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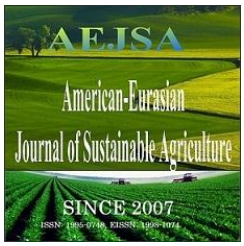

Genetic Parameter and Analysis of Traits Interrelationship in F2 Rice Generation of Inpago Unsoed 1 X Basmati Delta 9

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ABSTRACT

The rice improvement program in Indonesia is addressed to develop high-yielding varieties with long slender rice grain. The purpose of this study, therefore, was to estimate the genetic parameters, i.e., gene action, number of genes control, the magnitude of genetic variability, heritability, genetic advance and interrelationship of traits of yield components and yield were studied in the F2 generation of Inpago Unsoed 1 x Basmati Delta 9. The experiment was carried out at the experimental farm of Agriculture Faculty, Jenderal Soedirman University, Purwokerto, Central Java, Indonesia, from October 2018 - February 2019. The genetic material used was seeds of F2 populations derived from the crossing between Inpago Unsoed 1 and Basmati Delta 9, and the two parental genotypes. The estimates of Skewness, Kurtosis, genetic variability, heritability, genetic advance, and interrelationship were computed for yield and yield component traits. Broad genetic variability, high/medium heritability, and high genetic advance were found in the number of productive tillers, grains per, and grain yield per plant. The number of productive tillers and grains per panicle had a high correlation coefficient and positively direct effects on the grain yield per plant. It could be concluded that the number of productive tillers and the number of grains per panicle might be considered as criteria of selection for the development of high yield and long slender rice grain through pure line selection.

KEYWORDS

F2 population, genetic parameters, the interrelationship among traits, rice

INTRODUCTION

Rice is one of the most important food crops and the second-largest cereal crop in the world. Rice is a staple food for over half of the world's population and has a significant role in global food security [1]. Consequently, many countries worldwide develop strategies for self-sufficiency in rice production by expanding land area for rice cultivation and increasing output per unit area [2].

In Indonesia, rice is a staple food of more than 80% population, accounting for 62.1% of the energy intake [3]. National paddy production in 2019 is 56.60 million tons, and it is equivalent to 31,31 million tons of rice. In the same year, rice consumption in Indonesia is 29.6 million tons. Thus, the rice production surplus in Indonesia in 2019 is 1.53 million tons [4]. However, in Indonesia, the population growth is projected to grow from 270 million in 2020 to 330 million in 2050 and it results in the need for approx forty-two million tons of rice [5]. While, yield is still the main target of rice breeding programs, grain quality is now getting more attention due to increasing awareness of its importance. Rice grain quality has been the concern of people involved in the

production, processing, and consumption since it influences rice grains' nutritional and commercial value [6]. Improving rice grain quality has been a significant concern in rice breeding programs to meet consumer preference and market demand [7]. Grain size and shape largely determine the market acceptability of rice [8]. Long slender rice grain like basmati is the preferred rice shape in international markets, including Indonesia. Development of long slender grain rice in Agriculture Faculty of Jenderal Soedirman University was started with crossing Inpago Unsoed 1 (high-yielding rice, tolerant to drought, Indica type) and Delta 9 (long slender grain rice, a Basmati-like type) in 2017. The F_2 generation has been obtained and it is an ideal generation in which segregation and recombination are maximum for starting point of different selection methods [9].

Knowledge of genetic parameters and inter-correlation among traits is necessary for developing appropriate breeding methods and selection strategies to increase yield and grain shape. Genetic parameters' effectiveness is determined by genetic parameters that include gene action, number of gene control, magnitude of genetic variability, heritability, and genetic advance. Skewness and Kurtosis help us to draw a conclusion about the gene action and number of genes for a particular trait [10]. Studies on the estimation of gene action and the number of gene control were analyzed based on Skewness and Kurtosis values for yield and yield components of rice have been reported [11–13]. However, the findings can vary depending on the population used.

Knowledge on the nature and magnitude of genetic variability in any crop species plays an essential role in formulating successful breeding programs [14]. The coefficient of variation could be partitioned into the genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV). Heritability and genetic advance for yield attributing traits are significant concerns for any plant breeder and crop improvement programs [15]. It is valuable information in predicting the resultant effect in selecting the best genotypes for yield and its attributing traits [16]. Many studies were carried out to study genetic parameters of yield and yield component traits in rice. Many types of research have reported high, medium or low of GCV, PCV, heritability and genetic advance of yield and yield component of rice [17–23]. Information about the interrelationship among variables will improve selection effectiveness [24]. Coefficient correlation and path coefficient analysis are good statistical tools for studying the interrelationship among traits in many crop plants [25]. Interrelationship among yield and yield component traits in rice have been analyzed in many studies [17,26]. The study finding among yield and yield components has shown some variation in the correlation and yield component's degree of direct or indirect relationship with yield.

The purpose of this study was to estimate the genetic parameters, i.e., gene action, number of genes control, the magnitude of genetic variability, heritability, genetic advance and interrelationship of traits of yield components and yield that was studied in the F_2 generation of Inpago Unsoed 1 x Basmati Delta 9. The information so derived could be exploited in devising further breeding strategies and selection procedures to develop high yielding rice varieties with long slender grain rice in Indonesia

MATERIALS AND METHODS

Study area

The experiment was carried out at the experimental farm of Agriculture Faculty, Jenderal Soedirman University, Purwokerto, Central Java, Indonesia, in October 2018 - February 2019. The coordinate of this site is 7°24'28.7"S 109°15'13.3"E. The experimental site has an altitude of 110 meters above sea level. Seeds of F_2 populations derived from the cross between Inpago Unsoed 1 and Basmati Delta 9, and two parental genotypes were used as the genetic materials. Inpago Unsoed 1 was an Indonesian rice variety, while Basmati Delta 9 was an introduced variety from India.

Procedures

A total of 150 F_2 plants and 10 plants of each of the two-parent genotypes were grown for the study. Seeds were initially sown in a seedbox for 2 weeks before being transplanted to 35 cm x 40 cm polybag containing 9 kg of inceptisol soil. Each polybag was planted with one seedling. An augmented design with 3 replications was applied used to arrange the plant materials. A dosage of fertilizer of 1,21 g TSP-46 and 0,90 g KCL per polybag was applied 10 days before transplanting and 8.72 g NPK 2 weeks after transplanting. Weed, pest, and disease controls were carried out as needed. Harvesting was conducted when the plants are 101 days after seedling transplanting. Data of yield components and yield that included: plant height, number of productive tillers, days to flowering, days to maturity, panicle length, number of grains per panicle, the weight of 1000 grains, and grain yield per plant were recorded on an individual basis.

Data analysis

Estimation of gene action and number of gene control were analyzed based on Skewness and Kurtosis values, respectively, for each trait observed in the F_2 generation. The equation of Skewness and Kurtosis is as follows [27]:

$$\text{Skewness} = \frac{\sum_{i=1}^{n}(Yi-Y)^3}{(N-1)S^2}$$

$$\text{Kurtosis} = \frac{\sum_{i=1}^{n}(Yi-Y)^4}{(N-1)S^4}$$

where, Yi = genotype value, S = standard deviation, N = number of data. Skewness and Kurtosis value was tested using standard errors of the Skewness and Kurtosis test with statistical tests:

$$Z_S = \frac{S}{SE_S} \qquad Z_K = \frac{K}{SE_K}$$

Where, S = Skewness, K = Kurtosis, SE_S = standard errors of the Skewness, SE_K = common errors of Kurtosis. The critical value of two-way testing for Z_S and Z_K, namely $Z_{0.05/2} = 0.96$ and $Z_{0.01/2} = 2.57$. Skewness shows epistasis effected expression of a trait [28]. If Skewness equals to zero, it means there is no epistasis. Skewness > 0 means there is a complementary epistasis gene action, and Skewness < 0 means there is a duplicate epistasis gene action. Kurtosis describes the shape of the distribution curve and shows several genes controlling a trait [13]. When Kurtosis > 3, has a positive value, it shows the leptokurtic graph indicates a few gene controls trait. If Kurtosis < 3, has a negative value, it shows a platykurtic diagram and its trait is controlled by many genes. Interpretation Skewness and Kurtosis value refer to scheme in Jambormias research [29].

The data were analyzed to estimate the mean and variance using formulas as outlined by Steel and Torrie [30], is as follows:

$$\text{Mean } (\bar{X}) = \frac{\sum_{i=1}^{n} x_i}{n}$$

$$\text{Variance } (\sigma^2) = \frac{\sum_{i=1}^{n}(x_i-\bar{x})^2}{n-1}$$

where, X_i = the measurement of i-th individual and n = sample size.

The environmental variance (σ_e^2), phenotypic variance (σ_p^2) and genotypic variance (σ_g^2) were calculated using the following formula:

$$\text{Environmental variance } (\sigma_e^2) = \sqrt{\sigma_{P1}^2 \cdot \sigma_{P2}^2}$$

$$\text{Phenotypic variance } (\sigma_p^2) = \sigma_{F_2}^2$$

$$\text{Genotypic variance } (\sigma_g^2) = \sigma_p^2 - \sigma_e^2$$

where, σ_{P1}^2 and σ_{P2}^2 = parental variances of a particular F_2 population, and σ_{F2}^2 = variance of F_2 population for a trait.

The genetic variability was assessed based on the following parameters, i.e., phenotypic coefficient of variation (PCV), and genotypic coefficient of variation (GCV), which is computed using the formula suggested by Singh and Chaudhary [31]:

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sqrt{\sigma_p^2}}{\bar{X}}$$

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sqrt{\sigma_g^2}}{\bar{X}}$$

where, σ_p^2 = phenotypic variance, σ_g^2 = genotypic variance and $\bar{X}$ = mean of the population for trait X. Phenotypic (PCV) and genotypic (GCV) coefficient classified into three categories, i.e., if PCV and GCV values greater than 20% are regarded as high. In contrast, values between 10% and 20% is considered to be medium and value less than 10% are regarded to be low (Sivasubramanian and Menon, 1973).

Broad sense heritability was estimated for each F_2 population separately using the formula [32]:

$$\text{Broad sense heritability } (H^2) = \frac{\sigma_{F2}^2 - \sqrt{\sigma_{P1}^2 \cdot \sigma_{P2}^2}}{\sigma_{F2}^2} x\ 100\%$$

The heritability was categorized as high (values greater than 50%), medium (values between 50% and 20%), and low (values less than 20%) [33].

Expected genetic advance in each cross combination for the studied traits was estimated by using the formula [34]:

Genetic Advance (GA) $= i \cdot H^2 \cdot \sigma_p^2$

where, i = selection intensity. Value of 1 = 1.76 (at 10% selection pressure) was used in this study. Genetic advance is considered high when the values are greater than 14%), medium when the values are between 14% and 7%, and low when the value is less than 7% [35].

The interrelationship between traits was analyzed using simple correlation analysis and path analysis on a single plant basis. A simple correlation analysis was performed using Karl Pearson's coefficient of correlation, known as correlation coefficient r. The correlation coefficient is calculated as follows:

$$r_{xy} = \frac{Cov(x,y)}{\sqrt{\sigma^2(x) \cdot \sigma^2(xy)}}$$

Where, r_{xy} = correlation between x and y, Cov(xy) = the covariance between x and y, $\sigma^2(x)$ = the variance of x and $\sigma^2(y)$The following formula calculates = variance of Y. Variances and covariance:

$$\sigma^2(\mathrm{x}) = \frac{\sum_{i=1}^{n}(x_i - \bar{x})^2}{n-1}$$

$$\sigma^2(\mathrm{y}) = \frac{\sum_{i=1}^{n}(y_i - \bar{y})^2}{n-1}$$

$$Cov\ (x,y) = \frac{1}{2}\left[\sum xy - \frac{(\sum x)(\sum y)}{n}\right]$$

The significance of the correlation coefficient is tested with a t-test by the following formula:

$$t_{cal} = \frac{r\sqrt{n-2}}{1-r^2}$$

Where r = correlation coefficients and n = the number of pairs of observations. The calculated t-value can be compared with the tabulated t-value at (n-2) degree of freedom.

Path analysis with grain yield per plant as the dependent variable and plant height, number of productive tillers, days to flowering, days to maturity, panicle length, number of grains per panicle and weight of 1000 grains as independent variables was carried out to estimate the direct and indirect effects as suggested by Singh and Chaudhary [31]. It is given by:

$\frac{\sigma x_1}{\sigma Y} = P_{1y}$, the path coefficient from x_1 to Y

$\frac{\sigma x_2}{\sigma Y} = P_{2y}$, the path coefficient from x_2 to Y

$\frac{\sigma x_3}{\sigma Y} = P_{2y}$, the path coefficient from x_3 to Y

$r(x_1 Y) = P_{1y} + r(x_1, x_2)P_{2y} + r(x_1, x_3)P_{2y} + \cdots + r(x_i, x_n)P_{iy}$, i = 1, 2, 3, ... n

The above equation can be written in the form of the following matrix:

$$\begin{bmatrix} r_{x_1 y} \\ r_{x_2 y} \\ r_{3y} \end{bmatrix} = \begin{bmatrix} r_{x_1 x_1} & r_{x_1 x_2} & r_{x_1 x_3} \\ r_{x_2 x_1} & r_{x_2 x_2} & r_{x_2 x_3} \\ r_{x_3 x_1} & r_{x_3 x_2} & r_{x_3 x_3} \end{bmatrix} \begin{bmatrix} a \\ b \\ c \end{bmatrix}$$

A B C

Thus, the path coefficient values are estimates as C = B-1 A. The effect of residual factor (z), which measures the contribution of remaining traits not included in the path coefficient analysis, is estimated as follows:

$P_{zy} = \sqrt{1 - R^2}$

where, $R^2 = \sum_i P_{iY}^2 + 2\sum_i \sum_{i<j} P_{iY} P_{jy} r_{ij}$, R is the coefficient of multiple determinations.

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RESULTS

Skewness and Kurtosis Analysis

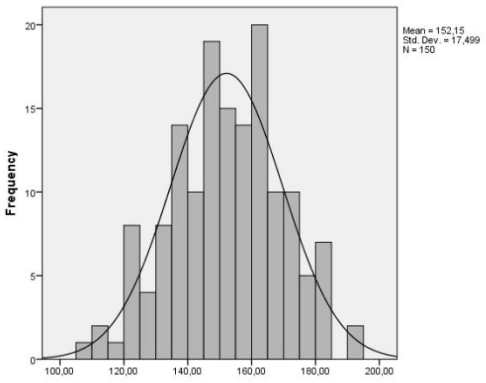
The Skewness and gene action of yield component and yield traits of F_2 populations are presented in Table 1 and Figure 1. No Skewness was found on plant height, days to flowering, days to maturity, panicle length, a number of grains per panicle, and weight of 1000 grains. Furthermore, the number of productive tillers and grain yield per plant had significant and positive Skewness.

Kurtosis and the number of gene control of the yield component and yield traits of F_2 populations are given in Table 1 and Figure 1. The Kurtosis estimations for a number of productive tillers, weight of 1000 grain and grain per yield showed significant and positive Kurtosis. The other traits i.e.: plant height, days to flowering, day to maturity, panicle length and the number of grains per panicle, had no significant Kurtosis.

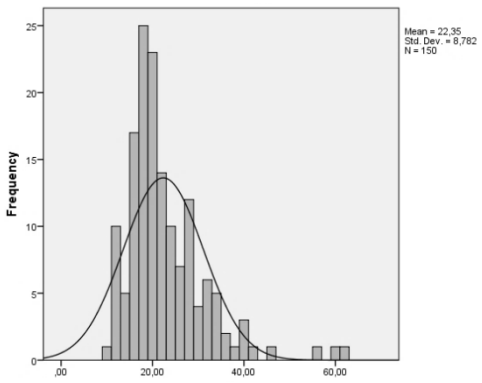
Table 1. Skewness, Kurtosis, gene action and the number of genes involved of yield component and yield traits of F_2 generation of Inpago Unsoed 1 x Basmati Delta 9.

Traits	Skewness		Kurtosis		Gene action	Number of Genes Control
Plant height	-0.144		-0.411		Additive	Many
Number of productive tillers	1.822	*	4.870	*	Complementary epistasis	A few
Days to flowering	-0.005		0.955		Additive	Many
Days to maturity	0.273		-1.169		Additive	Many
Panicle length	-0.294		0.263		Additive	Many
Number of grains per panicle	-0.024		0.509		Additive	Many
Weight of 1000 grains	-1.399		4.635	*	Additive	A few
Grain yield per plant	1.309	*	5.880	*	Complementary epistasis	A few

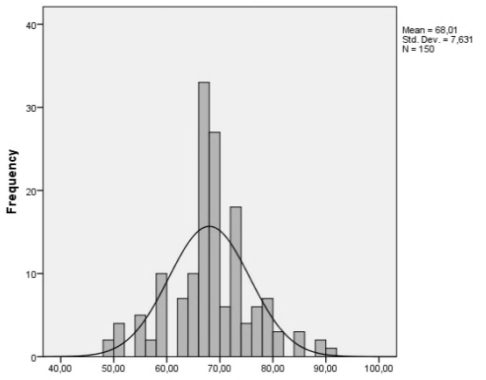
Note: * = significant at level of 0,5%.



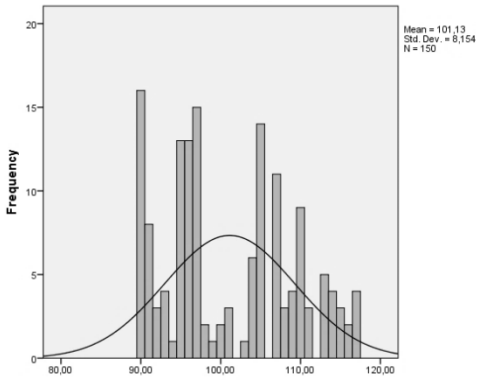
Plant height



Number of productive tillers



Days to flowering



Days to maturity

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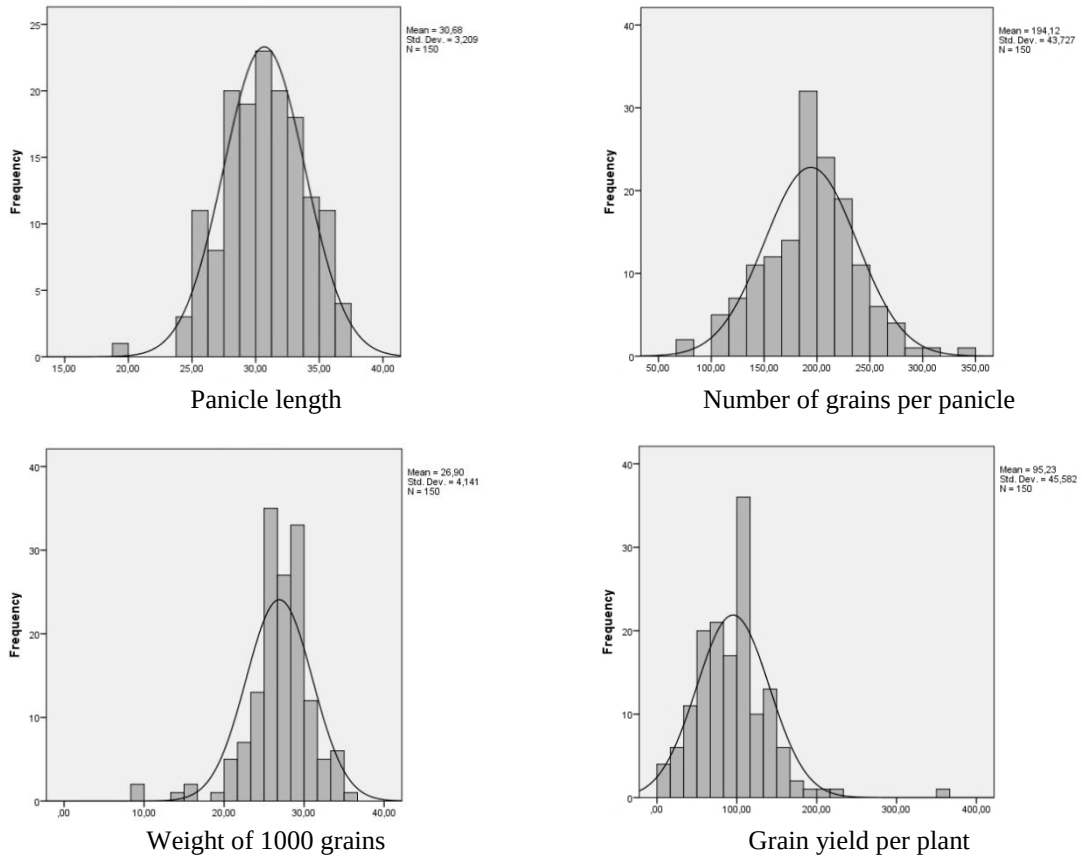

Figure 1. Distribution of yield component and yield traits of F_2 generation of Unsoed 1xBasmati Delta 9.

Genetic variability, Heritability and Genetic advance

In this study, genetic variability, heritability and genetic advance of yield components and yield were estimated in the F_2 generation. Estimates of phenotypic (σ^2p), genotypic (σ^2g), and environmental (σ^2e) variances, phenotypic coefficients of variation (PCV), and genotypic coefficient of variation (GCV), broad sense heritability (H^2) and genetic advance of yield component and yield traits of F_2 generation are presented in Table 2.

Genotypic variance of yield component and yield ranged from 5.97 for panicle length to 1208.48 for grain yield per plant, while phenotypic variance ranged from 10.29 to 2077.67 for panicle length and grain yield per plant, respectively. The genotypic coefficient of variation (GCV) ranged from 6.71 for days to maturity to 33.48 grain yield per plant. Similarly, phenotypic coefficients of variation (PCV) ranged from 8.06 for days to maturity to 47.86 for grain yield per plant. Furthermore, heritability estimation showed the lowest value at number of productive tillers (41,80%) and the highest at days to flowering (83,04). Lastly, genetic advance value of yield component and yield ranged from 9.82 to 41.21 for days to maturity and grain yield per plant, respectively.

Table 2. Phenotypic variance, genotypic variance, environmental variance, genotypic coefficient of variation, phenotypic coefficient of variation, broad sense heritability and genetic advance of yield component and yield traits of F_2 generation of Unsoed 1 x Basmati Delta 9.

Traits	σ^2g	σ^2p	σ^2e	GCV (%)	PCV (%)	H^2(%)	GA
Plant height	243,80	306,20	62,41	10,26	11,50	79,62	16,12
Number of productive tillers	32,24	77,13	44,89	25,41	39,30	41,80	32,30
Days to flowering	48,35	58,23	9,88	10,22	11,22	83,04	16,16
Days to maturity	46,00	66,49	20,49	6,71	8,06	69,19	10,08
Panicle length	5,97	10,29	4,32	7,97	10,46	58,01	10,67
Number of grains per panicle	1209,48	1912,09	702,61	17,92	22,53	63,25	25,01
Weight of 1000 grains	12,36	17,15	4,79	13,07	15,39	72,06	19,17
Grain yield per plant	1016,46	2077,70	1061,24	33,48	47,86	48,92	40,71

Note: σ^2p = phenotypic variance, σ^2g = genotypic variance, σ^2e = environmental variance, GCV = genotypic coefficient of variation, PCV = phenotypic coefficient of variation, H^2 = broad sense heritability and GA = genetic advance.

Interrelationship among Traits

Correlation and path analysis were the techniques used to elucidate the relationship between traits in this study. Correlation coefficients of yield component and yield traits of F_2 generation of Unsoed 1 x Basmati Delta 9 are presented in Table 3. The result showed that plant height (0.291), number of productive tillers (0.763), panicle length (0.359), number of grains per panicle (0.457) and weight of 1000 grains (0.395) had significant positive correlation with grain yield per plant. Day to flowering (-0.340) had a negative correlation with grain yield per plant, and no significant correlations between days to maturity and grain yield per plant.

Correlation coefficients were analyzed further by path coefficient analysis to determine the direct and indirect effects of yield component to yield. The direct and indirect effects of the grain yield Inpago Unsoed 1 x Basmati Delta 9 population related traits are presented in Table 4. It seemed that number of productive tillers, number of grains per panicle, and weight of 1000 grains was the traits which positively had direct effects on the grain yield per plant. The other traits i.e. plant height, days to flowering, days to maturity and panicle length have no direct effects on the grain yield per plant.

Table 3. Correlation coefficients of yield component and yield traits of F_2 generation of Unsoed 1 x Basmati Delta 9.

Traits	X1		X2		X3		X4		X5		X6		X7		X8
X1	1														
X2	-0.068		1												
X3	-0.192	*	-0.282	*	1										
X4	-0.320	*	0.089		0.302	*	1								
X5	0.693	*	-0.055		-0.165	*	-0.210	*	1						
X6	0.582	*	-0.035		-0.043		-0.153		0.728	*	1				
X7	0.320	*	0.167	*	-0.445	*	-0.065		0.258	*	0.102		1		
X8	0.291	*	0.763	*	-0.340	*	-0.065		0.359	*	0.457	*	0.395	*	1

Note: * = significant at level of 0,5%; X1 = plant height; X2 = number of productive tillers; X3 = days to flowering; X4 = days to maturity; X5 = panicle length; X6 = number of grains per panicle; X7 = weight of 1000 grains; and X8 = grain yield per plant.

Table 4. Path coefficient of yield component to yield of F_2 generation of Unsoed 1 x Basmati Delta 9.

Traits	Direct Effect	Indirect effect by						
		X1	X2	X3	X4	X5	X6	X7
X1	0,000		0,001	0,000	0,000	0,000	-0,006	-0,002
X2	0,558	0,001		-0,001	-0,003	-0,001	-0,012	0,028
X3	0,000	0,000	-0,001		0,000	0,000	0,000	0,000
X4	0,003	0,000	-0,003	0,000		0,000	0,004	0,001
X5	0,000	0,000	-0,001	0,000	0,000		0,006	0,001
X6	0,205	-0,006	-0,012	0,000	0,004	0,006		0,010
X7	0,051	-0,002	0,028	0,000	0,001	0,001	0,010	

Note: X1 = plant height; X2 = number of productive tillers; X3 = days to flowering; X4 = days to maturity; X5 = panicle length; X6 = number of grains per panicle; and X7 = weight of 1000 grains.

DISCUSSION

Skewness and Kurtosis Analysis

Skewness provides information about the nature of gene action [10]. In this study no Skewness was found on all traits except number of productive tillers and grain yield per plant. The similar findings were also observed by Vijaya and Shailaja [12] for plant height, days to flowering, days to maturity, and weight of 1000 grains; Herawati et al. [13] for panicle length and number of grains per panicle. No Skewness is associated with additive genes action [13]. This finding concluded that plant height, days to flowering, days to maturity, panicle length, number of grains per panicle and weight of 1000 grains are controlled by additive gene action. The existence of additive gene action on these traits indicates that the traits are stable and suggesting that selection may be effective for these traits in early generation [36].

Significant and positive Skewness found at number of productive tillers and grain yield per plant. These findings are in accordance with earlier reports by Savitha and Kumari [37] and Priyanka et al. [38]. Positive Skewness is associated with complementary gene action [39–41], so number of productive tillers and grain yield per plant are controlled by complementary epistatic gene action. The gain is slower with the mild selection and faster with intensive selection for that particular trait [42]. Maximizing the genetic gain with respect to traits with positively skewed distribution requires intense selection from the existing genetic variability [27,36].

Kurtosis statistical analysis provides information about number of genes controlling the trait [43]. Positive values of Kurtosis indicated leptokurtic curve and negative Kurtosis indicated platykurtic curve [42]. Significant and positive Kurtosis of number of productive tillers, weight of 1000 grain and grain per yield suggested these traits showed leptokurtic distribution in F_2 generation. This leptokurtic distribution suggested these traits are controlled by few of genes [39]. These results are in accordance with the findings of Savitha and Kumari [37].

Not significant or zero values of kurtosis indicates normal or mesokurtic distribution [44]. The traits with normal or mesokurtic distribution are controlled by many of genes [45,46]. In this study plant height, days to flowering, day to maturity, panicle length and number of grains per panicle had no significant kurtosis. Therefore, these traits demonstrated mesokurtic distribution indicated that these traits are controlled by many of genes. These findings are in agreement with Sheshaiah et al [11] for plant height, days to flowering, days to maturity, and panicle length; Kiran et al. [47] for number of grains per panicle. The number of genes controlling a trait will affect the level of difficulty in breeding programs [13]. The selection of traits that is controlled by many genes will be difficult. The number of genes controlling a trait affects the number of distribution classes. The more genes that control a trait, the more classes formed on the distribution and the greater variability among lines. Furthermore, the number of genes controlling a trait will affect the level of difficulty in breeding programs. Selection the traits controlled by a smaller number of genes seem to be more easy than traits controlled by many genes [28].

Genetic variability, Heritability and Genetic advance

This study showed that phenotypic variance was higher than genotypic variance for all the evaluated traits (Table 2). Phenotypic variance was higher than genotypic variance indicating a considerable influence of environment on the expression of these traits [48,49]. Therefore, selection for such traits sometimes might be misleading.

Table 2. showed that PCV estimates were higher than the GCV for all traits, indicating that the environment had an important role in the expression of these traits [21,23]. These phenomena have been reported in rice study everywhere, implying that the apparent variations are not singly attributed to the genetic constitution of the traits, but also due to environmental influence. A smaller difference between GCV and PVC indicates greater genetic determination and less environmental influence on the expression of the trait [17].

Based on the categories outlined by Sivasubramanian and Menon [50], number of productive tillers and grain yield per plant showed a high GCV**.** Likewise, the PCV of these traits. These results were in agreement with the findings of Chozin et al. [17]. Plant height, days to flowering, number of grains per panicle and weight of 1000 grains had medium GCV and PCV have medium GCV and PCV categories, except for number of grains per panicle. Number of grains per panicle has a high PCV value. These findings were in agreement with Anbanandan and Eswaran [18]. Days to maturity and panicle length has low GCF value but showed different PCF value, i.e.: low value for days to maturity and medium value for panicle length. Similar finding was reported by Singh et al. [16] and Bornare et al. [51] for days to maturity; Anbanandan and Eswaran [18] for panicle length.

Variations for traits in F_2 generation indicated a wide range of plant variation that provide a large scope and flexibility for selection on the basis of phenotypic performances [17]. Greater magnitude of variability in a population provides the opportunity for selection to assemble a variety having desirable traits [51]. Coefficient of variation along with variances gives a better picture of genetic variability [22] and its could be partitioned into genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV. High GCV and PCV indicated that selection might be effective based on these traits and their phenotypic expression would be a good indication of the genotypic potential [16]. The high values of GCV and PCV for number of productive tillers and grain yield per plant suggested the possibility of yield improvement through selection of these traits. Therefore, number of productive tillers and grain yield per plant can be used as a selection trait in F_2 population from the Inpago Unsoed 1 x Basmati Delta 9 crossing.

The phenotypic expression of the trait is the result of interaction between genotype and environment. Hence, the total variance should be partitioned into heritable and non-heritable components to assess the inheritance pattern of the particular trait under study [40]. Heritability indicates the relative degree of which a trait is transmitted from parent to offspring. Heritability is a ratio of genotypic variance to phenotypic variance and it is one of genetic parameters which is always included to choose a selection method [52].

Estimates of broad-sense heritability refer to the relative contribution of the genetic component to the variation of the observable trait [17]. According to Stansfield [33], heritability estimate resulted in this study was high for plant height, days to flowering, days to maturity, panicle length, number of grains per panicle and weight of 1000 grains. These findings are in accordance with Anbanandan and Eswaran [18]. High heritability value indicated a preponderance of additive gene action in the expression of the traits [3]. Additive gene action was also obtained in the Skewness test for the traits above (Table 1). Furthermore, high heritability values indicate that the traits under study are less influenced by environment in their expression and such traits could be improved by adopting simple selection methods [40,52]. In addition, selection against high heritability traits can be done at early generation because the genetic factors dominantly influence the plant phenotype [28].

The medium heritability was found on number of productive tiller and grain yield per plant (41.80% and 48.92%, respectively) suggests that both genetic and environmental factors gave effect on these two traits. These finding also reported by Choudhary et al. [22,23]. Medium heritability indicated favorable influence of environment rather than genotypes. Consequently, selection of number productive tiller and grain yield per plant would not be rewarding if to be done in early generations [53]. Therefore, another selection trait of yield component that correlated with yield is necessary.

Heritability of a trait is very important in determining the response to selection. Heritability indicates the effectiveness with which selection of genotypes could be based on phenotypic performance. Plant attributes with high heritability can be selected in earlier generations to accelerate the process of cultivar development. However, high heritability does not always indicate high genetic gain [54]. Hence, heritability values coupled with genetic advance would be more reliable than heritability alone [55]. Genetic advance provides information on expected genetic gain resulting from selection of superior individuals [18].

The genetic advances in this study are categorized according to Begum and Sobhan [35]. Number of productive tillers, number of grains per panicle and grain yield per plant could be categorized as to have high genetic advance. Whereas, plant height days to flowering, panicle length, weight of 1000 grains could be considered to have medium genetic advance, while days to maturity are considered to have low genetic advance. These findings are in agreement with Bornare et al. [51] for all traits.

High or medium heritability coupled with high genetic advance indicates simple selection favoring superior segregants for these traits will be effective and bred true in the next generation [17,56]. Number of productive tillers, number of grains per panicle and grain yield per plant has a high or medium heritability with high genetic advance so selection favoring superior segregants for these traits will be effective in the next generation. High heritability and medium genetic advance were observed for plant height, days to flowering, panicle length, and weight of 1000 grains. It can be attributed by favorable environment rather than genotype, and consequently, selection may not be rewarding [55], if the selection is carried out in an unfavorable environment because the phenotype will change. Furthermore, days to maturity showing high heritability with low genetic advance indicated the presence of non-additive gene action. Hence, selection could be postponed for these traits, or otherwise these traits could be improved by intermating of superior genotypes of segregating population from recombination breeding [16].

Interrelationship Among Traits

Yield is a complex trait that shows a chain of linear and nonlinear associations among yield components with varying degree of effects [53]. Interrelationship among traits is a guide in choosing the most important trait to select for the higher grain yield. Correlation and path analysis were the common techniques used to elucidate the relationship between traits in many of crop plants [25].

In this study, excep days to flowering and days to maturity several traits showed significant and positive correlations. These findings are reported by Hajiaqatabar et al. [26] and Chozin et al. [17] for plant height and number of productive tillers; Totok et al. [24] and Chozin et al [17] for panicle length and number of grains per panicle; Rajamadhan et al. [57] and Chozin et al. [17] for weight of 1000 grains. Positive correlation in many of traits relationship interprets to the similarity of direction of the trend association. It also indicates that compensatory effect was not found and competition among the traits may be ignored [25].

Negative correlation with grain yield per plant, and no significant correlations with grain yield per plant obtained on day to flowering and days to maturity, respectively. This is similar with findings by Bornare et al 2014 [51]. Negative correlation indicates the compensatory effects between traits [25]. It means that the increasing of the day to flowering may be followed by decreasing of grain yield per plant. On the contrary, the increasing of grain yield per plant may result in the decreasing of day to flowering.

Correlation coefficient analysis is used to measure the degree and direction of relationships among traits [58,59]. However correlation coefficient should be limited to describing the association between two variables that are not in a cause-and-effect relationship [26,60]. Therefore, other methods to describe a cause-and-effect relationship in the association between traits such as path analysis is needed.

Path analysis is a basic method that enables the drawing inferences about causal structure of data [61] and could give a better insight into cause-and-effect relationship between different pairs of traits [62]. Path coefficient analysis is a statistical technique of partitioning the correlation coefficients into its direct and indirect effects, so that the contribution of each trait to yield could be estimated [24,63].

In this study, several traits showed a direct effect on grain yield per plant. These findings was also reported by Bornare et al. [51] for plant height and days to maturity; Seneega et al. [64] for number of productive tillers and weight of 1000 grains; Chozin et al. [17] for days to maturity; Hajiaqatabar et al. [26] for panicle length and number of grains per panicle.

Number of productive tillers and number of grains per panicle showed the highest value of path coefficient (0.558 and 0.205, respectively). Relatively low counterbalance through other traits resulted in high value of its positive correlation to the grain yield per plant (0.763 and 0.457, respectively). It means that number of productive tillers and number of grains per panicle is the most influential trait to the seed yield by the strong direct effects and correlation to the grain yield per plant. Indirect selection for high yield genotype through selection of number of productive tillers and number of grains per panicle trait is therefore possible. Number of

productive tillers and number of grains per panicle as selection criterion traits also reported by other studies [20,21,38,64].

CONCLUSION

Summarizing the above result, broad genetic variability, high/medium heritability and high genetic advance were found on number of productive tillers, number of grains per and grain yield per plant. Number of productive tillers and number of grains per panicle had a high correlation coefficient and positively direct effects to the grain yield per plant. It could be concluded that number of productive tillers and number of grains per panicle might be considered as criteria of selection for the development of high yield and long slender rice grain through pure line selection of Inpago Unsoed 1 x Basmati Delta 9 generation.

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