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Single SNP- and Haplotype-Based Association Analysis of Anthracnose Disease Caused By *Colletotrichum Dematium* in Spinach (*Spinacia oleracea*)

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Partagas 2 (Tropicana Las Vegas)

Henry O. Awika, Texas A&M AgriLife Research, Weslaco, TX

Kimberly Cochran, Texas A&M AgriLife Extension, Uvalde, TX

Renesh Bedre, Texas A&M AgriLife Research, Weslaco, TX

Kranthi Mandadi, Texas A&M AgriLife Research, Weslaco

Carlos A. Avila, Texas A&M AgriLife Research, Weslaco, TX

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Anthracnose caused by *Colletotrichum dematium* is an important disease in commercial spinach fields resulting in up to 100% yield lost. Sources of genetic resistance need to be identified and molecular tools developed to expedite cultivar development. Unfortunately, since spinach has traditionally been treated as a minor crop, the development and use of genomic tools have been slow compared to more extensively cultivated crops. In this study we evaluated marker discovery for resistance to anthracnose by testing how well haplotype-based SNP-trait modelling compares to single-marker in identifying polymorphic features with strong association signal to anthracnose. Alleles in linkage disequilibrium (LD) were tagged in haplotype blocks, and the haplotype tag (ht) SNPs used in genome wide association study (GWAS). We also implemented the single marker testing to offer a comparison to haplotype-based tests in the same population. A diverse collection of 276 spinach accessions were inoculated and scored for disease severity. Anthracnose-associated molecular markers were identified using ddRADseq-generated single SNPs (SSNP), pairwise ht (htP) and multi-marker ht (htM). The results showed that after multiple testing correction, unique-marker anchoring genes identified by SSNP were 13, htP were 24 (~63% more) and htM were 34 (~162% more). Of these markers, 6 were uniquely identified using SSNP, 13 uniquely using htP, and 19 uniquely htP. The results suggest that resistance to anthracnose is polygenic and that haplotype-based analysis may have more power than SSNP. We recommend the use of a combination of these methods for molecular marker discovery in Spinach.

Key words: Anthracnose, *Colletotrichum dematium*, haplotype, Spinach, SNP

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