Manipulating gibberellin signalling in developing wheat grain for improved yield and quality

Aakriti Wanchoo-Kohli¹, Simon Vaughan¹, Michael Holdsworth², Andy Phillips¹ and Peter Hedden¹ ¹ Plant Biology and Crop Sciences, Rothamsted Research, ² Division of Plant and Crop Sciences, The University of Nottingham

During germination wheat embryos produce gibberellin (GA) which induces the production of α amylase by the aleurone layer that causes the subsequent hydrolysis of starch in the endosperm. Under certain environmental conditions GA can cause the premature induction of α -amylase resulting in degraded starch in the mature grain and poor quality flour. However, while GA is proposed to have a negative effect on flour quality, it is also essential for early grain development. As these effects are separated both temporarily and spatially in the grain, it may be possible to improve both grain yield and flour quality by manipulating GA signalling in specific tissues at specific times. We hypothesise that increasing GA content in early stages of development may promote grain size without having a negative impact on flour quality, while reducing GA content late in development, or conferring insensitivity to GA in specific tissues may improve flour quality, without affecting grain size. In order to test this and to obtain a better understanding of the role of GA in grain development, constructs were designed to alter GA metabolism or signalling in the seed-coat, endosperm, embryo or aleurone of developing wheat grains. The tissue and temporal specificity of each promoter was confirmed by cotransformation with GFP reporter constructs. To identify homozygous plants a reliable Q-PCR method using TaqMan assays was developed and zygosity determined in the T2 generation for each construct. Grain yield and quality in the transgenic lines were compared with azygous segregants in terms of grain number, weight, size and shape; α -amylase activity, protein content, grain hardness and moisture. Transcript levels of the transgenes were also measured using qRT-PCR to determine linkages between genotype and phenotype.