**Introduction**

Acetate is one of the most abundant intermediaries in an anaerobic microbial food web. In an anaerobic microbial community where carbon dioxide is the terminal electron acceptor, the degradation of acetate can be carried out in two ways, acetoclastic or syntrophically. To date, there are a few microorganisms described that are capable of syntrophic acetate oxidation, these are *Clostridium ultunense*, *Thermacetogenium phaeum*, *Thermatoga lettingae*, and strain ADR. In this study, we enriched and purified an anaerobic co-culture that is capable of syntrophic acetate and lactate degradation using sediments from a mechanochip and the serial dilution technique. Our molecular analysis of the DNA extracted from our culture fluids suggest that there is only one bacteria based on qPCR and that this organism belongs to the genus Syntrophus and contain the unique gene that codes for the flagellar cap protein that Syntrophus aciditrophicus has in its genome. Based on these data we conclude that we have an active culture of a Syntrophus that is capable of metabolizing acetate and lactate syntrophically with a hydrogenotrophic methanogen.

**Hypothesis**

Ho: Syntrophus aciditrophicus can degrade lactate and acetate in a syntrophic relationship.

H1: Syntrophus aciditrophicus can’t degrade lactate and acetate in a syntrophic relationship.

**Results**

- **Environmental sample in acetate (N)**: 25% of methanogens per *Bacteria*
- **SB CAP:** Methanospirillum and Methanobacterium. Similarly, the qPCR data using 16S rRNA (Universal Bacterial), 16S rRNA (genus specific, *Syntrophus*), and Cap (S. aciditrophicus specific) primers suggests that the bacterium in the culture belongs to the genus *Syntrophus* possibly a new strain of the previously described *Syntrophus aciditrophicus*. In conclusion, our consortium contains the first bacterium that belongs to the genus *Syntrophus* that is able to oxidize acetate and lactate syntrophically and use sulfate as electron acceptor.
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**Literature**