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Wind and biomass are promoted worldwide as sustainable forms of energy. Anaerobic digestion of biomass produces biogas with ~50–70% CH4 and 30–50% CO2. However, biogas with >90% CH4 content has higher heating value, can be injected into the natural gas grid or used as alternative to natural gas as vehicle fuel. Methods currently available for biogas upgrading mainly consists of physicochemical CO2 removal, requiring the use of chemical substances and energy input and, thus, increasing process costs. This PhD project proposes an alternative to existing biogas upgrading technologies, where H2, produced by water electrolysis, is coupled with the CO2 contained in the biogas to convert them to CH4. This process is defined as biological biogas upgrading and is carried out by hydrogenotrophic methanogenic archaea that couples CO2 with H2 to produce biomethane, via hydrogenotrophic methanogenesis. This reaction results in an increment of the total volume of CH4 produced avoiding any loss of CH4. Moreover, the CO2 is converted rather than being released to the atmosphere providing enhanced environmental benefits of biogas technologies. Moreover, hydrogenotrophic methanogenesis can operate in moderate operating conditions, without using chemical substances, and exploiting mixed culture, rather than pure culture, markedly reducing operation costs. The combination of these characteristics makes biomethane an energy carrier with exceptional potential, which could become a key element in the future renewable-based energy system. Nevertheless, the direct injection of H2 in the reactor (in-situ biogas upgrading) can cause scientific challenges, such as pH increase due to the CO2 removal and process inhibition due to higher H2 partial pressure. Therefore, ex-situ biogas upgrading emerged as a solution aiming at the optimization of the upgrading process in dedicated external reactors. In this concept, biogas and H2 are introduced into an anaerobic reactor containing a mixed hydrogenotrophic culture where the biogas is upgraded to higher CH4 content. To overcome the issues related to in-situ biogas upgrading, a two-stage Continuous Stirred Tank Reactor (CSTR) was designed. In this configuration, the biogas and the digestate produced in the first reactor were transferred to the second one, where H2 was injected, decoupling biogas production (mainly occurring in the first reactor) and biogas upgrading (occurring in the second reactor) and providing higher process efficiency. Moreover, biogas production and upgrading performances at mesophilic and thermophilic conditions were compared. The results demonstrate the feasibility of the biogas upgrading process, at both temperature conditions with higher biomethanation and CO2 conversion efficiency at thermophilic. Moreover, upon H2 addition, the produced biogas was upgraded to average CH4 content of 89% in the mesophilic reactor and 85% in the thermophilic. Nevertheless, H2 is known to be poorly soluble in aqueous media and its transfer to the reactors’ liquid phase represents a strong limiting factor for H2 availability for methanogens. Therefore, the optimization of H2 dispersion is crucial to ensure efficient biogas upgrading process. Gas transfer to the liquid phase is specific for given reactor configuration and operating conditions and can be modulated by adjusting on parameters such as mixing speed, gas recirculation and H2 diffusion device. This aspect has been investigated in a thermophilic granular up-flow anaerobic sludge blanket (UASB) reactor connected to a separate H2-injection chamber, for in-situ biogas upgrading. The effect of liquid and gas recirculation on gas-liquid transfer was evaluated. Moreover, the application of different packing materials in the separate chamber, as a mean to minimize gas bubble size and thus increase the gas dissolution in the liquid was discussed. Finally, the effect of gas retention time was evaluated in different chamber configurations to elucidate its role for CO2 and H2 conversion to CH4. It was observed that by distributing H2 through a stainless steel diffuser followed by a ceramic sponge in a separate chamber (having a volume of 25% of the reactor) and by applying a moderate gas recirculation, CO2 content in the biogas dropped from 42 to 10% and the final biogas was upgraded from 58 to 82% CH4 content. Based on these finding, further enhancement of the H2 gas-liquid mass transfer rate was investigated in four up-flow reactors for ex-situ biogas upgrading. The effect of different H2 distribution devices and different pore sizes on H2 uptake by methanogens was elucidated. Moreover, the role of input gas flow rate and gas recirculation on H2 and CO2 conversion to CH4 was investigated. The results showed that the configurations involving diffusion devices with larger pore size presented the best kinetics and output-gas quality and at the highest recirculation rate tested, they managed to convert all the input H2 and CO2 into CH4, up to a H2 loading rate of 3.6 L(Ch4)/L(REACTOR.d). Accordingly, the CH4 content in the reactor increased from 23 to 96% and the CH4 yield reached 0.25 CH4/LH2. Finally, to provide higher process control and efficiency, a better understanding of the biogas community composition is crucial. Previous studies have showed that in each microbial community there is a fraction of microorganisms that is always present and constitutes the core of the community and a fraction depending on operating conditions. Therefore, we hypothesized that the H2 addition would selectively stimulate the hydrogenotrophic pathway enhancing the CO2 consumption and thus the biogas upgrading. Based on this knowledge, different bioinformatics approaches, comprising the commonly utilized, 16S rRNA amplicon sequencing, but also Assembled Full-Length 16S rRNA gene sequencing and total random sequencing followed by de novo assembly and by a binning strategy, were applied to the study of biogas production and upgrading communities. Specifically, biogas core community was composed of several recurrent microbial groups, including resilient methanogenic archaea such as Methanoculleus and Methanotermobacter and bacteria belonging to phylum Proteobacteria and genus Syntrophomonas. Moreover, upon H2 addition, the concomitant proliferation of hydrogenotrophic methanogens and syntrophic bacteria, such as Desulfovibrio, and some Thermoanaerobacteraceae and Syntrophomonadaceae, and the reduction of acetlastic methanogens and fermentative bacteria state the role of the H2 moving biomethanation process toward the final steps stimulating CO2 consumption and therefore biogas upgrading.