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Do microbial communities in an anaerobic bioreactor change with continuous feeding sludge into a full-scale anaerobic digestion system?

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Abstract:

Microbial communities of sludge samples from a full-scale anaerobic digestion (AD) fed with primary sludge (PS) and excess sludge (ES) were analyzed using qPCR and MiSeq. The results showed that the microbial composition of digested sludge remained relatively stable but was partially changed by microbial immigration from feeding sludge. The dominant archaea in the digested sludge were largely the same as those in the feeding sludge, but their abundances differed markedly. The dominant fungal genera in the digested sludge were different from those in PS but were similar to those in ES. Various differences in bacterial community differences between digested sludge and PS/ES were observed. Notably, this study is the first to suggest *Verrucomicrobia* is

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