Identification of genes / QTLs for yellow rust resistance using association mapping in durum wheat

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INTRODUCTION

Durum wheat (Triticum turgidum L. cv. durum) is the raw material by excellence for pasta manufacturing. In Argentina, the cultivated area comprise 129,255 ha (2020/21), distributed in the Southeast of Buenos Aires, the Central and the Northwest regions. Diseases such as stripe rust or yellow rust (YR) caused by Puccinia striiformis f.sp. tritici (Pst) reduce the yield of the crop. The appearance of new highly virulent breeds has made YR a serious disease in Argentina and worldwide. Genetic resistance is one of the most effective methods to prevent these losses.

MATERIALS AND METHODS

A total of 197 cultivars and breeding lines were evaluated for: 1) yellow rust resistance at field conditions, under natural and controlled infection in four growing environments: Argentina (Pieres, Barrow [2017] Bordenave [2020]) and Mexico (Toluca 2019), inoculated with the race MX16-04, virulent on Yr24 / 26); 2) the response to infections at seedling stage using two races collected locally (Yr19-21, Yr19-48W). A matrix of 4,854 neutral SNPs (35K Axiom®) and nine KASP SNPs located in genes were used (Roncallo et al. 2021).

Association mapping was performed using the MLM (Q + K) method in Tassel 5.2 (Bradbury et al. 2007) and was validated in Gapit 3.0. The subpopulation structure was obtained by DAPC (Jombart et al., 2010).

RESULTS

A low linkage disequilibrium (DL) was estimated throughout the genome (13.37%, p <0.01), with a DL decay below 0.2 at 11.8 Mb.

The SNP markers identified over several environments are promising. The association analysis with annotated genes of the durum wheat genome assembly (cv Svevo) and the characterization of haplotypes continue. The detected regions at 1B and 7B are interesting candidates for fine mapping and KASP marker development.

CONCLUSIONS

The SNP markers identified over several environments are promising. The association analysis with annotated genes of the durum wheat genome assembly (cv Svevo) and the characterization of haplotypes continue. The detected regions at 1B and 7B are interesting candidates for fine mapping and KASP marker development.