Characterization of several collection genotypes of Cayenne Chili (Capsicum frustescens) in Aceh

S Hafsah1*, Nura1, M Rahmawati1, E Hayati1, M Syukur2 and Firdaus3

1 Department of Agrotechnology, Faculty of Agriculture, Universitas Syiah Kuala, Darussalam, Banda Aceh, 23111 Indonesia
2 Department of Agronomy and Horticulture, IPB University, Bogor, Indonesia
3 Assessment Institute of Agricultural Technology of Aceh, Banda Aceh, 23125, Indonesia

*E-mail: sitihafsah@unsyiah.ac.id

Abstract. The purpose of this study was to obtain information about genotypes characterization results of several IPB collection’s cayenne chili genotypes in Aceh. This research was conducted in the East Sector Experimental Field and the Laboratory of Genetics and Plant Breeding, Faculty of Agriculture, Syiah Kuala University from February 2019 to July 2019. This study used a one-factor randomized block design. This study used 11 IPB genotypes of cayenne chilli and 5 comparison varieties. Each treatment consisted of three replications and each experimental unit consisting of 20 plants. The result of cluster analysis on qualitative characters and quantitative characters in cayenne chilli produces two clusters. Cluster I consists of 10 genotypes which include F5 285290-237-6-1, F6 285290-6-10-1-1, F5 285290-290-2-1, F5 285290-290-9-1, F5 285290-290-9-3, F5 321290-40-2-1, F6 285290-123-6-15, F6 321290-252-10-8-4, F5 285290-38-6-3, F6 321290-252-10-8-2, Cluster II consists of five varieties and one genotype which includes the Bonita variety, Garut local varieties (290), Taruna (295), Cakra Putih (285) and Tabasco (321) and one tested genotype F6 321290-252-10-8-75. Mostly, the genotypes resulted from crossing has a different group with its parents, this is presumably due to the influence of genetic and environmental factors to the plant's growth.

1. Introduction
Cayenne chili (Capsicum frustescens L.) is a plant that is consumed by its fruit. Indonesian people consume a lot of cayenne chili both in raw form and as a food supplement. Cayenne chili contains many antioxidant vitamins such as vitamins A, C and E [1]. The capsaicin in chilies has a function as a source of spicy taste and as antibacterial [2]. The need for cayenne chilies increases continuously due to its use not only in the food sector, but also as raw material for medicine and cosmetics as well as an ornamental plant.

BPS data 2017 states that the productivity of cayenne chili in Aceh has fluctuated. This can be seen from the cayenne chili productivity in Aceh in 2014 of 13.87 tons ha−1 followed by an increase in 2015 of 16.36 tons ha−1 but in 2016 its productivity decreased to 15.17 tons ha−1. The decline of cayenne chili productivity in 2016 reached 7.08% from the previous year. The fluctuation on chili production is caused by the cayenne chili plant’s performance [3]. The performance of cayenne chili is influenced by genetic factors,
environmental factors and the interaction between them [4]. Chili plants that still have the tendency to cross-pollinate will have the potential to be pollinated by other pollens with different genetic makeup and causing high genetic diversity. This condition is one of the factors causing unstable production. Other obstacles in the development of chili plants in Indonesia are related to seed quality, cultivation techniques, pest and disease attacks, and the use of low yielding varieties [5]. Characterization of the chili genotype is one of the activities in the field of plant breeding. These activities include (i) collection of germplasm as a source of diversity, (ii) identification and characterization, (iii) increasing the diversity of germplasm, for example through crossing or by gene transfer, followed by (iv) a selection process, (v) testing and evaluation, (vi) release, distribution and commercialization of varieties. For the initial process of plant breeding activities, it is necessary to carry out the genotype characterization of chili plants. The purpose of this study was to obtain information on the qualitative and quantitative characters of chili plant germplasm and to classify genotypes based on qualitative and quantitative characters.

2. Materials and methods
This research was conducted at the East Sector Experimental Garden and observations were carried out at the Laboratory of Genetics and Plant Breeding, Faculty of Agriculture, Syiah Kuala University from February 2019 to July 2019. The experimental design used in this study was a one-factor randomized block design, namely genotype. This experiment used 11 IPB collection genotypes of cayenne chili and five comparison varieties. Each treatment consisted of three replications, so that there were 48 experimental units, each experimental unit consisting of 20 plants. Observations were made on five sample plants. Data on quantitative and qualitative variables were used for cluster analysis referring to Descriptors for Capsicum (IPGRI). The observed variables consist of quantitative and qualitative variables. The quantitative variables observed were plant height, dichotomous height, stem diameter, leaf width, leaf length, flowering age, harvest age, fruit skin thickness, fruit size, total weight per plant, weight per fruit, weight of 1000 seeds and productivity. The qualitative variables used were stem shape, stem color, leaf shape, leaf color, flower position, pistil color, anthers color, flower crown color, flower petal color, fruit shape, fruit tip shape, intermediate fruit color and ripe fruit color.

3. Results and discussion
Characterization is one of the basic methods in plant breeding to identify plant morphological characters that have the desired criteria for genetic improvement. The relationship between the characterization of the tested genotypes and some comparison varieties used for clustering is to make it easier for plant breeders to select parents prior to plant assembly to create New Superior Varieties. Genotypes that are in the same group or that have a high degree of similarity, so will not be made as parents, because crossing with genotypes that are in the same cluster will produce a low level of diversity. Meanwhile, plant breeders really expect a high level of diversity, making it easier to obtain the desired genetic characters. Therefore, the existence of clustering makes it easier for plant breeders to determine which genotypes are suitable to serve as parents in order to create high diversity.

3.1. Genotype test results tested
Measurement of stem diameter and dichotomous height was carried out at the first harvest. The stem diameter character in the genotype tested had the highest value on genotype F5 285290-237-6-1, F5 285290-290-2-1 and F6 285290-123-6-15 with an average value of 11.47 - 11.74 cm (Table 1). Plants that have a large stem diameter value will be stronger. Chili plants that are bearing fruit, the plants will be stronger to hold them, so that the stems or twigs do not break easily.

Measurement of dichotomous height, the genotype with the highest statistical value was genotype F5 285290-237-6-1 and F6 285290-123-6-15 which were significantly different from the five comparison
varieties (Table 1). [6] stated that the desired plant dichotomous height was approximately 20 cm. Plants with a dichotomous height that is too short, the fruit will be susceptible to disease, because the splash of rain water increases humidity. A dichotomous that is too short will also cause the fruit to become damaged or burnt due to direct contact with plastic mulch which reflects the heat of the sun.

Table 1. The mean value of the stem diameter and dichotomous height of the tested genotype against comparison varieties.

| Genotypes and comparison varieties | Parameters observed                  |
|-----------------------------------|--------------------------------------|
|                                   | Stem diameter (mm) | Dichotomous height (cm) |
| F5 285290-237-6-1                 | 11.74 c             | 13.30 cd               |
| F6 285290-6-10-1-1                | 9.77 b              | 10.19 bc               |
| F5 285290-290-2-1                 | 11.47 c             | 10.7 c                 |
| F5 285290-290-9-1                 | 8.74 a              | 8.51 bc                |
| F5 285290-290-9-3                 | 9.67 b              | 7.80 b                 |
| F5 321290-40-2-1                  | 8.64 a              | 6.01 ab                |
| F6 285290-123-6-15                | 11.72 c             | 14.48 d                |
| F6321290-252-10-8-4               | 8.53 a              | 5.57 ab                |
| F5 285290-38-6-3                  | 8.54 a              | 6.21 ab                |
| F6 321290-252-10-8-23             | 9.88 b              | 5.57 ab                |
| F6 321290-252-10-8-75             | 9.89 b              | 5.54 ab                |
| Bonita                            | 8.46 a              | 8.19 bc                |
| Local Garut (290)                 | 8.36 a              | 9.18 bc                |
| Taruna (295)                      | 8.59 a              | 5.28 ab                |
| Chakra Putih (285)                | 8.62 a              | 5.92 ab                |
| Tabasco (321)                     | 8.39 a              | 5.15 ab                |
| LSD value                         | 2.64                 | 2.82                   |

Note: The numbers followed by the same letter in the same column are not significantly different in the LSD test at 5% level.

For weight per fruit character, F5 285290-237-6-1, F5 285290-290-2-1, and F5 285290-290-9-1 are the genotypes that have the highest weight per fruit compared to the five comparison varieties (Table 1). Productivity is the potential for hybrid chilies to produce in tons per hectare. The genotypes resulting from crossing the Cakra Putih variety and the Garut local variety that showed significantly different productivity were genotype F5 285290-237-6-1, F5 285290-290-2-1, F5 285290-290-9-1, F6 285290-123-6-15, where the productivity value of Cakra Putih and Garut local varieties is 11.11-11.27 tons ha⁻¹ and the tested genotypes have a productivity of 11.55-15.77 tons ha⁻¹, with a difference of 4.5 ton ha⁻¹, then the tested genotypes have productivity values ranging from 40-45% higher than the parents. [7] stated that when plants grow in an environment with an optimum supply of growth factors, production will be high, but when the growth factors are very limited, there will be a large decrease in production. The plant like this can be categorized as having low adaptability.
Table 2. The average weight per fruit and the productivity of the tested genotypes against the comparison varieties.

| Genotypes and comparison varieties | Parameter observed | Weight per fruit (g) | Productivity (tons / ha) |
|-----------------------------------|--------------------|----------------------|-------------------------|
| F5 285290-237-6-1                 | 1.85 c             | 13.44 c              |
| F6 285290-6-10-1-1                | 1.54 bc            | 10.66 bc             |
| F5 285290-290-2-1                 | 1.79 c             | 15.77 c              |
| F5 285290-290-9-1                 | 1.43 ab            | 13.70 ab             |
| F5 285290-290-9-3                 | 1.71 c             | 11.29 c              |
| F5 321290-40-2-1                  | 1.26 a             | 9.39 a               |
| F6 285290-123-6-15                | 1.33 ab            | 11.55 ab             |
| F6 321290-252-10-8-4              | 1.69 bc            | 10.87 bc             |
| F5 285290-38-6-3                  | 1.73 c             | 10.49 c              |
| F6 321290-252-10-8-23             | 1.66 bc            | 8.24 bc              |
| F6 321290-252-10-8-75             | 1.59 bc            | 7.99 bc              |
| Bonita                            | 1.62 bc            | 13.84 bc             |
| Local Garut (290)                 | 1.55 bc            | 11.11 bc             |
| Taruna (295)                      | 1.53 bc            | 7.51 bc              |
| Chakra Putih (285)                | 1.50 bc            | 11.27 bc             |
| Tabasco (321)                     | 1.50 b             | 10.28 b              |
| LSD value                         | 0.19               | 0.19                 |

Note: The numbers followed by the same letter in the same column are not significantly different in the LSD test at 5% level.

3.2. Cluster analysis (cluster analysis)

The use of cluster analysis aims to group data (observations) into several classes (clusters) with grouping criteria based on the size of the dissimilarity [1]. The observed characteristics in a group have a low dissimilarity level, while between groups have a high dissimilarity level [8]. The dissimilarity between objects can be measured using distance measurements such as Euclid (feature root), the closer or smaller the Euclid distance between genotypes, the more similar the genotype [6].

The dissimilarity of highs and lows is reflected in the dendrogram (Figure 1). A value of 0-25 on the dendrogram indicates scaling based on Euclid's distance. The clustering of the genotype towards 0 (zero) indicates that the genotype has high or low genetic similarity. Cluster analysis was carried out on 11 genotypes and five varieties of cayenne chili using 26 characters at a dissimilarity value (Euclid distance) 10, all tested cayenne chili genotypes can be grouped into 3 groups (Figure 1). Cluster I consists of 11 genotypes which include F5 285290-237-6-1, F6 285290-6-10-1-1, F5 285290-290-2-1, F5 285 290-290-9-1, F5 285290-290-9-3, F5 321290-40-2-1, F6 285290-123-6-15, F6 321290-252-10-8-4, F6 285290-38-6-3, F6 321290-252-10-8-23, F6 321290-252-10-8-75. Cluster II consists of five varieties and one tested genotype which includes the Bonita variety, Garut local varieties (290), Taruna (295), Cakra Putih (285) and Tabasco (321) and one tested genotype, namely F6 321290-252-10-8-75.

Based on the results of cluster analysis (quantitative and qualitative chili), two groups of cayenne chili were obtained, namely a group consisting of the results of a cross (genotype) and a group consisting of several comparison varieties and one tested genotype of the results of the competition. These differences in genotype groups can be used to determine the similarities and relationships between genotypes. Genotypes that are in the same group have similarities and levels of close kinship. The genotypes that belong to...
different groups show quite a little of similarities and kinship. [9] states that in order to expand genetic diversity, crossing between genotypes that are far related will produce higher diversity compared to genotypes that are closely related.

Figure 1. Dendrogram analysis results cluster of 16 genotypes of cayenne pepper.

Based on research by Situmorang et al., [10] that there are wide differences in the genetic background of plants that can directly influence the magnitude of genetic variability in populations. Rosmaina et al., [11, 12] added that in selecting, the genotypes that were formed had to be quite a lot and had far-reaching kinship so that the genetic variation was higher. The high genetic diversity in the population indicates that a selection stage of the desired characters can be carried out in accordance with the objectives of plant breeding activities carried out.

4. Conclusion
Several IPB's cayenne pepper genotypes showed better characters than the comparison varieties. Genotype F5 285290-237-6-1 and genotype F6 285290-123-6-15 are genotypes with better plant growth than the five control varieties. Both genotypes had higher stem diameter and dichotomous height than the comparison varieties. Genotype F5 25290-237-6-1, F5 285290-290-2-1 and F5 285290-290-9-1 had the highest weight per fruit compared to the five comparison varieties. The highest productivity was obtained in genotype F5 285290-290-2-1 of 15.77 ton ha⁻¹ which is different from the comparative variety 4.5 ton ha⁻¹, the difference can reach 40-45%. The result of cluster analysis on qualitative characters and quantitative characters in cayenne chili plants produces two clusters, cluster I consists of 10 genotypes which include F5
Cluster II consists of five varieties and one genotype which includes the Bonita variety, Garut local varieties (290), Taruna (295), Cakra Putih (285) and Tabasco (321) and one tested genotype, namely F6 321290-252-10-8-75. The average genotype resulting from crossing has a different group with its parents, this is presumably due to the influence of genetic factors and the environment for the plant's growth. Genotypes F5 285290-237-6-1 and F5 285290-290-2-1 can be used as parent donors because they have good agronomic characters for all observed parameters, while the test genotype F6 321290-252-10-8-23 can be crossed with one of the F5 285290-237-6-1 or F5 285290-290-2-1 test genotypes, to improve agronomic characters and also to obtain high genetic diversity because they come from different cluster, so the degree of dissimilarity is also very high.

References

[1] Sulassih, Syukur M, Sobir S, Maharijaya A, Hakim A and Ratih 2017 Comm. Hortic. J. 1 26-33
[2] Ulya P D, Slamet W and Karno 2020 J. Agro Complex 4 23–31
[3] Lelang M A, Ceunfin S and Lelang A 2019 Savana Cendana 4 17–20
[4] Daryanto A, Sujiprihati S and Syukur M 2010 J. Agron. Indones. (Indonesian J. Agron. 38 113–21
[5] Kusmana, Kusandriani Y, Kirana R and Liferdi 2016 J. Hort. 26 133–42
[6] Syukur M, Sujiprihati S, Yunianti R and Kusumah D A 2014 J. Agron. Indonesia 42 32–8
[7] Arif A Bin, Sujiprihati S and Syukur M 2013 J. Hort. 22 103-110
[8] Hafsah S and Firdaus F 2020 J. of Trop. Hortic. 3 43-48
[9] Marpaung A E, Barus S and Musaddad D 2019 J. Hort. 29 33-44
[10] Situmorang H S, Zuhry E and Deviona 2014 J. Online Mahasiswa 1 1-13
[11] Rosmaina N-, Sobir N, Parjanto N and Yunus A 2020 J. Hort. 29 147-158
[12] Sudarjat, Kusumiyati, Hasanuddin, Munawar AA 2019 In: IOP Conference Series: Earth and Environmental Science. Institute of Physics Publishing.