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Single nucleotide polymorphisms linked to quantitative trait loci for grain quality traits in wheat

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ABSTRACT

Wheat (*Triticum aestivum* L.) grain quality traits that are controlled by quantitative trait loci (QTL) define suitable growing areas and potential end-use products of a wheat cultivar. To dissect QTL for these traits including protein content (GPC), test weight (TW), single kernel characterization system (SKCS)-estimated kernel weight (SKW), kernel diameter (KD), kernel hardness measured by near-infrared reflectance spectroscopy (NIRS) hardness index (NHI), and SKCS-hardness index (SHI), a high-density genetic map with single nucleotide polymorphism (SNP) and simple sequence repeat (SSR) markers was developed using recombinant inbred lines (RILs) derived from Ning7840 × Clark. The RILs were evaluated for these quality traits in seven Oklahoma environments from 2001 to 2003. A total of 41 QTL with additive effects on different traits were mapped on most wheat chromosomes, excluding 1A, 2A, 3D, 4D, 6D, and 7B. Seven chromosome regions showed either tightly linked QTL or QTL with pleiotropic effects on two to four traits. Ten pairs of QTL showed additive × additive effects (AA), four QTL were involved in additive × environment (AE) effects, and one was involved in AA/E effects. Two to eleven QTL for each of the six traits and 139 tightly linked markers to these QTL were identified. The findings shed light on the inheritance of wheat grain quality traits and provide DNA markers for manipulating these important traits to improve quality of new wheat cultivars.

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1. Introduction

Grain protein content (GPC), test weight (volumetric grain weight, TW), kernel weight (KW), kernel size (KS), and kernel

hardness (KH) are important grain quality traits in bread wheat (*Triticum aestivum* L.). Quantitative trait locus (QTL) analysis for GPC has been extensively studied and a large number of QTL were reported to cover all 21 wheat chromosomes

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