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Application of hyperspectral imaging to predict alpha amylase content and starch breakdown in pregerminated barley seeds

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Malting is the controlled germination of a cereal grain. In barley, malted grains provide the fermentable sugars necessary for brewing and distilling processes. Harvested barley must adhere to strict industry quality standards to be considered for malting including robust hydrolytic enzyme content, low protein content and high rates of germination. Failure to meet quality metrics results in significant loss of market value and presents a risk to growers considering malting barley. Modern cultivars of malting barley are susceptible to preharvest sprout (PHS), or germination of the seed prior to harvest, resulting in premature endosperm modification, reduced enzyme content and poor malthouse germination. Seeds with PHS damage fail quality assessments and are sold for feed at reduced prices. Most presprouted grain shows no visual signs of damage and accepted methods to assess PHS damage including Hagberg falling number and stirring number (Rapid Visco Analyzer), which are costly and destructive to the seed. To address this need, we applied time-series hyperspectral imaging of barley seeds with varying levels of PHS damage and used a deep neural network to predict stirring number and alpha amylase values, which are indicators of sprouting. Prediction models were generated for each of the seven genotypes tested individually and also for all genotypes when combined. Our prediction models had mean average errors from 10.5 to 23.9 and root mean square errors from 19.0 to 35.1 demonstrating the applicability of hyperspectral imaging as a high-throughput, nondestructive method for predicting levels PHS damage in malting barley.