Identification of quantitative trait loci associated with anthracnose resistance in sorghum [Sorghum bicolor (L.) Moench]

Nikhil Y. Patil1, William L. Rooney2, S. Delroy Collins2, A. Millie Burrell1, Patricia E. Klein1
1Department of Horticultural Sciences, Texas A&M University, College Station, TX 77843, USA
2 Department of Soil and Crop Sciences, Texas A&M University, College Station, TX 77843, USA

INTRODUCTION

Anthracnose in sorghum, caused by the fungal pathogen Colletotrichum sublineolum Henn. is a major biotic constraint to forage and grain production. Anthracnose is prevalent in hot, humid, tropical and subtropical regions and affects all parts of the plant making it one of the most damaging diseases of grain sorghum. Yield losses ranging from 50-70% have been reported in susceptible cultivars of sorghum. The variable nature of the fungus and limited knowledge of the genetics of host-pathogen interactions makes it a challenging task to control the disease. While agronomic practices have been proven inefficient, employment of host plant resistance is regarded as an effective means for controlling anthracnose. Multiple sources of genetic resistance to different races of the pathogen exist among the sorghum genotypes. Identifying and pyramiding these multiple anthracnose resistance genes into elite germplasm will provide effective and durable resistance against the pathogen.

The main objective of this study was to map at high resolution the genomic region harboring resistance to anthracnose using two mapping populations and develop molecular markers for use in marker-assisted breeding.

METHODS AND MATERIALS

Mapping population

Two mapping populations, each consisting of 100 recombinant inbred lines (RIL) were derived by crossing BTx623, an anthracnose susceptible line with two different anthracnose resistant lines, SC-414 and SC-155.

RESULTS

Phenotyping

The RIL populations were screened for anthracnose resistance in four environments: 2011, 2012 and 2013 in College Station (CS), TX and 2013 in Tifton, GA using a randomized complete block design with two replications.

Phenotypic data analysis indicates that the anthracnose ratings were consistent among the parental genotypes in different environments, however, the RILs displayed a wide range of disease severity. This is explained by highly significant genotype and genotype x environment effects. Linkage maps constructed for BTx623 x SC414 and BTx623 x SC155 RIL populations consisted of 857 and 514 SNPs spanning a total map length of 1732.6 cM and 498.5 cM, respectively. In the BTx623 x SC414 RIL population, a major QTL explaining 40% of the phenotypic variation was identified on chromosome 5 in three of the four environments having ~181 genes within 1 LOD interval and ~88 genes at the peak marker position. For the BTx623 x SC155 RIL population, a major quantitative trait locus (QTL) was identified on chromosome 10 in three of the four environments examined, which explained 10-20% of the phenotypic variation and had ~716 genes and ~124 genes within 1 LOD interval and at the peak marker position, respectively. The information provided by these QTLs will be of significance in marker-assisted pyramiding of multiple sources of anthracnose resistance into elite susceptible germplasm.

REFERENCES