

## GENETIC DIVERSITY OF PERENNIAL WEEDY *Ipomoea sp* L. as. WILD PROGENITOR FOR SWEET POTATO *Ipomoea batatas* L.

Tia Setiawati<sup>1)</sup>, and Agung Karuniawan<sup>2)</sup>

- <sup>1)</sup> Student of Graduate Program, Faculty of Mathematics and Natural Science, Universitas Padjadjaran Bandung, Indonesia
- <sup>2)</sup> Lecturer of Plant Breeding Program, Agricultural Faculty, Universitas Padjadjaran Bandung, Indonesia

Author for correspondence: akaruni1@unpad.ac.id

### ABSTRACT

Wild relative of sweet potato i.e. *I. trifida*, *I. cairica* and *I. triloba* originated from district Citatah in West Java are known as perennial weedy plants. However, these weeds are considered as potentially useful in breeding program to complement the special traits of cultivated-sweet potato. These perennial weeds carry genes for stress tolerance and/or resistance. For example, *I. triloba* has drought tolerance genes, *I. cairica* has virus resistance genes, while *I. trifida* has short duration characteristics. However, information in the genetic diversity and its relationships between the wild and cultivated *Ipomoea* is important due to breeding program. The objective of this research was to estimate the genetic diversity and the relation of 148 accessions of perennial weedy genus *Ipomoea* collected from Citatah West Java based on 29 morphological traits. Principal component analysis was employed to estimate the genetic diversity and to determine the relationship within the genus. The results indicated that dissimilarity coefficients were ranged between 0.00 to 5.60, and therefore they are considered as a high variation in the accessions studied. Furthermore, 2 clusters have been clearly observed, i.e. cluster A and B. Cluster A consists of 2 sub-clusters, i.e., A1 and A2. In sub-cluster A1 consisting of 145 accessions, most accessions gathered in cluster A1 (145 accessions). Cluster A2 consisted of 2 accessions of accession no 22 and no 169. Cluster B consists only one (accession no 41P) that have the greatest dissimilarity distance of 5.60. The morphological traits which played significant role as the determinant of the diversity were predominant vine colour, secondary vine colour, vine type pubescens, leaf lobus type, shape of central leaf lobe, abaxial leaf vein, pigmentation, mature leaf colour, petiole pigmentation, shape of limb, equality of sepal length, sepal shape, sepal apex, colour of stigma and stigma exertion. The pattern of the relations between the accessions of perennial weedy plants of wild *Ipomoea* can be used as base information for further sweet potato breeding program in the near future.

Keywords : genetic diversity, *Ipomoea* , perennial weedy plants

## INTRODUCTION

The existence of extensive genetic diversity is one of the essential factors, which have an important role in supporting plant breeding program. The availability of genetic resources or germplasm with a high level of diversity necessary to assemble the new plants with superior characteristics that benefit. Genetic resources can be obtained from the collections of cultivated plants or wild species such as weeds. Origin of genetic resources of wild species of *Ipomoea* known to have made valuable contributions in plant breeding programs (Renwarin *et al.*, 1994).

Indonesia is considered as a biodiversity center of sweet potato (*Ipomoea batatas*), second after Centre America. Hambali (1988) reported that the highest genetic and phenotypic diversity of perennial weedy *Ipomoea spp.* in Indonesia is located in Citatah which was calcareous area with dry climates, is in the province of West Java. These perennial weedy of *Ipomoea spp.* in Citatah known by local residents by name of *huhuian* or *boled areuy*.

Naturally, wild relatives of sweet potato founded in Citatah grow as a weed in farmland of cultivated-sweet potatoes, and the other calcareous slope regions. *Ipomoea trifida* is one wild relatives of sweet potato which can be found in Citatah (Greg Hambali, private comm., 2009), has been used as a source of genes for the assembly of superior cultivars of sweet potato to increase yield, dry matter, starch, resistance to the main pests and diseases, protein, early maturity, while *I. triloba* has drought tolerance genes, *I. cairica* has virus resistance genes.

Thus, efforts need to be done so the source of germplasm of these perennial weedy *Ipomoea spp.* to be maintained and conserved by doing the collection and characterization to determine the nature of the morphology and genetics in order to avoid duplication in the collection of germplasm. The study of wild relatives germplasm of sweet potato in supporting the breeding program is very important because the wild relatives of sweet potato to serve as a source of germplasm that can be used to complement the special characters of cultivated-sweet potato as well as to broaden the genetic diversity of species of sweet potato have been cultivated.

## MATERIALS AND METHODS

Materials examined were 148 accessions of wild relatives of sweet potato collection of Plant Breeding Laboratory, Agricultural Faculty, Universitas Padjadjaran. The experiment field was about 753 m altitude above sea level (asl), climate type according to Schmidt-

Ferguson (1951) included into the type C (rainfall). Planting done without design with 1 accession was represented by a crop, planted in a one-row-plot along the 5 m with space between plots 1 m, while spacing between plants in each plot was 25 cm.

Plants were fertilized with 100 kg / ha of urea, 75 kg / ha of SP36, 100 kg / ha of KCl and given twice. The first fertilization given at 1 week with a dose of 1 / 3 part fertilizer (Urea + KCl) and the entire dose of P while the second time was given at one month full after planting.

Characters observed consist of morphology traits of stems, leaf, flower, in accordance with the descriptor of sweet potato (CIP / were done by AVRDC / IBPGR, 1991). Genetic diversity analyzed using cluster analysis. Data were standardized to compile it. The result of the distance matrix through Agglomerative Hierarchical cluster analysis Sequential Nonoverlapping, used to create the cluster dendrogram UPGMA (Unweighted Pair Group Method Arithmetic). The calculation for cluster analysis was performed with aid of the software Numerical Taxonomy and Multivariate System (NTSYS) version 2.1. (Rolf, 2000).

## RESULTS AND DISCUSSION

Analysis of genetic diversity in 148 accessions of the wild relatives of sweet potato originated from Citatah-West Java with 29 morphological characters were analyzed using NTSYS-pc ver 2.10s, showed the characters which played significant role and dissimilarity coefficient among accessions were observed.

Table 1. Means Value, Standard Deviation, Minimum Value dan Maximum Value of 29 Morphological Characters (n=148)

	Morphological Characters	Means	Std.Dev		n	Min	Max
4.1	Vine internode length	4.4685	1.2091		143	1	9
4.2	Vine internode diameter	1.2238	0.6327		143	1	3
5.1	Predominant vine colour	6.9091	1.8648	*	143	1	9
5.2	Secondary vine colour	3.5664	1.7665	*	143	1	7
6	Vine tip pubescens	5.3287	1.8492	*	143	1	7
7.1	General outline of the leaf	4.6154	1.3211		143	3	6
7.2	Type of leaf lobe	2.2168	1.8770	*	143	0	7
7.3	Number of leaf lobe	2.4545	1.0396		143	1	5
7.4	Shape of central leaf lobe	2.4266	1.8251	*	143	0	6
8	Leaf size	3.0140	0.1672		143	3	5
9	Abaxial leaf vein pigmentation	2.9161	1.9841	*	143	1	9
10.1	Mature leaf colour	3.1818	1.5906	*	143	2	9
10.2	Immature leaf colour	3.0140	1.3108		143	1	7

11 Petiole 1.0000  
length

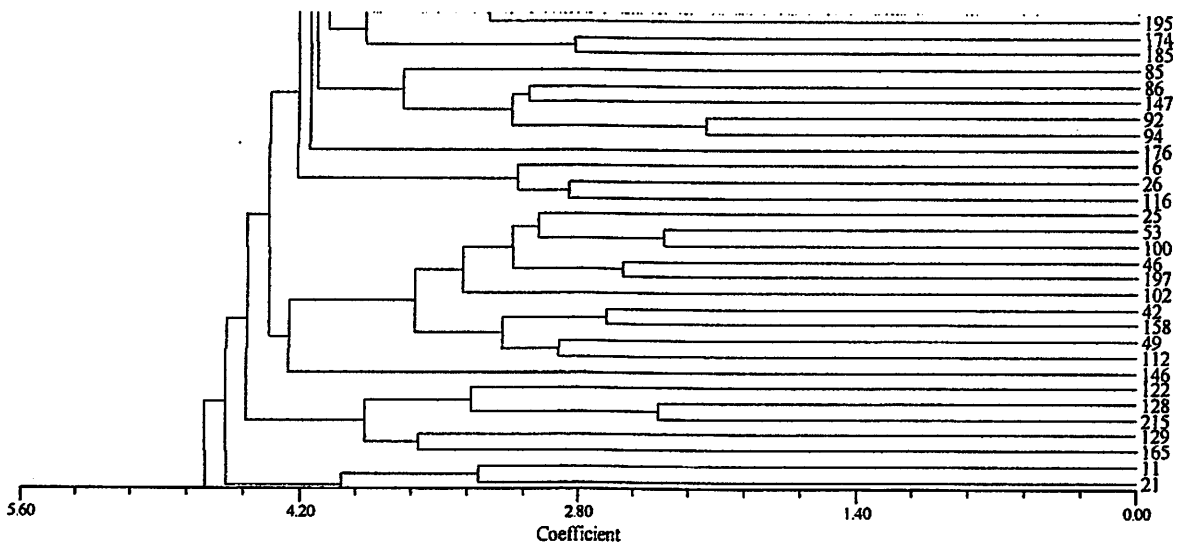
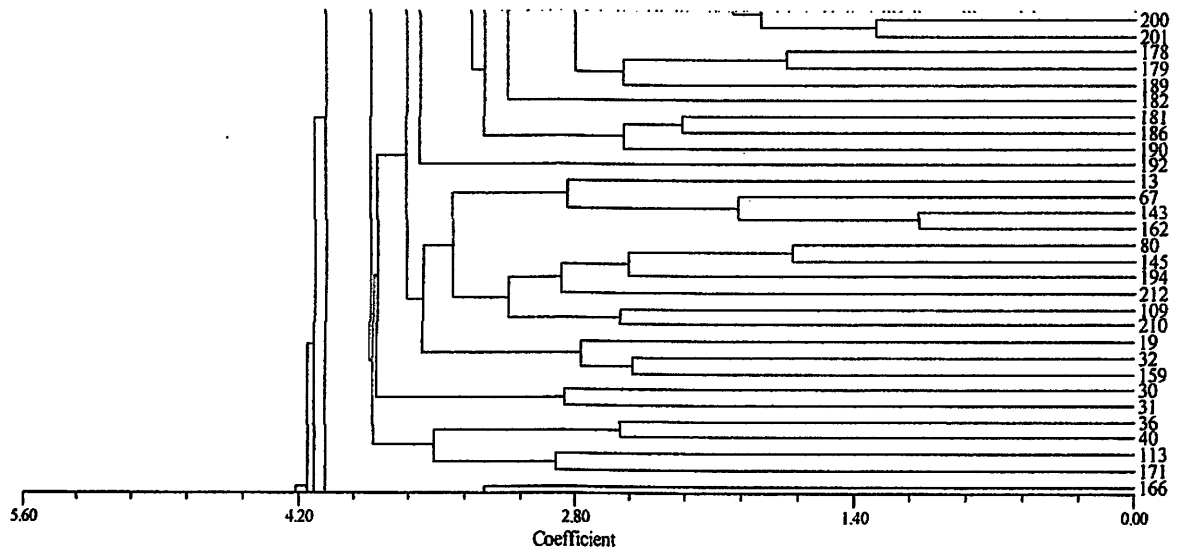
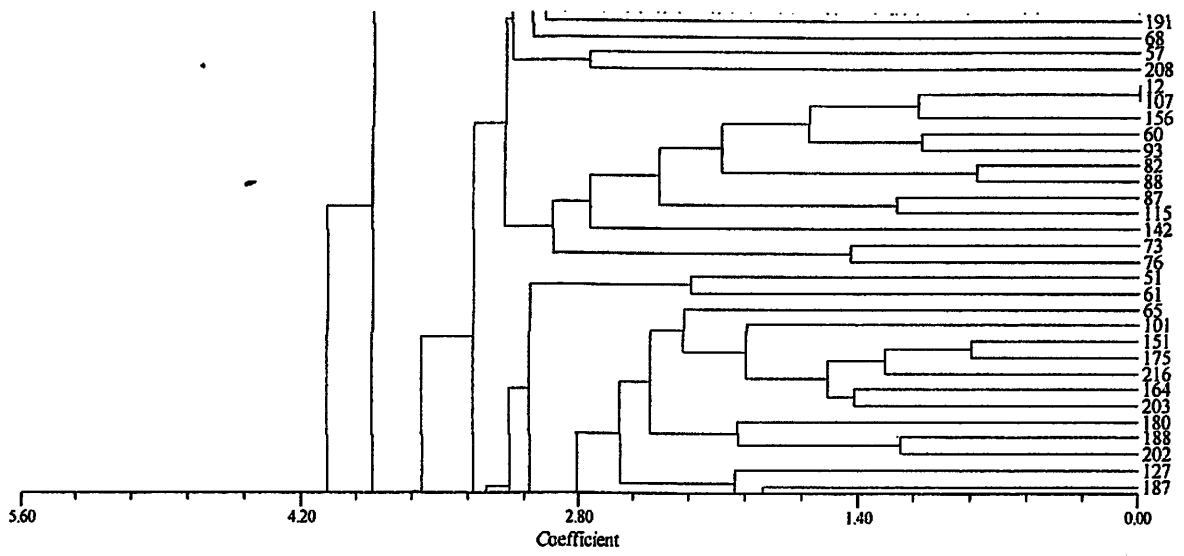
12	Petiole pigmentation	7.3357	2.3525	*	143	1	9
14.1	Number of flower	2.0968	0.9578		124	1	9
14.2	Flower colour	3.8800	0.6299		125	2	5
14.3.P	Flower length	3.2577	0.5750		123	2.1	5.5
14.3.L	Flower width	6.0161	1.4084		124	1	7
14.4	Shape of limb	4.1148	2.4936	*	122	1	9
14.5	Equality of sepal length	4.8211	1.8992	*	123	1	7
14.7	Sepal shape	4.8455	2.2067	*	123	0	7
14.8	Sepal apex	3.4553	2.1888	*	123	1	9
14.9	Sepal pubescens	1.0650	0.5080		123	1	5
14.10	Sepal colour	1.0000					
14.11	Colour of stigma	3.3415	2.0439	*	123	1	7
14.12	Colour of stylus	1.0000					
14.13	Stigma exercion	3.3415	2.0439	*	123	1	7
			SD=1.51				

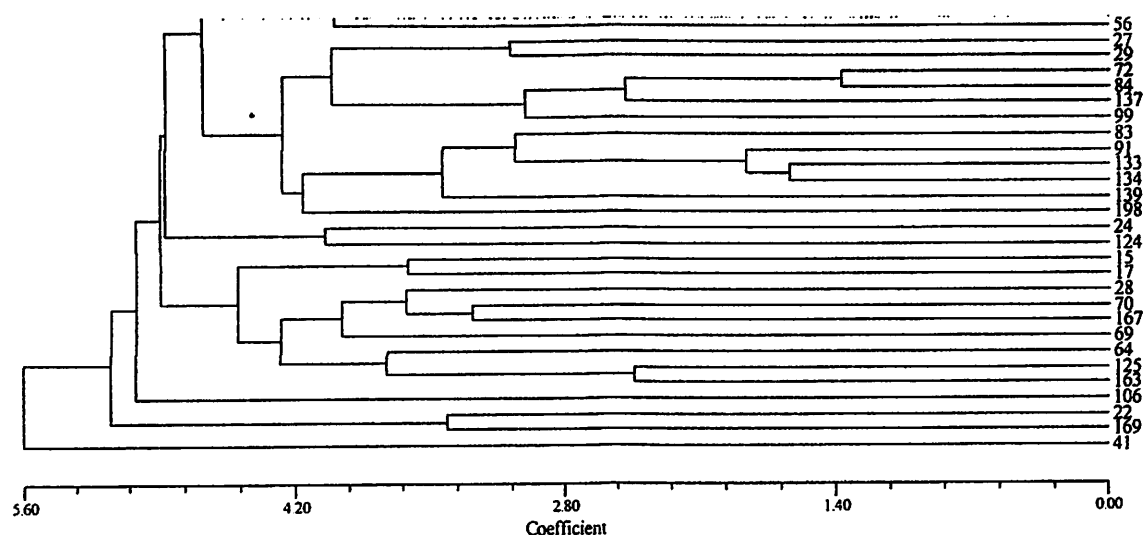
\*) characters which have high standard deviation value (significant)

Base on Table 1. showed that standard deviation values ranged from 0.1672 (character of mature leaf size) to 2.4936 (character of shape of limb) with average value of standar deviation of 1.51.

There were 14 morphological characters which played significant role as the determinant of the diversity i.e. predominant vine colour, secondary vine colour, vine type pubescens, leaf lobus type, shape of central leaf lobe, abaxial leaf vein, pigmentation, mature leaf colour, petiole pigmentation, shape of limb, equality of sepal length, sepal shape, sepal apex, colour of stigma and stigma exertion.

Base on data analysis of 29 morphological characters were observed in 148 accessions of perennial weedy *Ipomoea spp.* produced dissimilarity coefficient ranged between 0.00 to 5.60 (Fig.1). Generally, did not seem formed separate clusters significantly; however seemed the formation of clusters and sub clusters were seperates each other, although in the distance of dissimilarity coefficient that was not too far. This showed there were a very high genetic diversity among accessions were observed due to the formation of clusters and sub clusters (Kurniawan, 2002).





Cluster A consists of 2 sub-clusters, i.e., A1 and A2. In sub-cluster A1 consisting of 145 accessions, most accessions gathered in cluster A1 (145 accessions), this was because many morphological characters similarities in these accession, so that it can be assumed to have a close relationship. Cluster A2 consisted of 2 accessions i.e. accession no 22 and no 169. Cluster B consists only one (accession no 41P) that have the greatest dissimilarity distance of 5.60. This was because this accession has a morphological character, i.e. green main vein colour that was different from other accessions.

The research has been conducted by Tairo *et al.* (2008) on sweet potato germplasm in Tanzania showed that the dissimilarity coefficient ranged from 0.00 to 0.52. This showed a narrow genetic diversity and close relationships among accessions were observed. While the research on 26 *I. batatas* clones from Oceania, Peru, Phillipines and US, and 8 species of *Ipomoea sp.* represented a rich source of genetic diversity with similarity coefficient were ranged from 0.16 to 0.80 and 0.00 to 1.00, respectively (Jarret and Austin, 1994). As well as the result of this research, the dissimilarity coefficient of genetic diversity on 148 accession of perennial weedy *Ipomoea spp.* ranged between 0.00 to 5.60 that showed a high genetic diversity. So that can be used as the base of crossing for using these perennial weedy as wild progenitor in *Ipomoea batatas* improvement.

## CONCLUSION

Level of Genetic diversity of 148 accessions perennial weedy *Ipomoea spp.* observed bases of 29 morphological characters produced the dissimilarity coefficient ranged between 0.00 to 5.60, that showed the wide genetic diversity.

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