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Evaluation of the advanced yield trial on tropical wheat (*Triticum aestivum*) mutant lines using selection index and multivariate analysis

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Abstract. *Fadli M, Farid M, Yassi A, Nasaruddin, Anshori MF, Nur A, Suratman. 2021. Evaluation of the advanced yield trial on tropical wheat (*Triticum aestivum*) mutant lines using selection index and multivariate analysis. Biodiversitas 23: 540-547.* The development of adaptive wheat (*Triticum aestivum* L.) mutant lines in tropical climate is a long-term solution. The advanced yield trial is an important stage in this development, which is carried out using a selection index and multivariate analysis. This study aims to determine the selection effectiveness of tropical wheat mutant lines by using a selection index and multivariate analysis. the study was conducted in three locations, which included two locations for the follow-up yield test in Kelara Village and Ujung Bulu Village (South Sulawesi, Indonesia), and the third location for the selection validation in Padang Magek Village (West Sumatra, Indonesia). This study was designed by a nested Randomized Complete Block Design (RCBD), with replications nested in locations. The samples included 16 wheat genotypes (13 mutant lines and three comparison varieties) that were replicated three times. The result showed that the selection of tropical wheat mutant lines using selection index and multivariate analysis were considered effectively with high determination value of 0.57 (57%). The results of the selection index show that seven lines were recommended for multi-location trials since they had a better selection index potential than Dewata variety.

Keywords: Mutant lines, PCA analysis, selection index, *Triticum aestivum,* tropical climate

Abbreviations: 1000-GW: 1000 Grain weight, CD: Chlorophyll density, CV: Coefficient of variation, DF: Days to flowering, DH: Days to harvest, GFT: Grain Filling time, GWP: Grain weight Per panicle, NGP: Number of grain per panicle, NPT: Number of Productive tillers, NT: Number of tillers, PC: Principal component, PCA: Principal component analysis, PEF: Percentage of empty florets, PH: Plant Height, PL: Panicle length, RCBD: Randomized Complete blocked design, S: Spikilet, SD: Stomatal density, Vg: Genetic variability, Vp: Phenotypic variability

INTRODUCTION

Wheat (*Triticum aestivum* L.) is a primary food source in subtropical regions and a secondary food source in tropical regions, specifically wheat flour (Tharise et al. 2014). The availability of wheat promotes food security in Indonesia, since wheat flour is the second-largest source of carbohydrates after rice (Rafiuddin et al. 2020). Therefore, the increasing population growth of Indonesia has led to an annual increase in the demand for wheat, specifically wheat flour. The demand for wheat flour can be fulfilled by increasing wheat importation. According to Statistics Indonesia (2021), Indonesia imported about 10.29 million tons of wheat flour in 2020. However, this import danger to Indonesia food sovereignty. Therefore, the promotion of wheat farming is a better way of resolving the demand in Indonesia. Generally, wheat plants grow better in the highlands of Indonesia at 1000 m above sea level due to their optimal temperature ranging between 8-10°C (Farid et al. 2021). However, this condition is rare and only found in small areas of specific regions (Rafiuddin et al. 2020). The development of highland wheat will promote the growth of other products, such as vegetables, fruit, tea, coffee, etc. (Farid et al. 2020), which are considered to be more in demand and profitable than wheat farming (Rafiuddin et al. 2020). Therefore, wheat farming should be limited to the lower plains or the overall tropical climate.

Wheat farming in tropical lands is associated with the development of heat-resistant wheat varieties that require a diversity induction method for the selection process (Bovina et al. 2014). Irradiation mutation is one of the effective methods for developing such varieties randomly (Xiong et al. 2019). Furthermore, this method employs random abrasion of genes and chromosomes, which produces new viable variants (Sun et al. 2006; Farid and Ridwan 2018; Nasaruddin et al. 2018; Nur et al. 2018). Farid et al. (2020) have conducted the breeding procedure until it reached a preliminary yield test on several lines that are adaptive to the tropical lands. These lines have to continue to the following stage, namely the advanced yield trial. However, the effectiveness of the selection in advanced yield trials must be carried out with precision and accuracy. One method for improving the accuracy is by selecting based on a combination of primary and secondary parameters.

According to Wening et al. (2019), Fadhli et al. (2020), and Anshori et al. (2021), the yield test can be conducted effectively through a combination of primary and secondary characters in the form of a selection index, which is a method of selecting characters based on their weight (Simeao et al. 2015). Subsequently, the combination is substituted into a multiple regression formula. The order of the selection indices for each genotype serves as a guide in the selection process (Rajamani et al. 2016; Islam et al. 2017). According to Sabouri et al. (2008), Figueiredo et al. (2012), and Anshori et al. (2019), the selection index is effective and equivalent to the weight assigned to each character. The determination of the selection index can be conducted by multivariate analysis, which is used to interpret and simplify data containing a large number of variables (Mattjik and Sumertajaya 2011). Additionally, this analysis can aid breeders in determining the characteristics and weighting values for the selection process (Arain et al. 2018; Farid et al. 2020).

The cultivation of wheat in tropical lands requires advanced yield trialing of wheat mutant lines using a selection index based on multivariate analysis. Therefore, This study aims to determine the selection effectiveness of tropical wheat mutant lines by using a selection index and multivariate analysis.

MATERIALS AND METHODS

Study area

The study was conducted from July to October 2019 in three locations. The advanced yield trial was conducted in two locations, i.e. Kelara Village and Ujung Bulu Village, whereas, the validation of the selection was conducted in Padang Magek Village (Table 1).

Plant materials

A nested Randomized Complete Block Design (RCBD) was used in this study, where the replications were nested in the locations. The study included 16 wheat genotypes, which consisted of 13 wheat mutant lines irradiated by gamma radiation (1 line from Dewata variety, 4 lines from Selayar variety, 8 lines from Nias variety) and three control varieties (Dewata, Selayar, and Nias) (Table 2). Each variety was replicated three times at each location, for a total of 96 experimental units, and also each genotype consisted of three rows of plants cultivated in an array. Each experimental unit has ten clumps for observation samples.

Procedures

The procedure for planting wheat was in accordance with Nasruddin et al. (2018) and Farid et al. (2020). Plots were measured at 2.5x1 m with 0.5 m apart in each replication. Each plot consisted of three rows 0.25 cm apart. The seeds were planted in holes, which were formed from the array. Each of the wheat genotypes weighed 7 g and was planted in each row at 20x5 cm apart. The maintenance activities in wheat cultivation include watering, fertilizing, weeding, and controlling plant pest organisms. Watering was conducted every day, while the first and second weeding occurred on the fourth and sixth week after planting, respectively. Fertilization was performed twice on the tenth and thirtieth day after planting using Urea, SP36, and NPK fertilizer (16-16-16) at a dose of 150 kg ha^{-1}, 200 kg ha^{-1}, and 100 kg ha^{-1}, respectively. The second fertilization was conducted using Urea at a dose of 150 kg ha^{-1}. Subsequently, chemical pesticides (Deltamethrin 25 g L^{-1}, and Profenofos 500 g L^{-1}) were used to control plant pest organisms. Harvesting was performed when 80% of the plants in a plot were physiologically ripe, as indicated by yellowing panicles, stems, and leaves of the plant, as well as hardening of the wheat seeds.

Table 1. The detailed information of field locations

Aspects	Field locations		
	Kelara Village	**Ujung Bulu Village**	**Padang Magek Village**
Detailed location	South Tolo Sub-district, Jeneponto District, South Sulawesi, Indonesia	Rumbia Sub-district, Jeneponto District, South Sulawesi, Indonesia	Rambatan Sub-district, Tanah Datar District, West Sumatra, Indonesia
Altitude (asl.)	135 m	800 m	400 m
Coordinates	5º 34’59’’S 119º48’31” E	5º24’56’’S 119º54’19” E	0º29’37” S 100º34’04” E

Table 2. The detailed information of genotype used in this study

Genotype	Lines	Wild type mutant	Genotype	Lines	Wild type mutant
G1	N 200 2.3.3	Nias variety	G9	S 300 8.3.1	Selayar variety
G2	N 250 4.6.2	Nias variety	G10	N 200 2.4.6B	Nias variety
G3	D 200	Dewata variety	G11	N 200 2.5.2	Nias variety
G4	S 300 7.9.1	Selayar variety	G12	S 300 2.1	Selayar variety
G5	N 350 3.7.1	Nias variety	G13	N 350 3.6.2	Nias variety
G6	N 200 1.7.1	Nias variety	Dewata		Control variety
G7	N 350 3.1.3	Nias variety	Selayar		Control variety
G8	S 300 3.6.1	Selayar variety	Nias		Control variety

Parameters observations

The data used in this study were obtained from field observations in each experimental plot, such as plant height, number of tillers, number of productive tillers, stomatal density, chlorophyll index, days to flowering, days to harvest, grain filling time, panicle length, spikelet, floret, percentage of empty florets, number of grains per panicle, grain weight per panicle, 1000 grain weight, and the yield (Nasruddin et al. 2018; Farid et al. 2020).

Data analysis

Analysis of variance (ANOVA) and phenotypic-genetic correlation were used to analyze the observed data. The selected characters and correlations from ANOVA were subjected to in-depth analysis using path and principal component analysis (PCA), which served as the determinants of the optimal selection index based on index heritability as an early index validation technique (Anshori et al. 2019). Subsequently, the mutant lines were selected using the best selection index and a rating system. The ANOVA and PCA analysis used the STAR 2.0.1 software by IRRI. Meanwhile, path analysis used excel 2016 version and correlation analysis used META-R by CIMMYT. The selected mutant lines were propagated and validated using regression analysis by MINITAB 17 version (Anshori et al. 2020).

RESULTS AND DISCUSSION

Analysis of variance on the character of wheat growth in two locations

The analysis of variance results showed that there was a significant environmental influence on various characteristics, such as number of tillers, chlorophyll index, days to flowering, days to harvest, spikelet, percentage of empty florets, number of grains per panicle, grain weight per panicle, and the yield (Table 3). Genotype variance had a very significant effect (**) on plant height, number of tillers, number of productive tillers, flowering days, harvest days, time of grain filling, panicle length, grain, percentage of empty buds, the weight of grain per panicle, and yield. The stomata density, number of grains per panicle, and the weight of 1000 grains have affected significantly (*) on genotype variance, while chlorophyll index was not significantly affected by its variance (ns). The interaction variance is very significantly affected on plant height, stomatal density, days to flowering, grain filling time, percentage of empty florets, number of grains per panicle, and grain weight per panicle. The panicle length and the yield were just affected significantly by interaction variance. Identification of genetic parameters has focussed on heritability. Generally, the result of the heritability analysis showed that there was a high heritability of certain traits, such as the number of tillers, number of productive tillers, days to flowering, days to harvest, grain weight per panicle, and the 1000 grain weight. The panicle length, spikelet, and yield were all classified as having a medium heritability. However, the plant height, stomatal density, chlorophyll index, grain filling time, percentage of empty florets, and the number of grains per panicle of plants were all classified as having a low heritability based on the analysis of variance and the heritability of the yield.

Establishment of a selection index for lowland wheat yield test

The results of phenotypic and genotypic correlations on the yield are presented in Table 4. The results of phenotypic correlation showed that there was a significant relationship between the yield and other characteristics, such as the number of tillers, number of productive tillers, panicle length, stomatal density, spikelet, and grain weight per panicle of 0.81, 0.78, 0.86, 0.69, 0.66, and 0.89, respectively. Meanwhile, the results of genetic correlation showed that there was a significant relationship between the yield and other characteristics, such as the number of tillers, the number of productive tillers, spikelet, grain weight per panicle, and 1000 grain weight at a value of 1.00 each, as well as panicle length at 0.65.

Table 3. Analysis of variance (ANOVA) of growth characteristics in the test of the advanced yield of wheat mutants

Characters	MS				Genetic parameters		
	Environment (E)	Genotype (G)	E x G	CV	Vg	Vp	h^2
Plant height (cm)	119.93ns	64.88**	98.73**	7.65	0.00	16.45	0.00
Number of tillers (tillers)	43.34**	4.21**	1.20ns	15.89	0.50	0.70	71.39
Number of productive tillers (tillers)	5.59ns	3.26**	1.22ns	16.61	0.34	0.54	62.53
Stomatal density (mm^2)	214.05ns	72.09*	75.83**	14.53	0.00	12.64	0.00
Chlorophyll Index (CCI)	9618599.69**	42.17ns	38.69ns	1.33	0.58	7.03	8.25
Days to flowering (day)	2981.29**	28.30**	13.18**	1.89	2.52	4.72	53.45
Days to harvest (day)	3488.11**	10.33**	1.84ns	1.35	1.41	1.72	82.18
Grain filling time (day)	17.23ns	27.35**	27.35**	3.96	0.00	4.56	0.00
Panicle length (cm)	0.02ns	0.80**	0.58*	6.19	0.04	0.13	27.09
Spikelet (seed)	396.74**	3.72**	2.15ns	8.70	0.26	0.62	42.20
Percentage of empty florets (%)	3014.59**	92.49**	185.73**	8.92	0.00	30.95	0.00
Number of grains per panicle (seed)	2408.61**	23.80*	58.64**	15.41	0.00	9.77	0.00
Grain weight per panicle (g)	3.14**	0.10**	0.05**	20.35	0.01	0.02	53.22
1000 grain weight (g)	168.88ns	197.08*	55.31ns	30.93	23.63	32.85	71.94
The yield (ton)	249.39**	5.89**	3.59*	36.50	0.38	0.98	39.05

Note: MS: mean square, CV: coefficient of variance, Vg: genotypic variance, Vp: phenotypic variance, h^2: broad heritability, *: significant at level 0.05, **: significant at level 0.01, ns: no significant

The results of the path analysis on the yield is presented in Table 5 there was a very significant positive and direct effect on the yield by the number of productive tillers and the grain weight per panicle at 0.78 and 0.92, respectively. Conversely, the number of tillers had a very significant negative and direct effect on the yield at -0.78. Meanwhile, there was a high indirect effect by the number of productive tillers and grain weight per panicle on other characteristics related to the yield at 2.50 and 2.86, respectively. Lastly, the number of tillers had the most negative effect on other characteristics related to the yield at -2.61.

The results of the principal component analysis showed that four principal components had an eigen-value greater than 1 at a cumulative proportion of 0.8239 (Table 6). The greatest variance was observed in the principal component 1 (PC1) at 0.4707 (47.07%), which also showed the greatest variance of the yield eigenvectors at -0.3137. Therefore, PC1 could be used to determine the weight of the selection index. The weight of the modeled selection index consists of three formulations, which include: (i) Path analysis index = the yield + 0.78 number of productive tillers + 0.92 grain weight per panicle. (ii) PCA index= 0.314 the yield +0.332 number of productive tillers + 0.342 grain weight per panicle. (iii) Path – PCA index = 0.314 the yield + 0.259 number of productive tillers + 0.315 grain weight per panicle

Selection and validation selection index on wheat yield test in lowland

The actual value and standardization as the basis in forming the index value (Table 7). The results of selection index analysis showed that the PCA index has the highest heritability index (48.16%). Meanwhile, the path index and path-PCA have heritability index of 46.26 and 46.64, respectively. Therefore, the PCA index was used in selecting the tropical wheat genotypes. Based on this the PCA index selection, there were seven promising wheat lines, namely N 250 4.6.2 (G2), D 200 (G3), S 300 7.9.1 (G4), N 350 3.7.1 (G5), N 350 3.1.3 (G7), N 200 2.5.2 (G11), and N 350 3.6.2 (G13), which were better than the comparison Dewata variety and had a positive index value.

The validation results were analyzed using regression analysis (Figure 1). According to the analysis, the PCA index could be predicted the yield in Padang Magek Village with a formula as 2.126 + 0.2971 PCA index. Although the b or gradient value was not close to 1, the PCA index has a good determination value of 57.2% (Figure 1). Besides that, all the samples were within the prediction interval (PI) or the confidence interval (CI), whereas all mutant lines fell within or close to the CI. Therefore, the PCA index has been considered to have good validation.

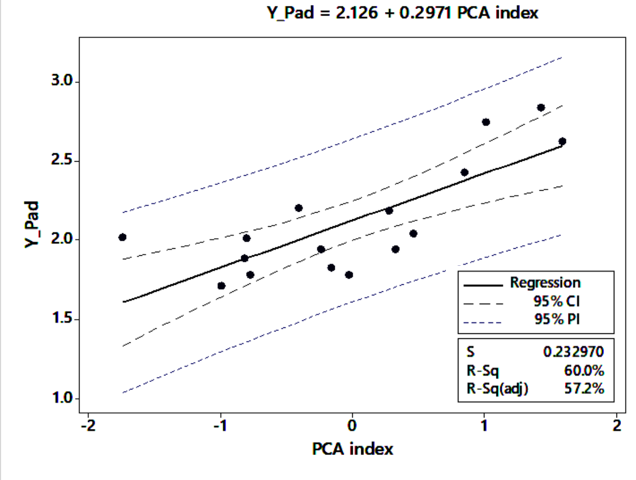

Figure 1. Regression analysis in index validation on the yield in Padang Magek Village, Rambatan Sub-district, Tanah Datar District, West Sumatra Province, Indonesia (note: Y_Pad: Yield in Padang Magek Village)

Table 4. Phenotypic and genotypic correlations for all wheat growth characters in the lowlands

Traits	PH	NT	NPT	SD	CD	FA	HA	GFT	PL	S	PEF	NGP	GWP	1000-GW
Phenotypic correlation														
The yield	0.50	**0.81****	**0.78****	**0.86****	0.35	0.15	0.06	-0.12	**0.69****	**0.66****	-0.28	0.48	**0.89****	0.42
Genetic correlation														
The yield	NA	**1.00****	**1.00****	NA	-0.4	0.51	0.22	-0.55	**0.65****	**1.00****	NA	NA	**1.00****	**1.00****

Note: PH: plant height, NT: Number of tillers, NPT: Number of productive tillers, SD: Stomatal density, CD: Chlorophyll density, DF: Days to flowering, DH: Days to harvest, GFT: Grain filling time, PL: Panicle length, S: Spikelet, PEF: Percentage of empty florets, NGP: Number of grain per panicle, GWP: Grain weight Per panicle, 1000-GW: 1000 Grain weight, **significant at level 0.01.

Table 5. Path analysis of wheat the yield based on characters that are significantly correlated with the yield

Characters	Direct effect	Indirect influence						Residual
		NT	NPT	PL	S	GWP	1000-GW	
Number of tillers	**-0.78****		0.75	0.26	-0.25	0.8	0.01	0.13
Number of productive tillers	**0.78****	-0.75		0.23	-0.25	0.76	0.01	0.13
Panicle length	0.37	-0.56	0.49		-0.21	0.59	0.02	0.13
Spikelet	-0.32	-0.62	0.62	0.24		0.71	0.01	0.13
Grain weight per panicle	**0.92****	-0.68	0.64	0.23	-0.24		0.02	0.13
1000 grain weight	0.4	-0.19	0.12	0.15	-0.1	0.04		0.13
Total		-2.61	2.50	0.96	-0.95	2.86	0.07	

Note: NT: Number of tillers, NPT: number of productive tillers, PL: panicle length, S: spikelet, GWP: grain weight per panicle, 1000-GW: 1000 grain weight, ** significant at level 0.01

Table 6. Analysis of the principal components of the growth character of wheat in the advanced yield trial

Characters	PC1	PC2	PC3	PC4	PC5
Plant height	-0.2051	-0.3049	0.3754	-0.2537	0.0580
Number of tillers	-0.3450	0.0123	-0.0732	-0.0447	0.2094
Number of productive tillers	-0.3322	-0.0149	-0.1458	-0.0086	0.1557
Stomatal density	-0.2499	-0.1964	0.1420	0.2229	-0.3218
Chlorophyll index	-0.2178	-0.3166	-0.2132	-0.1263	0.4796
Days to flowering	-0.0465	0.5253	0.2574	-0.2269	0.2459
Days to harvest	-0.0215	-0.0098	0.2470	-0.7761	-0.0535
Grain filling time	0.0421	-0.5514	-0.1025	-0.2453	-0.2707
Panicle length	-0.2796	0.1704	0.1915	0.0774	0.0530
Spikelet	-0.3268	-0.0405	-0.0958	0.0974	0.0437
Florets	-0.3268	-0.0405	-0.0958	0.0984	0.0435
Percentage of empty florets	0.1404	-0.3166	0.3149	0.2243	0.5826
Number of grains per panicle	-0.2627	0.2299	-0.3627	-0.1761	0.0504
Grain weight per panicle	-0.3415	-0.0145	0.0025	0.0206	-0.1936
1000 grain weight	-0.1371	0.0410	0.5566	0.2113	-0.0576
The yield	-0.3137	0.0227	0.1830	0.0484	-0.2625
Standard deviation	2.7442	1.6005	1.2912	1.1929	0.9075
Proportion of Variance	0.4707	0.1601	0.1042	0.0889	0.0515
Cumulative Proportion	0.4707	0.6308	0.735	0.8239	0.8754
EigenValues	7.5305	2.5617	1.6672	1.4229	0.8235

Note: PC: Principal component

Table 7. Selection index based on path analysis, PCA, and combination of path analysis and PCA

G	Actual value			Standardization			Index		
	Number of productive tillers	Grain weight per panicle	The yield	Number of productive tillers	Grain weight per panicle	The yield	Path	PCA	Path-PCA
G7	6.45	0.92	5.05	1.33	1.97	1.52	4.37	1.59	1.44
G5	6.39	0.84	5.25	1.26	1.38	1.73	3.98	1.43	1.3
G13	6.61	0.75	4.37	1.56	0.68	0.84	2.68	1.01	0.88
G4	6.39	0.76	4.05	1.25	0.8	0.52	2.23	0.85	0.74
G11	5.45	0.78	4.03	-0.03	0.93	0.49	1.33	0.46	0.44
G2	6.11	0.68	3.49	0.88	0.15	-0.05	0.78	0.33	0.26
G3	5.78	0.69	3.73	0.43	0.23	0.19	0.74	0.28	0.24
Dewata	5.22	0.65	3.87	-0.33	-0.05	0.34	0.03	-0.02	0
Nias	5.39	0.62	3.52	-0.1	-0.35	-0.02	-0.42	-0.16	-0.14
G10	4.89	0.58	4.27	-0.78	-0.62	0.73	-0.44	-0.24	-0.17
G6	5	0.64	3.08	-0.63	-0.15	-0.47	-1.1	-0.41	-0.36
G9	4.84	0.57	2.76	-0.85	-0.72	-0.79	-2.12	-0.78	-0.69
Selayar	4.39	0.63	2.79	-1.46	-0.24	-0.75	-2.12	-0.8	-0.69
G12	5.14	0.55	2.37	-0.44	-0.87	-1.18	-2.32	-0.81	-0.76
G1	5	0.52	2.22	-0.63	-1.08	-1.33	-2.81	-0.99	-0.92
G8	4.39	0.4	1.76	-1.46	-2.04	-1.79	-4.81	-1.74	-1.58
Heritability index							46.26	48.16	46.64

Discussion

Analysis of variance is used as a basis for evaluating the influence of genetic, environmental, and the interaction between both components on a population of genotypes in plant breeding (Syukur et al. 2015; Farid et al. 2020; Anshori et al. 2021). There are many pattern responses among genetic, environmental, and the interaction effect in ANOVA. The interactive pattern has in group 1 consists of plant height, stomatal density, grain filling time, and panicle length, and group 2 consists of the number of tillers, days to harvest, and spikelet. The first group was significantly affected by genetics and the interaction effect. However, it does not have an environmental variance. It means that the average environment of this group character relatively same, but there was a dynamic response pattern among genotypes in two environments. Group 2 is not significantly affected by interaction; however, the environment and genotype of these characters have a significant effect. It means that the changed response between environments is stable (Anshori et al. 2019). Although, the focus of analysis in advanced yield trials is the pure genotype effect that frees from the interaction effect (Hidayatullah et al. 2018; Liu et al. 2019; Akbar et al. 2021).

The genotype provides an early indication of the effectiveness of plant breeding experiments. According to Syukur et al. (2015), diverse genotypes facilitate the selection in plant breeding. This study showed that genotype had a significant effect on almost all parameters, which gave rise to effective selection. Selection in certain environments requires the existence of effective selection characteristics due to environmental factors or interactions between the genotype and environment (Anshori et al. 2019; Anshori et al. 2020; Farid et al. 2020). The yield is the main trait, which exhibits a significant response to the two sources of diversity. This shows that the selection process is based on relatively unstable yield, as supported by the heritability analysis, which indicates a moderate degree of inheritance. Heritability analysis is a type of genetic analysis, which is frequently used to determine the magnitude of the genetic influence on the observed phenotype diversity. According to Syukur et al. (2015), line selection is effective when carried out on highly heritable characteristics of populations. Therefore, the selection of the yield-enhancing and the yield-supporting characteristics is effective.

The application of multivariate analysis techniques, such as phenotypic and genetic correlation, path analysis, and PCA is an effective assessment package for character selection. These methods have been applied by Anshori et al. (2019) and Anshori et al. (2021) on salinity-tolerant rice, as well as Fadhli et al. (2020) on drought-tolerant rice and maize, respectively, and lastly, Farid et al. (2021) on hydroponic wheat selection. Correlation analysis was the fundamental concept of this analysis. Phenotypic-genetic correlation analysis was important in the selection process, specifically when genotypes are evaluated in several environments. Additionally, this was consistent with Lozada et al. (2019), which stated the critical importance of phenotypic-genetic correlation in the selection process, specifically when based on secondary characters. Generally, genetic analysis can separate environmental influences and interactions in the correlation analysis, such that the difference between phenotypic and genetic correlation becomes the basis for assessing environmental interactions (Singh and Chaudhary 2007; Anshori et al. 2019; Baye et al. 2020). Environmental interactions will affect the correlation analysis when there is a difference between phenotypic and genotypic correlation. Therefore, this concept often serves as the foundation for more detailed analysis (Anshori et al. 2019). Although, characters with significant genetic correlations are still included in the in-depth analysis. According to phenotypic-genetic correlation analysis, potential characteristics for further analysis included the number of tillers, the number of productive tillers, panicle length, the number of spikelets, grain weight per panicle, and 1000-grain weight.

The path analysis is quantified the direct effect of a certain trait on the diversity of its main characters or the yield (Singh and Chaudhary 2007). This analysis is very important in assessing selection characteristics due to the insufficiency of correlation analysis in this study. Fadhli et al. (2020) demonstrated the effectiveness of this analysis on maize during drought stress testing, while Baye et al. (2020), Bisht et al. (2020), Nada et al. (2021), and Farid et al. (2021) demonstrated the effectiveness of this analysis on wheat mutant. The number of productive tillers and grain weight per panicle were identified as characteristics with the potential to support the yield through path analysis. Therefore, both characteristics could be used to construct the selection index.

The number of productive tillers and grain weight per panicle were effective secondary characters for wheat and rice. This is also supported by Anshori et al. (2019), Akbar et al. (2021) and Anshori et al. (2021) for rice and Arya et al. (2017), Ibrahim (2019), Farid et al. (2020), and Farid et al. (2021) for wheat. Wheat and rice, as well as some Poaceae cereal crops, increase their growth area through the use of tillers or axillary shoots (Hussien 2014). Tiller growth becomes important in wheat and rice production patterns since each tiller has the potential to produce grains (Sidwell et al. 1976; Kato et al. 2000; Huang et al. 2003; Kumar et al. 2007). Meanwhile, the yield potential of cereal crops, such as corn and sorghum is largely determined by the size of the cob and panicle since they rely on apical dominance for growth (Dixit et al. 2014). According to Nukasani et al. (2013), Ayer et al. (2017), Bisht et al. (2020), Nada et al. (2021), and Farid et al. (2021), grain weight per panicle is another important trait that contributes to the wheat yield. The combination of these two characteristics with the yield is an optimal choice in developing the selection index. However, the selection index should be considered based on the priority value or diversity of the characteristics. This can be accomplished using the path analysis, principal component analysis (PCA), or a combination of PCA and path analysis (Path-PCA) (Table 5), which shows genotypic selection index. The selection index of the principal component is based on eigenvalues, which denote negative values. However, the eigenvalues of the three selection characteristics can be weighted by a positive sign since the negative sign is restricted to the direction of variance and not to the absolute value (Jollifle 2002). The effectiveness of the three indices was determined using the heritability analysis of the selection index, which shows the effectiveness of genetically weighted combinations (Ramos et al. 2014; Gazal et al. 2017). According to Table 3 and 7, the heritability of the selection index is greater than the heritability of the yield in isolation. Furthermore, the combination of several secondary characteristics with the yield can increase the genetic potential of the main characteristics, such as the yield, which increases the effectiveness of the selection over using only the yield. Farid et al. (2020) and Farid et al. (2021) reported similar effectiveness on wheat selection, Anshori et al. (2019) on rice under salinity stress, Rahajeng and Rahayuningsih (2017) on sweetpotato in two environments.

The selection index was then validated using regression analysis, which is used to determine the effectiveness of the model. In regression analysis, the determination value is an important component of the validation assessment (Al-Salim et al. 2017). The model is more suited to the selection accuracy at a higher determination value (Chun et al. 2021). The concept for the assessment was developed by Farid et al. (2021) and Anshori et al. (2021). The regression determination value shows that the selection index model was quite good since it exceeded 57% (Anshori et al. 2021; Farid et al. 2021). Additionally, none of the genotypes was outside the prediction interval, which is a time interval between two predictions in a model. The amount of selected tropical wheat mutant lines in this study also has the same amount reported by Sari et al. (2016). Besides that, these selected genotypes have a higher yield than the stable tropical wheat lines from Ashari et al. (2012). Therefore, this selection index was considered effective for use in multi-location wheat genotype selection.

In conclusion, the using selection index and multivariate analysis in the selection of tropical wheat mutant lines are considered effectively with high determination validation as 57%. Wheat the yield was strongly supported in this study by secondary characteristics, such as the number of productive tillers and grain weight per panicle. Also, PCA analysis was considered effective in constructing the selection index. The selection index in this analysis was calculated as follows: selection index = 0.314 the yield + 0.332 number of productive tillers + 0.342 grain weight per panicle. Consequently, seven lines were selected based on the yield, which included N 250 4.6.2 (G2), D 200 (G3), S 300 7.9.1 (G4), N 350 3.7.1 (G5), N 350 3.1.3 (G7), N 200 2.5.2 (G11), and N 350 3.6.2 (G13). These mutant lines would be recommended in multi-location testing to release tropical wheat varieties in Indonesia.

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