TROZ Centre for Agriculture in the Tropics and Subtropics

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ARRESTING THE SCOURGE OF *STRIGA* ON SORGHUM IN AFRICA BY COMBINING THE STRENGTHS OF MARKER-ASSISTED BACKCROSSING AND FARMER-PARTICIPATORY SELECTION

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Background

Sorghum (*Sorghum bicolor*) is one of the most important grain crops in Africa south of the Sahara. However its production in sub-Saharan Africa is seriously affected by the parasitic weed *Striga hermonthica*, with yield losses reported up to 100% (see Figure 1).

Figure 1. Devastating effect of *Striga hermonthica* on sorghum (R. Folkertsma, October 2005, Gezira, Sudan)

As part of an integrated *Striga* management, locally adapted farmer preferred sorghum varieties (FPSVs) are currently being introgressed with *Striga*-resistant quantitative trait locus (QTL) alleles from sorghum line N13 through marker-assisted backcrossing (MAB) in breeding programs by NARS in Eritrea (NARI), Kenya (KARI), Mali (IER) and Sudan (ARTC). Five *Striga* resistance QTL of line N13 have previously been validated across five different environments, over 2 years and independent genotype samples (Haussmann *et al.*, 2004) and thus are robust and excellent candidates for marker-assisted selection (MAS) (Figure 2).

In order to ensure the long term success of the project, it is important to identify appropriate channels for rapid seed dissemination to the farmers. In addition, farmers need to set-up self sustainable seed production systems. Therefore, along with the MAB program, a study of the seed system (for seed dissemination) as well as gene flow studies are important in order to prevent *Striga*-resistance dilution due to inflow of pollen from Striga susceptible sorghum from farmers diverse fields. The results of this study could also be used by commercial seed companies.

Set/ year	Percentage phenotypic variation (R^2) explained by the QTL in Position (linkage group /cM)															N QTL	V_e exp
	A 5	A 65	A 120	A 165	A 185	B 15	B 65	C 30	D1 50	E 50	F 100	H 125	I 90	J 5	J 70		
197	13		15	16	24		17	10			14	10	30	19	15	11	79
298		27			21	11	22		41	17			15	12	29	9	82
R^2 [%]	6-10		11-15		16-20		21-25		26-30		31-35		36-40		41-45		

Fig. 2 QTL for area under *Striga* number progress curve (ASNPC) in RIP2 (N13 × E36-1), combined across 5 test locations (Haussmann *et al.*, TAG 2004) (↑) arrow indicating the 5 common QTL present in both years.

Results and Project status

1a. Generating backcross generations

At the onset of the project, the NARS in Eritrea (NARI), Kenya (KARI), Mali (IER and UB) and Sudan (ARTC) each have identified FPSVs to be enriched with *Striga* resistance from resistant donor N13. Crosses were made between the FPSVs and N13 and up to two backcross generations have been generated during the first year (Figure 3).

1b. MAS

NARS in Kenya and Mali have optimized DNA extraction and PCR procedures for MAS of sorghum for SSR markers linked to the *Striga* resistance QTL. for the SSR markers linked to *Striga* resistance. SSR markers showing clear polymorphism between N13 and the FPSVs were identified and applied to confirm the hybrid status of the F1 seeds obtained. The NARS are currently

Objectives

1. Production of Striga resistant FPSVs through MAB.
2. Study outcrossing rates as well as pollen dispersal patterns of the selected FPSVs in order to develop guidelines of on-farm seed production by farmers.
3. Study farmer seed system from socio-economic and population genetic point of view.

Results and project status continued…….

screening the BC1F1 plants in order to identify plants with one or several QTL to be backcrossed with FPSV.

2a. FPSV outcrossing rates

For outcrossing rates of FPSVs, seed families (panicles) have been collected from farmer's fields in Eritrea, Kenya and Sudan in 2004. DNA has already been isolated from 30 families (8 progenies per family). The samples are currently being genotyped with SSR markers at ICRISAT, Nairobi (see Figure 4). Maximum likelihood algorithms will be used to infer the genotype of the mother plant and to estimate the extend of outcrossing in the FPSV.

2b. Pollen dispersal

In order to assess the extend of pollen dispersal of each of the FPSVs, an experiment has been set up during the long rains at Kiboko (Kenya). The FPSV from Kenya, Ochuti, has been planted in the centre of the field, with three different male sterile breeding lines (Atx623, ICSA404 and ICSA88006) radiating from the center in 8 directions, up to 100m. Seed set on each of the male sterile breeding lines will be assessed at different distances from Ochuti (0, 1, 5, 10, 25, 50, 100 meters) and their hybrid nature will be confirmed. The same experiment will be repeated with the other FPSVs in other locations.

3. Seed system analysis

The formal and informal sorghum seed sector has been poorly mapped in Eritrea, Kenya and Sudan. A socio-economic study is already underway in the main sorghum growing areas in Eritrea, Kenya and Sudan. Parallel to the socio-economic study, seeds will be sampled from target villages to study the genetic diversity of these samples to compare the results of the socio-economic study with population genetic data.

Fig.3 Crossing activity in October 2005, Halhale, Eritrea (R. Folkertsm)

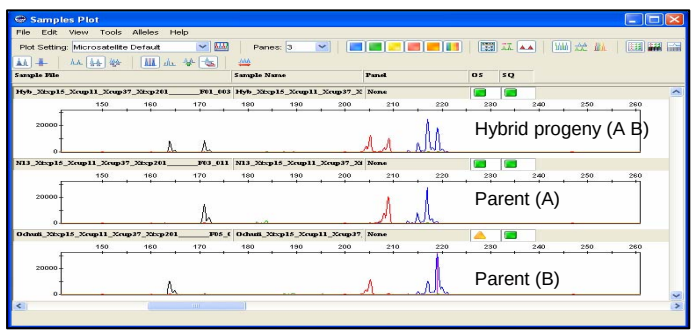

Fig. 4 Screening SSR markers with unequivocal detection of hybrids/ heterozygotes

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