

New APR QTL for leaf rust and stripe rust in seven genetic populations

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Leaf rust



Wheat leaf rust (LR, A) and stripe rust (YR, B), caused by the air-borne fungi *Puccinia triticina* (Pt) and *Puccinia striiformis* f. sp. *tritici* (Pst), respectively, are considered the primary biotic threats to bread wheat and durum wheat production globally.

Our study aimed to identify and locate adult plant resistance (APR) to leaf rust and stripe rust in both bread wheat and durum wheat based on 7 recombinant inbred line (RIL) populations

Materials & Methods

Plant materials and field trials

The genetic basis of resistance to both leaf rust and stripe rust have been analyzed in four bread wheat RIL populations derived from crosses Avocet/Francolin #1, Avocet/Kenya Kongoni, Avocet/Kundan, and Avocet/Sujata, while resistance to leaf rust in three durum wheat RIL populations of Atred#1/Bairds, Atred#1/Dunkle and Atred#1/Quetru

Phenotype and Genotype

The parents and RILs were phenotyped for leaf rust response at Ciudad Obregon, Mexico, and the bread wheat populations for stripe rust response at Toluca under artificial inoculations over 3-5 seasons. The parents and RILs were genotyped with 50K diversity arrays technology (DArT) sequence system and simple sequence repeat (SSR) markers.

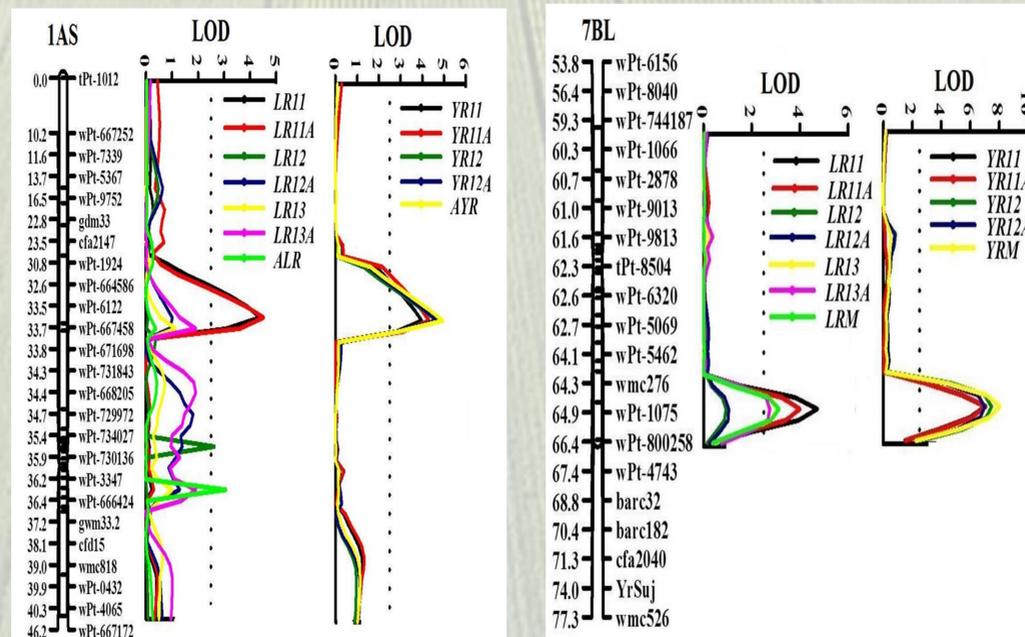
Map construction and QTL analysis

Linkage map and QTL analysis were generated using Joinmap 4.1 and IciMapping 4.0, respectively.

Abstract

Bread wheat lines Francolin #1, Kenya Kongoni, Kundan and Sujata, and CIMMYT-derived durum wheat lines Bairds, Dunkler and Quetru display an adequate level of APR to both leaf rust and stripe rust in Mexican field environments. Known pleiotropic APR genes *Lr46/Yr29* mapped in all of seven RIL populations, and explained 7.4-65.1% and 7.7-66.1% severity variations for LR and YR across different bread wheat populations and accounted for 12.4-60.8% of LR severity variations over three durum wheat populations. In addition, several new APR loci identified on chromosomes 1AS, 1DS, 2BS, 2BL, 3D and 7BL in bread wheat and QTL on chromosome 6BL in durum wheat. Among these loci, QTL on chromosomes 1AS and 7BL might be represent new co-located/pleiotropic loci conferring APR to LR and YR. RILs combining these APR loci can be used as sources of complex APR in both bread wheat and durum wheat breeding. In addition, the closely linked single nucleotide polymorphism (SNP) markers have been converted into breeder-friendly kompetitive allele specific PCR (KASP) markers and their diagnostic verified.

Results for bread wheat



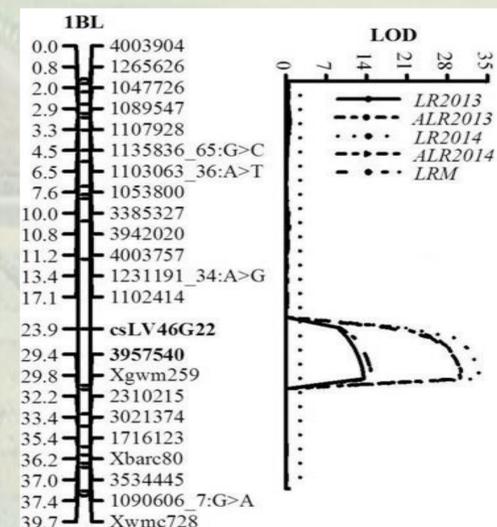
PVEs: YR for 10.5-13.8% and LR for 7.9-8.2%

PVEs: YR for 16.6-20.4% and LR for 5.7-13.0%

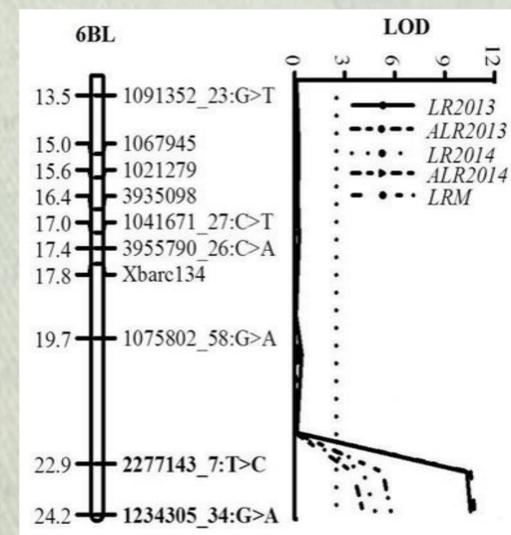
Table 1. list of developed KASP markers for rust breeding

KASP markers	Sequence	Chromosome
Td_c31624_230_A	aataataaccattagctcgaacA	1BL (Yr26)
Td_c31624_230_B	aataataaccattagctcgaacC	
Td_c31624_230_common	tctcatcAatcgccagagataC	
RAC875_c20775_540_A	gcatatGcattGgtttgaaacT	1BL (Yr26)
RAC875_c20775_540_B	gcatatGcattGgtttgaaacG	
RAC875_c20775_540_common	ctagttgtgataaacgggtgaC	
D_GB5Y7FA02JMPQ0_238_A	gcggagttcgtgctgtaT	4DS (Yr28)
D_GB5Y7FA02JMPQ0_238_B	gcggagttcgtgctgtaC	
D_GB5Y7FA02JMPQ0_238_common	cgaactcctcctgaactcC	
BS00108770_51_A	CTCTGCCCTTGGCGGT	4DS (Yr28)
BS00108770_51_B	CTCTGCCCTTGGCGGC	
BS00108770_51_common	CTGAGGGGGAGAGTTTGCCTA	
2277143_111:T>C_A	GGAACCTCCTGTTAGTAACG	6BL for LR (Bairds)
2277143_111:T>C_B	GGAACCTCCTGTTAGTAACA	
2277143_111:T>C_common	AAAAGACAAAGAAGAAAGAAGGA	
1234305_141:G>A_A	cctctaagctgggTcCaC	6BL for LR (Bairds)
1234305_141:G>A_B	cctctaagctgggTcCaT	
1234305_141:G>A_Common	gCagcttcagacgCTaagAttaG	
AX-95155193_A	GAAGGTGACCAAGTTCATGCTactgttcggccttctcta	6BL-LrQ (Quetru)
AX-95155193_B	GAAGGTGCGAGTCAACGGATTactgttcggccttctctatcC	
AX-95155193_Common	tgacggctaacttgactgtga	

Results for durum wheat



PVE: 22.9-92.3% for LR



PVE: 13.1-30.9% for LR

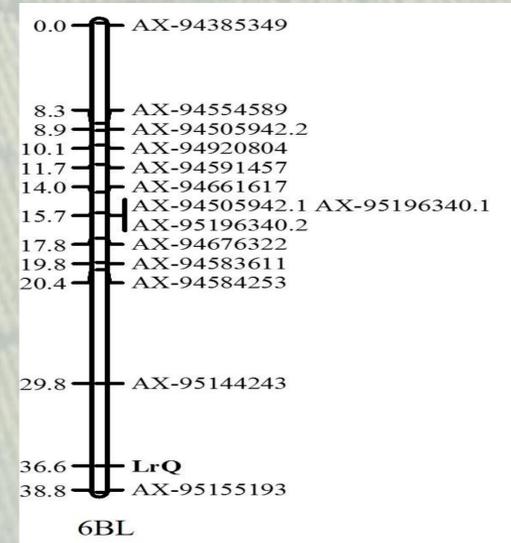


Fig.1. Linkage map of a new race-specific APR gene from Quetru

Acknowledgement

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