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Research Application Summary

Introgressing resistance to *Turcicum* leaf blight and mapping of associated quantitative trait loci in sorghum

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Abstract

Screening for *Turcicum* leaf blight was carried out in F_2 and $F_{2:3}$ segregating sorghum populations under field and controlled conditions. Disease severity as a percentage of leaf area covered by lesions was computed and the lesion type was characterized. The disease severity of F_2 plants indicated a major dominant gene for resistance while $F_{2:3}$ disease scores suggested quantitative inheritance. The two lesion types segregated monogenically among the $F_{2:3}$ lines. Single marker analysis showed that the major gene for the resistance to *Turcicum* leaf blight is probably located close to the sorghum plant's locus for colour and to Xtxp95 in the sixth chromosome in the sorghum genome map.

Key words: Inheritance, sorghum, SSR markers, *Turcicum* leaf blight

Résumé

Le test de dépistage pour la rouille de feuille de *Turcicum* a été effectué dans les populations de sorgho F_2 et $F_{2:3}$ séparées sur le champ et dans les conditions controlées. La sévérité de la maladie, prise comme le pourcentage de la surface de la feuille couverte par des lésions, a été calculée et le type de lésion a été caractérisé. La sévérité de la maladie des plantes F_2 a indiqué un gène dominant important pour la résistance tandis que les présents résultats de la maladie de $F_{2:3}$ ont suggéré une transmission de caractère quantitative. Les deux types de lésion se sont isolés d'une manière controlée par un seul gène parmi les lignées $F_{2:3}$. L'analyse du marqueur simple a prouvé que le gène principal pour la résistance à la rouille de feuille de *Turcicum* est probablement situé près de la position du gène de la plante de sorgho pour la couleur et à Xtxp95 dans le sixième chromosome dans la représentation du génome du sorgho.

Mots clés: Héritage, sorgho, marqueurs SSR, Rouille de feuille de *Turcicum*

Background

Sorghum [*Sorghum bicolor* (L.) Moench], a C4 grass that diverged from maize about 15 million years ago (Mullet, 2001), is the fifth major cereal crop in the world after wheat, rice, maize and barley (FAO, 2003). It has relatively small genome of 750 million base pairs (Arumuganathan and Earle, 1991). *Turcicum* leaf blight, which is caused by the pathogen *Exserohlium turcicum*, is one of the most destructive foliar diseases of sorghum (Ogliari1 *et al*., 2007). It is a fungal disease that originated under humid conditions (Mohan *et al*., 2009). The most feasible way to control *Turcicum* leaf blight is by breeding and deploying resistant sorghum genotypes, using for example, marker assisted breeding deploying genes that confer either qualitative or quantitative resistance (Ogliaril *et al*., 2007). Currently, however, there is limited information on use of molecular markers for improving sorghum for resistance to *Turcicum* leaf blight. The aim of this research was to determine the inheritance to *Turcicum* leaf blight found in Accession 9, and to identify molecular markers for marker- assisted breeding for *Turcicum* leaf blight resistance.

Literature Summary

Turcicum leaf blight is one of the most destructive foliage diseases of sorghum and can cause yield losses of up to 50% (Ogliari1 *et al*., 2007). The most observed symptom of Sorghum *turcicum* leaf blight are long elliptic lesions that develop first on the lower leaves and progress upward; and the lesions vary from small cigar – shaped lesions to complete destruction of the foliage (Welz, 2000). In Uganda, studies have shown that the disease epidemics are largely due to amounts of infested maize residues in farm fields (Adipala *et al*., 1993) although wind-blown conidia may cause widespread secondary spread. The mechanism of resistance in sorghum to single infection by *Exerohilum turcicum* is not yet fully confirmed.

One simple sequence repeat (Mittal *et al*., 2005) and one sequence characterized amplified regions (SCAR) (Boora *et al*., 1999) markers linked to the locus for sorghum *Turcicum* leaf blight resistance have been identified. In sorghum, a relationship between pigmented plant and resistance to foliar and panicle diseases has also been documented (Mohan *et al*., 2009). The genomic region flanked by plant colour locus (*Pclor*) and simple sequence repeat marker Xtxp95 on the sixth linkage group harbours disease response QTL for zonate leaf spot (ZLS), target leaf spot (TLS) and drechstera leaf blight (DLB) (Mohan *et al*., 2009).

Study Description

Field and laboratory experiments were conducted at Makerere University Agricultural Research Institute Kabanyolo in central Uganda. Population of F_2 plants and derived $F_{2:3}$ and $F_{2:4}$ lines were used to map quantitative trait loci (QTL) for resistance to TLB. Simple sequence repeats (SSR) were selected from the sixth chromosome on the sorghum genome map (Mace *et al*., 2009). The F_2 segregating population and $F_{2:3}$ and $F_{2:4}$ segregating families (from Accession 9, resistant, crossed with Epuripuri, susceptible) were inoculated. Disease severity (DS) was scored weekly as a percentage of leaf area covered by lesions, and the area under the disease progress curve (AUDPC) was computed. Appropriate statistical analysis (correlation, regression and Chi-square) were conducted using GenStat discovery edition 12.

Findings

The disease severity in F_2 plants in the screenhouse exhibited a bimodal pattern consistent with a major dominant gene for resistance ($\chi^2=0.04^{ns}$), despite there being no difference between the parents in that environment (Fig. 1a). In the field, the resistant parent showed a much lower severity of disease than did the susceptible parent. The $F_{2:3}$ disease scores almost matched a normal distribution, suggesting quantitative inheritance (Fig. 1b). There was no correlation between F_2 and F_3 scores, despite the fact that the F_3 showed highly significant differences between lines.

The two parents had distinctly different lesion types, with the resistant parent displaying narrow lesions with a distinctly red border (N) and the susceptible parent wider lesions with no red border (W). The two distinct lesion types segregated monogenically among the $F_{2:3}$ lines (73.4 (N): 131.6 (Segreg): 69 (W), $\chi^2= 0.57^{ns}$). Significantly, a higher number of individuals with low disease severity was associated with the N lesion type. A significant relationship was detected between the $F_{2:3}$ disease severity and the $F_{2:3}$ percentage for resistance lesion type (F=5.7*). The lack of consistency for disease severity between environments emphasizes the need for a carefully planned evaluation, and highlights the potential benefit of selection using molecular markers as selection criteria that are independent of the environment.

The polymorphic simple sequence repeat marker Xtxp95 showed a highly significant association with the lesion type for resistance (N) in $F_{2:3}$ segregating families (F=64.83***). Marker Xtxp95, which is linked to plant colour locus in

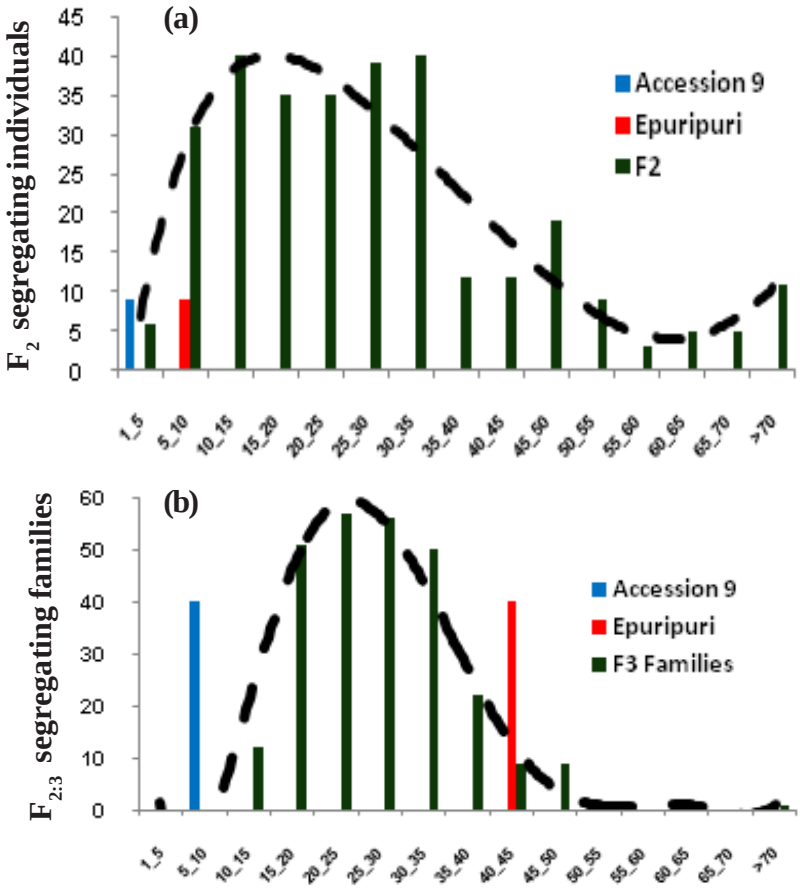

Figure1. F_2 segregating individuals' and $F_{2:3}$ segregating families' disease severity scores. (a) F_2 segregating population percentage disease severity scores skewed towards resistance disease severity scores. (b) $F_{2:3}$ segregating families' disease severity scores showing a normal distribution.

chromosome six, was used to screen the extracted DNA of the 304 F_2 segregating population. Single marker analysis for Xtxp95 showed that 26% of the variability in the resistant lesion type is linked with its segregation (R^2=26%***). $F_{2:4}$ data will be compared with the $F_{2:3}$ data and with several additional molecular markers.

Research Application

The major resistance gene to *Turcicum* leaf blight is probably located close to the sorghum plant's locus for colour and to Xtxp95 in the sixth chromosome in the sorghum genome map.

Recommendation

It is recommended that simple sequence repeat marker Xtxp95 be used in marker assisted breeding programmes. Also, using of resistant sorghum varieties is still the most feasible way to control *Turcicum* leaf blight.

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