

EARLY IDENTIFICATION ON THE GENETIC DIVERSITY OF INDONESIAN BUTTERFLY PEA ACCESSION AS COLORANT FOOD BASED ON MORPHOLOGICAL TRAITS

Karuniawan A.^{1*}, T.A. Ulimaz³, Kusumiyati¹, E. Yulia¹, F. Widiyanti¹, N. Wicaksana¹, Dudi², T. Suganda¹

¹Lecturer of Agriculture Faculty, Universitas Padjadjaran

²Lecturer of Animal Husbandry Faculty, Universitas Padjadjaran

³Magister Student, Graduate School, Universitas Padjadjaran

Jl. Dipatiukur No.35 Bandung, Graduate School, Universitas Padjadjaran

*Corresponding author: agung.karuniawan@unpad.ac.id

ABSTRACT

Butterfly pea is one of Indonesian origin plant species that is used as food coloring. Genetic diversity in butterfly pea of the origin of Indonesia is not known, so that the diversity of butterfly pea is needed to know the level of diversity. The objectives of this experiment was to obtain information on genetic diversity of butterfly pea origin Indonesia on morphological traits. The research was conducted in December 2016 until July 2017 at Ciparanje Experimental Farm Faculty of Agriculture, Padjadjaran University. The experiment used a randomized block design with three replications using ten accession butterfly pea from Indonesia (Aceh, Rancaekek, Jakarta, Kuningan, Madura, Lampung, Ciamis and Malang). The result showed that the genetic diversity of ten accessions of butterfly included extensive with dissimilarity coefficient from 0.00 to 4.79. Cluster analysis showed the division of groups into two clusters with accessions from Sumatra and Java spread in each cluster. In cluster A there was five accessions from Aceh, Ciamis, Jakarta, and Madura while cluster B has five accessions are Aceh, Malang, Lampung, Kuningan and Rancaekek. Based on Principal component analysis (PCA) showed eigenvalue ranged from 1.25 to 5.74 with a cumulative contribution of 87.43%. Traits that affect the diversity in this study are the age of flowering, the length of the pod, and the width of the flower.

Keywords: butterfly pea, genetic diversity, cluster, PCA

INTRODUCTION

Butterfly pea (*Clitoria ternatea* L.) is one of the horticultural plants used as a natural dye. The flower plants can be used as feed materials, medicines, and cover crops (Gomez and Kalamani, 2003; Sutedi, 2013). Butterfly pea is a type of legume that rich in protein. The blue color of the butterfly pea shows of anthocyanin content so it can be used as a dye (Suebkhampet & Sotthibandhu, 2011). Butterfly pea is also eaten as a vegetable in India and the Philippines (Lee *et al.*, 2011). Another advantage of butterfly pea is it can be used as a medicine because it contains flavonoids, alkaloids, saponins, and tannins (Kazuma, *et al.*, 2003; Chauhan *et al.*, 2012; Lijon, *et al.*, 2017). Butterfly pea has a great opportunity to develop because it has many benefits as food, and the medicine.

The need for dyes in the food processing industry is increasing. The use of synthetic dyes (textile substances) in Indonesia tends to be misused, because it is used for food (Synthetic dyes (textile substances) in Indonesia tends to be misused as coloring for food. The residue of heavy metals in synthetic dyes can endanger human health so that the need for dyes derived from natural sources. Utilization of plants as a source of color pigment producers have not been maximally utilized in Indonesia. One of the plants that can produce natural pigments that are used as natural dyes are butterfly pea. Besides being used as a natural dye, butterfly pea also contains anthocyanin which is good for health.

The development of butterfly pea in Indonesia is still very low both from the cultivation and utilization. The planting of butterfly pea buds is still irregular in most areas. Flower plants has not been developed much since there is no study of diversity of varieties butterfly pea so it becomes one of the factors of low quality anthocyanin information on the plants. Efforts that can be made to develop butterfly pea is by using superior varieties, proper cultivation mode, and improvement of genetic potential. Characterization and identification of morphological characters of butterfly pea can be done for the development.

Plant Breeding Laboratory of Padjadjaran University has a collection of germplasm butterfly pea from various Indonesia. Plant germplasm is a source of genetic material used by plant breeders to assemble or develop a superior cultivar of plants. The wealth of Indonesian germplasm including butterfly pea is still very open to be utilized all the potentials that exist in butterfly pea itself, both from the nutrient content, the utilization of plant organ parts and chemical content. So far the collection of germplasm or accession of butterfly pea has not been done comprehensively, so the studies related to genetic diversity based on morphological traits is needed. Genetic diversity is a measured genetic distance in a population (Hughes *et al.*, 2008). The success of plant breeding in the development of a plant can be seen from genetic diversity and heritability estimates (Poehlman, 1983). Extensive genetic diversity can facilitate the selection process on desired characters (Satoto & Suprihatno, 1996). Individuals in a relatively uniform population show a narrow genetic diversity. One of the factors needed to develop new varieties is high genetic diversity. In this research, genetic diversity analysis based on morphological traits of 10 accession of butterfly pea origin Indonesian.

MATERIALS AND METHODS

The research material used 10 accession of butterfly pea origin (Aceh, Rancaekek, Jakarta, Kuningan, Madura, Lampung, Ciamis, and Malang). The materials used in the form of seeds are germinated in Greenhouse Faculty of Agriculture UNPAD. The experiment was conducted from December 2016 to July 2017, at the Ciparanje Experimental field of the Faculty of Agriculture, Padjadjaran University. The experiment was conducted at an altitude of 753 m asl with type C rainfall according to Schimdt and Fergusson (1951).

The experiment was conducted by experimental method of randomized block design (RAK) with ten treatments and three replications. Observations made in this experiment include pod length (cm), pod width (mm), seed length (mm), seed diameter (mm), number of seeds per plant, weight of 100 seeds (gram), age of flowering, harvest (hst), length of flower (cm), and width of flower (cm). Analysis of genetic diversity using principal component analysis

(PCA) while for viewing genetic distance using cluster analysis. PCA analysis and cluster analysis using software NTSys 2.0.1.5.

RESULTS AND DISCUSSION

Analysis of genetic diversity in ten accessions of butterfly pea was done on the basis of Principal Component Analysis (PCA) on morphological traits. Exploration of the genetic diversity of different accessions in the geographic region is expected to have a real impact on the conservation and utilization of butterfly pea accessions. The genetic diversity shown in the main component analysis is eigenvalue.

Based on Table 1 shows the eigenvalue on 10 accession of the butterfly pea ranged from 1.25 to 5.74 with cumulative contribution to the diversity of 87.43%. The eigenvalue that explains the cumulative and diversity factors is more than 1 (Jeffers, 1967; Supranto, 2004). There are 10 characters that contribute to the diversity of the 10 accessions of butterfly pea. Traits that gives effect to the first component diversity (PC1) amounted to 8 traits including pod length, pod width, seed length, seed diameter, number of seeds per plant, flowering age, harvest age and length of interest with contribution value of variation 57.42% . In the second component (PC2) there are 2 characters that contribute to the diversity of 100 seeds and the width of the flower with the contribution value of variation 17.51%. The traits that contribute positively to the first component amount to seven while in the second component of the house one. According to Haydar *et al.* (2007), that the character that contributes positively is the maximum influence character of diversity. Traits that have both positive and negative contributions have an effect on diversity.

Table 1. Eigenvalue of morphological traits of 10 butterfly pea accessions origin in Indonesia

PCI	Eigenvalue	Percent (%)	Cumulative
1	5.74	57.41	57.41
2	1.75	17.51	74.92
3	1.25	12.50	87.43

Table 2. Principal component analysis of 10 butterfly pea accessions origin in Indonesia

Characters	PC1	PC2	PC3
Pod length	0.9218	0.1042	0.1933
Pod width	0.8816	-0.0353	0.4189
Seed length	0.8816	-0.0353	0.4189
Seed diameter	0.5619	0.0358	-0.6094
Number of seed per plant	0.8391	0.4114	-0.0471
Weight of 100 seeds	0.4511	-0.7300	-0.3645
Days to flower	0.9748	-0.0758	0.1731
Days to harvest	-0.6711	-0.3925	0.2561
Length flower	0.8238	-0.1053	-0.4827
Width flower	-0.1857	0.9296	-0.1641

Description: A bold number represents an influential character value due to discriminant > 0.5 or < -0.5 (Jolliffe, 2002)

The genetic distance in the ten accessions of butterfly pea is shown in the cluster analyst in the form of euclidean distance. Based on the cluster analysis on ten accessions of Indonesian flower shows a wide genetic diversity. This can be seen from the distance euclidean of 0.00 - 4.79. According to Setiawati *et al.* (2010) that the euclidean distance of 0.00 - 5.60 at 148 sweet potato accessions is expressed to have wide variations. To see the similarity or incompatibility between accessions can be seen from the value of euclidean distance. The distances of distant insignificance are marked by more than one euclidean distance (Sitepu *et al.*, 2011).

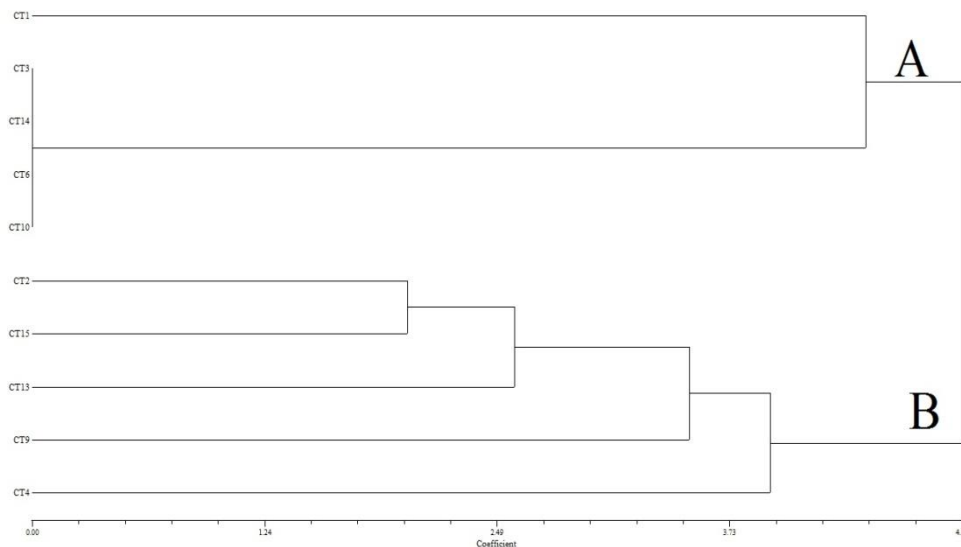


Figure 1. Dendrogram of 10 butterfly pea accessions origin in Indonesia based on morphological traits

The grouping of accession butterfly pea divides the accession of butterfly pea origin Indonesian into 2 main cluster clusters namely cluster A and B. There are five accessions in cluster A covering CT1, CT3, CT14, CT6, and CT10. In this group there are four accessions that have small inclination coefficient value that is CT3, CT14, CT6, and CT10 with euclidean distance 0.00. This is because the four accessions have similarities to the observed morphological traits. Research Tairo *et al.* (2008) showed that genetic diversity based on morphology of sweet potato germplasm has a narrow diversity and close genetic relationship with the coefficient of dissimilarity of 0.00 - 0.57. Accessions located on the same line tend to have low genetic diversity (Anas & Yoshida, 2004). Cluster B has five accessions are CT2, CT15, CT13, CT9, and CT4. Based on this grouping it is expected to assist in identifying the similarity and magnitude of the diversity of traits in each accession so as to support the development of butterfly pea in Indonesia. Understanding the genetic diversity of the flower accession in plant breeding programs is an important requirement for the development of flower plants. The existence of genetic diversity of butterfly pea is a requirement to do next stage of breeding is selection.

CONCLUSION

1. Principal component analysis results three main components with a cumulative contribution of 87.43%. Traits that influence the diversity in this study are the age of flowering, the length of the pod, and the width of the flower.
2. Genetic diversity in 10 accession of butterfly pea origin Indonesian based on morphological traits including wide with coefficient of inefficiency 0.00 - 4.79. There are 2 cluster groups with accession from Sumatera and Java spread in each cluster.

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