

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.

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

Table 1. SNPs markers associated with yellow rust resistance. na: not associated at field

Marker	Chr.	Position (bp)	Environments	YR race
AX-94517050	1A	292309850	2	Yr19-48W
AX-94470806	1A	292345413	2	Yr19-48W
AX-94415624	1A	358935538	3	
AX-94518188	1A	361869439	3	
AX-94492604	1A	521233447	na	Yr19-21
AX-94768537	1B	388487714	3	
AX-95174732	1B	389602791	3	
AX-95179739	1B	389834615	3	
AX-94563763	1B	390668095	3	
AX-94405550	1B	671592338	3	
AX-95240708	2A	82931331	2	Yr19-48W
AX-94620950	2A	742004273	3	
AX-94393920	2A	743529060	2	Yr19-48W
AX-95091262	2B	765289491	4	
AX-94566585	3A	659334984	3	
AX-94867205	4B	1400057	1	Yr19-21
AX-94926956	4B	624321352	2	Yr19-48W
AX-94535421	5B	654423508	3	
AX-94421698	6A	538525251	3	
AX-95629214	6A	538824385	3	
AX-95007288	6B	311521254	na	Yr19-21
AX-94626053	7B	112888785	4	
AX-94517805	7B	682322089	2	Yr19-48W
AX-95242246	7B	697128429	2	Yr19-21
AX-94750339	7B	703525207	3	
AX-94385063	7B	706052957	2	Yr19-21

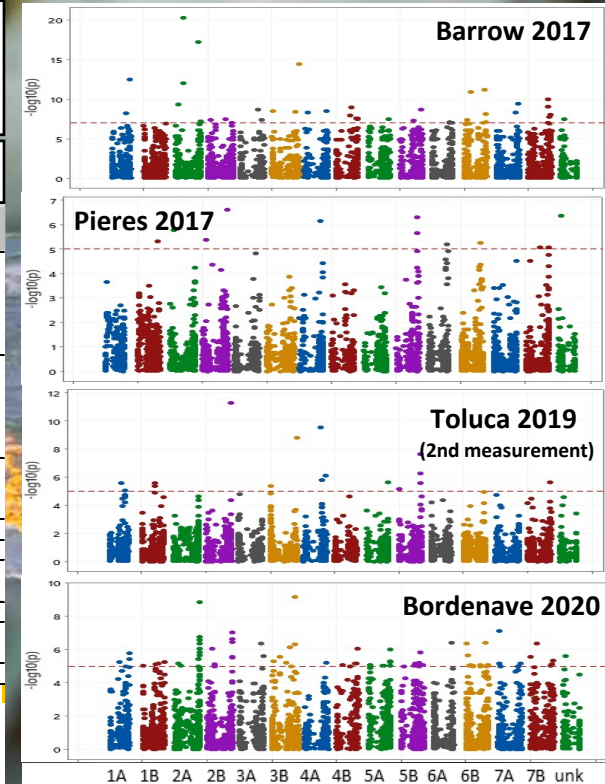


Fig. 2 Association mapping results (MLM [Q + K]) for yellow rust resistance in durum wheat

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.

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)

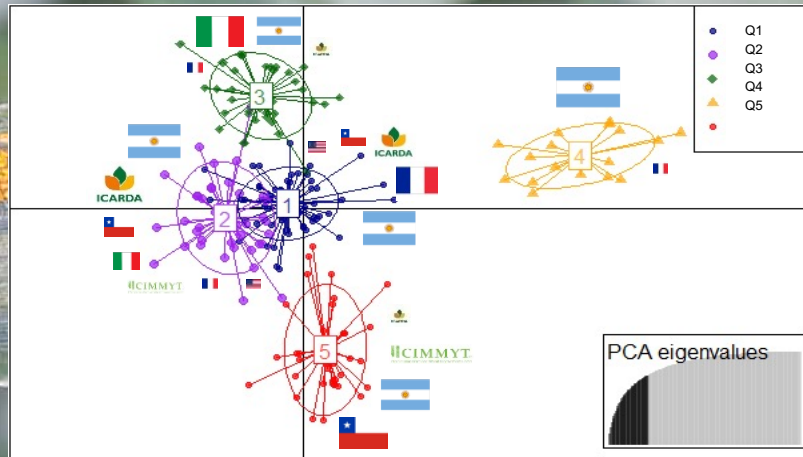


Fig. 1 Subpopulation structure of the durum wheat collection

SNPs associated with yellow rust resistance in adult plant and/or for a specific race at seedling stage were identified (Table 1, Fig. 2). Four SNPs were located in an interval of 2.18 Mb on chr. 1B. Two regions located on chr. 2B and 7B were mapped in the 4 field trials. The distal region of chr. 7BL was associated with SNPs close to a gene cluster encoding RPM1 and NBS-LRR resistance proteins. Eleven genotypes showed high levels of resistance in at least 3 environments and only 3 in the total of the environments.

Referencias:
 Bradbury PJ, et al., Buckler ES (2007). Bioinformatics 23:2633-2635.; -Jombart T, et al., Balloux, F (2010). BMC Genetics 11: 94.
 Roncallo et al. (2021). BMC Genomics