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Towards a genetic road map of wheat-processing quality

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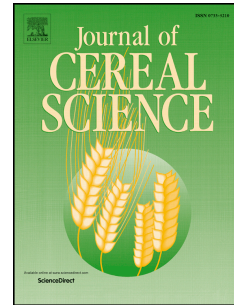
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**Short Communication** for J Cereal Science, invited by Fin MacRitchie

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## **Towards a genetic road map of wheat-processing quality**

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**Abstract:** The elucidation of wheat-quality genetics may be seen metaphorically as a road map to greater knowledge, and also as an interlocking jigsaw puzzle. Major genes relevant to the attributes needed for wheat-processing quality have been identified, namely, protein content, grain hardness, milling yield, dough strength, dough extensibility, baking quality, starch-paste viscosity and nutritional value.

**Key words:** Grain hardness; Milling yield; Dough quality; Baking quality; Nutritional value; Transcript profiling; Transcriptomic analysis; Arabinogalactan proteins.

The quality of wheat-based products depends on the quality of the grain from which the products have been made (Miskelly, 2017). Contributing factors are the interactions of genotype (G, variety) and growth environment (E), plus the effectiveness of the subsequent processing (P), summarised overall by  $G \times E \times P$ . The contribution of each factor may be major or minor, i.e., G or g, respectively, for the effect of growth environment. Eventual grain quality (the phenotype) for wheat-based products requires specific combinations of attributes: protein content (involving  $g \times E$  control), grain hardness (with  $G \times e$  control), milling yield ( $G \times e \times p$  control), dough strength ( $G \times e$  control), dough extensibility ( $G \times e$  control), baking quality ( $G \times e \times P$  control), starch-paste viscosity ( $G \times e$  control) and nutritional value (Howett and Miskelly, 2017; Nirmal, 2016). These attributes are listed across the bottom of Figure 1. Although already complex, the figure still does not include lipids or fibre.

The selection of genotypes with the appropriate combination of these attributes is most effective in breeding if a major gene can be identified that controls each attribute. Possession of that knowledge permits the breeder, early in the selection process, to discard lines that are unlikely to provide the desired grain-quality phenotype (depending on the subsequent contributions of growth and processing conditions). A research aim of the past few decades has been to identify the major genes responsible for these attributes. Advanced understanding and prediction of dough properties (strength and extensibility) are now available based on the alleles for glutenin subunits (both *Glu-1* and *Glu-3*) (e.g., Bekes and Wrigley, 2013). Alleles relevant to cereal starch-paste viscosity have also been recognised (e.g., Luo et al., 2015; Howett and Miskelly, 2017). However, the genes regulating other attributes in Figure 1 have been more difficult to identify.

Recent advances in DNA-sequencing technology have provided a new technology platform for cereal research (Henry, 2014). Research can now focus on extensive analysis of very large data sets rather than the now highly automated data collection (Rossetto and Henry, 2014). In particular, the study of transcriptomics permits the identification of the actual genes that are functional during grain filling, thereby focusing attention on the alleles that matter, in contrast to traditional correlation studies for which cause-and-effect conclusions have been

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