
Comparison of Structural Makeup of Four Hulless Barley Varieties Using Diffuse Reflectance Infrared Fourier Transform (DRIFT) Spectroscopy

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Abstract

The objective of this study was to determine molecular structural makeup features of 3 newer hulless barley varieties (CDC Fibar, CDC Rattan, and HB08302) in comparison to the conventional feed-type barley variety in Canada (CDC McGwire) using diffuse reflectance infrared fourier transform (DRIFT) spectroscopy. The items included IR absorbed intensity (IR intensity unit, KM) peak area attributed to protein amide I (ca. 1715-1575 cm^{-1}), amide II (ca. 1575-1490 cm^{-1}), total carbohydrate (CHO; ca. 1188-820 cm^{-1}), and structural carbohydrate (StCHO; ca. 1277-1190 cm^{-1}); and ratio of amide I to II, amide I to CHO, and CHO to StCHO. There were no differences among barley varieties in CHO. While, CDC Fibar was greatest in protein amide I and II peak areas, as well as the ratio of protein amide I to CHO among barley varieties. Newer barley varieties were similar to each other, but were different from CDC McGwire in protein amide I to II ratios. In summary, DRIFT spectroscopy associated with both univariate and multivariate techniques can be used as tool to discriminate and classify the inherent molecular structural features among the different barley varieties.

Introduction

Barley is (*Hordeum vulgare* L.) the fourth largest cereal crop produced in the world. Canada is among the top five barley producers and exporters in the world with the annual barley production close to 12 million tonnes (FAOSTAT, 2008). Canada has locally adapted and registered 200 varieties of barley. There are over 50 barley varieties produced in western Canada, including 8 hulless types, 13 malting types, and some others suitable for livestock industry. Recently, several new Canadian barley varieties, including hulless waxy genotypes such as CDC Fibar, and CDC Rattan as well as high amylose lines HB08302 have been developed specifically for food use. The objective of this study was to determine molecular structural features of the 3 newer hulless barley varieties using a DRIFT spectroscopy in comparison to CDC McGwire, the relatively conventional and feed-type hulless barley variety. The parameters assessed included (i) protein amide I, (ii) protein amide II, (iii) structural - (StCHO) and (iv) total carbohydrate

(CHO), and (v) their ratio (amide I to amide II, amide I to CHO, CHO to StCHO) profiles of hulless barley.

Materials and Methods

Four hulless barley varieties: (1) CDC McGwire, (2) CDC Fibar, (3) CDC Rattan, and (4) HB08302 were chosen. Barley samples were provided by Brian Rossnagel, Crop Development Center, University of Saskatchewan. Spectra's from samples were obtained using a FTS-40 Fourier transform vibrational infrared (FTIR) spectroscopy. Protein amides I and II, CHO, StCHO were identified according to published report (Wetzel and LeVine 2000). Spectral data were analyzed using both univariate and multivariate molecular spectral analysis (Yu et al. 2010). For the multivariate spectral analysis, agglomerative hierarchical cluster analysis (CLA) and principal component analysis (PCA) was performed using Statistica 7.0 software. Statistical analyses were performed using the MIXED procedure of SAS 9.2 (SAS Institute, Inc., Cary, NC).

Results and Discussion

CDC Fibar had the largest ($P < 0.05$) protein amide I and II peak area among the varieties, indicating higher concentration of protein in the CDC Fibar. While the amide I and II ratio for the newer barley varieties were similar ($P > 0.05$) to each other, they were lower (5.3, 5.5, and 4.9, CDC Fibar, CDC Rattan, and HB08302, respectively, $P < 0.05$) than the conventional variety (11.7). This indicates that newer varieties have similar protein profiles, but were different than conventional feed-type barley variety. Barley varieties did not differ ($P > 0.05$) in IR peak area attributed to structural carbohydrate; only exclusion was the CDC Rattan, which was lower ($P < 0.05$) than HB08302. IR absorbed intensity peak area values of CHO were 1307, 1519, 1180, and 1408, for the CDC McGwire, CDC Fibar, CDC Rattan, and HB08302, respectively; although ranges are large among varieties and were not statistically significant ($P > 0.05$). With regard to amide I to CHO ratio, CDC Fibar showed the highest (0.17; $P < 0.05$) value. The amide I to CHO ratio for HB08302 was lower (0.08; $P < 0.05$) than CDC McGwire (0.12), but was similar to CDC Rattan (0.10). CLA and PCA analysis detected no differences in protein or in carbohydrate molecular chemical makeup between CDC McGwire versus CDC Fibar, CDC Rattan or HB08302.

Conclusions

In conclusion, CDC Fibar, CDC Rattan, and HB08302 were smaller than CDC McGwire in protein amide I to II ratio, indicating that these varieties were different than conventional feed-type barley variety. Our result further suggested that, DRIFT spectroscopy associated with both univariate and multivariate spectral analytical techniques can be used as tool to discriminate and classify the inherent molecular and structural makeup of barley varieties.

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