Genetic control for agronomic characters of bread wheat

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Abstract. Indonesian wheat needs continue to increase from year to year. Some regions of Indonesia have the potential for wheat development. This study aimed to obtain gene action of wheat agronomic characters in the context of developing tropical wheat. The study was conducted at the Experimental Garden of the Indonesian Ornamental Plant Research Institute (1100 m asl), Cipanas, Cianjur Regency, West Java from July 2017 to January 2018. This study used F2 Ja/Se population and two-parent genotypes (Jarissa and Selayar) were planted in a randomized complete block design with three replications. Observations were made on plant height, days to flowering, days to harvesting, number of productive tillers, panicle length, number of spikelet, number of main panicle seeds, main panicle seed weight, number of seeds per plant and seeds weight per plant. Estimation of number and action genes used skewness and kurtosis approaches. The results showed that broad sense heritability was high except unfilled floret ratio. There were additive, dominant, epistasis gene actions controlling all observed characters. These characters were controlled by many genes.

1. Introduction
Wheat is one of cereal crops that widely consumed worldwide, including Indonesia. Wheat is consumed by ± 40% of the world population [1]. Wheat is the only food plant that contains gluten. The ability to expand from gluten is what distinguishes it from other food crops.

Wheat grown in Indonesia is a type of spring wheat. A good agroecosystem for the growth and development of wheat in Indonesia is an area with a temperature of 15-20°C [2]. Indonesia has a few wheat varieties, and most of them came from introduction varieties. The effort to increase the amount of wheat varieties is to do the tropical wheat assembly both conventionally and non-conventional. One way conventional breeding is through hybridization, which is the technique of combining superior traits with artificial crosses. This cross will produce a diverse derivative as a result of a pair of genes from both parents. The further the genetic distance of the elders then the diversity is getting higher. The high diversity in the population of F2 can be seen from the width of the value range of a character.

Genetic improvement of plants generally aims to increase plant production [3]. The right method of breeding a plant is decisive to achieve that goal. Therefore, information about genetic parameters is indispensable. Important genetic parameters such as heritability have always been the focus of breeding activities. Heritability describes the ability of plants to inherit a character in the next
generation. The heritability of wheat in agronomy characters has been widely reported by other researchers. [4] reported that seed weight per plant, plant height, seed weight per spike, and one thousand grain weight have high heritability.

The interaction of genes controlling a character affects the next stage of breeding. Gene action determines when selection is done [5],[6]. Gene action on agronomic characters of wheat crops has been widely reported by other researchers. Yield and yield component involved additive gene action, dominant and epistasis [5], [7], [8]. The study used Selayar varieties that had been released in 2003 and Jarissa (an introduced variety from Slovakia). Selayar is an adaptive variety in the lowland environment [9]. The cross of the two varieties is expected to obtain medium-maturity lines with more productive tillers and better adaptation to lowland environment. This study aims to estimate genetic parameters in the agronomic characters of F2 Ja/Se population.

2. Methodology

This research has been conducted at Balithi experimental site, Cipanas Regency, Cianjur, West Java in July 2017 - January 2018. The height of the study location is 1100 m above sea level. The genetic material used was population of F2 Ja/Se and its parents (Jarissa and Selayar). This study used a Randomized Complete Group Design with three replications so that there are 9 experimental units. The experimental unit is in the form of a plot measuring 1 m x 5 m with a spacing of 30 cm x 20 cm and obtained 75 individuals per plot. F2 populations consist of individual segregation having different genetics each other. Therefore, all individuals in F2 population were observed. There were ten samples for each replication of parent genotypes. Other materials used are manure, inorganic fertilizer (Urea, SP36, KCl), and Furadan 3G. Fertilizing was done twice, namely the first fertilization at the age of 10 days after planting at a dose of 150 kg ha\(^{-1}\) Urea, 200 kg ha\(^{-1}\) SP36 and 100 kg ha\(^{-1}\) KCl. Fertilization, watering, and controlling pests and diseases were done for maintenance. Application of pesticides based on symptoms in the field. Harvesting is done if the plant is 80% yellow and the seeds are hard when pressed with nails.

Observations included plant height, days to flowering, days to harvesting, seed filling period, number of productive tiller, panicle length, number of spikelets, number of main panicle seeds, unfilled florets ratio, number of seeds per plant, 100 grains weight, main panicle seeds weight, and seeds weight per plant. Estimating of variance follows to the formula, \(\sigma^2 = \frac{(X_i - X)^2}{n - 1}\).

Heritability of broad-sense followed [10]. The genetic variability coefficient (GVC) was calculated using the formulas: \(\sqrt{\frac{\sigma^2}{\bar{x}}} \times 100\%\). The GVC followed categorized [11], namely Narrow (0 - 10%), moderate (10-20%), and wide (> 20%).

Estimating of the action and number of genes using a descriptive approach through the value of skewness and kurtosis. Skewness shows the form of the sloping curve of a population. If skewness = 0, the character is controlled by the action of additive genes; skewness > 0 then the character is controlled by the action of additive genes with the effect of complementary epistasis; conversely, if skewness <0, it is suspected that the action of the gene is additive with the effect of duplicate epistasis. Kurtosis shows the height of the population curve. If kurtosis is positive then the graph is leptocurtic which indicates the character is controlled by a few genes whereas if kurtosis is negative then the graph is platycurtic which indicates that the character is controlled by many genes [12]. Interpretation of skewness and kurtosis values follows [13].

3. Result and Discussion

Hybridization is one way to increase diversity. Alleles from each parents will pair up when meiosis forms heterozygous homogeneous F1. The pairs of alleles will segregate to form genotypes that are similar to parents and recombinant in the F2 generation. Individuals in this generation have a phenotype with a wide range of values. The mean values of parent genotypes and the F2 Ja/Se
Table 1. Mean and standard deviation of agronomic characters

| Characters                      | Jarissa (P1)  | Selayar (P2) | p-value | F2            |
|---------------------------------|---------------|--------------|---------|---------------|
| Plant height (cm)               | 87.87±5.38    | 60.03±4.97   | **      | 70.14 ± 15.24|
| Days to flowering (days)        | 117.33±2.08   | 42.10±0.87   | **      | 81.83 ± 20.47|
| Days to harvesting (days)       | 167.33±2.08   | 82.33±1.53   | **      | 127.69 ± 15.43|
| Grain filling period (days)     | 50.00±3.61    | 40.23±1.14   | *       | 45.87 ± 15.42|
| Number of productive tiller     | 19.96±4.77    | 14.07±2.89   | **      | 23.58 ± 14.18|
| Spike length (cm)               | 11.40±1.63    | 8.66±0.72    | **      | 9.21 ± 1.84   |
| Number of spikelet              | 22.61±3.14    | 17.59±1.48   | **      | 19.07 ± 3.90  |
| Number seed of main spike       | 17.26±8.08    | 47.59±9.24   | **      | 49.24 ± 20.02|
| Unfilled seed ratio             | 0.75±0.16     | 0.36±0.19    | **      | 0.43 ± 0.17   |
| Number seed per plant           | 192.35±73.18  | 397.29±81.09 | **      | 933.43 ± 68.90|
| B100 (g)                        | 1.72±0.43     | 3.99±0.51    | **      | 3.04 ± 0.76   |
| Main spike seed weight (g)      | 0.27±0.19     | 1.94±0.55    | **      | 1.70 ± 0.77   |
| Seed weight per plant (g)       | 2.81±1.24     | 16.21±4.04   | **      | 26.63 ± 20.24|

Note: * means significantly different; ** means very significantly different

Jarissa genotype has a longer vegetative phase than Selayar (Table 1). The length of the vegetative phase of Jarissa provides opportunities for more photosynthetic accumulation to other plant organs. This is thought to have implications for higher plant height, a higher number of productive tillers, longer panicles, and longer days to harvesting. Jarissa generative phase occurred during the rainy season. Climatic conditions during the rainy season were not conducive to photosynthesis and pollination. In November 2017 the rainfall reached 624 mm and included in the very high category. The number of rainy days in the frost is 25 days [14]. [15] stated that Indonesia is a wet tropical climate country because it is between 5°LU and 5°LS. The wet tropical climate has the characteristics of rainfall that lasts all month and dew which produces an average rainfall of 15 cm for 11 months and average monthly temperatures between 25-31°C.

The grain filling period for Jarissa was longer than Selayar. This is expected to increase seeds weight per panicle and seeds weight per plant. [16] stated that there is a positive correlation between grain filling period and number of seeds per panicle and plant height.

Variation in F2 population are caused by the segregation of alleles that control a character. This can be seen from the standard deviation of each character shown in Table 1. The number of seeds per plant in population F2 has a wider range than other characters. Population F2 has a higher middle value than the two parents in the character of the number of productive tillers, number of seeds main panicle, number of seeds per plant, and seeds weight per plant. The other characters have a middle value between the two parents (Table 1).

Heritability is one of the important genetic parameters to determine the breeding method to be used. Heritability is the proportion of genetic variation to the phenotypic variation of a character. All observed characters have high broad-sense heritability values except the character of the unfilled seed ratio (Table 2). The low heritability of this character indicated that the unfilled seed ratio was very much influenced by the environment so that it was not passed on to the next generation.
Table 2. Variability and heritability of agronomic characters

| Character                        | $\sigma_p^2$ | $\sigma_s^2$ | $\sigma_g^2$ | $h_{bs}^2$ | Criteria | GVC     | Criteria |
|--------------------------------|-------------|-------------|-------------|-----------|----------|--------|----------|
| Plant height (cm)               | 232.21      | 26.84       | 205.36      | 88.44     | High     | 20.43  | Wide     |
| Days to flowering (days)        | 418.96      | 2.55        | 416.42      | 99.39     | High     | 24.94  | Wide     |
| Days to harvesting (days)       | 238.19      | 3.33        | 234.86      | 98.60     | High     | 12.00  | Medium   |
| Seed filling period (days)      | 237.72      | 7.15        | 230.58      | 96.99     | High     | 33.10  | Wide     |
| Number of productive tiller     | 200.94      | 15.57       | 185.37      | 92.25     | High     | 57.74  | Wide     |
| Spike length (cm)               | 3.38        | 1.58        | 1.79        | 53.11     | High     | 14.55  | Medium   |
| Number of spikelet              | 15.22       | 6.03        | 9.19        | 60.37     | High     | 15.90  | Medium   |
| Number seed of main spike       | 400.77      | 75.38       | 325.39      | 81.19     | High     | 36.64  | Wide     |
| Unfilled seed ratio             | 0.03        | 0.03        | 0.00        | 0.00      | Rendah   | 15.94  | Medium   |
| Number seed per plant           | 759640.64   | 5965.53     | 753675.11   | 99.21     | High     | 93.01  | Wide     |
| B100 (g)                        | 0.58        | 0.22        | 0.36        | 61.85     | High     | 19.70  | Medium   |
| Main Spike seed weight (g)      | 0.59        | 0.17        | 0.42        | 71.56     | High     | 38.36  | Wide     |
| Seed weight per plant (g)       | 409.61      | 8.92        | 400.69      | 97.82     | High     | 75.17  | Wide     |

Note: $\sigma_p^2$= phenotypic variability; $\sigma_s^2$= environment variability; $\sigma_g^2$= genetic variability; $h_{bs}^2$= broad sense heritability; GVC= genetic variability coefficient.

A high heritability is not always accompanied by genetic variability coefficient. Days to harvesting, spike length, number of spikelet, unfilled seed ratio, and weight of 100 grains had moderate genetic diversity coefficient (Table 2). [17] reported that plant height, days to 50 % flowering, spike length, grain yield and 1000 grain weight had high heritability. Furthermore, [11] found broad-sense heritability in his research ranging from 84.9% - 99.6%. The high value of heritability indicates the characters were controlled by genetic variance.

Table 3. Action and number of genes for agronomic characters

| Characters                        | S    | SE_s | Z_s  | K    | SE_K | Z_K  | Action and number of genes |
|-----------------------------------|------|------|------|------|------|------|---------------------------|
| Plant height (cm)                 | -0.78| 0.19 | -4.06| **   | 0.50 | 0.38 | Dom, M                    |
| Days to flowering (days)          | 0.06 | 0.19 | 0.32 | ns   | -0.25| 0.38 | Ad, M                     |
| Days to harvesting (days)         | 0.28 | 0.19 | 1.47 | ns   | 2.86 | 0.38 | AE,F                      |
| Grain filling period (days)       | 0.55 | 0.19 | 2.85 | **   | -0.02| 0.38 | -0.06                     |
| Number of productive tiller      | -0.38| 0.19 | -1.98*| 2.11 | 0.38 | 5.53 | ** DE,F                   |
| Spike length (cm)                 | -0.95| 0.19 | -4.97 | **  | 1.36 | 0.38 | 3.57 ** DE, F             |
| Number of spikelet               | -0.53| 0.19 | -2.75 | **  | -0.40 | 0.38 | -1.05                     |
| Unfilled seed ratio              | 0.82 | 0.19 | 4.26 | **  | 0.92 | 0.38 | 2.41 * CE, F              |
| Number seed per plant            | 1.84 | 0.19 | 9.61 | **  | 4.24 | 0.38 | 11.11 ** CE, F            |
| B100 (g)                         | -0.24| 0.19 | -1.27 | ns  | 3.01 | 0.38 | 7.90 ** AE, F             |
| Main Spike seed weight (g)       | -0.46| 0.19 | -2.42 | *   | -0.64 | 0.38 | -1.69                     |
| Seed weight per plant (g)        | 0.63 | 0.19 | 3.29 | **  | -0.26 | 0.38 | -0.68                     |

Note: S= skewness; K=kurtosis; ns= non significant; *= Significantly different; **= very significantly different; M=many genes; F= Few genes; Dom= dominant; Ad= additive; AE= additive epistatic; DE= dominant epistatic; CE= Complementary epistatic.
The coefficient of genetic diversity in the observed characters is in the medium-wide category. [18] stated that genetic diversity is important in germ plasm management and its use in plant breeding programs.

The agronomic traits observed in this study were partially controlled polygenic gene, namely the characters of plant height, days to flowering, grain filling period, number of a productive tillers, number and weight of main panicle seeds, and weight of seeds per plant (Table 3). Characters controlled by many genes have a platy curtic curve. Characters controlled by many genes have a continuous distribution [19]. The action of genes in the F2 Ja/Se population was non-additive genes (dominant and epistasis) except days to flowering (additives). [20] mentioned that characters controlled by the action of non-additive genes cause higher phenotypic mean values in the F2 generation, but not all of these characters are inherited. Plant height is controlled by the action of dominant genes. The same thing was reported by [8]. However other researchers reported that plant height is controlled by the action of additive genes [21].

4. Conclusions

All characters have high broad sense heritability except unfilled seed ratio. The GVC was in the medium-wide category. The characters observed were controlled by the action of additive, dominant, epistatatic genes. Days to flowering was controlled by the action of additive genes. Selection in the early generations using this characters can be done.

Acknowledgement

This research was supported by Directorate General of Higher Education, Ministry of Research Technology and Higher Education, Republic of Indonesia, Year 2018, Yudiwanti Wahyu.

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