Near infrared spectra indicate specific mutant endosperm genes and reveal a new mechanism for substituting starch with (1-->3,1-->4)-[beta]-glucan in barley

Near Infrared Reflectance spectroscopy was tested as a screening method to characterise high lysine mutants from a barley collection by classification through Principal Component Analysis (PCA). Mean spectra of the samples within each cluster identified gene-specific patterns in the 2270-2360 nm region. The characteristic spectral signatures representing the lys5 locus (Riso mutants 13 and 29) were found to be associated with large changes in percentage of starch and (1-->3,1-->4)-[beta]-glucan. These alleles compensated for a low level of starch (down to 30%) by a high level of (1-->3,1-->4)-[beta]-glucan (up to 15-20%), thus, maintaining a constant production of polysaccharides at 50-55%, within the range of normal barley. The spectral tool was tested by an independent data set with six mutants with unknown polysaccharide composition. Spectral data from four of these were classified within the high (1-->3,1-->4)-[beta]-glucan BG lys5 cluster in a PCA. Their high (1-->3,1-->4)-[beta]-glucan and low starch content was verified. It is concluded that genetic diversity such as from gene regulated polysaccharide and storage protein pathways in the endosperm tissue can be discovered directly from the phenotype by chemometric classification of a spectral library, representing the digitised phenome from a barley gene bank.
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