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Short communication

In vitro gas production and dry matter digestibility of malting barley grain sown with different seeding and nitrogen fertilization rates in Canada

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ABSTRACT

Two malting barley varieties, AC Metcalfe and CDC Copeland, were grown at seven sites in Canada with varying seeding rates (SR; 200 and 400 seeds/m^2) and nitrogen fertilization rates (NR; 0, 30, 60, 90, and 120 kg/ha) and were assessed for variation in chemical composition, gas production (GP), and dry matter digestibility (DMD) after 24 h of batch culture. The variety affected (P<0.01) the crude protein (CP) content of malting barley grain and interacted with SR or NR on DMD. The increase in NR quadratically increased (P<0.01) CP and fiber content but linearly (P<0.01) decreased starch content of malting barley grain. Variety, SR, and NR had limited impact on *in vitro* GP and DMD. This study showed substantial variation in CP content and DMD among samples and that the chemical composition of malting barley grain and its potential feed value could be altered by NR.

1. Introduction

In western Canada, barley grain (*Hordeum vulgare*) is the primary feed ingredient in ruminant diets. Approximately, 11–13 million tonnes of barley are grown in the Prairie provinces, of which 10 million tonnes are destined for use as livestock feed according to Canadian Barley Malting and Brewing Technical Guide (CBMBT, 2012), mostly by the cattle industry. However, over 7.2 million tonnes of barley in western Canada is grown for the value-added brewing market (Canadian Barley Malting and Brewing Technical Guide, 2012). Thus, less than half of the barley produced in western Canada qualifies for malting (Canadian Barley Malting and Brewing Technical Guide, 2012), with the remainder used as livestock feed. The feed value of malting barley grain is rarely considered by grain growers for malting production and as such, there is a paucity of

Abbreviations: CBMBT, Canadian Barley Malting and Brewing Technical Guide; CP, crude protein; CV, coefficient of variation; DM, dry matter; DMD, dry matter digestibility; EE, ether extract; GP, gas production; N, nitrogen; aNDF, neutral detergent fiber assayed with a heat-stable amylase and expressed inclusive of residual ash; NR, nitrogen fertilizer rate; PI, processing index; SR, seeding rate.

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information available on feeding value of malting barley. Cultivar type, agronomic practices, such as seeding rate (SR), nitrogen fertilizer rate (NR), and other management practices (*e.g.*, early seeding and maturity at harvesting) were the main factors influencing barley quality for malting purposes (O'Donovan et al., 2011). The information from western Canada on the effects of SR and NR on the quality of malting barley grain for malting use is limited (O'Donovan et al., 2012). McKenzie et al. (2005) found that the most beneficial agronomic practices for barley planted for malting in southern Alberta were early seeding and application of NR appropriate to the expected availability of moisture and soil nitrogen (N). Chemical and structural conformation and make-up of barley were affected by cultivars, environmental conditions during the growth of the crop, and agronomic practices (Kulp and Ponte, 2000). The increase in barley SR reduced protein concentration, as well as kernel plumpness (O'Donovan et al., 2011). In comparison, the increase in NR generally increased yield and protein content (McKenzie et al., 2005), yet decreased starch content (Jenner et al., 1991). The hypothesis was that agronomic practices of SR and NR can affect nutritive value and the ruminal digestion of malting barley grain. The objectives of the study were to investigate the effects of variety, SR and NR on dry matter (DM) digestibility (DMD), and gas production (GP) of malting barley grain in batch culture.

2. Material and methods

2.1. Barley sample collection

Two malting barley varieties of barley (*H. vulgare*), AC Metcalfe and CDC Copeland, were grown at seven sites across western Canada (Beaverlodge, Canora, Fortvermillion, Indian Head, Lacombe, Lethbridge, and Scott). Both varieties were early seeded in April–May at rates of 200 and 400 seeds/m^2. Nitrogen fertilizer was applied to each cultivar and each SR at rates of 0, 30, 60, 90, and 120 kg/ha. Malting barley grain was harvested at maturity of Zadoks stage 92 (O'Donovan et al., 2011). Four replicates of each of the 20 treatments (2 varieties × 2 SR × 5 NR) were grown at each site, with a total of 80 plots per site. A single sample (500 g) from each plot and each site, resulting in 560 samples in total, was collected following harvest and ground through a 6 mm sieve (standard model 4 Wiley Mill; Arthur H. Thomas, Philadelphia, PA, USA). Barley samples were coarsely ground to simulate the extent of processing for malting barley grain as it is fed to beef cattle in western Canada. Although coarsely processed malting barley grain will result in lower *in vitro* DMD, such an approach maintains kernel structure and considers responses to processing including particle size distribution, a factor that can be influenced by kernel uniformity. The particle size distribution of processed grain is associated with the physical features of kernels, processing method and degree of processing, and is considered to have major impact on rate and extent of DM digestion in the rumen of cattle.

2.2. In vitro batch culture incubations

In vitro batch culture incubations were performed in gas-tight culture vials (100 mL) based on the procedure of Mauricio et al. (1999). A total of 560 barley samples were incubated in one of 14 runs with 40 samples in each run plus an internal standard barley sample included in each run to enable among run correction. Ground sample (0.5 g) was weighed into acetone-washed and pre-weighed filter bags (F57; Ankom Technology, Macedon, NY, USA) in four replicate vials and sealed prior to incubation. Anaerobic media was prepared the day before the incubation according to the method of Mauricio et al. (1999). Rumen inoculum was obtained from two ruminally cannulated non-lactating Holstein cows 2 h after feeding a diet containing 700 g/kg barley silage and 300 g/kg barley-based concentrate (DM basis). Rumen contents were pooled between cows, and the liquid was filtered through 2 layers of cheesecloth and collected in an insulated thermos. Inocula was immediately transported to the laboratory in a sealed flask and kept at 39 °C in a water bath. Forty-five milliliters of pre-warmed medium and 20 mL of ruminal inoculum were added anaerobically to 100 mL bottles by flushing with oxygen free CO_2. Vials were immediately sealed with a 14 mm butyl rubber stopper plus aluminum crimp cap and placed on a rotary shaker platform (120 rpm, Lab-Line Instruments Inc., Melrose Park, IL, USA) in a shaking incubator at 39 °C for 24 h.

Negative controls that included only inoculum and buffer were incubated in triplicate for 4, 8, 12, 18, and 24 h of inoculation. These controls were used to correct for gas release and residual fermentation resulting directly from inoculum. Headspace GP was measured at 4, 8, 12, 18, and 24 h of incubation by inserting a 23 gauge (0.6 mm) needle attached to a pressure transducer (model PX4200-015GI, Omega Engineering, Inc., Laval, QC, Canada) into the vials. The pressure on the visual display (Data Track Technology plc, Christchurch, UK) was recorded. The transducer was then removed leaving the needle in place to permit venting, and the pressure (psi) on the visual display was recorded. Pressure values, corrected for the amount of substrate organic matter incubated and the gas released from negative controls, were used to generate volume estimates using the equation of Mauricio et al. (1999). After completing the incubation at 24 h, bags were removed from the vials, washed, and dried in an oven at 55 °C for 48 h to determine DMD. Values of GP and DMD were corrected from negative controls, and then further adjusted using the internal standard sample among runs. Average value from the internal standard sample over all runs was calculated and used as the reference value. The DMD was calculated as the differences between original and post incubation and expressed as a coefficient.