

The genetic basis of spectral reflectance indices in drought-stressed wheat

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Abstract Drought imposes a major constraint over the productivity of wheat, particularly in arid and semi-arid production zones. Here, the genetic basis of spectral reflectance indices was investigated in drought-stressed wheat by comparing, under two contrasting moisture regimes, the performance of an F₆ recombinant inbred line (RIL) population bred from a cross between the drought tolerant cultivar Pavon76 and the sensitive cultivar Yecora Rojo. The parents and RILs were genotyped with respect to both a set of microsatellite (SSR) loci and a number of known drought-responsive genes. In all, 28 quantitative trait loci (QTL) controlling dry weight per plant, water content of the above-ground biomass, leaf water potential, canopy temperature, and spectral reflectance indices traits were identified. The loci were distributed over 11 chromosomes, belonging to each of the three wheat sub-genomes. There were important location-flanking markers *Barc109* and *Barac4* on chromosome 5B relating to dry weight per plant accumulation under the limited irrigation

regime. The same region-harbored QTL associated with leaf water potential, canopy temperature, and ratio index under the limited irrigation regime. Linkage between the known drought-responsive genes and aspects of the drought response was established. Some of QTL were of substantial enough effect for their linked markers to be likely usable for the marker-assisted breeding of drought tolerance in wheat.

Keywords High throughput · Quantitative trait loci · Microsatellite · *Triticum aestivum*

Introduction

Drought imposes a major constraint over crop productivity in environments where moisture is limiting. In wheat, yield losses can vary from 10 to 90 %, depending on the timing and intensity of the stress and the addition pressure caused by the simultaneous presence of other stresses (Reynolds et al. 2004). Breeding for drought tolerance has proven to be difficult, largely because plants employ various mechanisms to cope with the stress (Tuberosa and Salvi 2006). The genetic basis of tolerance, therefore, is commonly described as highly polygenic (Ravi et al. 2011), reflecting both the major uncertainty surrounding the choice of traits to be measured and the difficulty of ensuring an appropriate and controllable experimental growing environment. Advances in genetic mapping and functional genomics technologies have nevertheless allowed some progress to be made in defining the genetic basis of tolerance (Worch et al. 2011; Saleh et al. 2014). The hope is that once linked markers and/or candidate genes have been identified, improvements can be made via marker-assisted breeding.

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