

# Analysis of genetic diversity in *Striga gesnerioides* (Willd.) Vatke, isolates from Senegal using AFLP markers

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## Introduction:

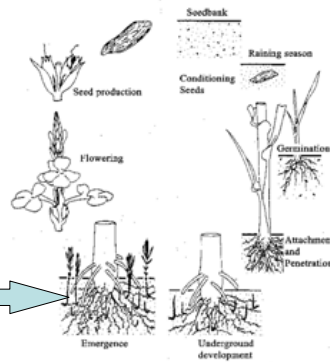
*Striga gesnerioides*, a root parasite of wild and cultivated legumes (photo 1) and non legume such as Ipomea, ... (Wade, 2000) is a major constraint to cowpea (*Vigna unguiculata*) production in Senegal. Control of the parasite by chemical means is not affordable by small farmers and presents some environmental hazards. Current controlling strategies are geared towards resistant varieties based on known differential resistance response of cowpea cultivars and breeding lines. Unfortunately, the genetic diversity of *S. gesnerioides* in Sub-Saharan Africa and in Senegal was evaluated based only on phenotypic reactions. A molecular characterization of *Striga* is needed for a better understanding of host-parasite interaction for successful genetic control of the pest.

## Materials and Methods:

- **Material:** *S. gesnerioides* seeds were randomly collected in bulk from 12 different localities during 2004 and 2005 growing seasons. The *Striga* seeds were used for molecular characterization of the 12 isolates and for differential host-parasite evaluation.



Photo: *Striga gesnerioides* on cowpea and infestation cycle



- **Differential host evaluation of Senegal isolates:** The differential host established with *Striga* races; SG1 through SG5, were evaluated in pots with the 12 isolates from Senegal.

## Molecular characterization

- **Host - parasite interactions** were established as follows: 250 ml pots filled with sand and metro-mix 250 (70:30), were planted with cowpea var. blackeye (3 seeds pot<sup>-1</sup>). Each pot was infested with *Striga* seeds. Each *Striga* isolate was present in 4 pots. Emerged *Striga* were monitored at 8-10 weeks post infestation.

- **DNA extraction and AFLP analyses.** Genomic DNA was extracted from a total of 215 individuals *S. gesnerioides* plants, using CTAB protocols (Botanga and Timko, 2005). AFLP analysis was carried using LI-COR-IR2 DNA Analyser. A total of 5 primers combinations were tested: EAAG-MCAA, EAGG-MCAT, EACA-MCAC, EACA-MCAT, EACA-MCAA.

- **Statistical analyses:** Group band AFLP frequencies were compared by a Chi-Squared test, and genetic distances between individuals were estimated using Dice's index with the NTSYS-pc 2.0. Cluster analysis was performed on the distance matrix with the unweighed pair-group method using arithmetic mean (UPGMA). Nei's between population differentiations (GST) was calculated using the POPGENE1.32.

## Results:

- From the results of the host evaluation experiment (Table 1), it appeared that the race of *Striga* present in Senegal is closely related to the race described in Mali (Lane *et al.*, 1996; Singh *et al.*, 1997).

- **Molecular diversity:** There was a clear separation between the 12 populations of *Striga* ( $\chi^2 = 15196$ ,  $df = 2475$ ,  $p < 0.0001$ ). Of the 226 AFLP bands, 148 bands explained up to 97% of the total diversity

- Comparison of AFLP profiles of individuals from different populations revealed that considerable inter-population variability exists within the race of parasite present in Senegal (Table 2). This genetic variability traduced well geographical distances between sampling locations. Genetic distances between isolates from Sindieng and other isolates were largest (Table 2).

Table 2: Differential resistance response of various cowpea cultivars and breeding lines to races of *Striga gesnerioides* in Senegal

Cultivars	West African race of <i>S. gesnerioides</i>					
	SG1 BurkinaFaso	SG2 Mali	SG3 Nigeria Niger	SG4 Benin	SG5 Cameroon	SG2 Senegal
IT81D-994	R	R	S	R	S	R
B301	R	R	R	S	R	R
58-57	R	S	S	R	R	S
Tvx-3236	S	S	S	S	S	S
Suvita 2	R	R	S	R	S	R
Blackeye	S	S	S	S	S	S
UVA-	S	S	S	S	S	S
UCR1115						

Table 2: Nei pairwise genetic distances between isolate of *Striga generioides* from Senegal

Population	Keur Boumi	Darou Alfa	Khandiar	Kourty	Maka Bira Gieye	Ndalame	Ndangalma	Ndatt Fall	Ngalbane	Ngoye	Pakhame Kouye	Sindieng
Keur Boumi	-											
Darou Alfa	0.4090	-										
Khandiar	0.2654	0.2562	-									
Kourty	0.3097	0.2616	0.2713	-								
Maka Bira Gieye	0.3683	0.2531	0.2456	0.1641	-							
Ndalame	0.2641	0.3132	0.2605	0.2900	0.1852	-						
Ndangalma	0.2585	0.3051	0.2548	0.3536	0.3100	0.2076	-					
Ndatt Fall	0.3344	0.2876	0.2395	0.3048	0.2535	0.2191	0.1847	-				
Ngalbane	0.2774	0.2763	0.1612	0.2791	0.2496	0.1805	0.1888	0.2094	-			
Ngoye	0.2741	0.2938	0.2788	0.3153	0.2371	0.1438	0.2208	0.2613	0.1824	-		
Pakhame Kouye	0.2292	0.3061	0.1485	0.2781	0.1995	0.2351	0.2297	0.2327	0.1343	0.2455	-	
Sindieng	0.5141	0.4628	0.3850	0.4874	0.3531	0.3156	0.3882	0.3895	0.4093	0.3085	0.3885	-

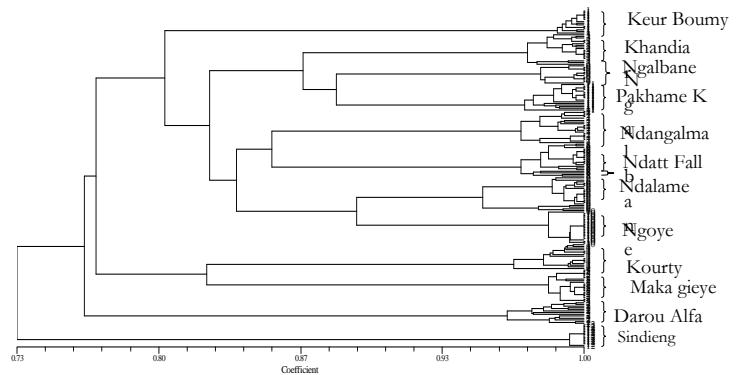


Fig.1. Dendrogram established on the basis of the UPGMA cluster analysis for Jaccard (1908) estimates of genetic similarity based on AFLP analysis with two selective primer combinations

The UPGMA cluster analysis divides the populations into 3 distinct clades sharing about 80% similarity. Two single clade contains the population from Sindieng and Darou Alfa while the other population tended to cluster together indicating their relative geographical proximity.

## Conclusion:

Race 2 of *S. gesnerioides* is present in Senegal. It is characterized by a relatively high within population genetic diversity allowing its adaptation to the varying local environment present in Senegal.

## References:

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- 3-Singh, B.B. and Emechebe A. M. 1997. Advances in cowpea research and *Alectra*. In *Advances in cowpea research*. Edited by Singh, B.B. Moha, Bani, K.F. Dehghani, A. IITA (IUPAS, P. 215-224)