BREEDING

Improving the nutritional quality and health benefits of wheat

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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 components in the grain: protein, starch and dietary fibre. It will also discuss strategies for developing new types of health outcomes and their distributions in grain tissues and fractions in the gluten protein fraction. Although high lysine mutations have been studied widely in maize and barley, they have achieved little in common wheat, where the effects of variations 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 Bhave & 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 peptides. 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; protein; dietary fibre; resistant starch.

References

Wheat grain hardness: multigenic basis and its implications

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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 helicoid 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 Bhave & 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 peptides. 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.

References