

Predicting alpha amylase content and starch breakdown in pregerminated barley seeds using hyperspectral imaging

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Abstract

Malting is the process of controlled germination of cereal grain that is steeped, germinated, and dry kilned to develop flavor compounds, fermentable sugars, the hydrolytic enzymes necessary for the brewing process. To meet the strict standards of the brewing industry, variation in the germination of barley grains need to be minimal but also maintain rapid germination and optimum levels of α and β amylase. Preharvest sprouting poses a significant threat to barley cultivars prior to harvest, resulting in premature endosperm modification, reduced enzyme content, and poor malthouse performance. Pregerminated grain is difficult to detect as there are often no signs of damage, and current methods such as the Hagberg falling/Stirring number, or pearling tests, each of which ultimately leads to the destruction of the seed. Here we used time-series hyperspectral imaging of barley seeds undergoing active and or pregerminated seed and used a deep neural network to predict stirring number and alpha amylase values, which are proxy measures for sprout damage. Prediction models were made for seven genotypes tested individually and with all genotypes combined. Stirring number assays ranged from 0 to 190 and our prediction models had mean average errors of 10.5 to 23.9 depending on the model. To increase the resolution and accuracy of the predictions we transitioned from using bulk conventional molecular assays to single seed assays and prediction models. These results demonstrate that hyperspectral imaging and machine learning models can be used to predict germinated grain in bulk and single seed assays.



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