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

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**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 the 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 different 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. *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, 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 was 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 Belgia, 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                     | V. biflora (1) | V. sesquipedalis (3) | V. unguiculata (1) | V. vexillata (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                      | 0.00                        |
| 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                      | 0.00                        |
| Pistil length (cm)         | 2.95           | 3.55                 | 3.50               | 5.10             | 51.86          | 48.14        | 77.04**                  | 0.294                       |
| Sament 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        | 2.39**                   | 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 ≥0.05, P ≤0.05, and P ≤0.01 respectively.
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 accessions, 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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