

Research Application Summary

**Strengthening breeding for resistance to Turcicum leaf blight in sorghum:  
Mapping of resistance quantitative trait loci**

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**Abstract**

Sorghum cultivars grown in East and Central Africa are susceptible to various foliar diseases, of which turcicum leaf blight, caused by *Exerohlium turcicum*, causes severe damage. The best way to control foliar diseases is by breeding resistant sorghum genotypes. This can be best done with the help of marker assisted breeding technology and also by deploying multiple genes that confer either qualitative or quantitative resistance. In this research project, we intend to identify quantitative trait loci and molecular markers tightly linked with resistance to *Exerohilum turcicum*.

Key words: Quantitative trait loci, resistance, sorghum, Turcicum leaf blight

**Résumé**

Les cultivars de sorgho cultivées en Afrique orientale et centrale sont susceptibles à diverses maladies foliaires, dont la rouille des feuilles turcicum, causée par l'*Exerohlium turcicum*, provoque de graves dommages. La meilleure façon de lutter contre les maladies foliaires est la reproduction de génotypes de sorgho résistant avec l'aide de la reproduction assistée par les marqueurs et aussi par le déploiement de plusieurs gènes qui confèrent une résistance qualitative ou quantitative. Dans ce projet de recherche, nous avons l'intention d'identifier les traits quantitatives de loci et les marqueurs moléculaires étroitement liés à la résistance aux *Exerohilum turcicum*.

Mots clés: les caractères quantitatifs de loci, la résistance, sorgho, la rouille de la feuille turcicum

**Background**

Sorghum (*Sorghum bicolor* L. Moench), which originated in tropical and subtropical regions of Africa (Doggett, 1988), is an important feed and fodder crop. It is grown in a total area of 47 million ha worldwide, with annual 69 million tons of grain

production and average of 1.45  $\text{tha}^{-1}$  productivity (FAOSTAT, 2012). Turcicum leaf blight is widespread and endemic in East and Central Africa (Ramathani *et al.*, 2011; Beshir *et al.*, 2012). Estimated sorghum losses caused by Turcicum leaf blight in Africa, Asia and the Americas are up to or greater than 50% in susceptible sorghum varieties (Beshir *et al.*, 2012). The best way to control this disease is by breeding resistant sorghum genotypes with help of marker assisted breeding (Mohan *et al.*, 2010). The effect of this disease can also be reduced by deployment of multiple genes that confer either qualitative or quantitative resistance (Ogliari *et al.*, 2007). Efficient introgression of targeted genomic regions with minimal linkage drag is the overall objective of this project. And to achieve this, there is need to characterise genomic regions such as quantitative trait loci (QTL) that have influence on turcicum leaf blight.

### Literature Summary

Molecular marker technology greatly facilitates the study of complex traits as fungal disease resistance (Paterson *et al.*, 2008). Resistance to sorghum Turcicum leaf blight is quantitative and its breeding is often compounded by genotype by environment interactions (Beshir *et al.*, 2012). Sequenced Characterised Amplified Region Marker (SCAR) and Simple Sequence Repeats (SSR) markers associated with Turcicum leaf blight resistance have been reported (Boora *et al.*, 1999; Mittal and Boora, 2005). A new plant resistance gene is located on chromosome five in sorghum (Martin *et al.*, 2011). DNA-based molecular markers delimiting disease resistance loci in sorghum have been reported for head smut, downy mildew, grain mold, and drechslera leaf blight, target leaf spot, zonate leaf spot (Mohan *et al.*, 2010). Characterisation of resistance loci associated with resistance to Turcicum leaf blight will support effective resistance breeding in sorghum. Success in breeding for disease resistance in sorghum will depend on complete understanding of the interaction of the genetics of sorghum foliar diseases resistance and other traits influencing disease resistance (Ramathani *et al.*, 2011).

### Study Description

Molecular characterisation of germplasm will be done at the International Crops Research Institute for Semi Arid Tropics in Kenya. In total, 160 recombinant inbred lines (RILs) from cross between MUC007/009; a resistant line to Turcicum leaf blight and Epuripuri; a farmer preferred susceptible variety will be evaluated.

The morphological characterisation of RILs were earlier evaluated at the National Semi-Arid Resources Research Institute (NaSARRI) and Makerere University Agricultural Research Institute Kabanyolo (MUARIK) both in Uganda. Disease severity and area under progress curve were computed and plant color and 50% dates to flowering (Beshir *et al.*, 2012) determined. The genetic analysis of materials and molecular marker identification will be done using the genotyping-by-sequencing protocol (Elshire *et al.*, 2011).

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