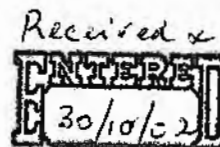


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Plain English Summary

The primary aim of this study was to investigate a range of strategies for the identification of molecular markers linked with Verticillium wilt response in cotton. The research was carried out on the parental *G. hirsutum* cultivars Sicala V-1 (wilt-tolerant) and Siokra 1-4 (wilt-susceptible) together with progeny derived by crossing these plants. A new disease grading system based on foliar symptoms, vascular discolouration and plant stunting was developed in order to compare plant responses to Verticillium wilt disease following pathogen inoculation. A study of inheritance showed for the first time that a single genetic locus, designated *VwRI*, was responsible for tolerance to Verticillium wilt in Sicala V-1.

The use of two different molecular marker techniques revealed a low but workable level of DNA polymorphism between the parental cultivars. Molecular marker analysis of progeny plants identified three markers (V8-180, V35-70 and V35-180) as being linked with Verticillium wilt tolerance. Although the markers were not tightly linked to *VwRI*, assays for various combinations of these markers enabled the differentiation of disease-tolerant and -susceptible plants with 100% and 82% reliability, respectively. These molecular markers therefore have the potential for use in marker-assisted selection during the breeding of disease tolerant cotton cultivars.