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

Fitriana Nasution[1]*, Sri Hadiati[1]

[1] Indonesian Tropical Fruit Research Institute
Jl. Raya SolokAripan Km.8
*Corresponding author:nasution79@gmail.com

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, and leaf diameter. 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.

This is an open access article under the CC–BY-SA license.

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 (H^2), 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 $\left(\sigma_g^2\right)$ $(M_2 - M_1)/r$

Phenotypic variance= $\left(\sigma_p^2\right)$ $\sigma_g^2 + M_1$

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), *cit.* Wahdah *et al.*, (1996):

$$\sigma_{\sigma^2 g} = \sqrt{\frac{2}{r^2}\left(\frac{M_2^2}{df\ genotype +2}+\frac{M_1^2}{df\ error +2}\right)}$$

$$\sigma_{\sigma_p^2} = \sqrt{\frac{2}{r^2}\left(\frac{M_2^2}{df\ genotype+2}\right)}$$

A character is considered to have had a broad variabilityif> an $\sigma_g^2 \tau_p^2$ $2\sigma_{\sigma_g^2}$ 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) *cit* Jalata et al. (2011):

GA = (K). (σ_p). (H),

where:

GA   = genetic advance

K   =the standardized selection differential at 5% selection intensity (K=2.06)

σ_p = phenotypic standard deviations

H   = heritability

According to Begum and Sobhan (1991) *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 gr, 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.

Table 1. Mean values of fruit weight, fruit length, fruit diameter, total soluble solids, leaf length and leaf width of water apple

Accessions	Fruit weight (g)	Fruit length (cm)	Fruit diameter (cm)	Total soluble solids (⁰Brix)	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

9.16	51.62 e	5.21 ab	4.81 d	7.79 a	21.48 bc	10.13 ab
CV (%)	6.17	9.01	2.89	24.64	4.29	13.81

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

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 Sanmukhiya (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	σ^2_g	$2\sigma_{\sigma^2_g}$	Criteria	σ^2_p	$2\sigma_{\sigma^2_p}$	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

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 addictive 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.

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 lettersin the same columns do not differ significantly as determined by DMRT test at 0.05 probability level

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.

REFERENCES

Allard, R.W. (1960). Principles of Plant Breeding.John Wiley and Sons, Inc. New York. Chichestor-Brisbane-Toronto-Singapore.

Bambang H, Purwati R.D, Marjani, dan Budi U. S. (1998). Genetic parameter of yield component and fibre component on potential accessions of kenaf (*Hibiscus cannabinus* L) (written in Indonesian language). *Zuriat.* 9(1) : 6 – 12.

Bitew, J. M. (2016). Estimation of genetic parameters, heritability and genetic advance for yield related traits in upland rice (*Oryza sativa* L. And *Oryza glaberrima* Steud) genotypes in North Western Ethiopia. World Scientific News. 47(2): 340-350.

Chaudhary, R. R. (2000). Genetic variability and heritability in sugarcane. Nepal Agric Res. J. Vol 4&5: 56-59.

Chaurasia, A. K., P. K. Rai, and A. Kumar. (2012). Estimation of genetic variability, heritability and genetic advance in aromatic fine grain rice. Romanian Journal of Biology. Plant Biology, 57(2): 99-104.

Cheong, M.L.S and V.M.R. Sanmukhiya. (2013). Phylogeny of Syzygium species using morphological, RAPD and ISSR markers. International Journal of Agricultural and Biology. 15: 511-516.

Das, S., A. Chattopadhyay, S. B. Chattopadhyay, S. Dutta, and P. Hazra. (2012). Genetic parameters and path analysis of yield and its components in okra at different sowing dates in the gangetic plains of eastern India. African Journal of Biotechnology, 11(95): 16132-16141.

Dilnesaw, Z., A. Seltene, and A. Getahun. (2013). Genetic variability and heritability of Soybean (*Glycine max* (L.) Merrill) genotypes in Pawe district, Metekel Zone, Benishangule Gumuz regional state, northwestern Ethiopia. Wudpecker Journal of Agricultural Research, 2 (9): 240-245.

Freitas, R. G., L. A. S. Dias, P. M. R. Cardoso, A. B. Evaristo, M. F. Silva and N. M. Araujo. (2016). Diversity and genetic parameter estimates for yield and its components in *Jatropha curcas* L. Genetic and Molecular Research, 15 (1): 1-10.

Idahosa, D. O., J. E. Alika, and A. U. Omeregie. (2010). Genetic variability, heritability and expected genetic advances as indices for yield and yield components selection in cowpea (*Vigna unguiculata* (L.) Walp). Academia Arena, 2(5): 22-26.

Jalata, Z., A. Ayana, and H. Zeleke. (2011). Variability, heritability and genetic advance for some yield and yield related traits in Ethiopian barley (*Hordeum vulgare* L.) landraces and crosses. International Journal of Plant Breeding and Genetics. 5 (11): 44-52.

Khan, S., Vaishali and V. Sharma. (2010). Genetic differentiation and diversity analysis of medicinal tree *Syzygium cumini* (Myrtaceae) from ecologically different regions of India. Physiol. Mol. Biol. Plants. 16(2): 149-158.

Manju, P. R., and I. Sreelathakumary. (2002). Genetic variability, heritability and genetic advance in hot chilli (*Capsicum chinenseja* (Q.)). Journal of   Tropical Agriculture. 40: 4-6.

Mc. Whirter   KS. (1979). Breeding of Cross Pollinated Crops. P. 79-110. *In*. R. Knight (eds). Plant Breeding.AA VCS, Brisbane.

Rahim, M. A., A. A. Mia, F. Mahmud, N. Zeba, and K. S. Afrin. (2010). Genetic variability, character association and genetic divergence in Mungbean (*Vigna radiata* L. Wilczek). Plant Omics Journal, 3 (1): 1-6.

Risvy, A. (2013). Morphological and molecular characterization of wax jambu (*Syzygium samarangense*). Unpublished master`s thesis, Bangladesh Agricultural University, Mymensingh.

Roychowdhury, R., S. Patta, M. Haque, T. K. Mukherjee, D. Maji, P. Gupta, D. Das and J. Tah. (2012). Effect of EMS on genetic parameters and selection scope for yield attributes in M_2 mugbean (*Vigna radiata* L.) genotypes. Romanian Journal of Biology. Plant Biology, 57(2): 87-98.

Singh, J.P., AK. Singh, A. Bajpai, I. Z. Ahmad. (2014). Comparative analysis of DNA polymorphisms and phylogenetic relationships among *Syzygium cumini* Skeels based on phenotypic characters and RAPD technique. Bioinformation. 10(4): 201-208.

Singh RK, and B.D. Chaudhary. (1979). Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publisher, New Delhi. p : 52 - 53.

Steel RGD, danJ.H. Torrie. (1989). Prinsip dan Prosedur Statistik (terjemahan oleh Bambang Sumantri). P.T. Gramedia. Jakarta.

Sujata, B., G. T. Basavaraja, and P. M. Salimath. (2011). Evaluation of narrow leaflet genotypes and genetic variability in segregating generation of soybean (*Glycine max* (L) Merrill). Electronic Journal of Plant Breeding, 2 (1): 124-131.

Verheij, E. W. M. And R. E. Coronel. (1992). Plant resources of South-East Asia. No 2. Edible fruits and nuts. Pudoc. Wageningen. 446 p.

Wahdah   R,   A. Baihaki, R. Setiamihardja, dan G. Suryatmana. (1996). Variability and heritability of accumulation rate of dry matter of on soybean (written in Indonesian language). *Zuriat*. 7(2) : 92 – 98.

Yaacob, O. And S. Subhadrabandhu. (1995). The production of economic fruits in South-East Asia. Oxford University Press, Kuala Lumpur. 419 p.

Zhigilla, D. A., A. A. Abdulrahaman, O. S. Kolawole, and F. A. Oladele. (2014). Fruit morphology as taxonomic features in five varieties of *Capsicum annum* L. Solanaceae. Journal of Botany, 1-6.