

# **A Mitogen-Activated Protein Kinase Kinase Kinase Gene Conferring Quantitative Foliar Disease Resistance in Maize**

Zhong, Tao<sup>1</sup>; Xue, Shang<sup>2</sup>; Olukolu, Bode<sup>1</sup>; Bian, Yang<sup>2</sup>; Wisser, Randall<sup>3,4</sup>; Holland, James<sup>2,5,6</sup>; Yang, Qin<sup>7</sup>; Balint-Kurti, Peter<sup>1,5</sup>

<sup>1</sup> Dept. of Entomology and Plant Pathology, North Carolina State University, Raleigh, NC, USA 27695

<sup>2</sup> Dept. of Crop and Soil Sciences, North Carolina State University, Raleigh, NC, USA 27695

<sup>3</sup> LEPSE, University of Montpellier, INRAE, Institut Agro Montpellier, Montpellier, FR 34000

<sup>4</sup> Dept. of Plant and Soil Sciences, University of Delaware, Newark, DE, USA 19716

<sup>5</sup> Plant Science Research Unit, USDA-ARS, Raleigh, NC, USA

<sup>6</sup> NC Plant Science Initiative, North Carolina State University, Raleigh, NC, USA

<sup>7</sup> State Key Laboratory of Crop Stress Resistance and High-Efficiency Production and College of Agronomy, Northwest A&F University, Yangling, China

Corresponding author: [tzhong3@ncsu.edu](mailto:tzhong3@ncsu.edu)

Southern leaf blight (SLB), caused by the necrotrophic fungal pathogen *Cochliobolus heterostrophus*, is a major foliar disease of maize worldwide. Here, we used an association mapping panel consisting of 270 diverse inbred lines with high-density genetic markers to dissect the genetic basis of SLB resistance. Fourteen single nucleotide polymorphism (SNPs) variants were significantly associated with SLB resistance, thirteen of which co-localized with previously reported SLB quantitative resistance loci (QRL), corresponding to ten candidate genes. Using a combination of mutant and transgenic analysis we demonstrated that one of the candidate genes, *ZmMAPKKK45*, encoding a mitogen-activated protein kinase kinase kinase (MAPKKK), was the causal gene conferring SLB resistance at a locus defined by two associated SNPs on chromosome 3. We additionally demonstrated that *ZmMAPKKK45* conferred resistance to two other foliar disease of maize, northern leaf blight (NLB) and gray leaf spot (GLS), and enhanced production of reactive oxygen species (ROS) during the defense response. Furthermore, we found *ZmMAPKKK45* enhances ROS production, probably by increasing the expression of maize respiratory burst oxidase homolog genes (*ZmRBOHs*) and we suggest that this is associated with its effect on multiple disease resistance.