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4 Screening Wild *Vigna* Species and Cowpea (*Vigna unguiculata*) Landraces for Sources of Resistance to *Striga gesnerioides*

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4.1 Introduction

Cowpea (*Vigna unguiculata* (L.) Walp.), also known as black-eyed or southern pea, belongs to the genus *Vigna*, section *Catiang*, species *unguiculata*. It comprises four subspecies, namely: *unguiculata*, *stenophylla*, *dekindtiana* and *tenuis* (Ng and Marechal, 1985). The subspecies *unguiculata* is the only one cultivated, while the other three are wild relatives. Subspecies *unguiculata* is itself subdivided into four cultivar groups (cv-gr) namely (cv-gr) *Unguiculata*, *Biflora*, *Sesquipedalis* and *Textilis* (Westphal, 1974). The cv-gr *unguiculata* is the most diverse of the four and is widely grown in Africa, Asia and Latin America. Cowpea is a grain legume grown in savannah regions of the tropics and subtropics.

Cowpea is a warm-season, annual, herbaceous legume. Plant types are often categorized as erect, semi-erect, prostrate (trailing) or climbing. There is much variability within the species. Growth habit ranges from indeterminate to fairly determinate, with the non-twining types tending to be more determinate. Cowpea generally is strongly taprooted.

It is grown mostly in west and central African countries. Its value lies in its high protein content, ability to tolerate drought and the fact that it fixes atmospheric nitrogen, which allows it to grow on and improve poor soils. It is an important protein supplement in the diet of many African people (Bressani, 1985). The dry seed contains approximately 51% carbohydrates, 23–25% protein, 13% fat and 3.5% minerals. It may contribute 60% of the total protein intake of the people of the western part of Nigeria (Rachie and Rawal, 1975). However, cowpea yield is affected negatively by different biotic and abiotic factors. Yield losses in cowpea associated with *Striga gesnerioides* have been reported to be as great as 83% and 100% (Cardwell and Lane, 1995). Emechebe *et al.* (1991) reported 100% yield losses on farmers' fields in the northern Guinea savannah of Nigeria in susceptible local varieties. Yield losses associated with *Alectra vogelii* (Benth.), an obligate, root-parasitic flowering plant of the family Orobanchaceae, range between 70% and 100% (Parker, 1991; Kureh *et al.*, 1999). Various control measures, including cultural practices, chemical and biological means and host plant resistance, have been suggested (Dube and Oliver, 2001; Boukar *et al.*, 2004), but no single field method seems to be fully adequate. Efforts have been made to identify

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natural sources of genetic resistance within cowpea germplasm and in the selection and breeding of improved lines with resistance to *Striga* and *Alectra* (Singh and Emechebe, 1997).

Fatokun and Singh (1987) crossed cultivated cowpea successfully with a hairy wild relative (*Vigna pubescens*). They used tissue culture techniques to rescue the hybrid embryos, which would otherwise have shrivelled and degenerated. The F_1 plants were vigorous in growth but partially sterile, with only about 32% pollen viability. Cytological investigations of F_1 plants showed meiotic abnormalities in the pollen mother cells. These abnormalities included a few univalents and quadrivalents, suggesting some structural differentiation in the chromosomes. Barone and Ng (1990) could not obtain an interspecific cross between *V. unguiculata* and *Vigna vexillata*. They concluded that the following were barriers to crossability: lack of fertilization and collapse of fertilized ovules 5–8 days after pollination. All attempts by Fatokun (2002) to cross *V. vexillata* with various cultivated and non-cultivated cowpeas were also unsuccessful.

4.2 Materials and Methods

The studies reported here were conducted on the experimental field of the International Institute of Tropical Agriculture (IITA) at Minjibir, Kano State, Nigeria (Sudan savannah, 12° 08.997′ N, 8° 39.733′ E) during the planting seasons of 2012 and 2013. In 2012, 350 accessions of wild *Vigna* belonging to 45 different species and from 32 countries of origin collected from the Genetic Resources Center (GRC) of IITA were used for the study. Accessions of wild *Vigna* species were planted in August 2012 on a single row of 2 m length, with 75 cm and 20 cm between and within rows, respectively, per accession per replicate in a randomized complete block design in three replications with two susceptible and one resistant check. Seed of *S. gesnerioides* was pre-mixed with oven-dried sandy soil at the ratio of 1.0 g *S. gesnerioides* seed to 1.0 kg oven-dried sandy soil, and each planting hole was inoculated artificially with one teaspoonful of the mixture. Three seeds of each accession were sown per hill and thinned to two plants per stand 2 weeks later. All management practices such as weed control, insecticide application to prevent pre- and post-flowering insects were done at regular intervals.

In 2013, 280 accessions of cowpea landraces that were geographically co-located with the resistant wild *Vigna* species from the *Striga* screening experiment in 2012 were selected from the cowpea core collection available in the GRC. Seeds of the 280 accessions of cowpea landraces were planted following the same planting, field maintenance and data collection procedures as in the previous experiment in the same location in August 2013.

4.3 Data Collection

Data were collected on a number of emerged *Striga*/plot (2 m²) at 9 weeks after planting (WAP) and at harvest to assess the host support for *Striga*, and the accessions were thereafter classified using the Singh *et al.* (1997) method as follows:

Resistant (R) = no *Striga* emergence on plot.
Moderately resistant (MR) = 1–2 *Striga* emergence per plot.
Susceptible (S) = 3–4 *Striga* per plot
Highly susceptible (HS) = 5 or more *Striga* emergence per plot.

4.4 Results

Twenty-one genotypes from 11 wild *Vigna* species (*Vigna ambacensis*, *Vigna davyi*, *Vigna glabrescens*, *Vigna marina*, *Vigna mungo*, *Vigna oblongifolia*, *Vigna parkeri*, *Vigna racemosa*, *Vigna reticulata*, *V. vexillata* and *V. unguiculata* subsp. *dekindtiana*) originating from Democratic Republic of Congo, Ghana, Kenya, Japan, South Africa, Equatorial Guinea, Republic of Benin, Zimbabwe, Namibia, Costa Rica, Zambia, Republic of Niger, Gambia and Philippines, showed resistance (R) to *S. gesnerioides* with no *Striga* emergence observed in their plots. One hundred and twenty-eight accessions showed moderate resistance (MR), 155 accessions were susceptible (S), with *Striga* counts per plot ranging from 3 to 4, while 35 accessions with high levels of susceptibility (HS) had *Striga* counts per plot ranging from 5 to 7. The 45 wild

Vigna species were classified on the basis of their varying degrees of reactions to *S. gesnerioides* (Table 4.1).

Sixteen landrace accessions of cowpea *V. unguiculata*, comprising of seven from Zambia, six from Niger, two from Kenya and one from Ghana, had no *S. gesnerioides* emergence and were classified as resistant (R). Two accessions showed moderate resistance (MR), 25 accessions were susceptible (S), while 237 showed high levels of susceptibility (HS), having *Striga* counts per plot ranging from 5 to 38.

Table 4.1. Reaction of wild *Vigna* species to *Striga gesnerioides*.

Species	Number resistant (R)	Number moderately resistant (MR)	Number susceptible (S)	Number highly susceptible (HS)
V. adenantha	0	1	1	0
V. ambascensis	4	2	3	0
V. baoulensis	0	4	6	0
V. benuensis	0	1	0	0
V. comosa	0	0	2	0
V. davyi	1	0	0	0
V. dekindtiana	0	1	0	0
V. filicaulis	0	1	1	0
V. fischeri	0	1	0	0
V. friesiorum	0	1	0	0
V. frutescens	0	2	0	0
V. gentryi	0	1	0	0
V. glabrescens	1	1	0	0
V. gracilis	0	0	0	2
V. heterophylla	0	1	0	0
V. hosei	0	0	1	1
V. juruana	0	0	0	1
V. kirkii	0	2	0	0
V. lasiocarpa	0	1	0	0
V. laurentii	0	0	0	1
V. linearis	0	0	0	1
V. lobatifolia	0	0	0	1
V.longifolia	0	0	0	1
V. longiloba	0	0	0	1
V. luteola	0	0	0	1
V. macrosperma	0	0	1	0
V. marina	2	0	0	0
V. membranacea	0	1	1	1
V. minima	0	1	0	0
V. multinervis	0	1	0	0
V. mungo	1	0	0	0
V. nigritia	0	0	0	2
V. oblongifolia	4	2	0	0
V. parkeri	1	0	0	0
V. peduncularis	0	0	0	1
V. racemosa	1	1	1	0
V. radiata	0	0	1	0
V. reticulata	2	3	0	1
V. trilobata	0	1	0	0
V. triphylla	0	0	0	1
V. unguiculata	1	92	128	28
V. venulosa	0	0	1	0
V. vexillata	2	5	3	2
V. wittei	0	1	0	0

4.5 Discussion

The results of the experiments indicate that 21 accessions from the following wild *Vigna* species – *V. ambacensis*, *V. davyi*, *V. glabrescens*, *V. marina*, *V. mungo*, *V. oblongifolia*, *V. parkeri*, *V. racemosa*, *V. reticulata*, *V. vexillata* and *V. unguiculata* subspecies *dekindtiana* – are potential sources of genes for resistance to *S. gesnerioides*. However, due to the strong cross-incompatibility between cowpea and *V. vexillata* reported by Barone and Ng (1990) and Fatokun (2002), it may be difficult to access these resistance genes for incorporation into cowpea using conventional crossing methods. Interspecific crosses between the following resistant species *ambacensis*, *parkeri*, *mungo*, *racemosa*, *oblongifolia*, *reticulata*, *glabrescens* and *marina*, with cowpea (*V. unguiculata*) have not yet been reported. Further studies on cross-compatibility between cowpea and these wild relatives would be needed in case any of them is crossable. *Striga*-susceptible cowpea landrace accessions showed more host support for *Striga* emergence by having higher *Striga* counts per plot ranging between 1 and 38 compared to the wild *Vigna* species, with lesser *Striga* counts per plot across both the resistant and the susceptible accessions.

These results indicate that cowpea landrace genotypes that are geographically co-located with the resistant wild *Vigna* species could be sources of resistance to *S. gesnerioides*. TVu-997, TVu-8788, TVu-8453, TVu-5478, TVu-4806, TVu-15474, TVu-15016, TVu-15011, TVu-14980, TVu-13485, TVu-13297, TVu-13035, TVu-12470, TVu-12449, TVu-12431 and TVu-12430 were identified as potential sources of resistance to *S. gesnerioides*. They have the same geographical origins of Ghana, Kenya, Niger, Zambia and Zimbabwe, with the wild *Vigna* accessions TVNu-1070, TVNu-1083, TVNu-585, TVNu-1535, TVNu-1537, TVNu-1589, TVNu-1647 and TVNu-491 belonging to the following species: *ambacensis*, *parkeri*, *oblongifolia*, *unguiculata* and *reticulata*, respectively. Of all these resistant wild *Vigna* species, only TVNu-1589 (*V. unguiculata* subsp. *dekindtiana*) is potentially cross compatible with cowpea (*V. unguiculata*).

4.6 Conclusions

- We identified some wild *Vigna* species and landrace germplasm lines as highly resistant to *S. gesnerioides*.
- Most of the resistant wild *Vigna* species are not members of section *Catiang*, where cultivated cowpea (*V. unguiculata*) belongs.
- Accessing the *Striga* resistance genes in these wild *Vigna* species may pose a great challenge as cross-incompatibility may be a problem.
- Studies have been initiated to establish if any of the *Striga* resistance genes found in the tested wild cowpea (*V. unguiculata* ssp. *dekindtiana*) and cowpea landrace germplasm lines are allelic to those previously used in the development of resistant cowpea varieties.

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