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Evolution of the pig's gut microbiota depends on the feed presentation.

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Abstract

If many studies have proven that a modification in the pig feed composition can alter its gut microbiota, the effect of feed presentation is still largely to be determined. A previous study (LeBel *et al.*, 2013) demonstrated that after 21 d of specific diet (varying only by their presentation) fecal bacteria (as many as 65 different genera) differ in proportion between the different diets. But to demonstrate the potential of the feed presentation to increase (or decrease) the presence of a given bacterial genus, a specific analyze of the evolution of the gut microbiota components must be made. To do so, 96 pigs were assigned a specific diet (24/diet) of the same composition varying only by their particle size (500 or 1250 µm) and/or texture (pellet or mash feed). Feces samples were taken at d 0 and 21. Non-specific PCR amplifications of the 16S gene from a DNA extraction of the feces were analyzed by an Ion-Torrent Semiconductor Sequencer (Illumina) and sequences were attributed using Ribosomal Database Project Pipeline. The proportion of the microbiota that represent a given bacterial genus obtained at d 0 was subtracted to the same data obtained at d 21 to measure the evolution of a given genus from one date to the other. For more than 30 different genera the evolution of the given genus was significantly different from one diet to the other between the 2 dates. While many genus containing potential pathogens seem to be advantaged ($P < 0.05$) by a small particle size (500 µm) and/or a pellet texture (for example: *Corynebacterium*, *Salmonella*, or *Treponema*) some, such as *Clostridium* cluster I, seem to be advantaged by a larger particle size (1250 µm) and a mash texture. It must be noted that many bacteria of the *Clostridium* genus are short-chain fatty acid producers which is reported to provide benefits to the animal by inhibiting some potential intestinal pathogens. Also, some of the reputed good gut health promoting bacteria genus (e.g., *Bifidobacterium* or *Lactobacillus*) have shown a significantly greater evolution ($P < 0.05$) in the pigs feed large particle size and/or mash feed. This study demonstrated that feed presentation alone is able to modify piglet's fecal microbiota, analyses indicated that mash or large particle size feed would promote a healthier microbiota.

Key Words: mash, pig, microbiota