

A study on the relationship between ruminal fermentation, milk production and
blood biochemical profiles in dairy cows during the transition period

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SOFYAN AHMAD

SUMMARY

Because dairy cows are usually faced with negative energy balance (NEB) in early lactation, dramatic changes in feed intake and metabolism during the transition period should be considered. Although high-energy diets applied to minimize NEB in early lactation, this feeding management may induce accumulation of lactate, depression of ruminal pH in the rumen and often causes subacute ruminal acidosis (SARA). Dietary changes during transition also presumably affect the structure of ruminal microbiota. Metagenomics analysis of ruminal microbiota could provide useful insight into diversity and function of rumen microbiota. Feeding management to regulate the ruminal microbiota structure is, therefore, expected to improve feed digestion, enhance microbial protein synthesis and minimize nutrient losses. Therefore, this study endeavored to define relationship between ruminal fermentations, milk production and metabolic profiles in dairy cows during the transition period in low-yield (LY) and high-yield (HY) dairy cows.

In this study, we observed that production of SCFAs in the transition period was similar in the both groups. Proportions of acetate (C2) and propionate (C3), and the C2:C3 ratio changed after parturition in the both groups. An increased proportion of C3 might be associated with the high proportion of concentrate in the lactating diet. Ruminal C2 was correlated with butyrate (C4) in the HY group. There was a significant relationship between ruminal C4 and blood beta-hydroxy butyric acid (BHBA) in the HY group after parturition, which might be assumed that ruminal C4 was converted into BHBA. Blood cholesterol, glutamic oxaloacetic transaminase and triglycerides (TG) of the HY group after parturition were higher than those in the LY group, which may contribute to high cholesterol requirement during milk synthesis. This study also showed that ruminal pH was closely correlated with non-esterified fatty acids (NEFA) in the LY group, and with C4, C2:C4 ratio, TG, BHBA:NEFA ratio in the HY group. These relationships indicated that ruminal pH might be associated with energy regulation during NEB.

Alterations of ruminal microbiota structure during transition in LY and HY dairy cows were investigated in this study. Although the diversity richness of ruminal microbiota in the both groups was not different, UniFrac distance of microbial communities was differently clustered into periods and groups. These differences might be associated with different adaptability of ruminal microbiota to the high-grain diet during transition. Moreover, rumen microbiota phyla in the both groups were dominated by *Bacteroidetes* (56-68%), *Firmicutes* (22-36%), *Proteobacteria* (1.3-4.4%), and other phyla (< 5%). In the HY group, abundance of *Bacteroidetes*, *Fibrobacteres* and *Bacteroidetes:Firmicutes* ratio were higher, but *Firmicutes* was lower than those in the LY group. At the genera level, *Bifidobacterium* and *Coriobacteriaceae* were increased in the LY group, whereas *Prevotella*, *Selenomonas*, *Succinivibrionaceae*, *Fibrobacter*, *Veillonellaceae*, and *Coprococcus* were increased in the HY group after parturition.

Patterns of relationships between ruminal microbiota, SCFAs and BHBA were different between the groups. Ruminal C3 was positively correlated with *Prevotella bryantii* in the both groups, with *Succinivibrionaceae* in the HY group, and with *Selenomonas ruminantium* in the LY group. Ruminal C4 was associated with *Megasphaera elsdenii*, *Ruminococcus albus* and

Butyrivibrio hungatei in the HY group, and with *Bifidobacterium* sp in the HY group. There was positive correlation between C4:BHBA ratio with *P. bryantii* and *Bacteroidales* bacterium in the HY group, whereas C4:BHBA ratio was negatively correlated with *P. ruminicola* and *Lachnospiraceae* bacterium in the LY group. C3:C4 ratio was positively correlated with *P. bryantii* and *Succinovibrionaceae* in the HY group, and *P. ruminicola* and *R. flavefaciens* in the LY group. Association of ruminal C3 with *P. bryantii* and *Succinivibriaceae* sp. in the HY group, and with *S. ruminantium* in the LY group indicated that production of C3 through succinate pathway was higher in the HY group than that in the LY group. In addition, positive correlation between C3:C4 ratio with *P. bryantii* and *Succinovibrionaceae* in the HY group, and with *P. ruminicola* and *R. flavefaciens* in the LY group presumably indicated that those bacteria contribute to energy regulation during lactation.

This study showed that abundance of gene families assigned by the Kyoto Encyclopedia Genes and Genomes (KEGG) orthology pathway in the both groups was composed of amino acid metabolism (10.5%), carbohydrate metabolism (10.5%), replication and repair (9.9%), membrane transport (8.7%), energy metabolism (6.0%), metabolism of cofactors and vitamins (4.7%), and others pathway (43.3%). Gene families responsible for metabolisms of amino acid, carbohydrate, lipid, vitamin and energy were accounted for 43% of genes in the both groups. High dominant abundance of gene families relating to metabolism of amino acids, cofactor and vitamin, and energy in the HY group may contribute to support milk protein synthesis. In conclusion, milk yield could be associated with ruminal fermentation and blood biochemical profiles during the transition period. Ruminal pH, ruminal fermentation and metabolic profiles, were associated with structural changes of ruminal microbiota. Cows in the HY group were appropriately adapted to high-concentrate diets rather than cows in the LY group.

This study concluded that milk yield could be associated with ruminal fermentation and blood biochemical profiles during the transition period. Ruminal pH, ruminal fermentations and metabolic profiles, were associated with structural changes of ruminal microbiota. Cows in the HY group appropriately adapted to high-concentrate diets rather than cows in the LY group. Although this study revealed that cows in the HY group likely have ability to maintain high absorption of ruminal metabolites and energy utilization during NEB, evidence of those mechanisms is unclear. Therefore, the further study is required to characterize the genomic expression related to absorption and utilization of the ruminal metabolites during the transition period.