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Diversity and Evolutionary Relationship Among Four Cultivated and Two Wild Species of Vigna

S. AUDILAKSHMI* AND K. P. S. CHANDEL**

National Bureau of Plant Genetic Resources, New Delhi

Cultivated Vigna *species*; mung *bean* (V. radiata *(L.) Wilczek*), urad *bean* (V. mungo *(L.) Hepper) and their wild occurring putative progenitors*; V. radiata *var.* sublobata *Verdc. and* V. mungo L. *var.* silvestris *Lukoki, Marechal and Otoul respectively were studied along with rice bean* (V. umbellata *(Thunb.) Ohwi and Ohashi) and* V. trilobata *Ait. The data from experimental biology demonstrated discrete variation among variable populations of different* Vigna *species. Four distinct groups emerged showing that all the four cultivated species are distinct and have diverse and independent origin, while var.* silvestris *showed continuous variation with* urad *bean suggesting close affinity and direct lineage from above putative progenitor.*

Mung bean (*V. radiata* (L.) Wilczek, *urad* bean (*V. mungo* (L.) Hepper, rice bean (*V. umbellata* (Thunb.) Ohwi and Ohashi and *V. trilobata* Ait. are cultivated in India as pulse and forage crops. While the two putative progenitors, *V. radiata* var. *sublobata* Verdc. and *V. mungo* L. var. *silvestris* Lukoki marechal and Otoul are predominently wild and occur in natural/disturbed habitats. The *mung* bean and *urad* bean have evolved directly from above wild types respectively (Lukoki *et al.*, 1980; Chandel, 1980, 1981, 1984; Chandel *et al.*, 1984.)

There are about 22 species of *Vigna,* both cultivated and wild that occur in India (Arora, 1984). *V. radiata* var. *sublobata, V. mungo* var. *silvestris, V. vexillata* and *V. umbellata* var. *major* and var. rumbaiya have been reported to occur sympatrically in sub-Himalayan region (Chandel, 1981) and some of these even show a very wide distribution occurring in the Western Ghats, Eastern Ghats, Central Deccan Plateau and North-Western Himalaya extending their distribution and adaptive range from Shiwalik hills, to Kamaon/Garhwal Himalaya, Chota Nagpur Plateau, Sikkim, North Bengal and North-Eastern Region of India (Arora, 1984). The distribution of some of these has also been documented recently from South-East Asia and Far East (Annishetty and Moss, 1987). Ironically, the taxonomic status of several Asian *Vigna* species is still in a confused state and needs critical studies (Verd-Court—personal communication, 1970). The present investigation is in the series of the studies to derive evidences from experimental biology. The genetic diversity and pattern of genetic variation (continuous or discrete) among the populations of

*Scientist, National Research Centre for Sorghum (ICAR), Rajendranagar, Hyderabad.

**Principal Scientist, National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi 110012.

six *Vigna* species would provide strong support about the evolutionary inter-relationships.

MATERIALS AND METHODS

The experiments were conducted on four culivatad *Vigna* species and two wild sub-species comprising variable populations from diverse agro-ecological habitats. The material consisted of *V. radiata* var. *sublobata* (6), *V. radiata* (2), *V. mungo* (2), *V. mungo* var. *silvestris* (8), *V. umbellata* (8) and *V. trilobata* (11). The material was grown during rainy season (July-November, 1980) at IARI farm. Each strain had 3 m long row and plants spaced 8-10 cm. Five randomely selected plants in each populations were scored for five important morphological characters. The data were averaged and plotted using metroglyph (Fig. I). Stipule index and cotyledon leaf index were used as ordinate and abcissa respectively and five characters, viz. cotyledon stalk, Ist leaf index, depth of hilum, length and density of hairs on pods were represented as rays emerging from each of the glyphs.

The interspecific crosses including reciprocals were also attempted between *V. radiata* and var. *sublobata*, *V. mungo* and var. *silvestris* (manuscript under preparation).

RESULTS

The careful observations on six *Vigna* species for germination habit and morphological characters showed that *urad* bean, *mung* bean and wild types, var. *sublobata*, var. *silvestris* and *V. trilobata* possessed epigeal germination habit and rice bean (*V. umbellata*) showed hypogeal germination. The comparative morphology of stipule showed that *V. mungo* and its wild type var. *silvestris* possess narrow linear stipules like that of *V. umbellata*. The hilum is also deep, furrowed and concave in structure. In contrast to above, *V. radiata* and its wild form *V. radiata* var. *sublobata* have broad stipules like that of *V. trilobata*. The hilum is long, linear and stretched like that of *V. umbellata*. These morphological similarities provide indications that they have close affinity. The present investigation provides experimental evidence that these are quite distinct species as they form independent groups. It is certain that they have not evolved from same common ancestor. Although sympatric variation pattern might have provided opportunities for occasional natural crossing and gene exchange. The apparent homology in morphological variation might have also been perforced by the ecological conditions.

A comparative study of the morphological characters exhibited conspicuous variation for cotyledon leaf stalk (0.05-1.3 cm), cotyledon leaf index (0.8-4.8 cm), first leaf index (0.7-4.8 cm), stipule index (1.2-5.5 cm), depth of hilum (7-50 mm), length of hairs on pods (short-long), and density of hairs on pod (very sparse-dense). The character association analysis of the *Vigna* species based on above morphological characters indicated existence of four broad groups (Fig I); group I comprised 54 plants belonging to *V. trilobata* which showed association of long cotyledonary leaf stalk (0.5-1.3 cm), broad cotyledonary leaf pair (0.8-1.7 cm.),

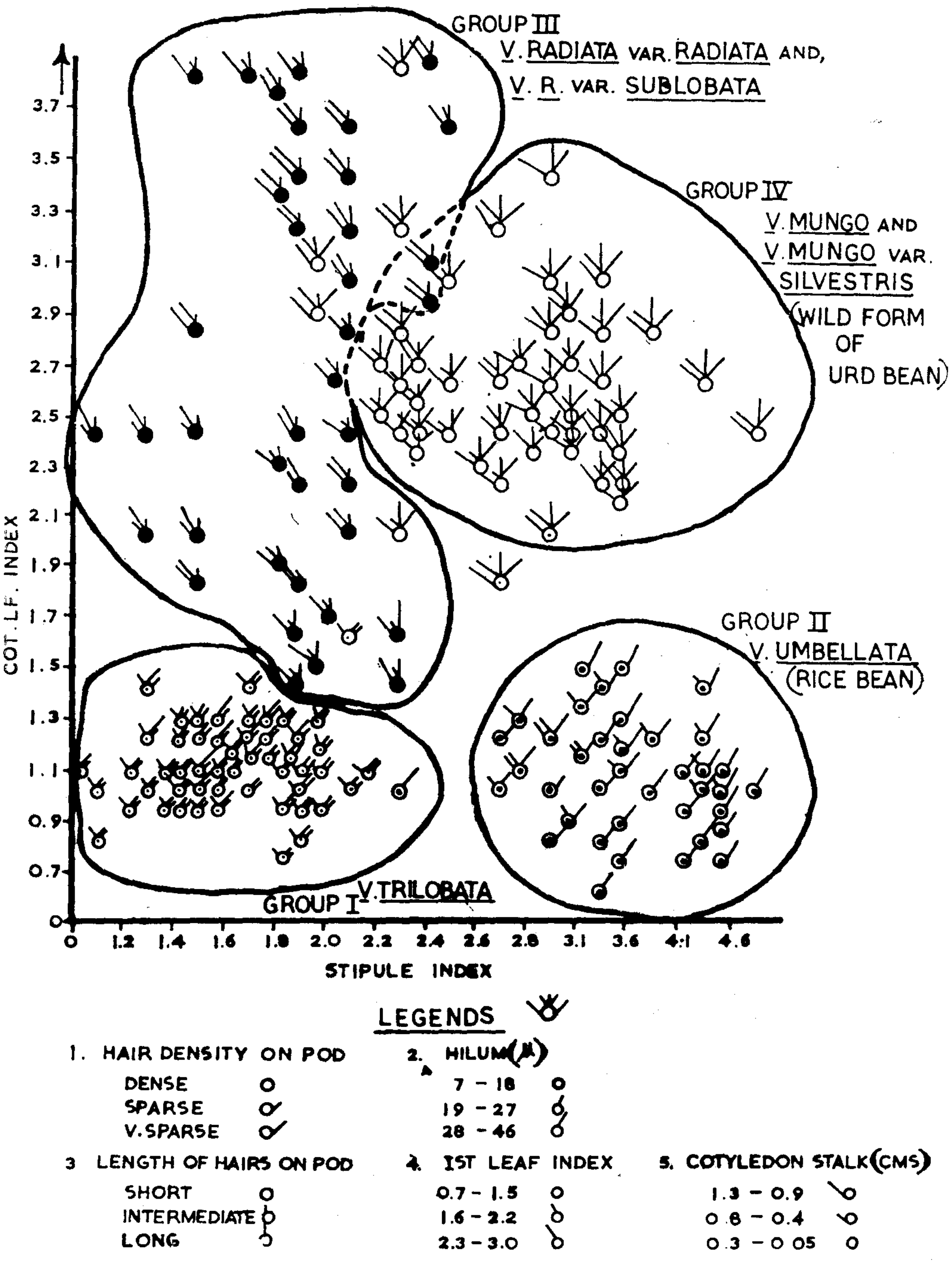

Fig. 1 Metroglyph showing inter relationships among *Vigna* species

and first leaf index (0.7-1.3 cm.), short and broad stipule (1.2-2.0 cm) very much raised hilum (19-35 mm.) and short sparse hairs on pods.

Group II consisted of 39 plants identified as *V. umbellata.* They possessed long stalk (0.6-1.3 cm), broad cotyledonary leaf pair (0.8-1.6 cm) and first trifoliate lateral leaflet (1.1-1.7 cm), narrow long stipule (2.5-4.5 cm), hilum not much raised (7-16 mm.), short and very sparse hairs on pods.

Group III comprised forty glyphs identified as *V. radiata* and its wild form *V. radiata* var. *sublobata.* They are more dispersed, showing some intermingling with *V. mungo* var. *silvestris* in one direction and *V. trilobata* on the other. The plants in this group have short cotyledonary stalk (0.05-0.4 cm), long and narrow cotyledonary leaf index 1.5-4.6 cm, first trifoliate leaf of moderate size (1.5-3.5 cm), short and broad stipule (1.3-2.5 cm), not much raised hilum (7-18 mm) and long, moderately dense hairs on pods.

Group IV comprised 50 plants which can be identified as *V. mungo* and its wild putative progenitor *V. mungo* var. *silvestris.* They have short coteledonary leaf stalk (0.05-0.2 cm), long and narrow coteledonary leaf (1.7-3.6 cm), first trifoliate leaf moderately long (1.8-3.5 cm), long and narrow stipule (2.0-5.5 cm), raised hilum (2.8-5.0 mm). and long dense hairs on pods.

DISCUSSION

The study of genetic variation showed the occurrance of intermediate forms between *V. radiata* var. *sublobata* and *V. mungo* var. *silvestris* for some morphological characters studied in the present studies. This suggests the possible natural chance outcrossing allowing introgression and restricted gene flow between the two wild putative progenitors with their respective cultigen species. It appears from the natural populations that outcrossing perhaps also occurred occasionally between the wild form of *V. radiata* var. *sublobata* and *V. radiata* var. *setulosus,* and *V. trilobata* as well as with wild forms of *V. umbellata* (var. *major* and *rumbaiya*). Normally, these species do not intercross in nature although occasional but restricted outcrossing has been documented (Chandel, 1984; Chandel *et al.*, 1988). Morphologically, the *Vigna* species were earlier grouped into three taxonomic complexes. First group included *V. trilobata* and *V. aconitifolia*; second complex consists of *V. radiata* var. *sublobata, V. mungo* and *V. mungo* var. *silvestris,* and third complex included *V. umbellata* and *V. angularis.* The species within each complex can be intercrossed and fertile hybrids are reported to have been obtained with *V. radiata* and *V. mungo* with *V. umbellata* or wi h *V. trilobata* (Dana, 1966a, 1966b; Ahn and Hartmann, 1978; Chandel, 1984). In some crosses, the F_1 hybrids are reported to be sterile despite the facts that 6-10 bivalents, out of the possible eleven were observed during meiosis (Dana, 1966a, 1966b). The detailed studies on Asian *Vigna* species (Chandel, 1980, 1984; Chandel *et al.*, 1984; Lukoki *et al*, 1980) have established conclusively the origin and evolution of *mung* bean and *urad* bean through extensive evidences from taxonomy, biochemical studies such as chromatography of leaf phenolics and protein gel electrophoresis, scanning electron microscopy of seed coat pattern and hilum structures. The quantitative data derived from independent sources was used in numerical taxonomy for drawing dendrograms each arriving at the same conclusion, (Chandel *et al.*, 1984). It was concluded that *V. radiata* and *V. mungo*, the two cultivated species in India, have independent lineage and were domesticated from two very distinct taxa namely, *V. radiata* var. *sublobata* and *V. mungo* var. *silvestris* respectively. The evidences were also supported by cytological relationship, crossing and hybridization studies, experimental biology, archaeology and phytogeographic distribution of cultivated types, their wild ancestral forms and weedy relatives. The possible area of domestications in Indian gene centre were also propounded (Chandel, 1984).

The present studies also indicated distinctness of different taxa under genus *Vigna* particularly *V. radiata* var. *sublobata*, *V. mungo* var. *silvestris*, *V. trilobata* and *V. umbellata*. The results further render support to previous investigations. The work is being intensified on all cultivated and related wild Asian species of *Vigna* using isozymes as well as cytological techniques such as DNA quantification and banding technique to elucidate relationships with other wild forms occuring in India. The evidences are likely to provide strong support and hopefully would pave the way for new opportunities in uitlization of wide genepool, particularly allowing inter-specific hybridization resulting in the improvement of cultivated *Vigna* species.

The study of the genetic variation and inter-relationship among large number of species of *Vigna* will be immensely valuable and rewarding as these species possess various useful agronomic traits, such as yellow mosaic virus disease resistance (*V. umbellata*), wide range of adaptability of *V. trilobata*, protein quality of *V. mungo* and balanced amino acids of *V. umbellata*. Such genepool offer tremendous opportunities in conventional breeding as well as in the application of biotechnology for crop improvement.

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