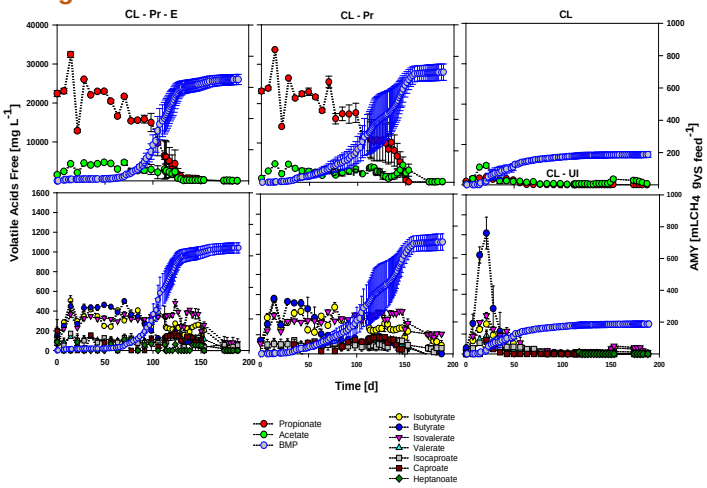
Role of microbiome on the performance of methane production via anaerobic digestion of chicken litter supplemented with propionate.

Flor de Maria Guerrero-Toledo, Teodoro Espinosa-Solares, David H. Huber, Sridhar Acharya Malkaram, Guadalupe Hernandez-Eugenio, Diana Guerra-Ramírez

Abstract

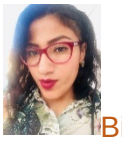
The objective of this work was to evaluate the influence of a consortium, obtained under selection pressure with high levels of propionate, on methane production, in a co-digestion system fed with chicken litter and propionate, under mesophilic conditions. The experiment was carried out in triplicate. The chicken litter 3 % of total solids (TS) with 22,592 ppm of propionate was degraded under mesophilic conditions using bioreactors with a working volume of 10 L, for 191 days. According to the modified Gompertz model, the best BMP (756.04 mL CH4 gvsfed-1) was obtained with the treatment CL – Pr, followed by the treatment with enrichment inoculum, CL – Pr - E (651.86 mL CH4 gvsfed-1), with a methane production rate (μm) of 18.35 mL CH4 gvsfed-1d-1 and a lag time (λ) of 88.05 d. This treatment increased the methane yield 3.55 times with respect to the control (CL, 183.66 mL CH4 gvsfed-1). In order to elucidate the role of the microbiome on the performance, sequencing and bioinformatic analysis of 48 DNA samples were necessary, the samples were taken at strategic points of the methane yield curve. The information obtained, using different bioinformatic tools, revealed that the dominant phylum was Firmicutes and that, the main microorganism responsible to produce methane is *Methanoculleus marisnigri* through the hydrogenotrophic methanogenesis pathway. While the methane produced by acetoclastic via was mainly attributed to *Methanosarcina mazei*. On the other hand, the degradation of propionate was carried out primarily by *Syntrophomonas wolfei* and *Pelotomaculum thermopropionicum*, increasing its population through the time of the experiment. In addition to this, the presence of reducing sulfate bacteria (SRB) could indicate the existence of an antagonistic relationship between this group of microorganisms and methanogens, this would explain the time of the lag phase in methane production in the treatments that were supplemented with propionate.

Image



Recent Publications

1. Ahlert, S., Zimmermann, R., Ebling, J. and König, H. (2016) Analysis of propionate-degrading consortia from agricultural biogas plants. MicrobiologyOpen 5(6), 1027-1037.Room R, BaborT, Rehm J (2005) Alcohol and public health. Lancet 365: 519-530.
2. Bayrakdar, A., Molaey, R., Sürmeli, R.Ö., Sahinkaya, E. and Çalli, B. (2017a) Biogas production from chicken manure: Co-digestion with spent poppy straw. International Biodeterioration & Biodegradation 119, 205-210.
3. Guerrero-Toledo, F., Espinosa-Solares, T., Balagurusamy, N., Guerra-Ramírez, D., Huber, D., & Hernández-Eugenio, G. (2019) Potencial bioquímico de metano de pollinaza adicionada con propionato en condiciones mesofílicas. Scientia Agropecuaria, 10(2), 307-311.
4. Kim, W., Shin, S.G., Han, G., Cho, K. and Hwang, S. (2015) Structures of microbial communities found in anaerobic batch runs that produce methane from propionic acid—Seeded from full-scale anaerobic digesters above a certain threshold. Journal of Biotechnology v. 214, pp. 192-198-2015 v.2214.
5. Meneses-Reyes, J.C., Hernández-Eugenio, G., Huber, D.H., Balagurusamy, N. and Espinosa-Solares, T. (2017) Biochemical methane potential of oil-extracted microalgae and glycerol in co-digestion with chicken litter. Bioresource Technology 224, 373-379.



Biography

Flor de Maria Guerrero-Toledo is a PhD student in bioprocess area at Universidad Autonoma Chapingo. Recently, she had a sequence analysis training at West Virginia State University. She has experience in waste management to methane production. She has worked specifically with chicken litter as substrate and propionate to enhance the methane production through of a process of anaerobic digestion. She has applied different molecular and bioinformatic tools to know the changes on the microbiome and the influence of these in the anaerobic digestion process and its efficiency.

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Notes/Comments: