EFFECT OF *GPC-B1* GENE ON GRAIN PROTEIN CONCENTRATION AND BREAD-MAKING QUALITY IN COMMON WHEAT

Bolesław Salmanowicz, Monika Langner

Institute of Plant Genetics of the Polish Academy of Sciences, Poznan, Poland

Presenting author: bsal@igr.poznan.pl
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Introduction. Quality traits are becoming increasingly important in wheat breeding programs due to higher standards imposed by millers, bakers, and consumers. Grain protein concentration (GPC) is an important quality trait in bread wheat, which determines processing properties, quality of the end products, nutritional and market value of the grain (1). The application of the *Gpc-B1* gene from *T. turgidum* ssp. *dicoccoides* (known to affect leaf senescence and nutrient retranslocation to the grain) into wheat breeding programs has the potential of improving protein, zinc and iron in a wide range of germplasm due to the absence of the functional allele in most of the commercial hexaploid cultivars (2-3).
Objectives. In this study, the effect of the wild-type allele of *Gpc-B1* locus on the grain properties and bread-making quality of dough was evaluated in 64 wheat double haploid (DH) lines.
Material and Methods. The samples were compared in respect of seed storage protein and starch composition, flour yield, rheological properties of dough, and loaf properties. The quantitative and qualitative composition of particular HMW- and LMW glutenin subunits in grain samples was determined by capillary zone electrophoresis (CZE). The rheological analyses were performed in micro-scale using 10g-mixograph, 10g-farinograph and the SMS-Texture analyzer with Kieffer gluten extensibility rig.
Results. In study material the *Gpc-B1* introgression was resulted in significant increase in GPC (6.2% - 14.1%) across genotypes. Farinograph characteristics of the wheat flour also showed a significant increase in water absorption in most genotypes, a trait known to be highly correlated with GPC (4.6% - 8.4% increase relative to control material). On the other hand, in some genotypes the functional *Gpc-B1* introgression was associated in reduction in grain weight and flour yield. The increase in GPC associated with the NAM-1 introgression was also paralleled with improved gluten quality. The obtained results showed that dough had better properties than that of the recurrent parent.
Conclusions. A positive effect on several bread-baking quality parameters was also observed in DH lines with the *Gpc-B1* gene. Significant gene x environment and gene x genotype interactions for most traits stress the need for evaluating the effect of this introgression in particular genotypes.
References:
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DETECTION OF LMW GLUTENIN GENES OF THE *GLU-3* LOCUS IN SOME POLISH WHEAT CULTIVARS BY CAPILLARY ELECTROPHORESIS AND RP-HPLC

Langner Monika, Franaszek Sławomir, Salmanowicz Bolesław

Institute of Plant Genetics, Polish Academy of Sciences, Poznań, Poland
E-mail address: mlan@igr.poznan.pl

Wheat is an important crop in most regions of the world due not only to its yield potential and plasticity, but also to the unique viscoelastic properties of its grain storage proteins (gluten) that can be processed into a large diversity of food products. Low-molecular-weight glutenin subunits (LMW-GS) are redounded to dough extensibility and gluten strength. These proteins are encoded by a multi-gene family located at the *Glu-A3*, *Glu-B3* and *Glu-D3* loci, located on the short arms of homoeologous group 1 chromosomes. The estimated number of LMW-GS gene copies varies from 15 to 35 in individual hexaploid wheat genotype. A large number of genes and abundant allelic variations at *Glu-3* loci and their tight linkage with gliadin genes make it difficult to elucidate the composition and function of LMW-GS genes in bread wheat. Therefore, it is important to develop more powerful methods to separate and characterize LMW-GS for better understanding of their complexity and heterogeneity in compositions.

A total of 50 Polish varieties and 15 world standard varieties of wheat with specific allelic variants LMW-GS were analyzed. For the separation of LMW-GS modern methods capillary electrophoresis (CZE) and reversed-phase high-performance liquid chromatography (RP-HPLC) were used. In total 52 isoforms LMW-GS encoded by 15 allelic variants of genes *Glu-3* (*GluA3b,df*; *Glu-B3a-e,h*; *Glu-D3a-c,e*) were distinguished in analyzed cultivars. Chromatographic and electrophoretic profiles obtained on the basis of RP-HPLC and CZE separations of wheat LMW-GS showed a similar number of major peaks. The results confirmed full compliance with the control varieties. During separation by CZE protein peaks were observed corresponding to LMW-GS in the range of 9-15 minutes time. The retention times of individual LMW-GS separated by RP-HPLC were ranged from 39-55 minutes. These data indicate the high resolution and good repeatability of both used methods (CZE and RP-HPLC). Main disadvantage of RP-HPLC is long retention times and high costs of the columns used for separation. On the other hands, obtained data indicate that CZE can be a powerful and alternative tool for genetic and proteomic studies of wheat grain proteins and fast identification or screening of desirable LMW-GS alleles in wheat quality improvement.

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