



# **QUALITY POTENTIAL OF GLUTEN PROTEINS IN HEXAPLOID WHEAT AND RELATED SPECIES**

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Vawser M-J and Cornish G B (2004) AJAR 55, 577-588 .....	
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## A B S T R A C T

Variation in quantity and quality of gluten proteins is largely responsible for the genotypic differences associated with the dough rheological parameters, maximum resistance ( $R_{max}$ ) and extensibility (Ext.). In the context of bread making, doughs characteristic of good quality have moderate to high extensograph maximum resistance ( $R_{max}$ ) and high extensibility (Ext.). The term usually applied to describe the balance between these two parameters is dough strength. Generally, weak doughs perform poorly in baking tests and as dough strength increases, bread making quality also increases. Important proteins that constitute the ‘gluten complex’ include high molecular weight glutenin subunits (HMW-GSs) and low molecular weight glutenin subunits (LMW-GSs). These proteins, which interact to produce large polymeric proteins, are coded at the *Glu-1* and *Glu-3* loci on group 1 chromosomes, respectively. Extensive allelic variation exists at each of the *Glu-1* and *Glu-3* loci. Field trials (4 years) and physical dough quality tests on harvested grain from a set of near-isogenic lines, differing in glutenin composition, were used to investigate the effect of numerous glutenin alleles on dough rheological parameters. Glutenin allele main effects were ranked as follows: *Glu-A1*  $a = p = b > c$  for  $R_{max}$  and *Glu-A1*  $a = b = p > c$  for Ext.; *Glu-B1*  $i \geq b = c > d = a$  for  $R_{max}$  and *Glu-B1*  $a = i = c \geq b \geq d$  for Ext.; *Glu-D1d*  $> Glu-D1a = Glu-D1b \geq Glu-D1f$  for  $R_{max}$  and *Glu-D1*  $a = b = f \geq d$  for Ext.; *Glu-A3*  $d = b \geq c = f \geq a > e$  for  $R_{max}$  and *Glu-A3*  $b = a = d = c = f \geq e$  for Ext.; *Glu-B3*  $g \geq b = m \geq d = i = h = f \geq a \geq c$  for  $R_{max}$  and *Glu-B3*  $i = d \geq g = f = m \geq b = c = h = a$  for Ext.; *Glu-D3*  $a - Gli-D1 = f \geq c = d = a \geq b$  for  $R_{max}$  and *Glu-D3*  $d \geq a - Gli-D1 \geq a \geq b = c = f$  for Ext. The influence of protein content and two-way glutenin allele interactions are also discussed.

Another aspect of this work investigated the relationship between HMW-GS expression

levels and quality. RP-HPLC was used to quantify the proportion (% area) of individual HMW-GSs relative to total HMW-GSs. Except for *Glu-B1d* (6+8\*), the B-genome contributed the highest percentage of HMW-GSs and was significantly higher ( $P<0.001$ ) in cultivars that contained the *Glu-B1al* allele. A high proportion of 1Bx subunits compared to 1Dx subunits ( $\approx 2.3$ , *Glu-B1al*) correlated with varieties reported to have extra strong dough properties, while a 1Bx:1Dx ratio of  $\approx 1.3$  (*Glu-B1 i, f, c, u* and *ak*) was typical of varieties with moderate to high dough strength characteristics. In varieties which contain *Glu-B1* alleles reported to produce weak doughs the 1Bx:1Dx value was  $\approx 1.0$  (*Glu-B1e*) and  $\approx 0.6$  (*Glu-B1d*). This suggests that the overall proportion of *Glu-B1* subunits has a major influence on dough strength and that the proportion of 1Bx relative to 1Dx subunits, as determined by RP-HPLC, could be used to predict dough quality. RP-HPLC analysis also enabled the identification of varieties that contained the *Glu-B1al* allele and over-expressed subunit *Glu-B1 7x*, including the most likely source of this allele in bread wheat cultivars.

Novel HMW-GS alleles in related wheat species with good quality potential were also identified. A simple small-scale screening assay was developed to efficiently assess the protein quality attributes associated with accessions of synthetic hexaploids, *T. tauschii* and *T. dicoccoides*. Development of the Turbidity assay is described and was used in conjunction with SE-HPLC and SDS-PAGE to confirm and characterise previously undescribed HMW-GSs. The HMW-GS composition of *T. dicoccoides* is discussed in detail where there were 49 HMW-GSs which combined to produce 54 different HMW-GS banding patterns. Accordingly, allelic designations were tentatively assigned to either individual or subunit pairs and these are also reported in this manuscript.