

Detection of QTLs for heat tolerance in wheat measured by grain filling duration

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ABSTRACT

Heat stress is a major environmental stress limiting wheat productivity in most cereal growing areas of the world. In order to map and characterize quantitative trait loci controlling heat tolerance, 144 recombinant inbred lines derived from the cross of Kauz and MTRWA116 along with the parents and ten local cultivars were evaluated by normal and late sowing in a rectangular lattice design in a very hot area. Grain filling duration was used as a measure of heat tolerance. One hundred and sixty six SSR and 3 AFLP markers were used to construct a linkage map containing 18 linkage groups and covering 16 chromosomes of wheat. With the method of composite interval mapping one major QTL was detected for heat tolerance, measured by grain filling duration, on chromosomes 2D. Closely linked to Xgwm484, the QTL was appeared in both normal and stressed conditions.

INTRODUCTION

Heat stress is a major limitation to wheat (*Triticum aestivum* L.) productivity in arid, semiarid, tropical, and subtropical regions of the world (Fischer, 1986). Consequently, development of heat-tolerant cultivars is of major concern in wheat breeding programs. Lower grain weight and altered grain quality result from heat stress during grain-filling due to the reduced availability and translocation of photosynthates to the developing kernel, decreased starch synthesis and deposition within the kernel (Bhullar & Jenner, 1985). Grain filling duration has been widely used as a measurement of heat tolerance (Fokar *et al.*, 1998). It is proved that heat tolerance is quantitatively inherited and continuously distributed (Blum 1988, Yang *et al.* 2002). QTL mapping offers important information on the number and location of the loci that control quantitative traits and may provide a useful method for marker assisted selection (Liu 1998). To our knowledge, the only study concerning QTLs for heat tolerance is that of Yang *et al.* (2002). They detected two QTLs for heat tolerance measured by grain filling duration with the method of single factor analysis in an F₂ population. They were, therefore, unable to map and localize the QTLs. The objective of this study was to map and characterize quantitative trait loci controlling heat tolerance measured by grain filling duration and to find the molecular markers associated with them.

MATERIAL AND METHODS

The plant population studied consisted of 144 F₉ recombinant inbred lines (RILs) originating from a cross between Kauz (Jupatco F73 / Blue Jay // Urest T81) and MTRWA116 (PI372129 / 2*Pondera). Kauz has been developed in CIMMYT, Mexico, and is known as tolerant to high temperature while MTRWA116 is an unreleased experimental line from Montana State University (USA) and is considered as thermo-sensitive (Fokar *et al.* 1998; Ibrahim and Quick 2001). 144 RILs along with the parents and ten local check cultivars were planted in two separate rectangular lattice designs under normal and late sowing conditions in a very hot province of Iran (Bushehr). Grain filling duration was used as a measure of heat tolerance.

The marker genotypes of 144 RILs were assessed with 166 wheat SSRs and 3 AFLPs. For the construction of the genetic map, linkage analysis was performed with the program MAPMAKER (Lander *et al.* 1987) using the Haldane mapping function. The genetic map used for QTL mapping comprised 81 marker loci (997.4 cM) with an average marker density of 6.6 cM. This covers 16 chromosomes of wheat including 1A, 1B, 2A, 2B, 2D, 3D, 4B, 4D, 5A, 5B, 5D, 6B, 6D, 7A, 7B and 7D. The QTL analysis was performed by the software package PLABQTL (Utz and Melchinger 1996) based on composite interval mapping (CIM). Co-factors were assessed by the procedure cov SELECT.

RESULTS AND DISCUSSION

Grain filling in both stress and normal condition showed transgressive segregation suggesting that a sufficient variation is present in the population for QTL analysis and that the alleles of both parents contribute to heat tolerance.

One major QTL was detected for grain filling duration, on chromosomes 2D (Table 1). Closely linked to Xgwm484, the QTL was appeared in both normal and stressed conditions (figure 1) with LOD >6 and R² >20. Negative effects indicate that the allele from Kauz contributes to a higher heat tolerance. It makes sense as it is the tolerant parent. Yang *et al.* (2002) reported two QTLs linked to gwm11 and gwm293 for heat tolerance which were not detected in our study. The reason might be: (1) the QTLs were detected in a F₂ population passing only one meiosis and the recombination might, therefore, happen during the subsequent generations, and

(2) these loci were possibly not segregating in our population. Further researches are needed to unravel the genetic structure of heat tolerance and to confirm the QTLs detected.

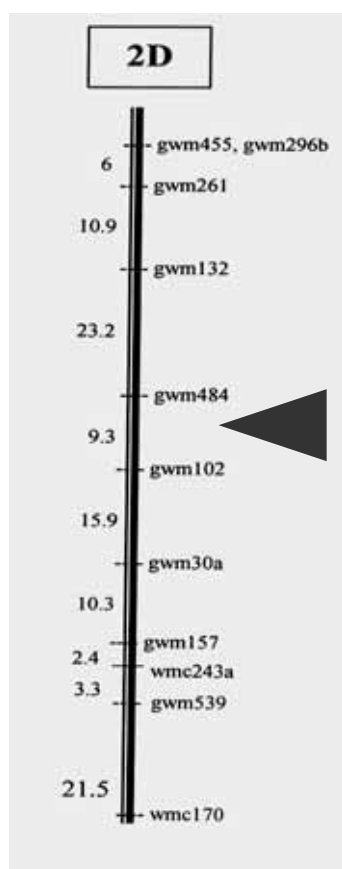


Fig.1. Position of QTL detected for heat tolerance measured by grain filling duration

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Table 1. QTLs for heat tolerance measured by grain filling duration under normal and heat-stressed conditions

Condition	Nearest marker	Position [†]	Confidence interval	LOD	R ²	Additive effects [£]
normal	Xgwm484	2D (42)	30-46	6.45	20.4	-1.58
stress	Xgwm484	2D (42)	40-46	7.53	22.5	-1.42

[†] The number in parenthesis shows the position on the chromosome of the QTL in cM

[£] Negative effects indicate that the allele from Kauz contributes to a higher heat tolerance