Estimation Of Genetic Parameters And Clustering Of Some Melon (*Cucumis melo* L) Strains Based On Qualitative And Quantitative Characteristics

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Abstract. Plant breeding programs in assembling high yielding varieties of melon need to know the qualitative and quantitative characters. The superior melon plants that people are interested in are fresh fruit, sweet taste, thick and durable fruit flesh. The study was to obtain character nine of strains melon, clustering analysis, determine the estimated value of genetic diversity and determine potential melon strains for future breeding programs. The research method was a field experiment in a Completely Randomized Block Design with a single factor and three replications. The treatments used were 9 strains of melons DS-1-2-10-21-11, DS-1-2-10-21-22, DS-1-2-10-21-31, DNG-1-47-13 , DNG-1-47-22, DNG-1-47-31, DNG-1-47-32, APL-11 and APL-12. The data were analyzed using Analysis of variance followed by Duncan's Multiple Range Test (DMRT) with a level 5%. Estimation of genetic diversity is done by calculating the coefficient of diversity and heritability values in a broad sense. Clustering was analyzed using the Agglomerative Hierarchical Clustering Method. The coefficient of similarity between strains was measured using the Euclidian Distance measurement transformation matrix. The character of the melon strains 1-2-10-21-31 is shorter, the stem diameter is large, the female flowering ages faster, the fruit diameter is large and the fruit flesh is thick. There are three clusters formed based on parameters. Variable plant height at 2 wap has a wide range of genetic diversity coefficients. A potential strains for further breeding programs is DS-1-2-10-21-31. Keywords : Genetic parameters, Melon strains, Qualitative characteristics, Quanlitative characteristics,Clustering analysis.

1 Introduction

Melon is a fruit plant that is sweet, fresh, contains vitamins A, B, and C, as well as protein, calcium, and phosphorus which has the potential to be developed and cultivated widely.

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Based on data from the Central Bureau of Statistics national melon production has increased over the 2018-2020 range. National production reached 118,708 tons in 2018, in 2019 it reached 3,397 tons, and in 2020 it increased by 16,072 tons [1]. Data from the Subdirectorate of Horticultural Statistics shows that the average productivity of melons has decreased, namely 18.55 tons/ha-1 (2019) down to 16.51 tons/ ha-1 [2]. Community demand for melon plants is increasing along with population growth. Increased production and cultivation of melon plants requires seeds with superior qualitative and quantitative properties. Efforts are being made to support the development of superior melon seeds through breeding programs. The superior characteristics expected of melon plants are high productivity, sweet fruit taste, early harvest time, long shelf life, fresh and smooth fruit appearance, and pest and disease resistance.

Morphological characters related to quality can be identified by observing the qualitative properties possessed by plants. The qualitative characters are influenced by many genes or slightly influenced by the environment. Research conducted by Sari et al [3] on the appearance of prospective melon hybrid varieties stated that there were several characters related to quality such as leaf shape, leaf color, fruit shape, net distribution, net intensity, and fruit flesh color. Franco et al. 2001 cit Novita et al [4] that studies on phenotype and genetic diversity are important to identify groups with the same genetic heritage for conservation, evaluation and use of genetic resources. How much phenotypic diversity will be inherited is measured by the heritability value.

Establishment of plant hybrids with superior morpho-physiological characteristics is the goal of a breeding program. Parental differences from different lines with far apart genetic distances provide the potential to form hybrid characters due to heterosis effects. The heterosis effect is a phenomenon in which the offspring of a cross between species show better morphological and physiological appearance compared to their parents. Two theories that are often used in heterosis effects are "dominance", in which the dominant alleles at a locus are complementary and "over-dominance" in which interactions between different alleles occur in hybrids resulting in an increase in plant vigor (physiological or morphological).[5] The degree of genomic differences between individuals within a species or population can be used as a basis for parental determination. This is because the greater degree among the selected parents, the greater of heterosis effect will be. The expression of hybrids is expanding along with an increase in genetic distance between parental inbreds, so that analysis of distances between strains or genomes can be a component of supporting analysis in determining parental inbreds.[5]

Information on genetic diversity is important to determine potential genotypes to be used as parents in hybrid breeding programs and improvement of melon cultivars through crosses. This study aims: to determine the growth, flowering and fruit of characteristics nine melon strains, to determine the estimated value of genetic diversity, heritability and clustering between strains formed by clustering analysis. Based on the research results, it is expected to be able recommend potential melon plant strains for further breeding programs.

2 Methods

The research was conducted at the SG commerce green house, the plants were grown hydroponically. The research method used a Complete Randomized Block Design with a single factor and three replications. The treatments used were 9 melon strains: DS-1-2-10-21-11, DS-1-2-10-21-22, DS-1-2-10-21-31, DNG-1-47 -13, DNG-1-47-22, DNG-1-47-31, DNG-1-47-32, APL-11 and APL-12. Each experimental unit contained 10 plants, with 3 sample plants.

The research materials were 9 strains of melon, cocopeat, AB Mix fertilizer, vegetable pesticides, Abamectin 36 g/l, Metomil 40%, Propineb 70%, Propamokarb hydrochloride 722 g/l, Difeneconazole 250 g/l, and Prefenofos 500 g/l. Research tools include: ruler, caliper, oil paper, tweezers, ziplock plastic, planter bag, scissors, sprayer, roll meter, timer, analytical balance, seedling tray, rope, sensor, PVC pipe, drip irrigation installation.

Activities include preparation of planting material, seeding, preparation of a fertigation system for transplanting, maintenance, harvesting, and data collection. Planting material in the form of melon seeds from several strains was sown in trays with cocopeat growing media. Then transplanted at 17 dap in a plantera bag containing

Plant maintenance includes twisting the main stem, pruning shoots on the 9th – 13th node, and controlling pests and diseases. Weed control is carried out physically by removing weeds around the planting area. Pest control is carried out physically using yellow sticky traps and chemically using insecticides. Pest and disease control is carried out by spraying insecticides with the active ingredients Metomil 40%, Abamectin 36 g/l, and Prefenofos 500 g/l; as well as fungicides with active ingredients Propineb 70%, Propamokacar hydrochloride 722 g/l, and Difenoconazole 250 g/l.

Harvesting is done when the fruit is around ± 60 – 75 HST, with the criteria that the plant has shown wilting of the leaves and color of the fruit has been fully formed. Harvesting is done by cutting the fruit stalks and leaving fruit stalks to form the letter "T" using a scissors/cutter. Parameters observed included growth characters (plant height, number of leaves, stem diameter), flower characters (male flowering age, female flowering ages, harvesting age) and fruit characters (fruit diameter, fruit weight, fruit flesh thickness and sweetness level).

Observational data were analyzed using Analysis Variants. To find out the significant difference between treatments, it was tested with the Duncans Multiple Range Test at a significance level at 5%. Calculation of genetic diversity coefficients, broad meaning heritability value and clustering formation using the Agglomerative Hierarchical Clustering Analysis method. The similarity coefficient between strains is measured using the Euclidian Distance measurement transformation matrix.

3 Result and discussion

The mean values of plant height at 2 wap, 4 wap, number of leaves at 2 wap, 4 wap, stem diameter at 6 wap in Table 1. The variable mean of plant height at 2 wap old showed that the DNG-1-42-32 strains was significantly higher, compared to strains DS-1-2-10-21-11, DS-1-2-10-21-22, DS-1-2-10-21-31, DNG-1-47-13, DNG- 1-42-31, APL-11 and APL-12 but not significantly different from DNG-1-47-22. Plant height at 4 wap showed that the DNG-1-42-31 strains was significantly higher than the DNG-1-47-13 strains. Yield characters of variable plant height at 2 WAP showed differences between the strains used. This shows that the differences are caused by factors from each of the genotypes of the strains tested. On the other hand, for the variable yield characters of plant height at age 4 wap the differences between lines were not too obvious. This is reinforced by the results of calculating heritability in a broad sense and the coefficients of genetic diversity in table 4.

Table 1. Average plant height, number of leaves and stem diameter (cm)

strains	PH 2 wap (cm)	PH 4 wap (cm)	NL 2 wap (pcs)	NL 4 wap (pcs)	SD 6 wap (cm)
DS-1-2-10-21-11	29,08 cd	140,07 ab	200,68 ab	25,11 bcd	5,52 ab

DS-1-2-10-21-22	34,43 bc	137,62 ab	187,07 b	25,00 bcd	6,24 a
DS-1-2-10-21-31	17,68 e	132,74 ab	184,12 b	25,67 abc	5,79 ab
DNG-1-47-13	20,22 de	122,81 b	175,06 b	21,44 d	5,11 b
DNG-1-47-22	40,06 ab	142,60 ab	191,84 ab	29,44 a	5,23 b
DNG-1-42-31	27,81 cd	164,60 a	239,50 a	28,67 ab	4,88 b
DNG-1-42-32	44,76 a	159,44 ab	195,58 ab	28,56 ab	5,45 ab
APL-11	36,28 bc	136,88 ab	195,24 ab	21,89 cd	5,40 ab
APL-12	35,08 bc	152,98 ab	200,78 ab	24,44 cd	5,26 b

Note: PH : plant height, NL : number of leaves, SD : stem diameter, wap : weeks after plant.The mean value followed by different letters in the same column showed a significantly different between genotype base on DMRT level of 0.05

The mean number of leaves at 2 wap and 4 wap showed that the DNG-1-47-22 strains was significantly larger than the other seven strains. This indicates that the potential of the two strains to increase photosynthate production is higher among the tested strains. Along with the increase in the formation of leaves as photosynthetic organs, photosynthate will also increase [6].

The aim of breeding in increasing the quality and quantity of plants can lead one of them to the characters related to the rate of photosynthesis and increase in biomass. Several aspects can be used as breeding targets including the rate of growth and development of leaves, the pattern of canopy arrangement, and the duration of leaf area in receiving sunlight. [7]

The variable mean stem diameter at 6 wap on the DS-1-2-10-21-22 strains was significantly greater than DNG-1-47-13, DNG-1-47-22, DNG-1-42-31 and APL-12, but was not significantly different with DS-1-2-10-21-11, DS-1-2-10-21-31, DNG-1-42-32 , and APL-11 strains. Melon strain DS-1-2-10-21-22 has a genotype that affects phenotype of the plant shown by the growth of a larger and stronger stem diameter. Growth can be elastic and reversible, for example what occurs in cell wall deformation which is plastic. This reversible nature of growth is often found as a result of interactions between genotypes and environment. The diameter of the fruit or stem increases during the growth period, but decreases when the evaporation rate in the environment is high. The availability of nutrients also affects increase in volume cells, number of cells, and tissues plant. [8]

The mean values of male flowering age, female flowering age and harvesting age in Table 2.

Table 2. Average male flowering age, female flowering age, and harvest age

strains	MFA (day)	FFA (day)	HA (day)
DS-1-2-10-21-11	28,00 b	37,00 a	69,22 bcd
DS-1-2-10-21-22	27,00 a	37,33 ab	69,78 cd

DS-1-2-10-21-31	28,00 b	36,67 a	70,44 d
DNG-1-47-13	34,00 d	41,67 cd	69,89 cd
DNG-1-47-22	29,67 c	40,33 c	64,89 a
DNG-1-42-31	32,67 d	42,67 d	67,00 abc
DNG-1-42-32	33,33 d	42,67 d	64,67 a
APL-11	30,33 c	38,67 b	66,00 ab
APL-12	30,33 c	38,67 b	65,33 ab

Note: MFA: Male Flowering Age; FFA: Female Flowering Age, HA: Harvesting Age; The mean value followed by different letters in the same column showed a significantly different between genotype base on DMRT level of 0.05

Melon strains DS-1-2-10-21-11, DS-1-2-10-21-22 and DS-1-2-10-21-31 showed a faster age of male and female flower formation than the other six genotype. Meanwhile, on the character of harvesting age, lines DNG-1-47-22 and DNG-1-42-32 showed a faster harvesting age than the other seven of genotype melon. Expression of deep genotype showing short flowering and harvest times is one of the targets in establishing early maturing varieties in plants.

The formation of flowers in plants is a process that indicates the right time and conditions for plants to form reproductive organs. The exact time of formation flowers can be influenced by the interaction between plants and the environment as well as competition in the use of photosynthates during transition from vegetative to flowering phase. Changes on ethylene levels affect the genetic trajectory that affects the signal regulation of flowering time (Simpson and Dean *cit.* Iqbal *et al.)* [9].

The mean values of fruit diameter, the thickness of fruit flesh, fruit weight, and fructose level can be seen in table 3. The DS-1-2-10-21-31 strain had a significantly larger fruit diameter and weight, but was not significantly different from the DS-1-2-10-21-11 and DS-1 -2 -10-21 – 22 strains. This indicates that there is a high potential for these strains to increase the size of the fruit circumference. The size of the fruit circumference is one of the parameters that can be included in the direction of increasing the quality of fruit yields. An increase in fruit size can be form of an increase in the number, volume, and density of cells in fruits. The direction of breeding to increase fruit size is the main thing, considering that genetic component of influences it is very wide (Janick and Moore *cit.* Callaha) [10]. The character of fruit weight can be influenced by a number of factors, including the potential genotype, environmental influences, and cultivation techniques. Plant phenotype is the interaction between genotype and environment.

Table 3. Mean fruit diameters, the thickness of fruit flesh, fruit weight and fructose level

Strains	FD (cm)	TFT (cm)	FW (g)	FD (^{o}brix)
DS-1-2-10-21-11	8,73 abc	1,97 ab	393,16 ab	9,07 c
DS-1-2-10-21-22	8,99 ab	2,25 abc	400,58 ab	8,62 c
DS-1-2-10-21-31	9,53 a	2,52 ab	448,14 a	9,64 c
DNG-1-47-13	8,47 bc	2,41 ab	362,44 bcd	8,89 c
DNG-1-47-22	7,67 c	2,13 bc	315,59 cd	8,67 c

DNG-1-42-31	7,98 bc	1,88 c	296,79 cd	8,11 c
DNG-1-42-32	7,76 c	1,94 c	291,16 d	11,44 b
APL-11	8,62 abc	2,20 abc	368,91 bc	12,00 ab
APL-12	8,52 bc	2,55 a	352,66 bcd	13,11 a

Note: FD: Fruit diameters, TFT : The thickness of fruit flesh, FW : Fruit weight, FL : Fructose level. The mean value followed by different letters in the same column showed a significantly different between genotype base on DMRT level of 0.05

The APL-12 strains has thickness flesh and a higher level of fructose than other strains. The thickness of the fruit flesh is one of variables in quality of melon fruit. The thickness of fruit flesh caused by the amount of fruit maintenance each plant. Maximum accumulation photosynthate in fruits can increase the thickness of the flesh which will directly increase fruit weight. [11]

The melon strains APL-12 and APL-11 respectively showed a higher level of fructose than other seven strains. This shows that there is potential in efforts to increase the amount of sugar contained in fruit juice. Sucrose, fructose, and glucose levels determine the sweet taste of fruit . [10]

There are two types of melon plants based on the accumulation of sucrose in the fruit, namely the type of plant with a high level of accumulation of sucrose and the type of plant with a low level of accumulation of sucrose. The first type shows a low concentration of sucrose in the early stages of fruit development, while the levels of fructose and glucose are relatively high. During later stages, sucrose accumulates rapidly to levels equal to or higher than hexose in some genotypes. Whereas in the low sucrose accumulation type, the sucrose concentration is maintained at a low level throughout all phases of fruit development [12].
The of the determinants of the success genetic improvement of hopeful characters is the existence of wide genetic diversity in these characters and inherited with high heritability values. The broad meaning of heritability can be estimated in indirect way from estimating the variance component [13] . The heritability value of the observed characters ranges from 15.84-96.83%. Based on the heritability value, nine characters are suspected to be inherited with a high heritability predictive value (57.67-96.83%), three characters are inherited with a fairly high heritability predictive value (24.64-44.42%) and two characters are inherited with a low heritability predictive value (15.84-16.51%). According to Wicaksana [14] characters that have high heritability values indicate that genetic factors are more dominant in the characters displayed by plants than environmental factors

The Coefficient of Genetic Diversity (CGD) values obtained for all the various variables are as in table 4, showing that the plant height of 2 wap has a high Coefficient of Genetic Diversity value of 26.75%. Coefficient of Genetic Diversity values are rather broad in the variable number of leaves 2 wap, number of leaves 4 wap, fruit weight, thickness of fruit flesh and fructose level. Based on the information on the alleged genetic diversity of 14 characters and their heritability values, selection can be made based on the characters of plant height 2 wap, thickness of fruit flesh, level of fructose and fruit weight.

Table 4. Predicted Value of Genetic Parameters, heritability

SK	$\sigma^2 g$	$\sigma^2 p$	$h^2 bs$ (%)	KKG (%)
PH 2 wap (cm)	71,970	92,483	77,82 h	26,753 b

PH 4 wap (cm)	66,259	401,344	16,51 l	5,680 n
PH 6 wap (cm)	117,751	743,513	15,84 l	5,518 n
NL 2 wap (pcs)	1,087	1,530	71,08 h	15,756 rb
NL 4 wap (pcs)	6,758	11,195	60,36 h	10.163 rb
NL 6 wap (pcs)	8,872	20,820	42,62 he	8,010 n
SD 6 wap (cm)	0,079	0,320	24,64 he	5,1762 n
MFA (day)	6,222	6,426	96,83 h	8,213 n
FFA (day)	5,491	6,194	88,64 h	5,930 n
HA (day)	4,475	7,760	57,67 h	3,135 n
FW (g)	2.181,771	3.642,678	59,89 h	13,017 rb
FD (cm)	0,253	0,569	44,42 he	5,947 n
TFT (cm)	0,051	0,088	57,78 h	10,237 rb
FL (^{o}brix)	2,877	3,703	77,70 h	17,045 rb

Notes : PH : plant height, NL : number of leaves, SD : stem diameter, MFA: Male Flowering Age; FFA: Female Flowering Age, HA: Harvesting Age, FD: Fruit diameters, TFT : The thickness of fruit flesh, FW : Fruit weight, FL : Fructose level, wap : weeks after plant. $\sigma^2 g$: Genetic Variance, $\sigma^2 p$: Phenotypic Variance, $h^2 bs$: Heritability in a broad sense, h : high, he : high enough, l : low, b: broad, rb : rather broad, n : narrow

Cluster analysis is a form of exploratory analysis aimed at grouping a multivariate data set into several groups or clusters so that the data in one group have similarities or differences compared to other groups. The cluster analysis assumption used is based on quantitative and qualitative variables which are a description of the phenotypic characteristics of the genotype and environmental influences. Clustering analysis can be performed on various types of data, including genetic data, but is not specifically related to measuring genetic distances. Analysis of genetic distance it self in the context of biology is the measurement of two loci on the same or different chromosomes based on the frequency of recombination between the two loci during meiosis. [15]

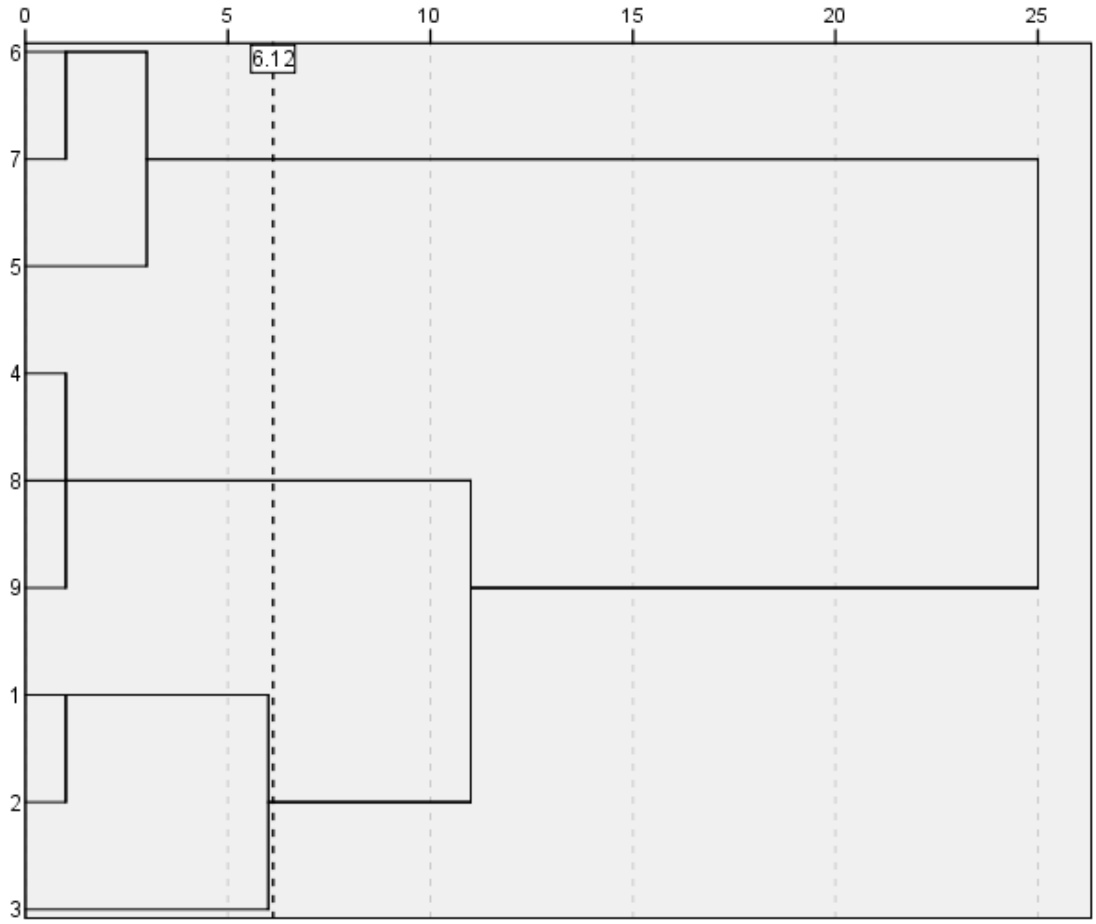

Fig. 1 Dendrogram of Fruit Yield Clustering Parameters.

Note : 1 = DS-1-2-10-21-11, 2 = DS-1-2-10-21-22, 3= , 4= DNG-1-47-13, 5= DNG-1-47-22, 6= DNG-1-42-31, 7= DNG-1-42-32, 8= APL-11, 9= APL-12

The fruit yield parameters consisted of fruit weight, fruit vertical circumference, fruit horizontal circumference, fruit diameter, the thickness of fruit, fructose level, fruit skin color, and fruit flesh color. Skin and fruit color transformation according to D'Andrade and Romney [16]. The similarity coefficient values of 9 melon strains using the multivariate approach range from 0-25, with a coefficient of 6.12 there three clusters can be formed. The first cluster group consists of the DNG-1-47-31, DNG-1-47-32, and DNG-1-47-22 strains. The second cluster group formed consisted of DNG-1-47-13, APL-11, and APL-12 strains. The third cluster group consists of DS-1-2-10-21-11, DS-1-2-10-21-22, and DS-1-2-10-21-31 strains.

The obtained Dendrogram showed the same number of genotype in the three clusters. Melon plants are cross-pollinated plants, so there will be a high chance that the parental genotypes and F1 selfing can be in different groups. This is thought to be due to segregation in offspring from heterozygous parents [4]. In addition, the effect of heterosis depends on the degree of genetic difference between the parents and the complementary nature of a parameter in the two parents. In general, the greater the genetic differences between parents, the greater the effect of heterosis. [13]

A cross between the two parents with a low genetic distance could theoretically provide a higher phenotypic variance compared to the parents with a high genetic distance. Progeny variance increases in parental crosses with greater distances due to the higher number of segregating loci. [17]

4 Conclusions

The character of the melon strains 1-2-10-21-31 is shorter, the stem diameter is large, the female flowering ages faster, the fruit diameter is large and the fruit flesh is thick. There are three clusters formed based on fruit yield. The characters with the estimated value of the oefficient of broad genetic diversity and high heritability values were found in plant height 2 wap. The melon was DS-1-2-10-21-31 of potential strains that can be used in further breeding programs.

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