ASSOCIATION MAPPING FOR DETECTING QTLS FOR FUSARIUM HEAD BLIGHT AND YELLOW RUST RESISTANCE IN BREAD WHEAT

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ABSTRACT

ASSOCIATION MAPPING FOR DETECTING QTLS FOR FUSARIUM HEAD BLIGHT AND YELLOW RUST RESISTANCE IN BREAD WHEAT

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Yellow rust (YR), caused by *Puccinia striiformis*, and Fusarium head blight (FHB), caused by *Fusarium graminearum*, are two of the most important wheat diseases in the world. Both pathogens cause severe losses in yield and in the case of FHB, there is an additional concern related with mycotoxin production, which induces serious toxicological problems in human and animals. Breeding for resistance for both diseases has been considered as the most practical strategy of control. To identify sources of resistance and detect regions responsible of resistance to these diseases in wheat germplasm, an association mapping panel (AMP) of 297 spring wheat lines developed by the International Maize and Wheat Improvement Center (CIMMYT) was assembled. The AMP was evaluated for resistance to *P. striiformis* and *F. graminearum* in Mexico and Ecuador over two years. The AMP was screened with 8,632 SNP markers included in the wheat 9K chip from Illumina® and 66 SSR markers from the wheat consensus map. A total of 3,701 SNP and 33 SSR markers were informative and were used to perform analyses in the wheat AMP. Genotypic data was used to estimate the population structure and determine the extent of linkage disequilibrium in the panel. Genotypic and phenotypic data was used to identify marker trait associations.
The structure analysis determined that the panel can be separated in three sub-populations. The extent of LD was different for each genome with major differences between linkage groups in the D-genome. Association analysis with GLM method

detected significant regions associated with yellow rust resistance on chromosomes 1A, 2A, 5A, 6A, 7A, 2B, 5B, 6B, 7B, and 3D, however, the analysis with the MLM method detected significant regions on chromosomes 1A and 2A. The association analysis conducted for Fusarium head blight resistance using the GLM detected regions significantly associated with resistance on chromosomes 4A, 7A, 2B, 5B, and 7B and using the MLM method the regions associated with resistance were located on chromosomes 2B and 7B. In the association analysis for DON concentration with GLM the regions associated with resistance were detected on chromosomes 4A, 5B, 7B, and 2D. However, no significant regions were detected with the MLM method.

This study allowed the identification of several sources of resistance for yellow rust and Fusarium head blight as well as the identification of several molecular markers linked to regions responsible for resistance to these two important diseases. Additionally, the wheat AMP panel showed to be a source of genetic diversity. The findings reported here can be applied to wheat breeding by different programs interested in spring wheat. Finally, the SNP chip utilized to conduct the genotypic analysis was found to be a very useful tool to conduct association analysis studies. However, more coverage on the D-genome might be necessary in spring wheat populations.