

# Effects of Different Dietary Fiber Sources on Short-Chain Fatty Acid & Gas Production by *In Vitro* Fermentation Models of the Pregnant Sow Intestinal Microbiota

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**Keywords:** pregnant sows; dietary fiber; *in vitro* fermentation; microbial community; short chain fatty acids; gas production

Effective utilization of dietary fiber (DF) during gestation on alleviating inflammatory responses and ensuring normal metabolism and immune is critical to the performance of the sows and offsprings. Variations in the contents and compositions of DF in the feedstuffs determine their physicochemical properties and in turn affect the fermentation characteristics of the intestinal microbiota in the hindgut of sows. Due to the single research variable, the controllable process, and the ability to monitor the fermentation dynamics in real time, numerous studies have adopted the *in vitro* fermentation to investigate the interaction between nutrients and gut microbiota in recent years. The objective of this study is to evaluate the fermentation characteristics of different fiber sources (control, without fiber sources, CON; beet pulp, BP; commodity concentrated fiber, CCF; alfalfa meal, AM) in an *in vitro* methods using fecal microbiota from pregnant sows, and their effects on short chain fatty acids (SCFAs), gas production at 8, 12, 24, and 36 h of fermentation and bacterial community at 36 h. The results showed the fermentation of AM showed higher total gas and H<sub>2</sub> production than BP, CCF, and CON, at different time points. CH<sub>4</sub> and CO<sub>2</sub> production increased significantly in all DF groups, especially the AM group was significantly higher than the BP and CCF. In addition, total SCFAs production was higher in AM in comparison with BP, CCF, and CON. At the phylum level, the most abundant bacteria were *Firmicutes*, *Bacteroidetes*, and *Actinobacteriota* in AM and BP. *Firmicutes*, *Bacteroidetes*, and *Fusobacteriota* were the dominant phyla in CCF. Compared to CON, *Fimicutes* was significantly higher in AM and *Fusobacteriota* was markedly decreased in all DF. At the genus level, *Lactobacius* in AM was significantly higher than that in CON, while all DF significantly reduced *Fusobacterium*. Furthermore, correlation analysis showed that *Acidaminococcus*, *norank\_f\_Muribaculaceae*, *Prevotellaceae\_NK3B31\_group*, and *Lactobacillus*, *Holdemanella* *Collinsella* were positively correlated with total gas, H<sub>2</sub>, and SCFAs production. In conclusion, this study implicated that different sources of DF exerted divergent physiological functions in regulating microbial composition, SCFAs and gas production, providing new prospects for targeting host health by choosing fiber-rich AM diets.

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