Genetic and Heritability Estimation of Water Apple (*Syzygium aqueum* (Burm.f.) Alston)

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**ABSTRACT**

Nine different accessions of water apples were evaluated at Indonesian Tropical Fruit Research Institute (ITFRI), Solok, West Sumatera from January 2013 to December 2014. This present study was aimed to evaluate the variability, heritability, genetic advance and its characters in nine different accessions to provide useful information in the improvement program of water apples. The research used Randomized Complete Block Design (RCBD) with two replications. The ANOVA results exposed significant differences at 5% probability level for all characters. Genotypic variance on fruit weight, fruit length, fruit diameter, leaf length were broad. However, the genotypic variance on total soluble solids, leaf width were narrow. The phenotypic variation for all characters was broad. The heritability estimation was categorized as low, moderate, and high. High heritability estimation was recorded for fruit weight, fruit length, fruit diameter; leaf length. Moderate heritability estimation was noticed for total soluble solids. Leaf width had low heritability estimation. High heritability and high genetic advance were observed on fruit weight.

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Water apples; Variety; Heritability; Genotypic; Phenotypic;

**1. INTRODUCTION**

Water apple has a good prospect in the market. This tree is cultivated in the whole of the tropical countries and also grows naturally (Yaacob and Subhadrabandhu, 1995). Various parts of water apple such as leaves were useful for traditional medicine, as snacks wrap and it’s wood for construction purposes. This fruit is used as a salad (rujak) and pickling (asinan) in Indonesia. However, there is limited information on germplasm collection, so it is difficult for the selection of superior forms (Verheij and Coronel, 1992). Selection is a major and important process for the hybridization program because this is a process to store desired genotypes and eliminate of undesirable genotypes. Dilnesaw et al. (2013) revealed that germplasm collection is a basic step of improvement in any crop. Genetic variability is considered as one basis for selection because it is one of the criteria of parent selection in a breeding program. Thus genetic variability is a crucial activity and must be exploited by plant breeders (Idahosa et al., 2010; Sujata et al., 2011; Jalata et al., 2011; Rahim et al., 2010). Manju and Sreelathakumary (2002) stated that genetic variability is a prerequisite for improvement work of breeding and high variability necessary to improve the yield of any crop.

The information of genotypic and phenotypic, along with heritability, will determine the effectiveness of selection because it selects character whether the desired or undesired objectives (Chaudhary, 2000; Manju and Sreelathakumary, 2002). Heritability and genetic coefficient of variation are found out by the statistical tool. Phenotypic and genotypic variances, phenotypic and genotypic coefficient variation (PCV and GCV), broad-sense heritability (H²), are formulated to genetic improvement of any crop (Roychowdhury et al., 2012), then calculated by using Analysis of Variance (ANOVA). The estimations of genetic variability and heritability are necessary for initiating an efficient breeding program to develop high yielded genotypes (Chaurasia et al., 2012; Das et al., 2012). The heritability estimates, coupled with genetic advance, are more meaningful to determine the method of selection (Sujata et al., 2011). Freitas et al. (2016) revealed that knowledge of the genetic diversity would identify the success of the breeding program. As a result, the present study was aimed to evaluate variability, heritability, genetic advance and its characters in nine water apple accessions to provide information which could be useful for improvement program of water apple.
2. MATERIALS AND METHODS

The research was conducted at Indonesian Tropical Fruit Research Institute (ITFRI), Solok, West Sumatra, from January 2013 to December 2014. Nine accessions viz., 9.6; 9.8; 9.9; 9.10; 9.11; 9.13; 9.14; 9.15; 9.16 were selected to evaluate their parameters. The experiments used Randomized Complete Block Design (RCBD) with two replications. The characters observed were fruit weight (g), fruit length (cm), fruit diameter (cm), total soluble solids (Brix), leaf length (cm), and leaf width (cm). Collected data were statistically analyzed using Analysis of Variance (ANOVA). Mean values were compared by using Duncan’s Multiple Range Test (DMRT) test at 5\% probability level.

Those genotypic and phenotypic variabilities were estimated by variance components analysis (Steel and Torrie, 1989) where the formula for these variances was suggested by Singh and Chaudhary (1979).

Genotypic variance  \( \sigma_g^2 = (\bar{M}_2^2 - \bar{M}_1^2)/r \)

Phenotypic variance  \( \sigma_p^2 = \sigma_g^2 + \sigma_p^2 \)

Where:

\( M_2 \) : the mean sum of squares for the genotypes
\( M_1 \) : error in the analysis of variance
\( R \) : the number of replications

Genotypic and phenotypic coefficient variations of a character were calculated using the formula by Anderson and Bancroff (1952), \( \text{cit. Wahdah et al., (1996)} \):

\[ \sigma_g^2 = \frac{2}{r^2} \left( \frac{M_2^2 - M_1^2}{f \text{ genotype }+ 2} - \frac{M_1^2}{f \text{ error }+ 2} \right) \]

\[ \sigma_p^2 = \frac{2}{r^2} \left( \frac{M_2^2}{f \text{ genotype }+ 2} \right) \]

A character is considered to have a broad variability if \( \sigma_g^2 > 2\sigma_p^2 \) and conversely.

Heritability (H) of the accessions was estimated using ANOVA and it was calculated based on the method of "broad-sense" used by Allard (1960) and the criteria of heritability values according to the following formula by McWhirter (1979) respectively:

\[ H = \frac{\sigma_g^2}{\sigma_p^2} \]

Where:

\( H(\%) \): 0 - 20 (low), 20 < \( H \) ≤ 50 (moderate), \( H > 50 \) (high)

Expected genetic advances (GA) at 5\% were calculated using the following formula by Johnson and Robinson (1955) \( \text{cit Jalata et al. (2011)} \):

\[ GA = (K)(\sigma_p)(H) \]

where:

\( GA \) = genetic advance
\( K \) = the standardized selection differential at 5\% selection intensity (K=2.06)
\( \sigma_p \) = phenotypic standard deviations
\( H \) = heritability

According to Begum and Sobhan (1991) \( \text{cit Bambang et al., (1998)} \), criteria of genetic advance percentage (GA (\%)) were classified as: 0-7\% (low), 7.1 - 14\% (moderate) and >14.1\% (high).

3. RESULTS AND DISCUSSIONS

The ANOVA results showed a significant difference (P<0.05) for all characters (Table 1), indicating there was genetic variation in water apples. This study is similar to Khan et al. (2010). They reported that there were genetic differentiation and diversity on Syzygium cumini (Mrytaceae) in India. Risvy (2013) found the same result; namely there was a genetic variation on Syzygium samarangense in Bangladesh. Singh et al. (2014) noted that Syzygium cumini Skeels in India significantly varied on fruit weight, length, breadth, length: breadth ratio, pulp weight, pulp content, seed weight, and pulp: seed ratio in different observed accessions.

From the results obtained, the fruit weight ranged from 35.69 to 86.15 g, fruit length from 3.97 to 5.99 cm, fruit diameter from 4.17 to 6.60 cm, total soluble solids (TSS) from 4.24 to 7.79-Brix, leaf length from 17.52 to 24.04 cm, and leaf width from 7.85 to 11.14 cm.

| Accessions | Fruit weight (g) | Fruit length (cm) | Fruit diameter (cm) | Total soluble solids (Brix) | Leaf length (cm) | Leaf width (cm) |
|------------|------------------|-------------------|---------------------|-----------------------------|-----------------|---------------|
| 9.6        | 53.75 de         | 4.89 abc          | 5.59 c              | 6.25 ab                     | 19.42 def       | 9.47 ab        |
| 9.8        | 66.59 bc         | 5.99 a            | 5.13 d              | 6.46 ab                     | 21.07 bcd       | 9.72 ab        |
| 9.9        | 53.07 de         | 5.80 a            | 5.11 d              | 7.24 ab                     | 24.04 a         | 11.14 a        |
| 9.10       | 31.70 f          | 4.56 bc           | 4.41 e              | 4.29 ab                     | 19.27 def       | 7.85 b         |
| 9.11       | 61.21 cd         | 3.97 c            | 6.60 a              | 4.24 b                      | 22.40 ab        | 9.17 ab        |
| 9.13       | 86.15 a          | 5.90 a            | 6.23 b              | 4.98 ab                     | 18.14 ef        | 8.21 ab        |
| 9.14       | 35.69 f          | 5.44 ab           | 4.17 e              | 5.48 ab                     | 17.52 f         | 9.90 ab        |
| 9.15       | 70.09 b          | 5.41 ab           | 5.79 c              | 4.42 ab                     | 19.70 cde       | 8.81 ab        |
An agro-economical value such as fruit weight, fruit length, fruit diameter, leaf length, leaf width, etc as metrical traits is complex in nature because these traits are influenced by polygenic inheritance and environmental fluctuation. Analysis of variance (ANOVA) of the mean value of agro-economical traits as genetic parameters affects the genetic improvement of any crop (Roychowdhury et al., 2012). Fruit size is an important character to be evaluated in breeding because this character will distinguish the size of fruit as large, medium and small (Zhigilla et al., 2014). Leaflet size is also important character. Cheong and Sanmukhya (2013) observed the morphological characteristics of the leaf on Syzygium species in Mauritius. Sujata et al. (2011) stated that leaflet shape has a correlation with a single gene. This trait is qualitative, and the environment did not influence it. In soybean, the performance of narrow leaflet genotypes contributed to the yield and variability of the crossing population.

The estimation of genotypic and phenotypic variances was given in Table 2. Broad genotypic variation was observed for fruit weight, fruit length, fruit diameter; and leaf length, while total soluble solids and leaf width had narrow of genotypic variance. Broad phenotypic variance was noticed for all characters. Broad genetic variability is important in breeding (Freitas et al., 2016). The phenotypic variance was found to be higher than genotypic variance for all characters. It indicated that the expression of those characters was influenced by the environmental aspect (Rahim et al., 2010; Bitew, 2016).

### Table 2. Genotype variance ($\sigma^2_g$) and phenotypic variation ($\sigma^2_p$) of six characteristics in water apple

| Characteristics       | $\sigma^2_g$ | $2\sigma_{c_1^2}$ | Criteria | $\sigma^2_p$ | $2\sigma_{c_2^2}$ | Criteria |
|-----------------------|-------------|-----------------|----------|-------------|-----------------|----------|
| Fruit weight          | 276.88      | 126.63          | Broad    | 289.28      | 126.59          | Broad    |
| Fruit length          | 0.44        | 0.19            | Broad    | 0.45        | 0.19            | Broad    |
| Fruit diameter        | 0.64        | 0.29            | Broad    | 0.66        | 0.29            | Broad    |
| Total soluble solids  | 0.76        | 0.88            | Narrow   | 2.72        | 0.78            | Broad    |
| Leaf length           | 3.98        | 1.96            | Broad    | 4.74        | 1.95            | Broad    |
| Leaf width            | 0.17        | 0.58            | Narrow   | 1.85        | 0.45            | Broad    |

### Table 3. Broad-sense heritability estimation (H) and genetic advance of six characteristics of water apple at 5%

| Characteristics       | Heritability (H) | Criteria | Genetic Advance (GA) | Criteria |
|-----------------------|------------------|----------|----------------------|----------|
| Fruit weight          | 95               | High     | 33.53                | High     |
| Fruit length          | 96               | High     | 1.34                 | Low      |
| Fruit diameter        | 97               | High     | 1.63                 | Low      |
| Total soluble solids  | 28               | Moderate | 0.95                 | Low      |
| Leaf length           | 84               | High     | 3.77                 | Low      |
| Leaf width            | 9                | Low      | 0.26                 | Low      |

**Note:** Means followed by the same letters in the same columns do not differ significantly as determined by DMRT test at 0.05 probability level.

The estimation of heritability is presented in Table 3. In this study, the heritability estimation ranged from 9 to 97. The estimation of heritability was categorized as low, moderate, and high. High heritability was recorded for fruit weight, fruit length, fruit diameter, and leaf length. Moderate heritability was noticed for total soluble solids. Leaf width had a low of heritability estimate. Greater role of the environment affected the trait which had low heritability (Bitew, 2016). Genetic advance (GA) for fruit weight was higher than was fruit length, fruit diameter, total soluble solids, leaf length, and leaf width. High heritability, followed by high genetic advance, was observed on fruit weight.

Environment factors influenced heritability. The high heritability estimation is useful in plant breeding because phenotypic performance is considered as a basis for the selection (Roychowdhury et al., 2012). High heritability estimation was indicated by the presence of a large number of fixable additive factors. Rahim et al. (2010) stated that superior genotypes selection based on phenotypic performance could be found by high heritability estimation. The information on the magnitude of inheritance of metrical attributes is given by heritability (Roychowdhury et al., 2012). Therefore, selection can improve these characters (Manju and Sreelathakumary, 2002). Bitew (2016) confirmed that high heritability coupled with high genetic advance is good condition to increase this trait using these accessions. The data in this research showed the possibility of improving water apple by selection. These accessions could be the materials for breeding programs.
4. CONCLUSION
The analysis of variance showed significant differences (P<0.05) for all characters. Genotypic variations on fruit weight, fruit length, fruit diameter, leaf length were broad however, the genotypic variance on total soluble solids and leaf width were narrow. Phenotypic variations for all characters were broad. The heritability estimation was categorized as low, moderate, and high. High heritability estimation was recorded on fruit weight, fruit length, fruit diameter, and leaf diameter. Moderate heritability estimation was noticed in total soluble solids. Leaf width had low heritability estimation. High heritability, coupled with high genetic advance, was observed on fruit weight.

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