

**BREEDING****Improving the nutritional quality and health benefits of wheat**P.R. Shewry<sup>1</sup>, D. Lafiandra<sup>2</sup> & Z. Bedo<sup>3</sup><sup>1</sup> Rothamsted Research, Harpenden, Hertfordshire AL5 2JQ, UK<sup>2</sup> University of Tuscia, Via SC De Lellis, Viterbo 01100, Italy<sup>3</sup> Agricultural Research Institute of the Hungarian Academy of Sciences, Brunszvik u. 2, Martonvásár HU-2462, Hungary

Wheat is an important source of calories (derived from starch), protein, dietary fibre, minerals, vitamins and health-promoting phytochemicals to the human diet. However, many of the beneficial components are concentrated in the outer layers of the grain (bran) and embryo (germ). Consequently, whereas the consumption of whole grain products has health benefits in reducing the risk of a number of medical conditions including the metabolic syndrome, the consumption of highly refined products derived from the starchy endosperm (white flour) may be associated with increased risk. This work will therefore discuss the composition of the wheat grain, focusing on components which positively or negatively affect health outcomes and their distributions in grain tissues and fractions. It will also discuss strategies for developing new types of wheat with improved health benefits, focusing on the three major components in the grain: protein, starch and dietary fibre. Classical plant breeding can be used to increase the content and improve the composition of dietary fibre in flour and wholemeal, exploiting the existence of wide variation in composition and high genetic heritability (Ward *et al.* 2008; Shewry *et al.* 2010), and using molecular markers for selection. In particular, increasing the content of soluble fibre content leads to increased intestinal viscosity and reduced glycaemic index (with reduced risk of type-2 diabetes). The glycaemic index of wheat products can also be reduced by increasing the amylose content of starch, and increases from 25% to 40% amylose can be achieved by combining naturally occurring or induced mutations in genes controlling the synthesis of amylopectin (Sestili *et al.* 2010). The nutritional quality of wheat protein is limited by the low contents of essential amino acids, notably lysine, in the gluten protein fraction. Although high lysine mutations have been studied widely in maize and barley, they have achieved little commercial success and this approach has not been adopted in hexaploid bread wheat. However, lessons learned from studies in these cereals should allow the use of genetic engineering to improve the protein quality of wheat. The combination of these traditional and novel approaches will allow the development of new types of wheat with enhanced nutritional quality and health benefits for wholegrain and white products.

**Keywords**

wheat; protein; dietary fibre; resistant starch.

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**Wheat grain hardness: multigenic basis and its implications**M. Bhavé<sup>1</sup>, E. Palombo<sup>1</sup>, A. Ramalingam<sup>1</sup>, A. Niknejad<sup>1</sup> & D. Webster<sup>2</sup><sup>1</sup> Faculty of Life and Social Sciences, Swinburne University of Technology, Vic 3122, Australia<sup>2</sup> School of Biological Sciences, Monash University, Vic 3800, Australia

The grain hardness (or texture) of common wheat (*Triticum aestivum* L.) is an important measure of grain quality and significantly influences the end-use of wheat and its commercial value. The two puroindoline genes, Pina-D1 and Pinb-D1, located at the Ha locus on chromosome 5D only of common wheat, are key genetic determinants of grain hardness. These encode small molecular weight (~13 kDa) proteins called puroindoline A and B (PINA and PINB), respectively, which are lipid-binding proteins with a distinct 10-cysteine backbone, a heliocoid structure and a unique tryptophan-rich domain (TRD). When both PINs are in wild-type, they are proposed to lead to soft grain texture, while diverse mutations in either/both genes have been associated with grain hardness of common wheat and deletion of Pin genes in both genomes associated with the very hard texture of durum (reviewed in Bhavé & Morris, 2008). The recently reported Pinb-2 gene on chromosome 7 of common and durum wheat may also have a role in texture (Wilkinson *et al.*, 2008; Chen *et al.*, 2010). We aimed to analyse the Pinb-2 gene diversity in a number of Chinese land races as China is the secondary centre of origin of wheat. The alleles of Pina-D1 and Pinb-D1 were also analysed to get a complete Pin genotype, and durum wheats were included to test their Pinb2 genotypes. Synthetic peptides designed on the PINB-2 TRD were also tested for any antimicrobial activity. The genes were amplified from genomic DNAs using degenerate primers to allow amplification of variants, the PCR products cloned, and a number of clones sequenced to identify individual sequences. The Pinb-2 genes were identified in all wheats tested and comprised a small family with variations in the putative proteins. A new Pina-D1 allele, Pina-D1t, with a tryptophan-to-stop codon mutation, was also identified. Taken together, the results suggest that the final texture of common wheat could be determined by three interactors: the PINA and PINB (in wild type or altered/null forms) and PINB2 variants, while the texture of durums could be influenced by PINB2 variants. In addition, the PINB2-based peptides exhibited antimicrobial activity, as we noted for PINA and PINB-based peptides, suggesting likely seed defence roles for the whole PIN family.

**Keywords**

wheat; grain texture; puroindolines; antimicrobial peptides.

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