

Genotypic Differences between Indonesian Accessions of Wild Cowpea (*Vigna vexillata*) and Related *Vigna* Species Based on Morpho-agronomic Traits

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ABSTRAK

Penelitian ini bertujuan untuk menguji perbedaan genotipe berdasarkan karakter morfo-agronomi di antara aksesori 'wild cowpea' (*Vigna vexillata*) dan kerabatnya dalam genus *Vigna*. Penelitian dilakukan di Kebun Percobaan Fakultas Pertanian Universitas Padjadjaran Bandung di Sumedang, Jawa Barat, mulai dari Oktober 2005 sampai Maret 2006. Pengujian meliputi 16 genotipe dengan dua ulangan dalam rancangan acak kelompok. Setiap genotipe ditumbuhkan dalam satu baris tanam sepanjang 6 m. Terdapat variasi yang luas dalam karakter morfo-agronomi di antara genotipe yang diuji. Analisis keragaman menunjukkan bahwa untuk beberapa karakter, aksesori *V. vexillata* serupa dengan kerabatnya dalam genus *Vigna*. Namun, beberapa tipe *V. vexillata* budi daya asal Bali menunjukkan hubungan yang jauh dengan kerabat liarnya asal Afrika.

Kata kunci: *Vigna*, plasma nutfah, karakter morfo-agronomi.

ABSTRACT

This research examined genotypic differences in morpho-agronomic traits among 'wild cowpea' (*Vigna vexillata*) accessions and related groups in the genus *Vigna*. The traits were observed under natural, open field conditions at the field experimental station of The Faculty of Agriculture of Padjadjaran University, West Java, Indonesia, between October 2005 and March 2006. sixteen genotypes studied were planted in two replications and arranged in randomized complete block design. The plants of each genotype were grown in a single row plot of 6 m long. Large variations in morpho-agronomic traits were observed between genotypes. Analysis of genotypic differences showed that for certain traits, the *V. vexillata* accessions were similar to their relatives within the genus *Vigna*. However, some cultivated forms of *V. vexillata* from Bali exhibited some distinct differences from related wild genotypes of African origin.

Key words: *Vigna*, germplasm resources, morpho-agronomic traits.

INTRODUCTION

The 'wild cowpea' (*Vigna vexillata*) is native of Africa, Asia (including Australia) and central America. The species is morphologically variable and widely distributed across Tanzania to South Africa (Garba and Pasquet 1998) and from Yunnan in China to South-East Asia and northern Australia (Wong 1997, Lawn and Watkinson 2002). *V. vexillata* often has fleshy roots and is occasionally used as food by indigenous people in times of scarcity due to drought in particular parts of Africa, Australia and Asia (FAO 1979, NRC 1979, Wong, 1997). A cultivated form of *V. vexillata* has been reportedly used for their fleshy tubers for food in some localities in Bali and Timor (Karuniawan *et al.* 2006).

The adaptive responses of the putative wild progenitors of cultivated crops are of interest, since they are potentially useful adjunct to the cultivated ones (Smartt 1978). Nonetheless many wild traits are undesirable in cultivated legume crops and have been selected against during their domestication (Smartt 1978, Donald and Hamblin 1984). Effective strategies for exploiting wild germplasm, therefore, need to identify potentially useful adaptive traits and at the same time discriminate against undesirable wild type traits. The development of such strategies can benefit from a better understanding of the morpho-agronomic basis of adaptation of the wild relatives to natural environments. This same information can also be potentially useful for targeting the collection of specific adaptive traits (Chapman 1989), as well as for developing strategies for *in situ* conservation of genetic resources.

Cultivated accessions of *V. vexillata* from Bali can be hybridized with wild relatives of the same species from Timor and Australia (Lawn, Pers. Comm. 2007). Morpho-agronomic and phenological traits (i.e. date to flower, date to mature etc.) are important factors conditioning adaptation to both natural and agricultural environments. For example, phenology is important in determining how well the plant's life cycle is matched to periods generally favorable to growth (Richards 1991), and hence, the potential of its yield.

The present study was undertaken to examine the extent of genotypic differences in morpho-agronomic traits between Indonesian *V. vexillata* accessions and related *Vigna* species, and whether differential genotypic performance might be attributed to these differences

MATERIALS AND METHODS

Plant Materials

Sixteen genotypes representing four *Vigna* groups (species or subspecies) were involved in the study. Accessions within the *V. vexillata* group comprised three wild types obtained from IITA Ibadan Nigeria i.e. TVNu-4670, TVNu-3189, and TVNu-3193 and eight cultivated types of *V. vexillata* collected from Bali Indonesia i.e. JIM-1, JIM-2, JIM-3, JIM-4, TAB-1, TAB-2, TAB-3, and TAB-4. The second group, yard long bean (*V. sesquipedalis*) was represented by three accessions i.e. NI-146 (*V. unguiculata* subsp. *unguiculata* cv *sesquipedalis*) obtained from Meise Gene Bank Belgium, and two accessions from the Research Institute for Tuber and Legume Crops (RILET) at Malang Indonesia i.e. MLG-15151, and a modern cultivar of *Hijau Super*. The third group comprised a single accession of cowpea i.e. *V. unguiculata* subsp. *unguiculata* cv *unguiculata* (NI-479), while the fourth group comprised a single accession of the wild species, *V. unguiculata* cv. gr. *Biflora* (NI-478), both obtained from Meise Gene Bank Belgium.

Experimental Design and Plant Culture

The plants were grown in single row plots of 6 m long with 70 cm distance between rows, in the field at the Padjadjaran University Research Station at Jatinangor, Sumedang, West Java from October 2005 to March 2006. The plants were spaced 20 cm apart in the rows. A border row of mungbean was grown around the perimeter of each sowing. Bamboo sticks 2.0 m long were provided for each plant as plant supporter, around which they were hand-trained to prevent inter-twinning. The experiment was arranged in a randomized complete block design with two replications and with the 16 *Vigna* genotypes as treatments. Sowings were located randomly in the field, with two replicate blocks within each sowing. The plants were grown under generally favorable conditions of nutrients and water supply from natural rainfall, and with chemical protection to avoid damage from weeds, insect pests and disease.

Measurements

Twenty morpho-agronomic traits, based on the Cowpea Descriptors (IPGRI 1983) were used to identify genotypic differences, i.e. leaf traits (ratio of length/width of terminal leaflets, petiole length, outline of terminal leaflets, length of leaflet hairs, petiole colour, colour of petiole bases, leaflet midrib, and leaflets). Floral traits measured were length of corolla, width of corolla, length of sepallum, outline of sepallum, length of pistil, length of stamen, corolla colour, number of stamen, stylus colour, stigma colour, position of stigma and keel. Yield components (i.e. 100 seed weight and number of seed per pod) were also measured.

Analysis of Data

Analysis of variance (GENSTAT IV) was used to examine the differences between accessions, both between and within the four *Vigna* groups. The relationship between the *V. vexillata* accessions and the other *Vigna* accessions were analyzed using Euclidean distance and UPGMA clustering confirmed by NTSYS program 2.10q version (Rohlf 2001). Means across replicates and standardized data were used in these analyses.

RESULTS AND DISCUSSION

Means for the four *Vigna* groups across accessions for the *sesquipedalis* and *vexillata* groups, are shown in Table 1, together with key statistical data. For almost all of the 20 morpho-agronomic traits observed, there were significant differences between groups, and among accessions within groups. For several traits (100 seeds weight, sepal width, trifoliolate terminal length, date to flowering) most of the variation (>60% of sums of squares) was associated with differences between the four groups. For several other traits (pedunculus length, leaf hair length, left trifoliolate length, and widths of all 3 leaflets, sowing to emergence, stamen length), there was more variation between the accessions within groups than between groups, as indicated by the fact that >60% of sums of squares were associated with variation between accessions within groups. For the rest of the 20 traits, there was as about as much variation between the accessions in the *vexillata* and *sesquipedalis* groups as there was between the four groups.

Among groups, the *sesquipedalis* accessions flowered earliest, while the single *biflora* accession

tested flowered latest. Among groups, *sesquipedalis* possessed bigger seed size than the other groups. The *vexillata* genotypes (both cultivated and wild forms) were relatively late flowering and along with *biflora*, had small seed size relative to the other two groups. Interestingly, the *vexillata* genotypes possessed the biggest floral set size compared to the three other groups. In general, the differences between the groups, as well as between the accessions within groups, in the number of seeds per pod, were relatively small, especially when compared with the large differences in seed size (Table 1).

In interpreting the observed variation between groups, caution is needed in that for two of the groups (*unguiculata* or cowpea, and the closely related wild species, *biflora*), only 1 accession each was evaluated. Inevitably, there would have been greater variation among accessions within groups had more accessions in these groups been evaluated.

Cluster analysis of the 16 accessions, based on the variation in the 20 traits observed in the study, is illustrated in Figure 1. The yard long bean (*sesquipedalis*) group, comprising NI-146 from Meise Gene Bank Belgium, and the two accessions

Table 1. Genotypic diversity for 20 morpho-agronomic traits in four *Vigna* groups, as indicated by groups means, variance components and Anova statistics.

Traits	Group means (and no. of accessions examined)				Sums of Squares (%)		Anova statistics	
	<i>V. biflora</i> (1)	<i>V. sesquipedalis</i> (3)	<i>V. unguiculata</i> (1)	<i>V. vexillata</i> (11)	Between groups	Within groups	F-ratio for group effects	Standard error of difference
Corolla length (cm)	1.80	2.17	1.97	2.72	42.85	57.15	n.a	0.000
Corolla width (cm)	2.65	2.83	2.50	3.58	53.25	46.75	47.78**	0.191
Sepal length (cm)	0.90	1.33	0.95	1.25	42.12	57.88	5.28**	0.168
Sepal width (cm)	0.73	0.97	0.63	1.30	71.29	28.71	n.a	0.000
Pistil length (cm)	2.95	3.55	3.50	5.10	51.86	48.14	77.04**	0.294
Stamen length (cm)	3.10	3.43	3.25	4.18	35.65	64.35	51.31**	0.182
Sowing to emergence (day)	9.50	8.33	7.00	10.05	23.66	76.34	2.39ns	1.949
Sowing to 50 % flower (day)	89.50	47.17	61.50	70.59	61.72	38.28	117.39**	3.278
Trifoliolate left length (cm)	8.35	12.94	12.31	10.68	9.70	90.30	15.79**	0.944
Trifoliolate terminal length (cm)	9.34	14.28	13.20	11.26	64.83	35.17	27.94**	0.841
Trifoliolate right length (cm)	8.54	13.05	12.28	10.68	49.83	50.17	15.62**	0.954
Trifoliolate left width (cm)	5.95	7.99	8.62	6.91	17.38	82.62	10.18**	0.645
Trifoliolate terminal width (cm)	6.68	8.84	9.47	7.39	19.54	80.46	14.23**	0.653
Trifoliolate right width (cm)	5.77	7.83	8.56	6.94	16.31	83.69	7.53ns	0.717
Leaf hair length (cm)	2.00	2.00	2.00	2.18	6.49	93.51	3.01*	0.000
Petiolus length (cm)	10.13	11.65	14.93	9.10	59.06	40.94	28.35**	0.985
Petiolulus length (cm)	2.75	3.62	4.21	2.78	41.92	58.08	42.83**	0.223
Pedunculus length (cm)	31.50	27.67	33.00	30.45	4.56	95.44	3.01*	2.554
No. of seed per pod	16.50	15.62	18.00	15.33	51.13	48.87	8.60*	0.926
100 seed weight (g)	2.40	19.79	8.32	4.03	96.63	3.37	641.29**	0.796

ns, *, ** = indicate statistical significance at $P \geq 0.05$, $P \leq 0.05$, and $P \leq 0.01$ respectively.

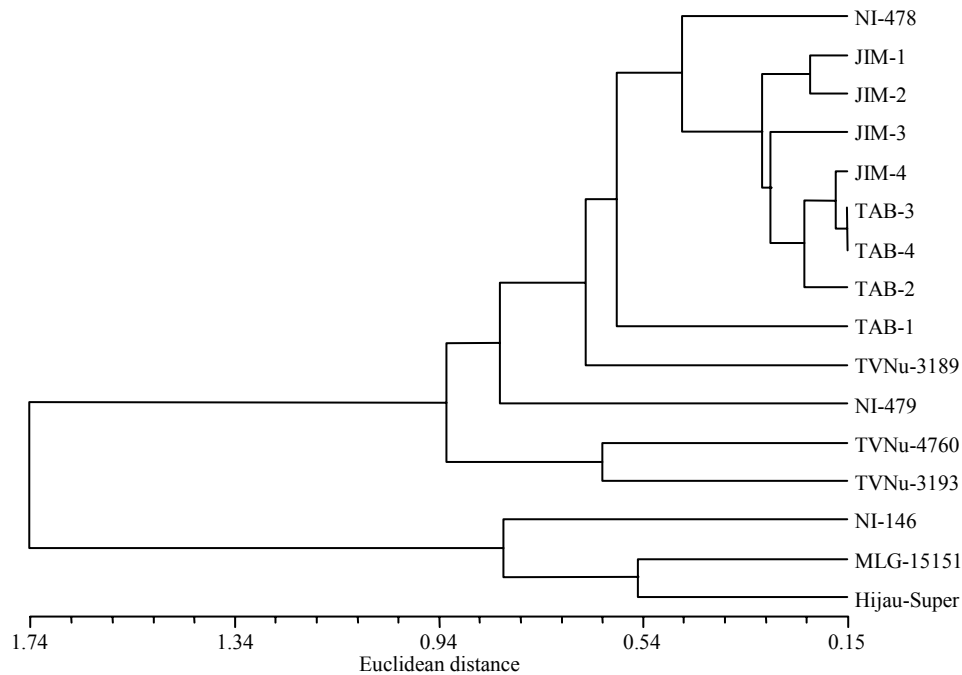


Figure 1. Genetic relationship between *V. vexillata* and other *Vigna* accessions, based on the observed variation in morpho-agronomic traits.

from RILET Indonesia, MLG-15151 and *Hijau Super*, were the most distinctly separated from the other three groups (*vexillata*, *biflora*, and *unguiculata*). Within the latter cluster (cluster 1 in Figure 1), two of the wild *vexillata* accessions (TVNu-4760 and TVNu-3193) were the next to cluster out separately, followed by the *unguiculata* line, NI-479 and the other wild *vexillata* accession, TVNu-3189. The eight cultivated *vexillata* accessions from Bali, and the *biflora* accession, NI-478, formed a relatively tight cluster with only relatively small inter-accession variation, especially among 7 of the 8 cultivated *vexillata* accessions (Figure 1).

It is highly likely that those traits where there was greatest between-group variation, like 100 seeds weight, time from sowing to flowering and terminal leaflet length (Table 1), contributed most to the clustering observed in Figure 1.

Particular interest was the fact that the eight accessions of cultivated *vexillata*, from two traditionally known areas of cultivation in Bali i.e., district Jimbaran in Southern Bali (JIM-1, JIM-2, JIM-3, and JIM-4) and of Tabanan in Central Bali (TAB-1, TAB-2, TAB-3, and TAB-4), were apparently very closely related. These Balinese acces-

sions, except TAB-1, were closer to the *biflora* accession NI-478 than to cowpea NI-479 or to the three wild *vexillata* accessions from IITA (TVNu-4670, TVNu-3189, and TVNu-3193). The lack of variation between the cultivated *vexillata* accessions from Bali is of concern, because it indicates there may be very little genetic variation available that could be exploited in a breeding program to improve the cultivated *vexillata*. To some extent, the fact that the 3 wild *vexillata* accessions from IITA clustered less closely with the Bali accessions suggests that these accessions may provide a source of genetic variation in a breeding program. In particular, the wild *vexillata* accessions may be useful as a source of traits for enhancing the tolerance of cultivated *vexillata* to environmental stresses.

CONCLUSION

1. Large variations in morpho-agronomic traits were observed between genotypes.
2. Cultivated forms of *V. vexillata* from Bali exhibited some distinct differences from their related wild genotypes of African origin.

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