Plant Science 252 (2016) 222–229

Contents lists available at ScienceDirect

Plant Science

journal homepage: www.elsevier.com/locate/plantsci

Genome wide association mapping of stripe rust resistance in Afghan wheat landraces

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ARTICLE INFO

Article history:
Received 14 April 2016
Received in revised form 28 July 2016
Accepted 30 July 2016
Available online 1 August 2016

Keywords:
Afghan wheat landraces
Stripe rust
GWAS
Genotyping-by-sequencing

ABSTRACT

Mining of new genetic resources is of paramount importance to combat the alarming spread of stripe rust disease and breakdown of major resistance genes in wheat. We conducted a genome wide association study on 352 un-utilized Afghan wheat landraces against stripe rust resistance in eight locations. High level of disease variation was observed among locations and a core-set of germplasm showed consistence performance. Linkage disequilibrium (LD) decayed rapidly ($R^2 \approx 0.16$ at 0 cM) due to germplasm peerless diversity. The mixed linear model resulted in ten marker-trait associations (MTAs) across all environments representing five QTL. The extensively short LD blocks required us to repeat the analysis with less diverse subset of 220 landraces in which R^2 decayed below 0.2 at 0.3 cM. The subset GWAS resulted in 36 MTAs clustered in nine QTL. The subset analysis validated three QTL previously detected in the full list analysis. Overall, the study revealed that stripe rust epidemics in the geographical origin of this germplasm through time have permitted for selecting novel resistance loci.

1. Introduction

Stripe rust, caused by *Puccinia striiformis* f. sp. *tritici* (*Pst*), is one of the most destructive fungal diseases that can limit wheat production worldwide. Grain yield losses can reach 40% and up to 100% under severe infections [1]. Moreover, the recent breakdown of the race-specific resistance gene *Yr27*, a gene present in several commercial varieties in Asia and Africa, caused yield losses between 10% and 80% in many countries of Central West Asia and North Africa (CWANA) region [2]. Managing stripe rust epidemics is difficult and using resistant cultivars carrying both major and minor resistance genes is the best way to control stripe rust [3]. The continuous evolution of pathogens creates a need to develop new resistance cultivars through time. Two type of wheat resistance genes have been found and deployed in different breeding programs which are 1) race-specific and 2) race-nonspecific genes [4,5]. Race specific genes usually shows major resistance against *Pst* while race nonspecific genes are minor genes that are usually expressed in the adult stage and supposed to be affective against all *Pst* races, theoretically. Due to the rapid evolution of the rust pathogen population, different breeding programs are now focusing on pyramiding both race-specific and race nonspecific resistance genes to improve the resistance durability [6,7]. So far, about 67 designed and 42 temporarily named stripe rust resistance

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http://dx.doi.org/10.1016/j.plantsci.2016.07.018
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