

Dynamic Changes of Wheat Quality during Grain Filling in Waxy Wheat WX12

J. NI, B. FENG, Z. XU and T. WANG

Chengdu Institute of Biology, Chinese Academy of Sciences, 610041 Chengdu, China;
e-mail: wangtao@cib.ac.cn

Abstract: Changes of quality traits such as grain sugar, starch, and protein content in full waxy and normal wheat in field grown samples was studied during grain filling. Compared to the normal line, the soluble sugar, sucrose and pentosan contents were higher in the waxy isolate. The highest pentosan content in waxy wheat was 22–27 days after flowering (DAF), while the highest fructan content was 7–12 DAF. In addition, the quality dynamic changes of two wheat lines were similar except for starch content during grain filling, the V_{\max} of starch synthesis were highest at 17–22 DAF in the waxy line, while this was at 22–27 DAF in the normal line. The results indicated that according to the different dynamic changes between waxy and common wheat, the quality of waxy wheat may be improved by optimum cultivation measures.

Keywords: filling stage; protein; starch; sugar; waxy wheat

Granule-bound starch synthase (GBSS), also known as the waxy (Wx) protein, is a key enzyme for amylose synthesis in wheat. Common wheat has three genes, *Wx-A1*, *Wx-B1* and *Wx-D1*, located on chromosome 7AS, 4AL and 7DS, respectively, that encode GBSS. Full waxy wheat (amylose-free) is deficient in all three GBSS, while partial waxy wheat lacks one or two waxy proteins (NAKAMURA *et al.* 1993a, b; MIURA & TANII 1994; YAMAMORI *et al.* 1994). After full waxy wheat was produced by combining three null alleles at *Wx* loci (NAKAMURA *et al.* 1995), researchers have focused on the processing quality of waxy wheat (HOSHINO *et al.* 1996; KIRIBUCHI-OTOBE *et al.* 1997; YASUI *et al.* 1997; ZHAO & SHARP 1998). However, less attention was paid to waxy wheat sugar, starch, protein changes during grain filling in waxy wheat.

In this study, a full waxy wheat line Nuomai 12 (WX12) and its near isogenic line (NIL) common wheat Chuanyu 12 (CY12) were used to identify waxy wheat grain sugar, starch, protein content,

and the differences of dynamic changes on quality between waxy and common wheat during grain filling. This research could provide useful information for improving waxy wheat quality by cultivation techniques.

MATERIAL AND METHODS

Full waxy wheat line Nuomai 12 (WX12) and common wheat Chuanyu 12 (CY12) were chosen for the study as they are near-isogenic lines.

The field experiment was conducted in the farm of the Chengdu Institute of Biology (CIB) from year 2008 to 2009. Plots were 5 × 1 m, with row spacing of 20 cm and plant spacing of 10 cm. WX12 and CY12 were grown, and the plants were managed with recommended high-yield practices until maturity. Plants were sampled at 7, 12, 17, 22, 27, 32, 37, and 42 days after flowering (DAF). The kernel samples were killed immediately at 105°C

Table 1. Grain soluble sugar, starch and protein content in WX12 and CY12 (in %)

Variety	Soluble sugar	Sucrose	Pentosan	Fructan	Starch	Protein
WX12	4.35 ^a	3.91 ^a	5.77 ^a	1.62 ^a	71.46 ^a	11.49 ^a
CY12	3.48 ^b	2.93 ^b	5.10 ^b	1.49 ^a	73.08 ^a	11.60 ^a

Different small letters meant significant difference at 0.05 probability level

and oven-dried at 80°C to constant weight, and the grain were then milled and used for the determination of sugar, starch and protein content.

Starch was determined by polarimetric analysis (GB/T15685-1995). Soluble sugar and sucrose were determined by Anthracenone Colorimetry (Experimental Manual on Plant Physiology 1985). Phloroglucinal Spectrophotometric Method was used to determine pentosan content (DOUGLAS 1981). Fructan content was determined by AOAC method 999.03.

Statistical analyses were done with SPSS statistical software.

RESULTS AND DISCUSSION

Comparison of soluble sugar, starch and protein contents in WX12 and CY12

The soluble sugar, sucrose, and pentosan contents in the seeds of WX12 were significant higher than that of CY12. However, the starch and protein contents in the seeds of WX12 were measured as lower than that of CY12 (Table 1), but were not statistically significant. These differences may result from the mutations in the three GBSS genes, which could affect the starch and protein synthesis in the grains.

Dynamic change of grain sugar, starch during grain filling stage in WX12

The soluble sugar decreased most at 17–22 DAF in WX12, while it decreased most at 17–27 DAF in CY12 (Figures 1 and 2). The soluble sugar was higher in seeds of WX12 than that of CY12 at the latter period of grain filling. The dynamic change of sucrose content in WX12 and CY12 were similar during the filling stage, while this content in WX12 seeds was lower at the middle of grain filling and were higher at the latter stage than that of CY12.

The changes of fructan in seeds of WX12 and CY12 were nearly the same (Figure 3). The fructan content had no significant variations during the latter period of filling, however, the maximum content of fructan in WX12 were higher than that of CY12 at the middle filling stage.

The changes of pentosan levels in seeds of WX12 and CY12 were similar, while these values in seeds of WX12 were higher than that of CY12 during the filling stage (Figure 4).

The dynamic change of starch content in seeds of WX12 was similar to that of CY12 (Figure 5). However, the V_{max} was detected at 17–22 DAF in seeds of WX12 and at 22–27 DAF in that of CY12 (Figure 6).

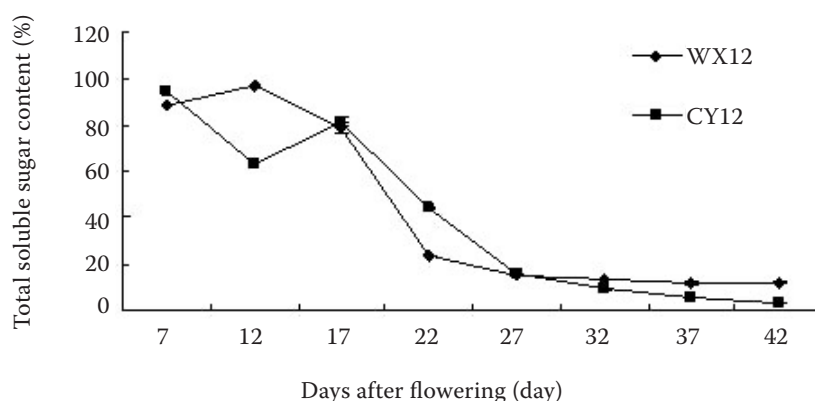


Figure 1. Dynamic changes of total soluble sugar content in the grains of WX12 and CY12 during grain filling

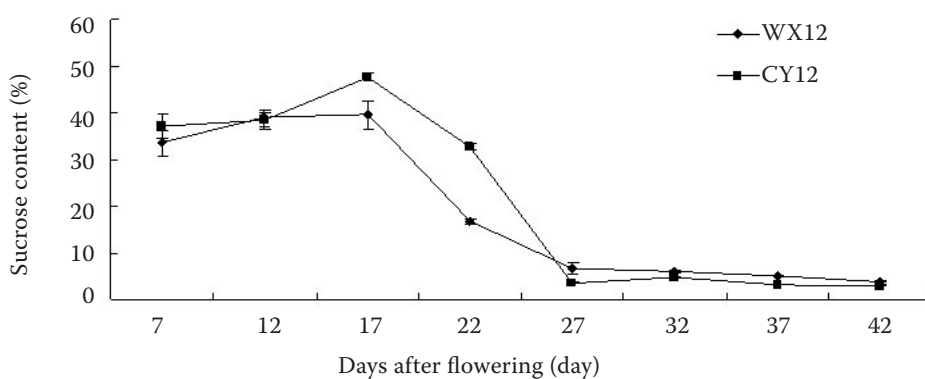


Figure 2. Dynamic changes of sucrose content in the grains of WX12 and CY12 during grain filling

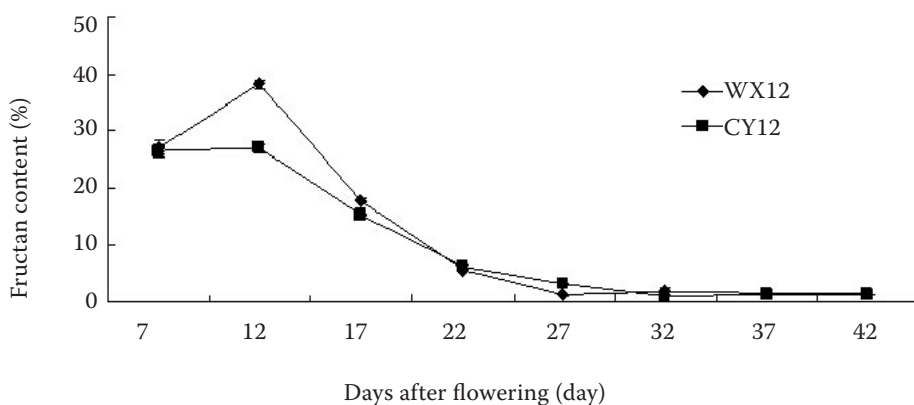


Figure 3. Dynamic changes of fructan content in the grains of WX12 and CY12 during grain filling

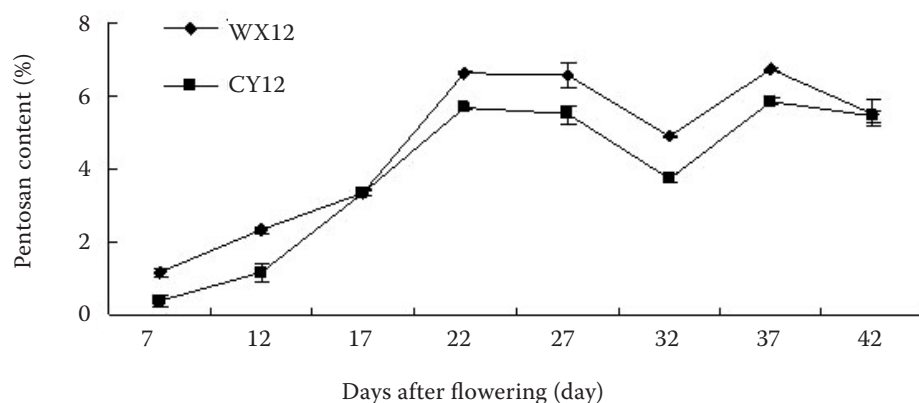


Figure 4. Dynamic changes of WX12 and CY12 pentosan content during grain filling

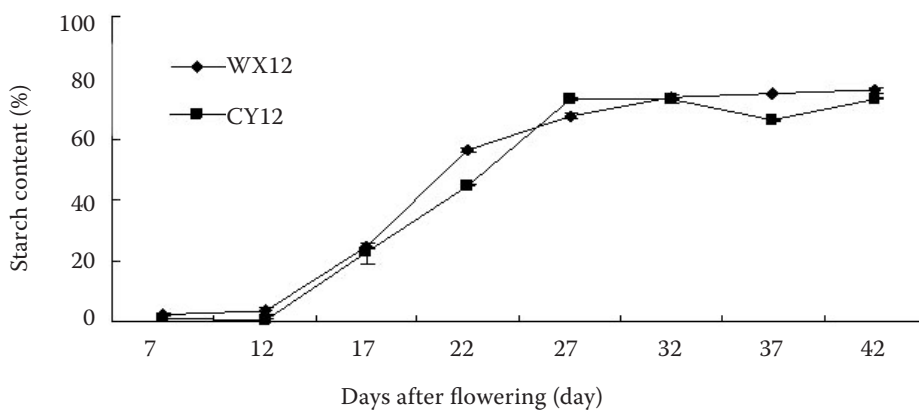


Figure 5. Dynamic changes of WX12 and CY12 starch content during grain filling

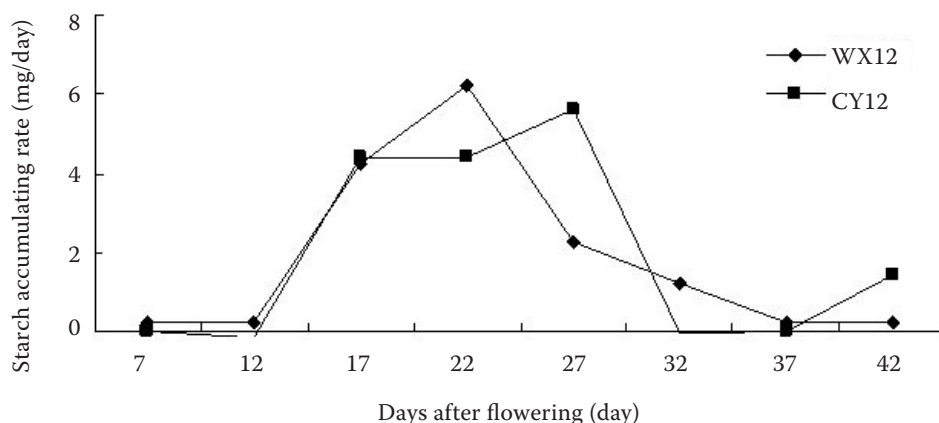


Figure 6. Dynamic changes of WX12 and CY12 starch accumulation rate during grain filling

CONCLUSIONS

Field trial results showed that the V_{\max} of starch synthesis was highest at 17–22 DAF in WX12, while this value in CY12 was at a maximum at 22–27 DAF. The dynamic changes of two wheat lines were similar except for starch content during the filling stage. Compared to CY12, the soluble sugar, sucrose and pentosan contents were higher in WX12. The highest pentosan content in WX12 was 22–27 DAF, while the highest fructan content was 7–12 DAF.

This research reveals that there were differences in quality between waxy and common wheat during the grain filling stage. These could be used as cultivation techniques to improve the quality of waxy wheat for various purposes.

Acknowledgements. This work was supported by the Knowledge Innovation Program of the Chinese Academy of Sciences (Grant No. KSCX3-EW-N-02) and the National Key Project of Transgenic Biologic Varieties Breeding of China (2009ZX08009-053B). We thank Dr. R. GRAYBOSCH for providing waxy wheat germplasm for breeding.

References

DOUGLAS S.G. (1981): A rapid method for the determination of pentosans in wheat flour. *Food Chemistry*, **7**: 139–145.
 HOSHINO T., ITO S., HATTA K., NAKAMURA T., YAMAMORI M. (1996): Development of waxy common

wheat by haploid breeding. *Breeding Science*, **46**: 185–188.
 KIRIBUCHI-OTOBE C., NAGAMINE T., YANAGISAWA T., OHNISHI M., YAMAGUCHI I. (1997): Production of hexaploid wheats with waxy endosperm character. *Cereal Chemistry*, **74**: 72–74.
 MIURA H., TANII S. (1994): Endosperm starch properties in several wheat cultivars preferred for Japanese noodles. *Euphytica*, **72**: 171–176.
 NAKAMURA T., YAMAMORI M., HIRANO H., HIDAKA S. (1993a): Identification of three Wx protein in wheat (*Triticum aestivum* L.). *Biochemical Genetics*, **31**: 75–86.
 NAKAMURA T., YAMAMORI M., HIRANO H., HIDAKA S. (1993b): Decrease of waxy (Wx) protein in two common wheat cultivars with low amylose content. *Plant Breeding*, **111**: 99–105.
 NAKAMURA T., YAMAMORI M., HOSHINO H. (1995): Production of waxy (amylase-free) wheats. *Molecular and General Genetics*, **248**: 253–259.
 Shanghai Society for Plant Physiology (1985): *Experimental Manual on Plant Physiology*. Shanghai Scientific and Technical Publisher, Shanghai, 134–138.
 YAMAMORI M., NAKAMURA T., ENDO T.R., NAGAMINE T. (1994): Waxy protein deficiency and chromosomal location of coding genes in common wheat. *Theoretical and Applied Genetics*, **89**: 179–184.
 YASUI T., SASAKI T., MATSUKI J., YAMAMORI M. (1997): Waxy endosperm mutants of bread wheat (*Triticum aestivum* L.) and their starch properties. *Breeding Science*, **47**: 161–163.
 ZHAO X.C., SHARP P.J. (1998): Production of all eight genotypes of null alleles at “waxy” loci in bread wheat. *Plant Breeding*, **117**: 488–490.