Search for Search All Journals TEXT SIZE + −

Plant Breeding and Biotechnology

Open Access

ISSN 2287-9358 (Print)
ISSN 2287-9366(Online)

Home | Articles | Online First | Authors | Reviewers | About this Journal

Search for Title Author Keyword ::: Volume ::: ::: Issue ::: SEARCH

CURRENT ISSUE

Plant Breed. Biotech. 2020;8:307-444

Research Articles

Development of a Mutant Population of Micro-Tom Tomato Using Gamma-Irradiation

Jae-In Chun, Heejin Kim, Yeong Deuk Jo, Jin-Baek Kim, Jin-Ho Kang
Plant Breed. Biotech. 2020;8:307-315
https://doi.org/10.9787/PBB.2020.8.4.307 Full Text (PDF) Free Supplementary File(s)

Trait Association, Genetic Analyses and Fatty Acid Profiles in Oilseed Producing Rapeseed-Mustard (Brassica spp.) Genotypes

Md. Abir Ul Islam, Juthy Abedin Nupur, Arif Hasan Khan Robin
Plant Breed. Biotech. 2020;8:316-326
https://doi.org/10.9787/PBB.2020.8.4.316 Full Text (PDF) Free Supplementary File(s)

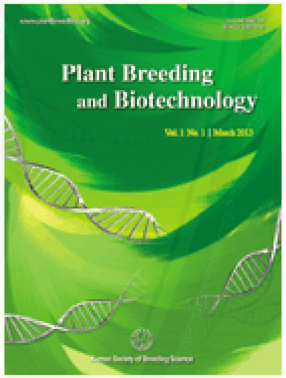
Genetic Analysis Reveals a Major Effect QTL Associated with High Grain Zinc Content in Rice (Oryza sativa L.)

Shaikh J. Mohiuddin , Md. Ashraful Haque , Md. Manjurul Haque , Md. Tofazzal Islam , Partha S. Biswas
Plant Breed. Biotech. 2020;8:327-340
https://doi.org/10.9787/PBB.2020.8.4.327 Full Text (PDF) Free Supplementary File(s)

Genetic Diversity of Fatty Acids, Tocols, Squalene, and Phytosterols in Grains of

PLANT BREEDING AND BIOTECHNOLOGY
e-Submission »»

Aims and Scope | Editorial Board



Plant Breeding and Biotechnology (Plant Breed. Biotech.) publishes original and peer-reviewed research and review articles in all areas of basic and practical researches in the field of plant breeding and biotechnology including breeding methodologies, genetics, and genomics of ......

Editor-in-Chief
Tae-Jin Yang
Seoul National University

MORE

Most Read | Archives

Gene-Based Markers for the Tomato Yellow Leaf Curl Virus Resistance Gene Ty-3

157 Rice Cultivars Bred in Korea

Young-Sang Lee , Kyu-Won Kim , Yong-Jin Park
Plant Breed. Biotech. 2020;8:341-353
https://doi.org/10.9787/PBB.2020.8.4.341
Full Text (PDF) Free | Supplementary File(s)

Two Complementary Genes, SBE3 and GBSS1 Contribute to High Amylose Content in Japonica Cultivar Dodamssal

Cheryl C. Adeva, Hyun-Sook Lee, Sun-Ha Kim, Yun-A Jeon, Kyu-Chan Shim, Ngoc Ha Luong, Ju-Won Kang, Chang-Soo Kim, Jun-Hyeon Cho, Sang-Nag Ahn
Plant Breed. Biotech. 2020;8:354-367
https://doi.org/10.9787/PBB.2020.8.4.354
Full Text (PDF) Free | Supplementary File(s)

Genetic Parameters and Multivariate Analysis to Determine Secondary Traits in Selecting Wheat Mutant Adaptive on Tropical Lowlands

Muh Farid, Nasaruddin Nasaruddin, Yunus Musa , Muhammad Fuad Anshori, Ifayanti Ridwan, Jekvy Hendra ,Gatot Subroto
Plant Breed. Biotech. 2020;8:368-377
https://doi.org/10.9787/PBB.2020.8.4.368
Full Text (PDF) Free | Supplementary File(s)

Genetic Analysis of Anthocyanin Pigmentation in Sterile Lemma and Apiculus in Rice

Woo-Jin Kim, Cheryl Adeva, Hyun-Sook Lee, Yun-A Jeon, Kyu-Chan Shim, Sang-Nag Ahn
Plant Breed. Biotech. 2020;8:378-388
https://doi.org/10.9787/PBB.2020.8.4.378
Full Text (PDF) Free | Supplementary File(s)

FISH Karyotype Comparison of Platycodon grandiflorus (Jacq.) A. DC. 'Jangbaek' and Its Colchicine-Induced Tetraploid 'Etteumbaek

Eliazar Alumbro Peniton Jr., Yurry Um, Hyun Hee Kim
Plant Breed. Biotech. 2020;8:389-395
https://doi.org/10.9787/PBB.2020.8.4.389
Full Text (PDF) Free

Detection of Whole-Genome Resequencing-Based QTLs Associated with Pre-Harvest Sprouting in Rice (Oryza sativa L.)

Seong-Gyu Jang, San Mar Lar, Hongjia Zhang, Ah-Rim Lee, Ja-Hong Lee, Na-Eun Kim, So-Yeon Park, Joohyun Lee, Tae-Ho Ham, Soon-Wook Kwon
Plant Breed. Biotech. 2020;8:396-404
https://doi.org/10.9787/PBB.2020.8.4.396
Full Text (PDF) Free | Supplementary File(s)

Panpan Dong, Koeun Han, Muhammad Irfan Siddique, Jin-Kyung Kwon, Meiai Zhao, Fu Wang, and Byoung-Cheorl Kang
Received January 12, 2016; **Accepted** February 11, 2016.

A Simple DNA Preparation Method for High Quality Polymerase Chain Reaction in Rice

Sung-Ryul Kim, Jungil Yang, Gynheung An, and Kshirod K. Jena
Received January 4, 2016; **Accepted** February 4, 2016.

High-Throughput SNP Genotyping to Accelerate Crop Improvement

Michael J. Thomson
Received September 19, 2014; **Accepted** September 23, 2014.

A New Approach for Glutinous Rice Breeding through Dull Genes Pyramiding

Ji-Yoon Lee, Ju-Won Kang, Su-Min Jo, Youngho Kwon, So-Myeong Lee, Dong Jin Shin, You-Chun Song, Dong Soo Park, Jong-Hee Lee, Jong-Min Ko, Jun-Hyeon Cho
Plant Breed. Biotech. 2020;8:405-412
https://doi.org/10.9787/PBB.2020.8.4.405 Full Text (PDF) Free

Genome-Wide Association Study for Flowering Time in Korean Cowpea Germplasm

Eunju Seo, Kipoong Kim, Ryulyi Kang, Gyutae Kim, Aron Park, Woon Ji Kim, Hokeun Sun, Bo-Keun Ha
Plant Breed. Biotech. 2020;8:413-425
https://doi.org/10.9787/PBB.2020.8.4.413 Full Text (PDF) Free Supplementary File(s)

Analysis of Chronological Variation in Pedigree and Agronomic Traits of 325 Korean Rice Varieties

Gihwan Yi
Plant Breed. Biotech. 2020;8:426-433
https://doi.org/10.9787/PBB.2020.8.4.426 Full Text (PDF) Free

Rapid Communications

Screening of Salinity Tolerance and Genome-Wide Association Study in 249 Peanut Accessions (Arachis hypogaea L.)

Kunyan Zou, Dongwoo Kang, Ki-Seung Kim, Tae-Hwan Jun
Plant Breed. Biotech. 2020;8:434-438
https://doi.org/10.9787/PBB.2020.8.4.434 Full Text (PDF) Free Supplementary File(s)

Complete Chloroplast Genome of a Milk Thistle (Silybum marianum) Acc. ‘912036’

Jeehyoung Shim, Jae-Hyuk Han, Na-Hyun Shin, Jae-Eun Lee, Jung-Sook Sung, Yeisoo Yu, Sanghyun Lee, Kwang Hoon Ahn, Joong Hyoun Chin
Plant Breed. Biotech. 2020;8:439-444
https://doi.org/10.9787/PBB.2020.8.4.439 Full Text (PDF) Free

The Korean Society of Breeding Science, National Institute of Crop Science, RDA, Suin-ro 126, Gwonseon-gu, Suwon 16429, Republic of Korea
Phone: +82-2-880-4547 **E-mail**: pbb@plantbreedbio.org / Powered by INFOrang Co., Ltd

Plant Breed. Biotech. 2020 (December) 8(4):368~377
https://doi.org/10.9787/PBB.2020.8.4.368

Online ISSN: 2287-9366
Print ISSN: 2287-9358

RESEARCH ARTICLE

Genetic Parameters and Multivariate Analysis to Determine Secondary Traits in Selecting Wheat Mutant Adaptive on Tropical Lowlands

Muh Farid[1], Nasaruddin Nasaruddin[1], Yunus Musa[1], Muhammad Fuad Anshori[1]*, Ifayanti Ridwan[1], Jekvy Hendra[2], Gatot Subroto[3]

[1]Department of Agronomy, Faculty of Agriculture, Hasanuddin University, Makassar 90245, Indonesia
[2]Institute for Agriculture Technology Assessment and Application, West Sumatera 27365, Indonesia
[3]Department of Agronomy, Faculty of Agriculture, Jember University, Jember, East Java 68121, Indonesia

ABSTRACT One of approaches to maintain the yield stability of the lowland tropical wheat is the use of secondary traits in the selection process. The identification of these characters requires a statistical approach in the form of genetic parameter analysis and multivariate analysis. The objective of this study was to determine the secondary traits of adaptive wheat mutants in the lowlands through the use of genetic parameters and multivariate analysis on the parameters. The study consisted of three field trials conducted in three different regencies, namely Jeneponto (135 m above sea level (asl)), Maros (100 m asl) and Bantaeng (125 m asl). The study used a nested design, where replications were nested in the environments. The genotype factors consisted of 20 genotypes repeated three times. 11 characters were observed including vegetative and reproductive characters. The analysis used consisted of repeatability, correlation, cluster analysis, principal component analysis, factor analysis, and cross print analysis. The overall results of the analysis indicate that the number of productive tillers is the main secondary trait for the selection of adaptive wheat in the lowlands. The character can be recommended for selection criteria in testing wheat lines in the lowlands to make an effective selection.

Keywords Genetic parameters, Multivariate analysis, Productive tillers, Secondary traits, Tropical wheat

INTRODUCTION

Wheat is the main raw material widely used in making flour and bread (Kumar *et al*. 2011). In the developing countries, such as in Indonesia, more people consume bread made from wheat flour not only for its dietary fibre but also to obtain beneficial components such as protein, vitamins, and other phytochemicals (Shewry and Hey 2015). However, the development of these plants is generally not suitable for the tropical climate in Indonesia (Farid 2018). This makes Indonesia import wheat from other countries, especially from subtropical countries. The high volume of wheat import of Indonesia, reached 8.1 million tons in 2016, making Indonesia very dependent on other countries and burden the country's foreign exchange (APTINDO 2016). Therefore, the development of wheat in the tropics, including Indonesia, is a long-term solution to reduce the proportion of imports and dependence on other countries.

Development of tropical wheat can be done through the development of plant varieties. In general, there are several accessions of wheat grown in Indonesia (Nur *et al*. 2018). However, the accession only grows optimally in the highlands. It is considered less able to compete with

Received September 16, 2020; Revised October 9, 2020; Accepted October 22, 2020; Published December 1, 2020
***Corresponding author** Muhammad Fuad Anshori, fuad.pbt15@gmail.com, Tel: +62 853-1123-6019, Fax: +62-853-1123-6019

horticultural commodities that have high selling values. Hence, it is necessary to develop an optimal tropical wheat in the lowlands (Nasaruddin *et al*. 2018). One way to induce these characteristics is through initiation of mutation. This has been developed by Nur *et al*. (2018), Farid (2018), and Nasaruddin *et al*. (2018). Therefore, the continued development of this research is important for obtaining wheat varieties adaptive under the lowlands.

Decrease in the growing environmental elevation of wheat plants will result in an increase in environmental temperature which causes the plants to experience heat stress (Akter and Islam 2017; Farid 2018). In general, this condition will reduce the growth rate of wheat production components and have an impact on wheat yield (Bányai *et al*. 2014; Akter and Islam 2017). One solution can be done is to include secondary traits related to wheat yield in the selection process. Selected secondary traits are expected to have high heritability and specific variability in yield (Madhav *et al*. 2013). This will support the dynamic stability of wheat yield when planted in different environments (Fellahi *et al*. 2018; Anshori *et al*. 2019). The use of secondary traits in selection under stress conditions has been reported by Anshori *et al*. (2019) and Anshori *et al*. (2018) in rice under salinity stress, by Fadhli *et al*. (2020) in corn under drought stress, Sareen *et al*. (2014), Bennani *et al*. (2016) and Ahmed *et al*. (2019) in wheat against drought stress, Sareen *et al*. (2014) and Sharma *et al*. (2018) of wheat against high temperature stress.

The best secondary trait identification can be done with several approaches, such as the use of genetic parameters (Erkul *et al*. 2010; Joshi *et al*. 2018) and multivariate analyses (Awan *et al*. 2015; Arzu *et al*. 2018). Genetic parameters are aimed at predicting the proportion or variety of genetic roles to the response of the phenotypic characters, so this parameter is used as a general indicator in the selection process (Arief *et al*. 2015). The most widely used genetic parameters are heritability or repeatability (Bhushan *et al*. 2013; Joshi *et al*. 2018; Anshori *et al*. 2019), genetic correlations (Bhushan *et al*. 2013; Malek *et al*. 2014; Anshori *et al*. 2019; Meier *et al*. 2019) etc. The multivariate analysis is an analysis conducted on many variables to assess, visualize, and simplify the related relationships between each variable (Mattjik and Sumertajaya 2011). It is very useful in analyzing the nature of growth that is related to one another (Awan *et al*. 2015; Arzu *et al*. 2018). Based on this, the best estimation of secondary traits that support lowland wheat yield can be identified through genetic parameters and multivariate analysis. The aim of the study was to determine the secondary trait of adaptive wheat mutants in the lowlands through analysis of genetic and multivariate parameters.

MATERIALS AND METHODS

The study was conducted in three growing environments. The first environment was conducted in Kelara Village, South Tolo District, Jeneponto Regency, South Sulawesi province, Indonesia (latitude 5°24'58.0"S, longitude 119º54'58.2"E, and 135 m above sea level (asl)) from March to June 2018. The second experiment was conducted in Allopolea Village, Lau District, Maros Regency, South Sulawesi province, Indonesia (latitude -4º-58'-55.1"S, longitude 119º34'27.4"E, and 100 m asl) in the same time frame of the first experiment. The last and third experiment was carried out in Bonto Manai Village, Bissappu District, Bantaeng Regency, South Sulawesi province, Indonesia (latitude 5º32'03.0"S, longitude 119º54'17.5"E, and 120 m asl) from July to October 2018. The plant conditions in each environment was shown in Fig. 1.

Experimental design and observation

The experiment used a nested randomized complete block design (RCBD) with two factors namely genotype and environment. The replications were three times and nested in the environment. 20 genotypes were used consisting of 16 mutant lines and 4 control varieties, namely Dewata, Selayar, Nias, and Munal. Based on the design, the total experimental units were 180. Each plot is 1 m × 4 m divided into 4 rows. Each genotype was planted with spacing of 25 cm × 2 cm (12 g / row according to CIMMYT standards).

Fertilization was conducted twice during plant growth. The first fertilization was carried out 10 days after planting (DAP) with 150 kg/ha Urea, 200 kg/ha SP36, and 100 kg/ha NPK. The second fertilization was at 30 DAP using

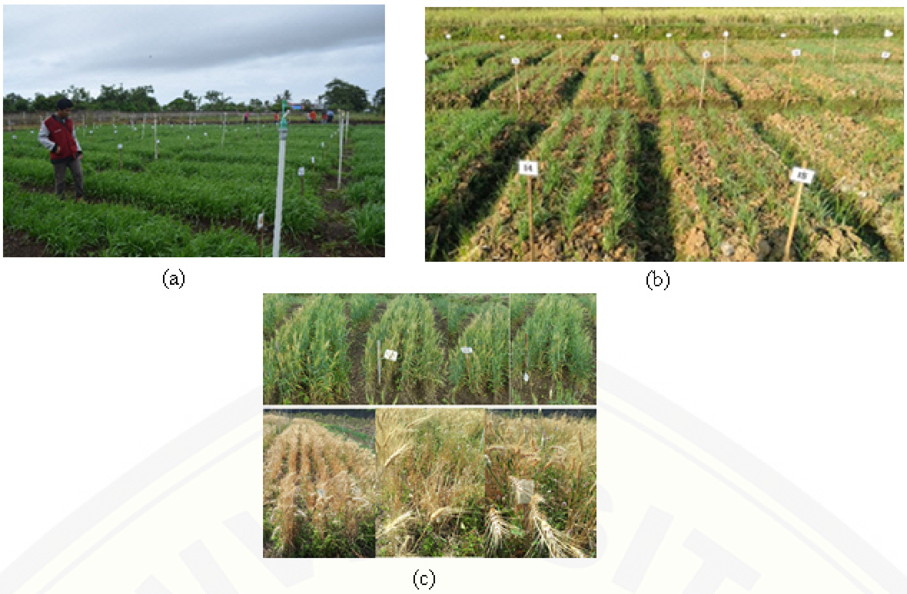


Fig. 1. The general plant condition in each study environment, (a) Kelara village, (b) Allopolea Village, and (c) Bonto Manai Village.

150 kg/ha Urea. Weeding was done twice, at 30 and 45 DAP. Pest control was conducted by spraying insecticide on wheat. Harvesting was conducted when the plants reached its physiological maturity, marked 80% of panicles, stems and leaves of plants have turned yellow, and the seeds have hardened. Harvesting was done by cutting the base of the stem above the soil surface using a sickle. Panicles that have been harvested are then dried and seeded. Observations were carried out for plant height before harvest, number of productive tillers, days to flowering, days to harvest, number of spikelet, panicle length, number of seeds per panicle, seed weight per panicle, weight 100 seeds, percentage of unfilled grains, and yield.

Data analysis

Data analysis conducted on the observed data in this study consists of analysis on the genetic parameters and multivariate analysis. Data analysis carried out were analysis of variance using STAR 2.1, and identification on genetic variability, repeatability, genetic correlation and phenotypic correlation for each character using META-R software (Anshori *et al*. 2019).

Four analyses were conducted in the multivariate analysis on the genotypes average values at the three locations consisted of cluster analysis, principal component analysis, factor analysis and path analysis (Mattjik and Sumertajaya 2011). Cluster and path analysis were carried out using Rstudio software with Cluster Maechler *et al*. (2019) and Agricolae packages (Mendiburu 2014), respectively. Meanwhile, the analysis of the principal component analysis and factor analysis were carried out with minitab v 17. For PCA visualitation in 3D, the three principal component were analized by scatterplot3d package in Rstudio (Ligges and Mächler 2003), respectively. Finally, all the results of genetic parameters and multivariate analysis were evaluated by scoring secondary characters in each analysis. The score consisted of three scores, 1, 3 and 5. The nearer of score indicated that the character has a stronger relationship to the yield. All scores on all characters were summed and formed as for the percentage of conformity. This value served as a quantitative benchmark of the suitability of a character to be a character of the selection. The formula of conformity explained below:

$$C = (1 - ((X_k - X_{min}) / (X_{max} - X_{min}))) \times 100\%$$

Note: C = conformity value

X_k = number of character scores

X_{min} = minimum number of scores

X_{max} = maximum score

RESULTS

Analysis of variance in Table 1 showed that all responses to growth character were influenced by environmental variability, genotypes and their interactions ($P \leq 0.01$), except for the characters of the number of productive tillers and yield (Table 1). Besides that, the repeatability also showed that the characters of the number of productive tillers and yield had the highest value of repeatability of 89.38% and 87.92%, respectively. Other characters also classified as having high repeatability were grain weight per panicle (61.98%), the number of spikelets (55.41%), and panicle length (51.96%). Meanwhile, the character of 100 grains weight was classified as medium repeatability (27.36%) and the rest were classified as low repeatability (Table 1). The information of wheat mutant morphology

Table 1. Analysis of variance and repeatability of the characters of wheat mutant adaptive to tropical lowland.

Character	Location (E)	Genotype (G)	G × E	CV	Vg	R
PH	2211.88**	64.97**	55.31**	8.63	0.02	14.86%
NPT	30.55*	5.97**	0.55ns	20.05	0.37	89.38%
DF	181.52**	19.44*	31.12**	5.48	0.00	0.00%
DH	1886.16**	15.97**	17.84**	2.76	0.00	0.00%
NS	202.43**	7.0**	3.13**	7.95	0.09	55.41%
PL	46.12**	1.15**	0.55**	5.46	0.08	51.96%
NGP	778.65**	57.61**	45.56**	16.32	0.04	20.92%
WPG	1.821**	0.085**	0.032**	19.1	0.13	61.98%
W100	0.28**	0.32**	0.23**	8.51	0.07	27.36%
PUG	411.84**	133.96**	175.34**	12.05	0.00	0.00%
Yield	7.49**	1.59**	0.19ns	22.07	0.38	87.92%

CV: coefficient of variance, Vg: genetic varaince, R: repeatability, ns: not significant. *: significant at $P \leq 0.05$, **: significant at $P \leq 0.01$, DF: Days to flowering, DH: Days to harvest, NGP: Number of grains per panicle, NPT: The number of productive tillers, NS: Number of spikelet, PH: Plant height, PL: Panicle length, PUG: Percentage of unfilled grains, W100: Weight of 100 grains, WGP: Weight of grains per panicle.

Table 2. Analysis genetic correlation (above the diagonal line) and phenotypic correlation (below diagonal line) on the yield of wheat mutant adaptive to tropical lowland.

Traits	PH	NPT	DF	DH	NS	PL	NGP	WGP	W100	PUG	Yield
PH		0.599	NA	NA	0.999	0.999	0.999	0.999	0.999	NA	0.999**
NPT	0.167		NA	NA	0.682	0.364	0.797	0.441	0.423	NA	0.835**
DF	−0.508	0.019		NA	NA	NA	NA	NA	NA	NA	NA
DH	0.057	−0.380	−0.287		NA	NA	NA	NA	NA	NA	NA
NS	0.606	0.443	−0.315	−0.379		0.822	1.000	1.000	1.000	NA	0.999**
PL	0.632	0.216	−0.241	−0.173	0.745		0.550	0.978	1.000	NA	0.705**
NGP	0.386	0.247	−0.331	−0.172	0.755	0.377		1.000	1.000	NA	0.999**
WGP	0.671	0.262	−0.228	0.054	0.667	0.765	0.633		1.000	NA	0.921**
W100	0.729	0.189	−0.198	−0.180	0.642	0.669	0.517	0.749		NA	0.999**
PUG	−0.108	−0.011	0.176	0.011	−0.366	−0.020	−0.874	−0.424	−0.325		NA
Yield	0.503**	0.771**	−0.137	−0.413	0.831**	0.559**	0.674**	0.663**	0.645**	−0.386	
Difference	0.497	0.065			0.169	0.146	0.326	0.258	0.355		

ns: not significant, *: significant at $P \leq 0.05$, **: significant at $P \leq 0.01$, Difference: (genetic correlation- phenotypic correlation), DF: Days to flowering, DH: Days to harvest, NGP: Number of grains per panicle, NPT: The number of productive tillers, NS: Number of spikelet, PH: Plant height, PL: Panicle length, PUG: Percentage of unfilled grains, W100: Weight of 100 grains, WGP: Weight of grains per panicle.

was attached in Supplementary Table S1.

The results of phenotype and genotype correlation analysis showed that plant height (0.503, 0.999), number of productive tillers (0.771, 0.835), number of spikelets (0.831, 0.999), panicle length (0.559, 0.705), number of grains per panicle (0.674, 0.999), grain weight per panicle (0.663, 0.921), and weight of 100 grains (0.645, 0.999) have significant correlations with yield. On the other hand, days to flowering, days to harvest and percentage of unfilled grains had a low phenotype correlation and are undefined in the genetic correlations. Based on Table 2, the number of productive tillers (0.065) was the character showing the lowest difference between phenotype and genetic correlations compared to other characters, followed by characters of panicle length (0.146) and number of spikelets (0.169).

The results of the cluster analysis showed that there were two large groups with a degree of dissimilarity and agglomerative coefficients reaching values of 0.6 and 0.89, respectively (Fig. 2). The yield as the main character was grouped in group 2. In general, group 2 was divided into two sub-groups with a degree of dissimilarity of 0.2. Based on the division of the subgroups in group 2, the yield was in subgroup 1 together with the number of productive tillers, the weight of 100 grains, seed weight per panicle, and panicle length. On the other hand, the number of spikelets and number of grains per panicle were in subgroup 2. Meanwhile, plant height, days to flowering, percentage of unfilled grains, and days to harvest were in group 1.

The results of the principal components analysis were visualized in the 3D plot form (Fig. 3). Based on Fig. 3, the yield was in quadrant 2 together with the number of productive tillers, panicle length, number of spikelets and weight of 100 grains. On the other hand, days to harvest was in quadrant which is opposite to quadrant 2 or there was in quadrant 8. Meanwhile, the closest quadrant that has a vector close to the yield was quadrant 3 (plant height and weight of grains per panicle) and 7 (number of grains per panicle).

Factor analysis in this study showed representative results. This was supported by a total variance of data that reached 85.58% and the overall character trait that was above 0.8, except for plant height (0.774) and days to harvest (0.698) (Table 3). Based on the factor loading values, panicle length and weight of 100 grains were the determinants of the first-factor variance represented 34.2% of the total initial data variance. Then the second factor, which represented 19.9% of the total data variance, had a variance direction that was largely determined by the number of grains per panicle and the percentage of unfilled grains in the opposite directions. The greatest variance of the yield, as the main character, was in the third factor with a factor loading value of 0.321. Besides the yield, another main character in factor 3 was the number of productive

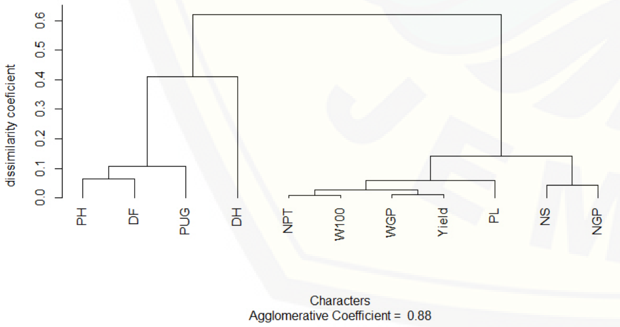


Fig. 2. Dendrogram of characters of wheat mutant adaptive to lowland. DF: Days to flowering, DH: Days to harvest, NGP: Number of grains per panicle, NPT: The number of productive tillers, NS: Number of spikelet, PH: Plant height, PL: Panicle length, PUG: Percentage of unfilled grains, W100: Weight of 100 grains, WGP: Weight of grains per panicle.

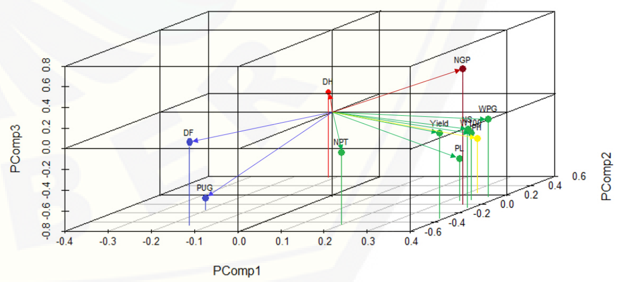


Fig. 3. 3D plot of principal component analysis (PCA) of the character of wheat mutant adaptive to lowland. DF: Days to flowering, DH: Days to harvest, NGP: Number of grains per panicle, NPT: The number of productive tillers, NS: Number of spikelet, PH: Plant height, PL: Panicle length, PUG: Percentage of unfilled grains, W100: Weight of 100 grains, WGP: Weight of grains per panicle.

Table 3. Factor analysis of wheat mutant adaptive to tropical lowland character.

Variable	Factor1	Factor2	Factor3	Factor4	Communality
PH	0.218	0.14	−0.017	−0.233	0.774
NPT	−0.185	0.121	**0.592**	−0.219	0.86
DF	0.127	−0.027	−0.126	0.775	0.878
DH	0.015	−0.011	−0.293	−0.364	0.698
NS	0.105	−0.034	0.152	−0.035	0.836
PL	0.366	0.202	−0.086	0.118	0.85
NGP	−0.067	−0.43	0.011	−0.03	0.976
WPG	0.274	−0.068	−0.163	0.101	0.841
W100	0.326	0.001	−0.167	0.203	0.805
PUG	0.135	0.59	0.125	−0.069	0.978
Yield	0.002	−0.043	**0.321**	−0.035	0.946
Variance (Var)	3.764	2.1886	2.177	1.3137	9.4433
% Var	0.342	0.199	0.198	0.119	0.858

DF: Days to flowering, DH: Days to harvest, NGP: Number of grains per panicle, NPT: The number of productive tillers, NS: Number of spikelet, PH: Plant height, PL: Panicle length, PUG: Percentage of unfilled grains, W100: Weight of 100 grains, WGP: Weight of grains per panicle.

Table 4. Path analysis on yield of wheat mutant adaptive to tropical lowland.

Character	Direct effect	JAP	JS	JBM	BBM	B100	Residual
NPT	0.563		0.104	0.051	0.017	0.045	0.044
NS	0.237	0.248		0.142	0.041	0.153	0.044
NGP	0.189	0.152	0.178		0.039	0.122	0.044
WGP	0.061	0.152	0.157	0.121		0.179	0.044
W100	0.239	0.107	0.152	0.096	0.046		0.044

R^2 = 79.01%. NPT: the number of productive tillers, NS: Number of spikelet, NGP: Number of grains per panicle, WGP: Weight of grains per panicle, W100: Weight of 100 grains.

tillers (0.592).

Path analysis showed fairly representative results with a determination value of 79.01% (Table 4). Based on the path analysis, the number of productive tillers was the character that had the greatest direct influence value with a value of 0.563. As for the other characters that have a significant direct effect were the weights of 100 grains (0.239) and the number of spikelets (0.237). However, the direct influence of the two characters was only half of the direct effect of the number of productive tillers.

Evaluation of conformity of all multivariate analysis results and genetic parameters was shown in Table 5. The number of productive tillers was a character with the highest degree of conformity value of 91.67%. Meanwhile, other characters that have a suitability value above 50% were the number of spikelets (75%), weight of 100 grains (75%), weight of grains per panicle (66.67%) and panicle length (66.67%). Based on these results, the number of productive tillers, number of spikelets, weight of 100 grains, weight of grains per panicle, and panicle length could be used as a selection character in the development of tropical wheat in Indonesia. However, the number of productive tillers was the best selection character highly recommended in developing wheat under the lowland.

DISCUSSION

Based on the analysis results of variance and repeatability, the number of productive tillers and yield

Table 5. Conformity value of secondary trait on the yield of wheat mutant adaptive to tropical lowland.

Character	R	CA	Dr	PCA	FcA	PA	Total	Conformity
Plant height	5	3	5	3	5	5	26	16.67
Number of productive tillers	1	1	1	3	1	1	8	91.67
Days to flowering	5	5	5	5	5	5	30	0.00
Days to harvest	5	5	5	5	5	5	30	0.00
Number of spikelet	1	1	3	1	5	1	12	75.00
Panicle length	1	1	3	1	3	5	14	66.67
Number of grains per panicle	3	3	3	3	5	3	20	41.67
Weight of grains per panicle	1	3	1	1	5	3	14	66.67
Weight of 100 grains	3	3	1	1	3	1	12	75.00
Percentage of unfilled grains	5	5	5	5	3	5	28	8.33
Max score	5	5	5	5	5	5	30	
Min Score	1	1	1	1	1	1	6	

R: Repeatability, CA: Correlation analysis, Dr: Dendrogram, PCA: Principal component analysis, FcA: Factor analysis, PA: path analysis.

were genetically stable characters in the lowlands (Table 1). This was also reported by Erkul *et al*. (2010), Tripathi *et al*. (2011) and Bhushan *et al*. (2013) which stated that the number of tillers or the number of productive tillers and yield had high repeatability. A different result reported by Joshi *et al*. (2018) showed the number of productive tillers had moderate repeatability and the yield had high heritability. The not significant character in interaction effect indicate that the different environment relative does not change the rank of genotype or in general all genotype have the same pattern to environmental alteration. Moreover, if characters also showed high repeatability or heritablity (Arief *et al*. 2015; Anshori *et al*. 2019). Based on these, the characters who have high repeatability deserve to be used as selection characters. However, the determination of secondary traits in selection need to do some data analysis testing on the yield, so that the precision of secondary traits could increase the effectiveness of lowland wheat selection.

Phenotypic and genetic correlation is one way to determine the stability of a selection character (Garg *et al*. 2017). The large difference in the two correlations shows the magnitude of the influence of environmental and interactions effect affecting the correlation (Manjunatha *et al*. 2017; Anshori *et al*. 2019). In Table 2, genetic correlations had a greater value than phenotypic correlations for most growth characters. This result explained that there was a negative influence of the environments and their interactions, so that the value of phenotypic correlations to be lower than their genetic correlations (Patil and Lokesha 2018). Based on these, the character considered very stably in this study was the number of productive tillers followed by panicle length and number of spikelets. These characters had low correlation subtraction between the two correlations, especially the number of productive tillers. This result has also been reported by Bhushan *et al*. (2013), Malek *et al*. (2014), and Meier *et al*. (2019). Therefore, the three characters, especially the number of productive tillers, are recommended as selection characters in the lowland wheat selection based on phenotypic and genetic correlation analysis.

Cluster analysis is a semi-qualitative and subjective multivariate analysis (Mattjik and Sumertajaya 2011). The results of this analysis are groupings with a certain degree of closeness based on the grouping method chosen by the researcher (Malek *et al*. 2014; Awan 2015). However, the analysis is quite effective and easy to understand, so it is widely used in determining selection (Arain *et al*. 2018). Based on Fig. 2, the number of productive tillers, weight of 100 grains, the weight of grains per panicle have a pattern of mean values almost identical to all 20 genotypes tested. Therefore, the number of productive tillers, weight of 100 grains and weight of grains per panicle can be considered as selection characters in selecting the lowland wheats based on cluster analysis.

The principal component analysis is a multivariate analysis used by many researchers to reduce and simplify character dimensions with still maintaining most of the initial data variance (Awan *et al*. 2015; Anshori *et al*. 2018). It is very useful in determining secondary traits which have the same variance direction as the main characters without overlapping variations (Mattjik and Sumertajaya 2011; Awan *et al*. 2015). Based on Fig. 3, the number of productive tillers in this analysis had a vector quite far towards the yield character compared to the characters of panicle length, the weight of 100 grains, and the number of spikelets. Nevertheless, the number of productive tillers remained representative to be categorized in one group with the yield because of the cumulative percentage between PComp1 and PComp3 reached 60% and had a vector direction that was consistent with the yield. On the other hand, the plant height and seed weight per panicle were still considered as different groups, even though both characters had a small vector angle to the yield. This is due to the consistency of the vectors of the two characters towards the yield. Therefore, based on the principal component analysis, the number of productive tillers, panicle length, weight of 100 grains, and number of spikelets can be considered as selection characters in the selection of lowland wheats.

Factor analysis is a multivariate analysis that has similarities with the principal component analysis (PCA) (Mattjik and Sumertajaya 2011). The difference in this analysis lies in the process of reducing the variance of the non-specific covariates and optimizing variances on specific characters that have high covariance in a factor dimension (Mattjik and Sumertajaya 2011; Dormann *et al*. 2013; Awan *et al*. 2015). This is indicated by the low loading factor value on non-specific characters and conversely the high factor loading value on the main character dimensions of the factor (Dormann *et al*. 2013; Yong and Pearce 2013; Rocha *et al*. 2018). Based on Table 3, the number of productive tillers and yield characterizes factor 3 with a loading factor value exceeding 0.32 (Yong and Pearce 2013). This value is a standard loading factor based on the principal component. Based on this, the number of productive tillers had the same directional relationship with the yield. It is strong proof that the number of productive tillers was a very suitable character to be used as a selection character on lowland wheat plants.

Path analysis is a multivariate analysis used to divide a multivariate correlation into direct and indirect effects (Carvalho *et al*. 2017; Anshori *et al*. 2018). The direct effect is one indicator in projecting how large a character variance influences the total variance of the main characters (Yagdi 2009). The results of this analysis are often used as a standard in determining selection characters (Anshori *et al*. 2019). Based on Table 4, the number of productive tillers is very suitable as a selection character compared to other characters. This result was also reported by Arya *et al*. (2017) and Ibrahim (2019) who stated that the number of productive tillers and number of spikelets had a large direct effect on the yield in F6 wheat lines. This completed the evidence in the previous multivariate analysis. Besides that, the number of spikelets and weights of 100 grains also could be considered as a selection character. However, both characters were not better than the number of productive tillers. Based on all the analyses, the evaluation of all results needs to be done as a systematic consideration in the selection of secondary traits in lowland wheat.

Productive tillers become one of the main keys in supporting wheat yield (Monpara 2011). Every tiller may not be a productive one (Moral and Moral 1995). This is due to the competition of the energy distribution in initiating flowering apparatus including the spikelet formation (Xie *et al*. 2016). Based on the results of this study, wheat grown in lowland areas will make the formation of tillers efficiently to be productive tillers. It made the number of tillers less than that of the highlands (Bányai *et al*. 2014) so that plants can be more effective in supporting their production and yield components in the lowlands. Therefore, the number of productive tillers was strongly recommended as the main secondary trait in the lowland wheat selection.

In conclusions, the number of productive tillers, number of spikelets, panicle length, weight of 100 grains and weight of grains per panicle can be used as secondary traits in the selection of lowland wheats. The number of productive tillers is the main secondary trait for adaptive wheat in the lowlands. These characters can be recommended for selection criteria in testing wheat lines in the lowlands to make selection effective.

REFERENCES

Ahmed HG, Sajjad M, Li M, Azmat MA, Rizwan M, Maqsood RH, *et al*. 2019. Selection criteria for drought-tolerant bread wheat genotypes at seedling stage. Sustainability 11: 2584.

Akter N, Islam MR. 2017. Heat stress effects and management in wheat. a review. Agron. Sustain. Dev. 37: 37.

Anshori MF, Purwoko BS, Dewi IS, Ardie SW, Suwarno WB. 2018. Determination of selection criteria for screening of rice genotypes for salinity tolerance. SABRAO J. Breed. Genet. 50: 279-294.

Anshori MF, Purwoko BS, Dewi IS, Ardie SW, Suwarno WB. 2019. Selection index based on multivariate analysis for selecting doubled-haploid rice lines in lowland saline prone area. SABRAO J. Breed. Genet. 51: 161-174.

Arain SM, Sial MA, Jamali KD, Laghari KA. 2018. Grain yield performance, correlation, and cluster analysis in elite bread wheat (*Triticum aestivum* L.) lines. Acta Agrobot. 71: 1747.

Arief VN, DeLacy IH, Crossa J, Payne T, Singh R, Braun HJ, *et al*. 2015. Evaluating testing strategies for plant breeding field trials: redesigning a CIMMYT international wheat nursery. Crop Sci. 55: 164-177.

Arya VK, Singh J, Kumar L, Kumar R, Kumar P, Chand P. 2017. Genetic variability and diversity analysis for yield and its components in wheat (*Triticum aestivum* L.). Indian J. Agric. Sci. 51: 128-134.

Arzu K, Onder O, Bilir O, Kosar F. 2018. Application of multivariate statistical analysis for breeding strategies of spring safflower (*Carthamus tinctorius* L.). Turk. J. Field Crops 23: 12-19.

Asosiasi Produsen Terigu Indonesia (APTINDO). 2016. Asosiasi Produsen Terigu Indonesia. Available at http://bataviase.co.id/node/436332. (accessed 18 December 2017).

Awan SI, Ahmad SD, Ali MA, Ahmed MS, Rao A. 2015. Use of multivariate analysis determining characteristics for grain yield selection in wheat. Sarhad J. of Agric. 31: 139-150.

Bányai J, Karsai I, Balla K, Kiss T, Bedő Z, Láng L. 2014. Heat stress response of wheat cultivars with different ecological adaptation. Cereal Res. Commun. 42: 413-425.

Bennani S, Nsarellah N, Birouk A, Ouabbou H, Tadesse W. 2016. Effective selection criteria for screening drought tolerant and high yielding bread wheat genotypes. Univers. J. Agric. Res. 4: 134-142.

Bhushan B, Bharti S, Ojha A, Pandey M, Gourav SS, Tyagi BS, *et al*. 2013. Genetic variability, correlation coefficient and path analysis of some quantitative traits in bread wheat. J. Wheat Res. 5: 21-26.

Carvalho IR, Nardino M, Follmann DN, Demari GH, Olivoto T, Pelegrin AJ, *et al*. 2017. Path analysis of grain yield associated characters in Brazilians wheat genotypes (*Triticum aestivum* L.). Aust. J. Crop Sci. 11:1406-1410.

del Moral MG, del Moral LG. 1995. Tiller production and survival in relation to grain yield in winter and spring barley. Field Crops Res. 44: 85-93.

Dormann CF, Elith J, Bacher S, Buchmann C, Carl G, Carré G, *et al*. 2013. Collinearity: a review of methods to deal with it and a simulation study evaluating their performance. Ecography 36: 27-46.

Erkul A, Ünay A, Konak C. 2010. Inheritance of yield and yield components in a bread wheat (*Triticum aestivum* L.) cross. Turkish J. Field Crops 15: 137-140.

Fadhli N, Farid M, Rafiuddin, Effendi R, Azrai M, Anshori MF. 2020. Multivariate analysis to determine secondary trait in selecting adaptive hybrid corn lines under drought stress. Biodiversitas 21: 3617-3624.

Farid M. 2018. Growth and production of various wheat genotypes at various PEG concentration in hydroponic. Agrotech J. 3: 21-26.

Fellahi ZE, Hannachi A, Bouzerzour H. 2018. Analysis of direct and indirect selection and indices in bread wheat (*Triticum aestivum* L.) segregating progeny. Int. J. Agron. 2018: 1-11.

Garg HS, Kumar R, Kumar B, Singh AK. 2017. Screening and identification of rice genotypes with drought tolerance under stress and non-stress condition. Int. J. Chem. Stud. 5: 1031-1042.

Ibrahim AU. 2019. Genetic variability, correlation and path analysis for yield and yield components in F6 generation of wheat (*Triticum aestivum* Em. Thell.). IOSR J. Agric. Vet. Sci. 12: 17-23.

Joshi A, Kumar A, Budhlakoti V, Bhatt N, Tabassum. 2018.

Estimation of genetic variability parameters for yield and its components in bread wheat (*Triticum aestivum* L. em. Thell) genotypes. J. Pharmacogn. Phytochem. 5: 87-90.

Kumar P, Yadava RK, Gollen B, Kumar S, Verma RK, Yadav S. 2011. Nutritional contents and medicinal properties of wheat: a review. Life Sciences and Medicine Research 2011: 1-10.

Ligges U, Mächler M. 2003. Scatterplot3d - an R package for visualizing multivariate data. J. Stat. Softw. 8: 1-20.

Madhav MS, Laha GS, Padmakumari AP, Somashekar N, Mangrauthia SK, Viraktamath BC. 2013. Phenotyping rice for molecular plant breeding, p. 1-40. In: SK. Panguluri, AA. Kumar (Eds.). Phenotyping for plant breeding: applications of phenotyping methods for crop improvement. Springer Science and Business Media, Heidelberg, Germany.

Maechler M, Rousseeuw P, Struyf A, Hubert M, Hornik K. 2019. Cluster: cluster analysis basics and extensions. R package version 1: 56.

Malek MA, Rafii MY, Afroz SS, Nath UK, Mondal M. 2014. Morphological characterization and assessment of genetic variability, character association, and divergence in soybean mutants. Sci. World J. 2014: 1-12.

Manjunatha GA, Kumar MS, Jayashree M. 2017. Character association and path analysis in rice (*Oryza sativa* L.) genotypes evaluated under organic management. J. Pharmacogn. Phytochem. 5: 1053-1058.

Mattjik AA, Sumertajaya IM. 2011. Multivariate analysis using SAS. Statistika F-MIPA IPB Press, Bogor, Indonesia.

Meier C, Meira D, Marchioro VS, Olivoto T, Klein LA, de Souza VQ. 2019. Selection gain and interrelations between agronomic traits in wheat F5 genotypes. Revista Ceres. 66: 271-278.

Mendiburu FD. 2014. Agricolae. The comprehensive R archive network. https://cran.r-project.org.

Monpara BA. 2011. Grain filling period as a measure of yield improvement in bread wheat. Crop Improv. 38: 1-5.

Nasaruddin, Farid M, Musa Y, Iswoyo H. 2018. Assessment and selection of M3 generation of wheat mutants adaptive in lowland. IOP Conf. Ser. Earth Environ. Sci. 157: 012051.

Nur A, Syahruddin K, Azrai M, Farid M. 2018. Genetic by environment interaction and stability tropical wheat lines in Indonesia medium-plains. IOP Conf. Ser. Earth Environ. Sci. 157: 012049.

Patil MK, Lokesha R. 2018. Estimation of genetic variability, heritability, genetic advance, correlations and path analysis in advanced mutant breeding lines of sesame (*Sesamum indicum* L.). J. Pharmacogn. Nat. Prod. 4: 1-5.

Rocha JR, Machado JC, Carneiro PCS. 2018. Multitrait index based on factor analysis and ideotype-design: proposal and application on elephant grass breeding for bioenergy. Bioenergy 10: 52-60.

Sareen S, Tyagi BS, Sarial AK, Tiwari V, Sharma I. 2014. Trait analysis, diversity, and genotype × environment interaction in some wheat landraces evaluated under drought and heat stress conditions. Chil. J. Agric. Res. 74: 135-142.

Sharma D, Jaiswal JP, Singh NK, Chauhan A, Gahtyari NC. 2018. Developing a selection criterion for terminal heat tolerance in bread wheat based on various mopho-physiological traits. Int. J. Curr. Microbiol. Appl. Sci. 7: 2716-2726.

Shewry PR, Hey SJ. 2015. The contribution of wheat to human diet and health. Food Energy Secur. 4: 178-202.

Tripathi SN, Marker S, Pandey P, Jaiswal KK, Tiwari DK. 2011. Relationship between some morphological and physiological traits with grain yield in bread wheat (*Triticum aesticum* L. em. Thell.). Trends Appl. Sci. Res. 6: 1037-1045.

Xie Q, Mayes S, Sparkes DL. 2016. Optimizing tiller production and survival for grain yield improvement in a bread wheat x spelt mapping population. Ann. Bot. 117: 51-66.

Yagdi K. 2009. Path coefficient analysis of some yield components in durum wheat (*Triticum durum* Desf.). Pak. J. Bot. 41: 745-751.

Yong AG, Pearce S. 2013. A beginner's guide to factor analysis: Focusing on exploratory factor analysis. Tutor. Quant. Methods Psychol. 9: 79-94.