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Characterization and Similarity Analysis of 15 Tomato Genotypes in Lowlands Based on Morphological Characters

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Abstract

This study aimed to obtain information about the characteristics of 15 genotypes and to study a genetic similarity of each genotype that will be used for producing superior tomato varieties in lowlands. The research was conducted from March to August 2012 at the Experimental Field Leuwikopo Bogor Agricultural University, Darmaga Bogor. The experiment used The Randomized Complete Block Design (RCBD) using a single factor of genotype with three replications. Characterization and similarity analysis used the method of principal component analysis and cluster analysis. Based on principal component analysis and cluster analysis of tomato genotypes, it can be classified into three groups: group I (IPBT1, IPBT4, IPBT8, IPBT13, IPBT58, IPBT83 and IPBT84), Group II (IPBT3, IPBT23, IPBT30, IPBT33, IPBT34, IPBT53 and IPBT57) and group III (IPBT80). Characters with an influence on the genetic diversity of each component are the size of the cork layer between the scar stalk and the size of the center of the fruit in transverse slices. The genotypes with a high genetic similarity were IPBT1 and IPBT8, while IPBT30 with IPBT80 had a low genetic similarity.

Keywords: genotype, characterization, genetic similarity, morphology, tomato

A. Introduction

The low productivity of lowland tomatoes encourages breeders to improve tomato characters in lowlands. Efforts to improve these characters require several stages such as the expansion of genetic diversity. High genetic diversity greatly determines the success of breeding to get a superior variety and also provides a great opportunity to get the best combination of crossings with a combination of good characters. Thus, the collected genotypes were then characterized as well as analyzed for diversity and similarity to facilitate plant breeding activities.

Analysis of genetic similarity is conducted using the principal component analysis (PCA) and cluster analysis. The use of both methods is often performed to see the classification between genotypes. Genotypes belonging to a group or cluster indicate a close similarity or close genetic relationship, whereas intergroup genotypes indicate a distant similarity or distant genetic relationship. The analysis of the principal component and cluster is often used for various plants such as tomatoes (Albrecht *et al*., 2010, Aguire and Cabrera 2012) and chili (Yunianti *et al*., 2010).

The objective of the study was to obtain information about the characteristics of 15 genotypes as well as to obtain genetic similarity of each genotype to be used for the assembling of superior tomato varieties in lowlands.

B. Methodology

The research was conducted from March to August 2012 at the Experimental Field Leuwikopo Bogor Agricultural University, Dramaga, Bogor (230 m asl). Plant material used was 15 genotypes of tomato collection of Tomato Breeding Team of Genetics and Plant Breeding Division, Department of Agronomy and Horticulture Bogor Agricultural University namely; IPBT1, IPBT3, IPBT4, IPBT8, IPBT13, IPBT23, IPBT30, IPBT33, IPBT34, IPBT53, IPBT57, IPBT58, IPBT80, IPBT83, and IPBT84. The genotypes were collected from landraces in several locations in Indonesia and IPB collections.

The research was conducted using The Randomized Complete Block Design (RCB) with a single-factor of 15 tomato genotypes with three replications so that there were 45 experimental units. Each experimental unit consisted of 20 plants and 10 of the plants used as plant samples.

Preparation of land and beds was performed at the same time during the seeding activities. Planting was carried out at 30 days after seedling. Plots of beds were made with the size of 5 m x 1 m for each experimental unit with a distance between beds of 50 cm. Furthermore, each bed was treated with 20 kg manure and 0.5 kg dolomite lime.

Maintenance activities included watering, fertilization, pesticide application and weeding. Fertilization was carried out once a week after the plants aged one week after planting (1 WAP) using NPK fertilizer (16:16:16) with a concentration of 10 g l^{-1} as much as 250 ml/plant. Pesticide application was carried out twice a week using a fungicide with an active compound of 80% mancozeb and 70% prophinep with a concentration of 2 g l^{-1}, insecticide with the active compound of profenofos 500 g l^{-1} with a concentration 2 ml l^{-1} and acaricides with active compound of dicofol with concentration 2 ml l^{-1}. Weed control was carried out manually. Harvesting was performed to the fruit with the criteria of yellow reddish, twice a week for six weeks.

Characterization was divided into qualitative and quantitative characteristics. Qualitative characters refer to The Individual Testing Guides in the form of novelty, uniqueness as well as tomato Uniformity and Stability (PPVT 2007) and UPOV (2011). Quantitative characters included plant height, length and width of the leaf (in a third of the middle plant), the age of flowering, harvest age, the number of fruits per plant, fruit weight per plant, fruit length, fruit diameter, fruit pulp, fruit hardness and moisture content. The value of the quantitative character was set based on Descriptor for Tomato (*Lycopersicon* spp.) for quantitative characters (IPGRI 1996).

The pattern of clustering and diversity between genotypes was obtained based on qualitative and quantitative character data analyzed using Principal Component Analysis and Cluster Analysis using the software of SPSS version 20.

C. Result and Discussion

1. Principal Component Analysis

The numerous number of character observation in the characterization can be reduced to a few principal components that were in smaller dimensions and independent. The number of principal components formed can be determined by the Eigenvalue. According to Santoso

(2004), the Eigenvalue indicates the relative importance of each factor in calculating the diversity of the variables analyzed. The calculation of the amount of the principal components formed based on the valid Eigenvalue which is more than one whereas the value less than one might be ignored (Simamora 2005; Yunianti *et al*., 2007; Maxisella *et al*., 2008; Bhartaya *et al*., 2011). Based on the principal component analysis with 32 characters of 100% diversity, it formed 14 components, however, the number of valid components based on Eigenvalue was only 8 components with the diversity percentage of 90.96% (Table 1). The component with the largest eigenvalue was obtained by component 1 of 10.080, while component 2 reached 5,339. Each genotype can be grouped according to each component. The number of Principal Components (PC) was used to describe the diversity of characters based on the cumulative proportions of total diversity (Yunianti *et al*., 2007 and Mattjik and Sumertajaya 2011, Undang *et al*., 2015). The grouping of each genotype based on the proportion of total diversity. The components with the largest proportion of diversity are component 1 and component 2 which reached 48.18%, thus, grouping was made based on components 1 and component 2 (Figure 1).

Tabel 1. The Eigenvalue of each component based on principal component analysis

Component	Eigenvalue			Quadratic Root Extraction		
	Total	% Diversity	% Cumulative	Total	% Diversity	% Cumulative
1	10.080	31.501	31.50	10.080	31.501	31.501
2	5.339	16.683	48.18	5.339	16.683	48.185
3	3.801	11.879	60.06	3.801	11.879	60.064
4	2.663	8.322	68.38	2.663	8.322	68.386
5	2.611	8.159	76.54	2.611	8.159	76.545
6	1.823	5.697	82.24	1.823	5.697	82.242
7	1.659	5.185	87.42	1.659	5.185	87.428
8	1.131	3.534	90.96	1.131	3.534	90.961

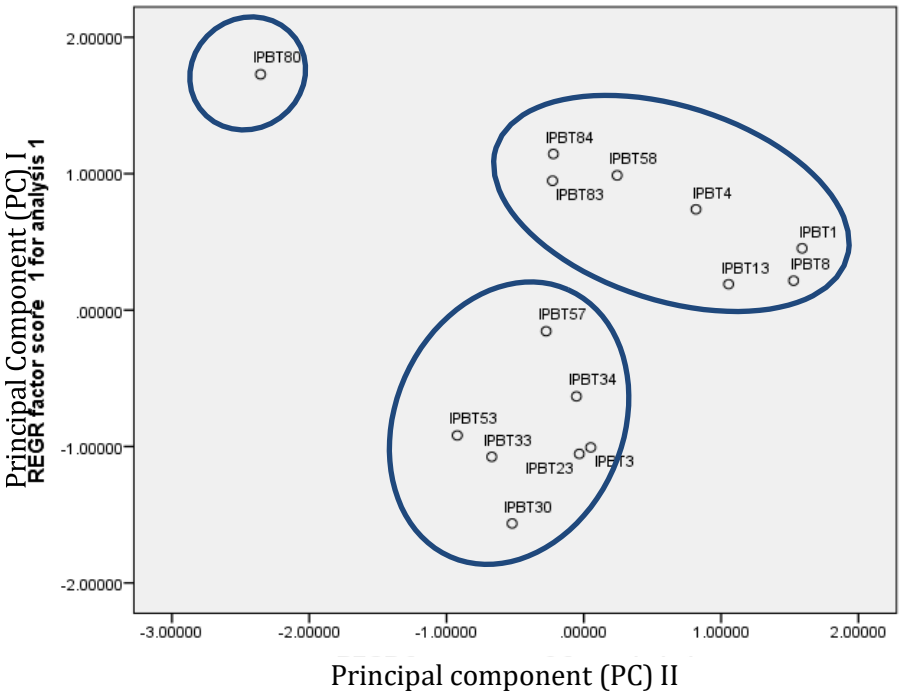

Figure1. Cluster of 15 tomato genotypes based on PC I and PC II

Characters that affect genetic diversity in the principal components are determined by the value of eigenvector. The characteristic vector value > 0.5 indicates that the character affected the diversity (Yunianti *et al*., 2007; Maxisella *et al*., 2008; Undang *et al*., 2015). The characters affecting principal component (PC) I consisted of 9 characters including fruit size, fruit depression at the end of the fruit stalk, the size of the cork layer between the fruit stalk, the size of the middle of the fruit in transverse slices, fruit length, fruit diameter, thickness of the pulp, the length and width of leaf . PC II consisted of 8 characters including the division of leaf blade, abscission layer, pedicel length, size of the cork layer between the fruit stalk, The size of the scar

at the end of pistil stalk, the size of the middle of the fruit in transverse slices, the number of fruit cavities and the color of ripe fruit (Table 2). Based on the eigenvector of two principal components, it indicated that there are two characters affecting the genetic diversity on each component that were the size of the cork layer between the scar stalk and the size of the centre of the fruit in transverse slices.

Table 2. Eigenvector of two principal components

Character	Component	
	I	II
Leaves position	0.463	-0.381
Division of leaf blade	-0.586	**0.628**
Intensity of green leaf color	0.272	-0.064
The position of leaflet on the main leaf bone	-0.288	0.494
Type of flower bunches	0.189	-0.321
Branch on flower bunches	-0.258	0.269
Abscission layer	-0.478	**0.651**
Pedicel length	-0.503	**0.540**
Size of fruit	**0.872**	0.160
The shape of the fruit in a longitudinal state	0.458	-0.050
Transverse slices	0.428	-0.695
Depression of fruit on the tip of the fruit stalk	**0.525**	0.434
The size of the cork layer between the fruit stalk	**0.682**	**0.577**
The size of the scar at the end of pistil stalk	-0.070	**0.606**
The shape of the fruit tip	-0.476	0.384
The size of the center of the fruit in transverse slices	**0.555**	**0.608**
The number of fruit cavities	-0.053	**0.601**
The shoulder of green fruit before fruit ripening	-0.761	-0.310
shoulder width of the green fruit	-0.761	-0.310
The intensity of green color on the shoulders of the fruit	-0.777	-0.310
The Intensity of green color of fruit	-0.233	-0.222
The color of ripe fruit	-0.530	**0.509**
The color of the pulp	-0.341	0.076
Number of fruits per plant	-0.814	-0.323
The weight of fruit per plant	0.346	0.401
Fruit length	**0.897**	0.292
Fruit diameter	**0.797**	0.317
Thickness of pulp	**0.812**	-0.256
flowering time	0.396	-0.211
Leaf length	**0.692**	-0.254
Leaf width	**0.680**	-0.218
Hardness of fruit	0.393	0.327

Note: bold numbers are the values of influential characters.

The tested genotypes was grouped into three groups based on PC I and PC II with a proportion of total diversity of 48.18% (Figure 12). Group I consisted of seven genotypes including IPBT1, IPBT4, IPBT8, IPBT13, IPBT58, IPBT83 and IPBT84. Group II consisted of seven genotypes including IPBT3, IPBT23, IPBT30, IPBT33, IPBT34, IPBT53 and IPBT57. Group III consisted of IPBT80. The genotypes clustered in one group had a high genetic similarity compared to the cluster that was not in one group.

2. Cluster Analysis

The similarity between genotypes can also be determined by Euclidean distance and able to form clusters which based on the dissimilarities level (Yunianti *et al*. 2007; Nisya 2010). The greater the value of the Euclidean distance between genotypes indicated the more low similarity of the genotype (Yunianti *et al*. 2007; Mattjik and Sumertajaya 2011). The cluster analysis of 15 genotypes obtained the Euclidean distance of 13.57-145.24 (Table 3). IPBT1 and IPBT8 had the smallest Euclidean distance of 13.57, while the largest Euclidean distance was obtained by IPBT30 and IPBT80 of 145.24. The Euclidean distance suggested that IPBT1 and IPBT8 had a low dissimilarity, whereas IPBT30 and IPBT80 had a high dissimilarity. The High and low of dissimilarity are reflected in the dendrogram presented in Figure 2. The value of

Euclidean distance of 13.57-145.24 scaled to 0-25 on the dendrogram. The cluster of genotypes which more closely to 0 indicated the genotype has a high genetic similarity or a low dissimilarity.

Table 3 Euclidean distance (Eigen Value) of each genotype based on cluster analysis

	Euclidean distance (Eigen value)														
Genotype	IPB T1	IPB T3	IPB T4	IPB T8	IPB T13	IPB T23	IPB T30	IPB T33	IPB T34	IPB T53	IPB T57	IPB T58	IPB T80	IPB T83	IPB T84
IPBT1	.00														
IPBT3	57.33	.00													
IPBT4	55.44	60.91	.00												
IPBT8	**13.57**	44.41	58.29	.00											
IPBT13	48.97	53.86	45.91	34.84	.00										
IPBT23	80.10	32.67	79.35	56.82	48.05	.00									
IPBT30	87.29	24.74	98.27	64.01	68.94	28.80	.00								
IPBT33	68.94	34.75	89.82	69.67	67.52	48.29	24.38	.00							
IPBT34	62.15	18.59	43.50	50.00	43.69	45.30	32.27	44.97	.00						
IPBT53	83.93	30.3	74.81	78.15	79.63	58.71	35.22	43.53	34.69	.00					
IPBT57	68.25	44.02	60.00	52.46	50.87	40.19	51.05	66.57	49.99	34.19	.00				
IPBT58	63.59	70.15	39.14	49.92	56.21	83.00	89.61	90.93	67.55	65.50	44.87	.00			
IPBT80	13.35	24.50	05.61	13.20	09.93	30.57	**45.24**	22.23	09.13	26.07	05.13	3.46	0		
IPBT83	2.32	9.05	7.61	5.67	2.98	7.09	6.52	7.78	0.98	8.53	1.83	0.84	3.76	00	
IPBT84	2.69	1.44	3.18	0.71	4.37	7.73	1.22	4.58	3.08	8.05	6.14	3.65	9.29	6.55	0

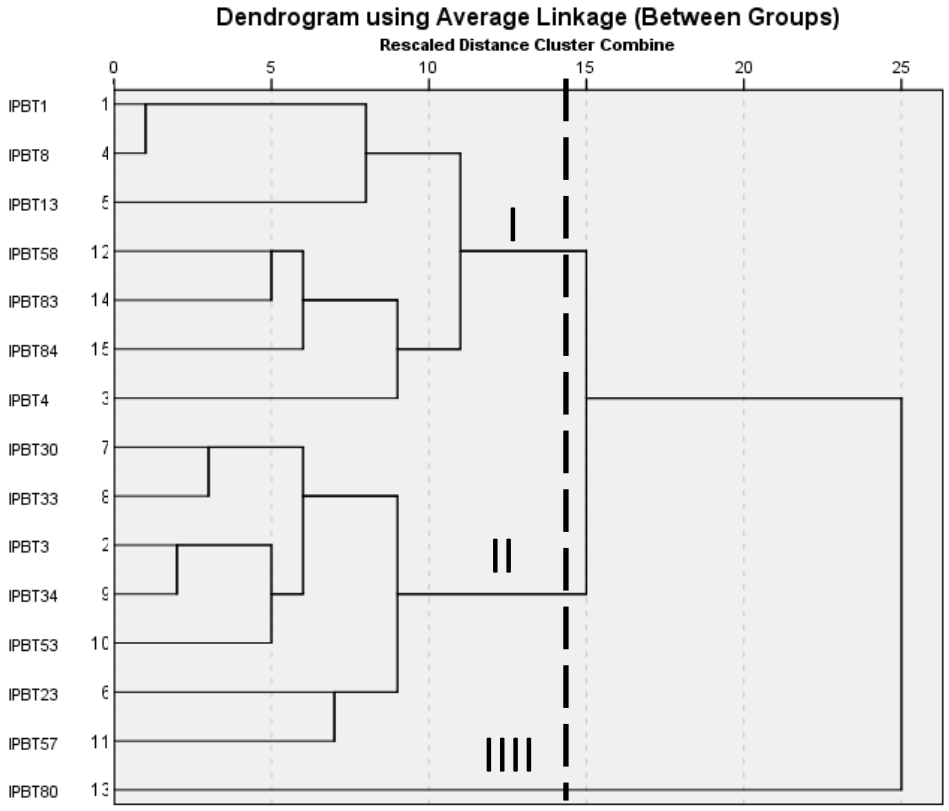

Figure2. Dendrogram analysis of 15 tomato genotypes

Cluster analysis on 15 tomato genotypes used 32 characters. Dissimilarity value (Euclidean distance) in dendrogram is the scaling of the original Euclidean distance (Appendix 3), for example, IPBT58 and IPBT83 had a Euclidean distance of 30.84 while IPBT3 and IPBT53 had a Euclidean distance of 30.36. Based on the original Euclidean distance, it was made resize with a maximum value of the Euclidean distance of 25 as presented in the dendrogram (Figure 2), thus the Euclidean distance between IPBT58 and IPBT83 as well as IPBT3 and IPBT53 were 5. On the dissimilarity value (Euclidean distance) 15, all tested genotypes could be grouped into three clusters. Cluster I consisted of seven genotypes including IPBT1, IPBT4, IPBT8, IPBT13, IPBT58, IPBT83 and IPBT84. Cluster II consisted of seven genotypes including IPBT3, IPBT23, IPBT30, IPBT33, IPBT34, IPBT53 and IPBT57. Cluster III was only one genotype of IPBT80. The grouping was the same as grouping produced by PC I and PC II.

D. Conclusion

The morphological characters of 15 genotypes are divided into three groups. Group 1 consists of IPBT1, IPBT4, IPBT8, IPBT13, IPBT58, IPBT83, and IPBT84, Group II consists of IPBT3, IPBT23, IPBT30, IPBT33, IPBT34, IPBT53, and IPBT57 as well as Group III consists of IPBT80. There are two characters that effect on the genetic diversity that exists on each component that are the size of the cork layer between the fruit stalk and the size of the middle of the fruit in a transverse slice. Genotypes with high genetic similarity are IPBT1 and IPBT8 while genotypes with low genetic similarity are IPBT30 and IPBT80.

E. Conclusion

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