Effect of Gene Modification on Protein and Energy Values in New Alfalfa for Dairy Cattle

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Lignin deposited in the secondary cell walls of alfalfa (*Medicago sativa*) plant negatively affects the digestibility of nutrient fiber. It is possible to modify lignification process by employing RNAi-mediated approaches to suppress single or multiple genes in second cell wall synthesis. Recently, two novel lignin-modified transgenic alfalfa were developed by scientists at Agriculture and Agri-Food Canada by down-regulating the expression of *TRANSPARENT TESTA 8* (*TT8*) and *HB12* genes. The objective of this study was to detect the effect of gene modification on protein and energy values in dairy cattle. The results showed that protein profiles differed among TT8, HB12 and non-transgenic alfalfa plants. TT8 alfalfa was higher in CP (22.6 vs 19.5 and 20.8 %DM; $p<0.05$), and lower in NPN (34.3 vs 36.7 and 36.2 %CP; $p<0.05$) than HB 12 and non-transgenic alfalfa. According to Cornell Net Carbohydrate and Protein System (CNCPS V 6.5), CP was partitioned into five sub-fractions. TT8 alfalfa was higher in moderately degradable CP fraction than HB 12 alfalfa (PB1: 49.0 vs 42.6 %CP; $P<0.05$), but similar to non-transgenic alfalfa. Rumen degradable PB1 fractions (RDPB1) and rumen degradable peptides (PDPEP) were both higher in TT8 alfalfa, compared to non-transgenic alfalfa ($p<0.05$).The values of HB 12 alfalfa was significantly lower than the other two groups ($p<0.05$). TT8 alfalfa had the highest rumen undegradable PB1 (RUPB1) among three alfalfa trial groups ($p<0.05$). The results of energy value estimated based on NRC dairy 2001 showed that gene modification had no significant impact on energy values (TDN, DE, ME, NE_m, NE_g, DE_{3X}, ME_{3X}, NEL_{3X}) of both transgenic and non-transgenic alfalfa plants.

Implications: Down-regulating the expression of *TT8* and *HB12* genes in alfalfa could affect protein nutrient availability for dairy cattle. The cultivation of gene modified alfalfa may promote the improvement of forage quality by transforming synthesis pathway of anti-quality compound in forages.