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Methane is a potent greenhouse gas and a major contributor to climate change, with a global warming potential (GWP) much greater than CO_2. Thus, understanding the various biological sources and sinks of methane is critical. One such sink is the anaerobic oxidation of methane (AOM) carried out by microbes that oxidize methane to CO_2. AOM is commonly linked to nitrate reduction in freshwater environments, and sulfate reduction in marine environments by sulfate reducing bacteria (SRB). Studies on AOM are limited as these anaerobic methane oxidizers (ANME) have never been successfully isolated, so there is no direct way to test various theories concerning potential methane oxidation pathways. A well characterized methane-producing archaeon, *Methanosarcina acetivorans*, exhibits limited methane oxidizing capabilities and is closely related phylogenetically to ANME organisms. In an effort to make a genetically tractable AOM system, here we show that a co-culture of *M. acetivorans* and *Desulfosarcina variabilis*, an SRB commonly found with ANME in nature, oxidizes methane and reduces sulfate. In addition, this co-culture exists in an aggregate formation similar in size and shape to ANME-SRB aggregates found in nature. We also identified an oxidase in *M. acetivorans* that could allow methanogens like *M. acetivorans* to oxidize methane anaerobically by coupling it to oxygen reduction or by transferring electrons to its syntrophic partners in nature. Given that *M. acetivorans* is very genetically similar to an ANME strain, this co-culture is a viable substitute for an ANME-SRB co-culture, and will be used to test various theories about the specific energetic and metabolic pathways for methane oxidation, and the morphological and energetic basis of the ANME-SRB syntrophic relationship.