per hill, filled grain percentage, 1000 seed weight, number of spikelets per panicle, harvest index and yield per plant exhibited highly significant differences indicating the existence of genetic variability among the improved rice lines. There was not much variability in panicle length. Seed yield per plant was positively and significantly correlated with days to reach 50% flowering, plant height, the number of effective tillers per hill, filled grain percentage, number of spikelets per panicle and the harvest index at phenotypic and genotypic levels. This shows that indirect selection on these traits would be effective in improving grain yield. At the genotypic level, path coefficient analysis shows that number of spikelets per panicle, the 1000 grain weight, filled grain percentage, number of effective tillers per hill, plant height and harvest index has a positive influence on seed yield. The selection index based on the combination of number of effective tiller per hill, filled grain percentage, number of spikelets per panicle and seed yield per plant (ETPP+FGP+SPP+SYPP) has the highest genetic advance and relative efficiency. This indicated that indirect selection via these traits would be more efficient than direct selection using yield alone. Therefore, the genotypes; YAU-1215-S-S-S-41-1-1, YAU-1211-9-3-1, YAU-1211-71-1-1, YAU-1211-118-2-1 and YAU-1201-151-1-1 could be selected based on multiple traits selection for further evaluation.

Keywords correlation, genotypic, path analysis, phenotypic, selection index

INTRODUCTION

Improving grain yield is one of the main objectives of many breeding programs. Seed yield is linked to a complex inheritance and it is an ultimate expression of different factors. It is highly affected by environmental variations. The knowledge of the interrelationship among various yield and yield component traits is necessary for an effective breeding program (Sarwar et al., 2004). Path coefficient analysis can estimate the causes and measurement of the relative importance of each of the yield components can also separate the direct effects from the indirect ones that are due to other characters (Ibrahim et al., 2012). Moreover, the effectiveness of a plant breeding programs depends on the ability of a breeder to select superior individuals or families for many traits of interest (Strefeler and Wehner, 1986a).

The economic value of a plant depends on the value of its different traits, therefore, plant breeders should consider simultaneous selections for several traits to maximize the economic value of a plant (Rabiei et al., 2004). Moreover, breeding and selection programs often incorporate several

characters simultaneously (Hill et al., 1998). It is necessary to choose individuals with the best combination of desirable traits when considering several traits. The basis for this selection is a selection index, which is a combination of traits to select, according to their relative weighting. Gains from selection for any given trait is expected to decrease as additional traits are included in the index, therefore the choice for traits to be included must be done accurately (Hallauer and Miranda, 1981).

The Smith Hazel index is considered the optimum index when accurate estimates of variances and covariance are available (Hazel, 1943; Strefeler and Wehner, 1986b). However, this index requires a quantitative genetic study to estimate genetic variances and covariance and the assignment of relative economic weights to each trait (Strefeler and Wehner, 1986a). The Smith (Smith, 1936) and Hazel (Hazel, 1943) index and its various modifications (Kempthorne and Nordskog, 1959; Tallis, 1962; Elston, 1963; Pešek and Baker, 1969) have been shown to be the most efficient methods to achieve aggregate genetic progress compared with any other direct single trait selection methods.

OBJECTIVE

The objectives of this study were to determine the interrelationship between yield and yield contributing characters and to select the rice line(s) based on the selection indices and their relative efficiencies in providing improvement in yield.

MATERIALS AND METHODS

Fifty rice genotypes developed at Yezin Agricultural University (YAU), Myanmar were used in this study. These genotypes were developed by crossing parental lines such as Sin Thwe Latt, Yadanar Toe, Sin Thu Kha, Long 8, Shwe Thwe Yin and Long 6. Pedigree, bulk and single seed descent methods were used to develop these lines. The genotypes were evaluated at the Department of Plant Breeding, Physiology and Ecology at YAU during the 2017 dry season. The experiment site was located in Yezin Agricultural University, Zeyar Thiri Township, Nay Pyi Taw, Myanmar, latitude 19° 10' N and longitude 96° 07' E with an elevation of 102 m above sea level.

These genotypes were grown in a randomized complete block design, with three replications. The spacing was 20 cm × 20 cm with 100 hills per block. Standard agronomic practices and plant protection measures were applied to ensure good crop growth and complete grain development. The data collected were; days to 50% flowering (days) (DTF), plant height (cm) (PH), number of effective tillers per hill (no.) (ETPP), panicle length (cm) (PL), filled grain percentage (FGP), 1000 grain weight (g) (TGW), number of spikelets per panicle (no.) (SPP), harvest index (HI) and seed yield per plant (g) (SYPP). All the traits were measured following the guidelines provided by the Standard Evaluation System for Rice (SES) prepared by the International Rice Research Institute, Philippines (IRRI, 2002).

Analysis of variance (ANOVA) and correlations were generated using STAR v.2.0.1 (STAR, 2014). Path coefficient analysis was worked out using SPAR v 2.0 (Statistical Package for Agricultural Research, Version 2.0) software and R programs. Selection indices were constructed using the method developed by (Smith, 1936) based on the discriminate function of (Fisher, 1936). The economic weight for Smith Hazel Index was used to evaluate the direct effects from path analysis. The 10 % selection intensity was used to estimate genetic advances. The estimates of genetic advance were expressed as a percentage of the genetic progress obtained from seed yield per plant alone, which was assumed to initially be 100%, and it was used to compare the relative efficiencies of the different selection indices.

RESULTS AND DISCUSSION

Mean Performances and Analysis of Variances for Yield and Yield Component Traits

The analysis of variance revealed statistically significant differences at 0.1% probability level among the genotypes, for all traits except panicle length (Table 1). This indicates that there is much genetic variation among genotypes in all characters.

Table 1 Analysis of variance for yield and yield components in 50 rice genotypes

Trait	Replication	Genotype	Error
Days to 50% flowering	2.007	79.728**	5.367
Plant height	179.554	657.449**	294.131
Panicle length	6.125	5.679	4.012
No. of effective tillers per hill	4.903	6.509**	0.747
Filled grain percentage	14.992	94.504**	4.966
No. of spikelets per panicle	534.068	2422.678**	102.384
1000 grain weight	3.079	28.801**	1.013
Harvest index	0.0009	0.0067**	0.0004
Seed yield per plant	19.227	145.634**	7.989

** Significant at 1% probability level

Correlation Coefficient Analysis

There were 12 positive and 3 negatively significant correlations at phenotypic level and 14 positive and 4 negatively significant correlations at genotypic level for the nine traits measured (Fig. 1 a and b). At genotypic and phenotypic levels, seed yield per plant was positively and significantly correlated with days to 50% flowering, plant height, number of effective tillers per hill, filled grain percentage, number of spikelet per panicle and harvest index. This showed that indirect selection based on these traits will improve grain yield.

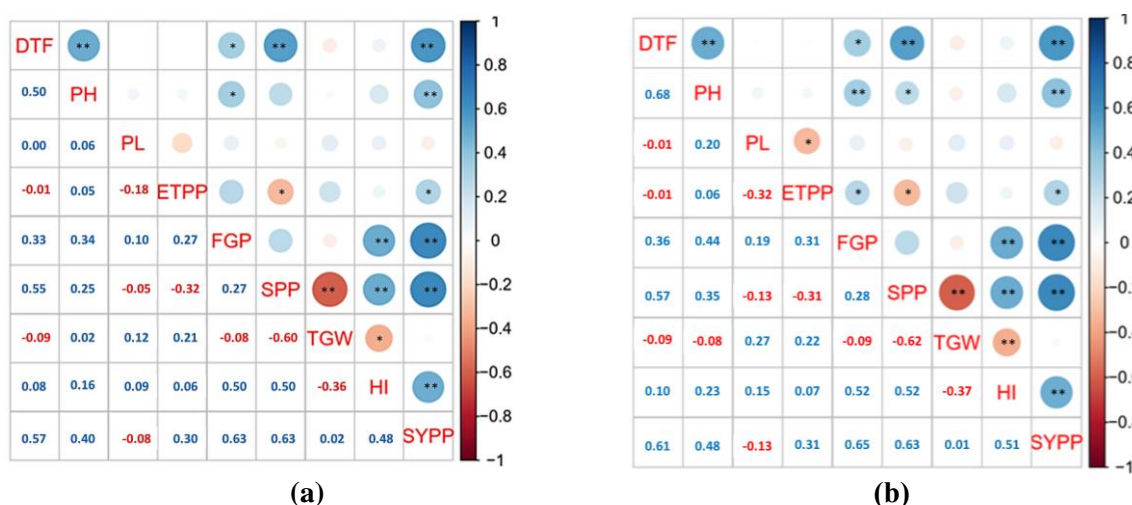


Fig. 1 Phenotypic correlation (a) and genotypic correlation (b) among agronomic traits in 50 rice genotypes

The tests of significance were indicated as **, * at 1% and 5 % probability level, respectively. The blue colour shows the positive association and red colour indicates the negative association and the intensity of the colour indicates the degree of association.

Path Coefficient Analysis

At phenotypic level and genotypic level, all of the direct effects, with the exception of one, were below one, suggesting that inflation due to multicollinearity was minimal (Fig. 2). At both levels, the direct effects for number of spikelets per panicle were positive and of greater magnitude than direct effects for the other traits. At phenotypic level, number of spikelets per panicle (1.07), 1000 grain weight (0.60), number of effective tillers per hill (0.42), filled grain percentage (0.30), plant height

(0.04) and harvest index (0.01) showed a significant positive direct effect with seed yield per plant. At genotypic level, path coefficient analysis showed that number of spikelets per panicle (1.05), 1000 grain weight (0.67), filled grain percentage (0.34), number of effective tillers per hill (0.32), plant height (0.14) and harvest index (0.02) influenced seed yield directly in a positive direction. These are the primary yield components in tested genotypes. In other words, when there is an increase in the performance of these characters, seed yield per plant can also increase. However, days to 50% flowering (-0.15) and panicle length (-0.17) had direct negative effect on seed yield per plant.

At genotypic level, days to 50% flowering (0.61) followed by harvest index (0.55), plant height (0.37) and filled grain percentage (0.30) exhibited a high order of positive indirect effect on seed yield per plant via number of spikelets per panicle. The remaining estimates of indirect effects in this analysis were too low to be considered of any consequence. The estimates of residual factors (0.0581) were negligible in the present study. The residual effect determines how best the causal factors account for the variability of the dependent factor such as the standard evaluation score. Residual effect indicated that the characters which are selected in this study contributed 94% of variability of the standard evaluation score.

Therefore, the number of effective tillers per hill, filled grain percentage and number of spikelets per panicle had significant positive correlation with seed yield as well as exercising a positive direct effect on seed yield, suggesting the selection for these traits would be helpful for the improvement of seed yield. Path analysis studies revealed that the traits, such as the number of effective tillers per hill, filled grain percentage and number of spikelets per panicle can be considered as selection criteria in improving the seed yield of rice as these have a prominent direct effect. Hence, selection for these traits will improve the yield.

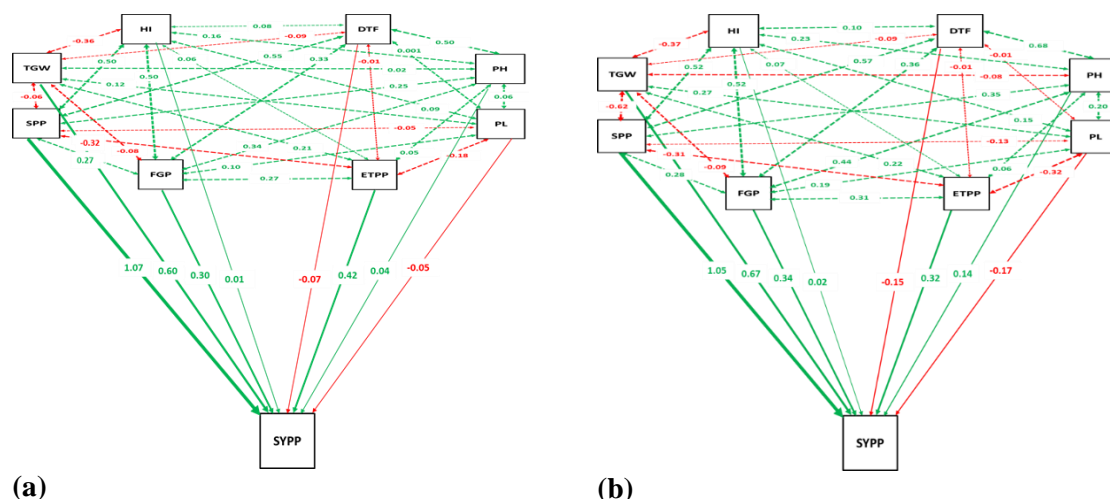


Fig. 2 Direct and indirect effects of seed yield and other related traits in path analysis at (a) phenotypic level and (b) genotypic level

Selection Indices

Fifteen selection indices containing two or more traits simultaneously were constructed. Out of fifteen, four selection indices were more efficient than direct selection for seed yield per plant. Using different combinations of yield and yield contributing traits, different selection indices were formulated and their expected genetic gain and relative efficiencies were estimated (Table 2). It was observed that among all selection indices, the index based on number of effective tiller per hill + filled grain percentage + number of spikelets per panicle + seed yield per plant (ETPP+ FGP+ SPP+ SYPP) had the maximum genetic advance (57.79) with relative efficiency (498.65). Among the others, the indices based on filled grain percentage + number of spikelets per panicle + seed yield per plant (FGP+SPP+SYPP), number of effective tillers per hill + number of spikelet per panicle + seed yield per plant (ETPP+SPP+SYPP), number of spikelets per panicle + seed yield per plant

(SPP+SYPP) showed high genetic gain with relative efficiency over straight selection for grain yield alone. Therefore, an improvement of grain yield is suggested through these selection indices.

Table 2 Selection indices for seed yield and their relative efficiency in YAU promising rice genotypes

Index	Genetic advance (g)/plant	Relative efficiency (%)
ETPP + FGP + SPP + TGW + SYPP	55.94	482.63
FGP + SPP + TGW + SYPP	55.93	482.54
ETPP + SPP + TGW + SYPP	54.51	470.36
ETPP+ FGP + TGW + SYPP	13.82	119.20
ETPP + FGP + SPP + SYPP	57.79	498.65
SPP + TGW + SYPP	54.60	471.10
FGP +TGW + SYPP	13.51	116.57
FGP + SPP + SYPP	57.67	497.61
ETPP + TGW + SYPP	11.68	100.80
ETPP+ SPP + SYPP	56.36	486.32
ETPP+ FGP + SYPP	13.54	116.84
ETPP + SYPP	11.25	97.03
FGP +SYPP	13.28	114.55
SPP + SYPP	56.31	485.83
TGW + SYPP	11.40	98.33
SYPP	11.59	100.00

Table 3 Comparison between relative genetic score of 50 rice genotypes based on the best selection index (ETPP + FGP + SPP+ SYPP)

Rank	Genotypes	Selection Index (Selection Score)	Rank	Genotypes	Selection Index (Selection Score)
1	YAU-1215-S-S-S-41-1-1	187.776	26	YAU-1201-187-1-1	127.507
2	YAU-1211-9-3-1	185.773	27	YAU-1215-B-B-B-168-1-1	126.567
3	YAU-1211-71-1-1	173.982	28	YAU-1215-B-B-B-10-1-1	125.120
4	YAU-1211-118-2-1	172.725	29	YAU-1201-206-2-1	122.602
5	YAU-1201-151-1-1	171.689	30	YAU-1211-121-2-1	122.587
6	YAU-1201-151-1-3	169.348	31	YAU-1201-202-2-1	122.458
7	YAU-1215-S-S-S-78-3-1	168.001	32	YAU-1214-B-B-B-33-1-1	122.174
8	YAU-1211-116-3-4	165.081	33	YAU-1201-90-2-2	120.390
9	YAU-1211-26-1-2	164.421	34	YAU-1201-90-1-1	117.818
10	YAU-1201-1-2-1	162.572	35	YAU-1214-183-3-3-1-1-1	117.552
11	YAU-1215-S-S-S-40-2-1	160.616	36	YAU-1201-202-2-2	116.408
12	YAU-1211-22-2-1	158.096	37	YAU-1201-61-3-3	115.993
13	YAU-1201-39-2-1	155.626	38	YAU-1215-188-3-1-2-1-1	115.741
14	YAU-1215-S-S-S-55-2-1	138.238	39	YAU-1215-B-B-B-139-3-1	112.413
15	YAU-1211-223-3-1	137.691	40	YAU-1215-B-B-B-134-1-1	112.031
16	YAU-1215-B-B-B-153-3-1	137.037	41	YAU-1214-183-3-4-1-1-1	109.247
17	YAU-1215-S-S-S-77-2-1	134.943	42	YAU-1201-61-3-1	107.198
18	YAU-1215-73-2-3-1-1-1	134.882	43	YAU-1215-S-S-S-115-1-1	103.131
19	YAU-1201-74-1-2	134.623	44	YAU-1215-B-B-B-141-3-1	102.619
20	YAU-1201-187-1-2	132.461	45	YAU-1201-16-2-1	101.812
21	YAU-1214-S-S-S-77-1-1	131.854	46	YAU-1201-121-3-1	99.830
22	YAU-1215-188-3-1-1-1-1	129.958	47	YAU-1215-80-1-2-1-1-1	95.564
23	YAU-1201-202-1-2	129.379	48	YAU-1215-B-B-B-52-3-1	95.304
24	YAU-1201-9-1-1	129.155	49	YAU-1215-S-S-S-113-1-1	79.839
25	YAU-1214-183-35-1-1-1-1	127.852	50	YAU-1214-187-1-1-1-1-1	77.424

Selection based on yield alone may be often misleading due to high environmental influence and multiple traits selection can improve selection efficiency and can attain largest economic gain. Therefore, utilizing the best selection index (number of effective tiller per hill + filled grain percentage + number of spikelets per panicle + seed yield per plant) (ETPP+FGP+SPP+SYPP), the relative genetic score of each genotype was determined (Table 3). It was found that the genotypes YAU-1215-S-S-S-41-1-1, YAU-1211-9-3-1, YAU-1211-71-1-1, YAU-1211-118-2-1 and YAU-

1201-151-1-1 were superior among all genotypes tested, having the optimal combination of attributes. These genotypes should be used for further evaluation.

CONCLUSION

Except panicle length, all the tested genotypes have a high variation in all studied traits. Number of effective tillers per hill, filled grain percentage and number of spikelets per panicle had significant positive genetic correlation with seed yield as well as employed positive direct effect on seed yield at genotypic and phenotypic levels. The selection index based on the combination of number of effective tiller per hill, filled grain percentage, number of spikelets per panicle and seed yield per plant (ETPP+FGP+SPP+SYPP) resulted the highest genetic advancement and relative efficiency. This indicates that indirect selection via these traits would be more efficient than direct selection considering yield alone. Therefore, the genotypes; YAU-1215-S-S-S-41-1-1, YAU-1211-9-3-1, YAU-1211-71-1-1, YAU-1211-118-2-1 and YAU-1201-151-1-1 are superior among all genotypes and could be selected for further evaluation.

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