

Effect of Different Roughages on Milk Protein and Milk Fat Synthesis in Dairy Cows

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Abstract: The main purpose of this study was to determine the effect of a corn straw or mixed diet on milk production, milk composition and the expression of genes associated with lactation in mid-lactation Chinese Holstein cows. In this study, 10 healthy Chinese Holstein cows were randomly assigned to two groups and fed with different diets respectively, corn straw (CS) or mixed forage (MF) diet. CS group was fed roughage consisting of 53.8% corn straw only and the forage to concentrate (F : C) ratio [dry matter (DM)] was about 40: 60. MF group was fed roughage consisting of 3.7% Chinese wildrye and 23.4% alfalfa hay, the forage to concentrate (F : C) ratio (DM) was 70: 30. All the cows were fed 8 weeks and body weight, dry matter intake, body condition score, fat, protein, lactose, milk yield, total solid and somatic cell count (SCC) were recorded. Quantitative real-time PCR (qRT-PCR) was used to analyze cow mammary gland samples representing two different diets. The results suggested that different diet types had significant effects on milk yield, lactose, milk fat, milk protein, dry matter intake and somatic cell count in dairy cows, and cows fed MF diet improved milk production and lactation performance clearly ($P < 0.05$). In addition, mRNA expression of genes *ACC*, *mTOR*, *STAT5*, *CSN2*, *PPAR γ* , *FABP3* and *PTEN* in MF group was extremely significantly higher than that in CS group ($P < 0.05$). mRNA expression of *AKT1*, *FAS*, *SCD* and *SREBP1c* in MF group was significantly higher than that in CS group ($P < 0.01$). In summary, the milk yield and composition in mixed forage group were significantly improved than those in corn straw group.

Key words: dairy cow, different roughages, milk production, milk composition

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Introduction

It has been known for many years that various dietary factors, such as roughage type and proportion can affect rumen fermentation, milk production and composition (Weng *et al.*, 2012). The roughage is critical to the cow general health, milk production and quality. Roughage type as a key factor is widely used to improve milk production and milk fat and protein to increase economic genetic efficiency (Peres *et al.*,

2012). Corn straws are widely used as main roughage sources for most dairy farms in China, but the amount and nutrient quality of corn straws are not enough for livestock production. In recent years, Chinese wildrye and alfalfa hay as main mixed forage are used as basic components in feeding programs for dairy cows in most areas of China. It is well known that Chinese wildrye and alfalfa hay provide highly nutritious forage in terms of proteins, vitamins and minerals for ruminant animals. There are series of studies on the effects of different roughages on lactation performance

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and metabolic changes in dairy cows. The effect of a corn straw or mixed forage diet on endocrine, metabolism and lactation performance was reported in periparturient Holstein cows (Qin *et al.*, 2013). The influence of roughage types on ruminal metabolite profile that correlated with feeding on different roughage types was investigated (Zhao *et al.*, 2014). Some studies investigated the effects of dietary replacement of grass silage (GS) with forage millet silages that were harvested at two stages of maturity on milk production, apparent total-tract digestibility and ruminal fermentation characteristics of dairy cows (Brunette *et al.*, 2015).

The aim of this study was to evaluate the effects of two different forage quality diets on milk production, milk composition and expression of genes associated with lactation in dairy cows. This study was also aimed at exploring a more suitable dietary type for lactation cows to improve milk production and quality. It is critical to the general health of cows and the development of milk industry and nutrition research for the future.

Materials and Methods

Animals and tissue samples

Twelve healthy mid-lactating Holstein cows [(550±25) kg of body weight at the start of the experiment] were randomly divided into two groups: corn straw group (CS) and mixed forage group (MF). Corn straw group cows ($n=5$) were fed 53.8% corn straw only and F : C ratio [dry matter (DM)] was 40 : 60; and mixed forage group cows ($n=5$) were fed mixed forage consisting of 3.7% Chinese wildrye and 23.4% alfalfa hay, F : C ratio (DM) was 70 : 30. Ingredient and nutrient composition of the diets used in this study are presented in Table 1. They were fed twice at 6: 00 a.m. and 6: 00 p.m., and milked at 6: 00 a.m. and 6: 00 p.m. Other feeding conditions were the same and nutrition was abundant for two group cows, according to the College of Animal Sciences, Northeast Agricultural University, Harbin, China.

Throughout the experimental period, milk yield of each cow was recorded at each milking, and stored at 4°C with a preservative until analyzed for fat, protein, lactose, total solid and dry matter intake. Cows were slaughtered and mammary parenchymal tissues were aseptically excised 5 cm from the base of the nipple and 3 cm from the half line that divides the glandular quarters of each animal. The samples of mammary tissues were aseptically excised and immediately frozen in liquid nitrogen and stored at -80°C until further analyses.

Table 1 Ingredient and nutrient composition of corn straw (CS) and mixed forage (MF) diet

Item	Corn straw	Mixed forage
Ingredient (g·100 g ⁻¹ of DM)		
Chinese wildrye	–	3.70
Alfalfa hay	–	23.40
Corn straw	53.80	–
Corn silage	24.60	24.60
Soybean meal	14.80	14.80
Cotton seed	5.10	5.10
CaHCO ₃	0.60	0.60
NaCl	0.50	0.50
Mixed feed	0.60	0.60

mRNA level of genes by quantitative real-time PCR

The total RNA extraction and cDNA synthesis. The total RNA was isolated from the mammary tissue samples by Trizol Reagent (Invitrogen, Carlsbad, CA). Concentration and purity of the isolated RNA were measured in Nanodrop spectrophotometer (Thermo Scientific, USA). RNA integrity was evaluated by the observation of 18S and 28S ribosomal bands after electrophoresis on 1% agarose gel in the presence of ethidium bromide. Complimentary DNA (cDNA) was reverse transcribed from total RNA samples, using oligo dT primers and cDNA synthesis premium kit (TaKaRa, Tokyo, Japan) following the manufacturers' instructions.

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