



Dynamic QTL analysis of protein content and glutamine synthetase activity in recombinant inbred wheat lines

H.M. Li^{1,2}, H. Liang¹, Z. Li¹, Z.X. Tang¹, S.L. Fu¹, Y.Y. Geng², B.J. Yan¹ and Z.L. Ren¹

¹Sichuan Agricultural University, Chengdu, Sichuan, China

²Hebei University of Engineering, Handan, Hebei, China

Corresponding authors: B.J. Yan / Z.L. Ren

E-mail: yanbenju@sicau.edu.cn / renzllab@sicau.edu.cn

Genet. Mol. Res. 14 (3): 8706-8715 (2015)

Received October 30, 2015

Accepted April 28, 2015

Published July 31, 2015

DOI <http://dx.doi.org/10.4238/2015.July.31.19>

ABSTRACT. Protein content (PC) is a crucial factor that determines the end-use and nutritional quality of wheat (*Triticum aestivum*). Glutamine synthetase (GS), which is a major participant in nitrogen metabolism, can convert inorganic nitrogen into organic nitrogen. Although many studies have been conducted on PC and GS, a dynamic analysis of all of the filling stages has not been conducted. Therefore, 115 F₉₋₁₀ recombinant inbred wheat lines of 'R131/R142' were used to analyze PC and GS activity during different developmental stages, using the conditional quantitative trait loci (QTL) mapping method. Twenty-two and six conditional QTL were detected for PC and GS activity, respectively. More QTL in leaf PC were detected during the early filling stages than in the later filling stages. Grain PC QTL displayed different dynamic variations to leaf PC QTL during the entire grain-filling stages. All of the QTL were expressed differently over time, and nine conditional QTL were detected across two filling stages. QTL with similar functions may have tended to group in specific locales. This study provides dynamic

genetic information on protein accumulation during grain-filling stages.

Key words: Wheat; Protein content; Conditional QTL; Glutamine synthetase; Dynamic QTL mapping