

Importance of inoculum source and initial community structure for biogas production from manure and lignocellulose rich material

Tong Liu, Li Sun, Bettina Müller and Anna Schnürer

Uppsala Biocenter, Dept. Microbiology, Swedish University of Agricultural Sciences, Uppsala, Sweden, SE-750 07



Background:

Agriculture residuals and manure represent a big biogas potential. However, the complex structure with high level of lignocellulose limits the overall degradation efficiency of these materials. Cellulose is degraded by extracellular or complex cell-bonded cellulases, called cellulosome, produced by microbes. The genes encoding the cellulase glycoside hydrolase are wide spread and are grouped in many families, of which family 5 and family 48 have been used as functional target genes to screen the potential lignocellulose degraders in different biogas reactors (Pereyra, Hiibel et al. 2010). In a previous study using this approach the degradation efficiency of cellulose and straw in batch cultures initiated with inoculum from 10 different biogas plant were shown to vary, indicatively caused by a difference in the composition of the cellulose degrading community.

Aim and method

In this study, inoculum from three different industrial biogas plants in Sweden were selected with the aim to investigate the importance of inoculum source and initial community structure for the start up and operation of lab-scale semi-continuous digesters (named GA, GB and GC) using grass-manure mixture as substrate (GS). The full-scale plants were different in regard to both substrate and operational parameters. During start up and operation the performance of the processes were followed by chemical analyses. The cellulose degrading microbial community were analysed by terminal restriction fragment length polymorphism analysis (T-RFLP) targeting glucoside hydrolase family 5 (cel5) and 48 (cel48) and the total microbial community were targeted by illumina sequencing targeting the 16S RNA. The digester were operated at 37°C, with an OLR of 2.8 VS/L and HRT at 30 days.

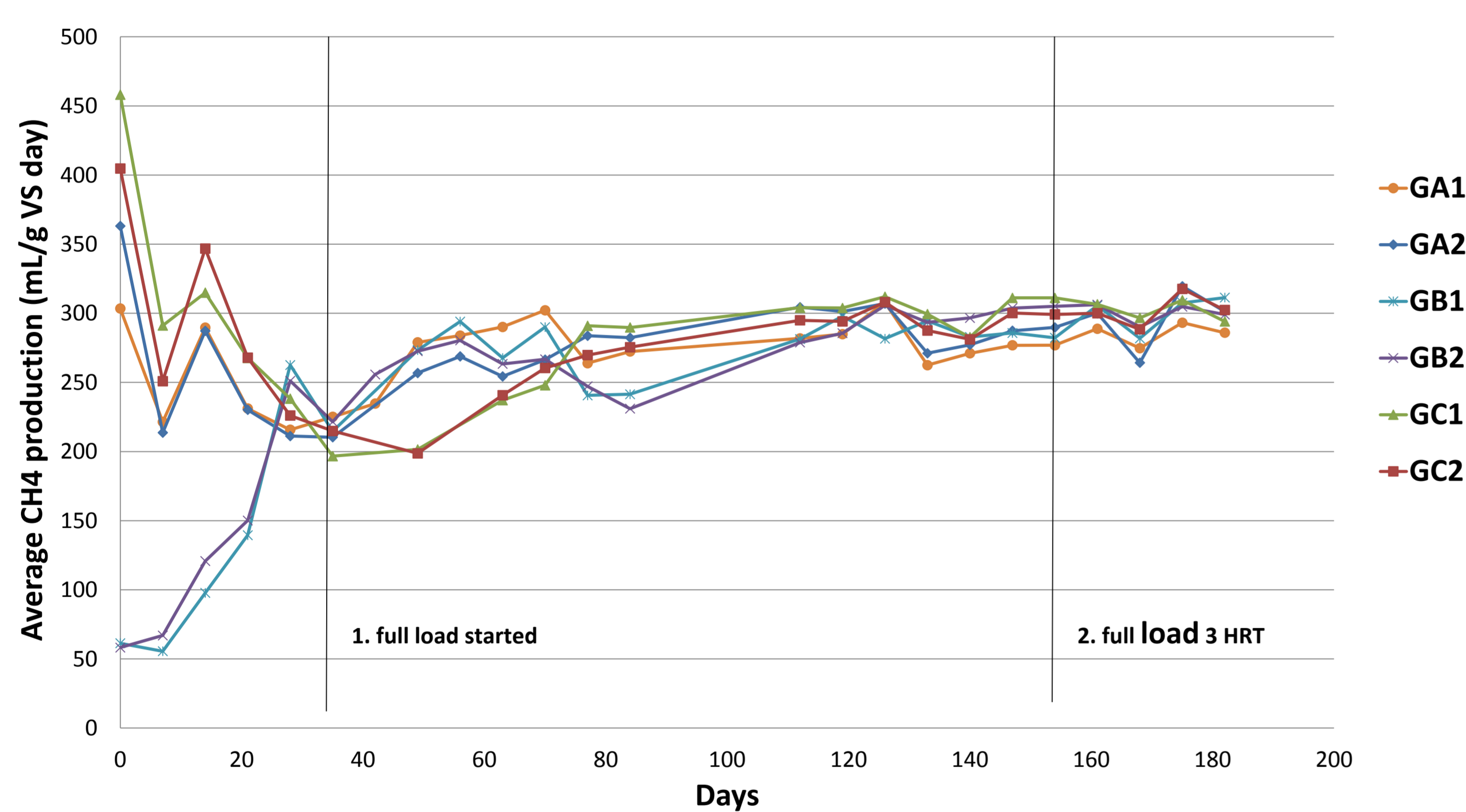


Fig 1. Average CH₄ production (NmL/g VS day) of the lab-scale biogas reactors.

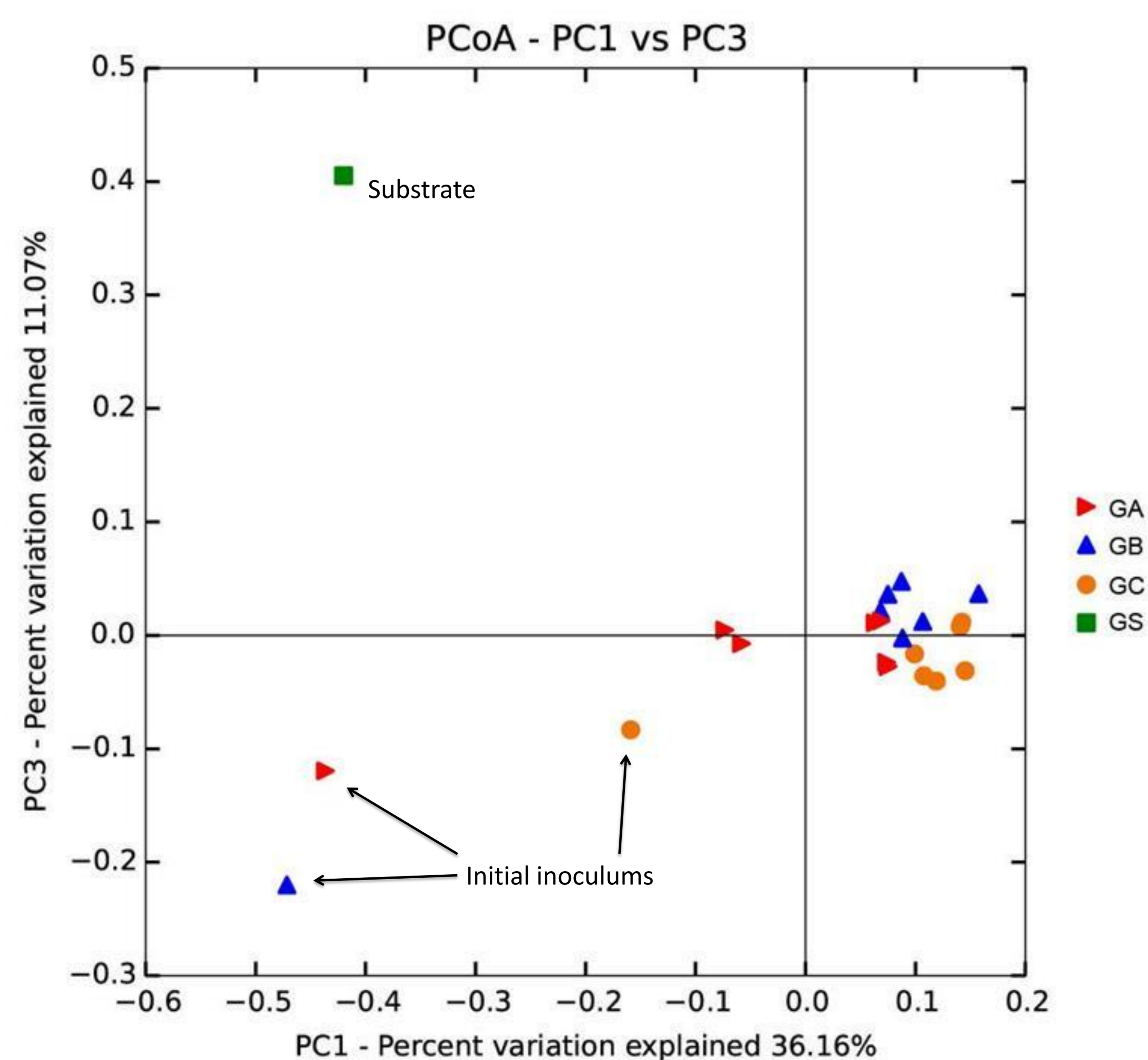


Fig 2. Unweighted UniFrac principal coordinate analysis (PCoA) of the total microbial community

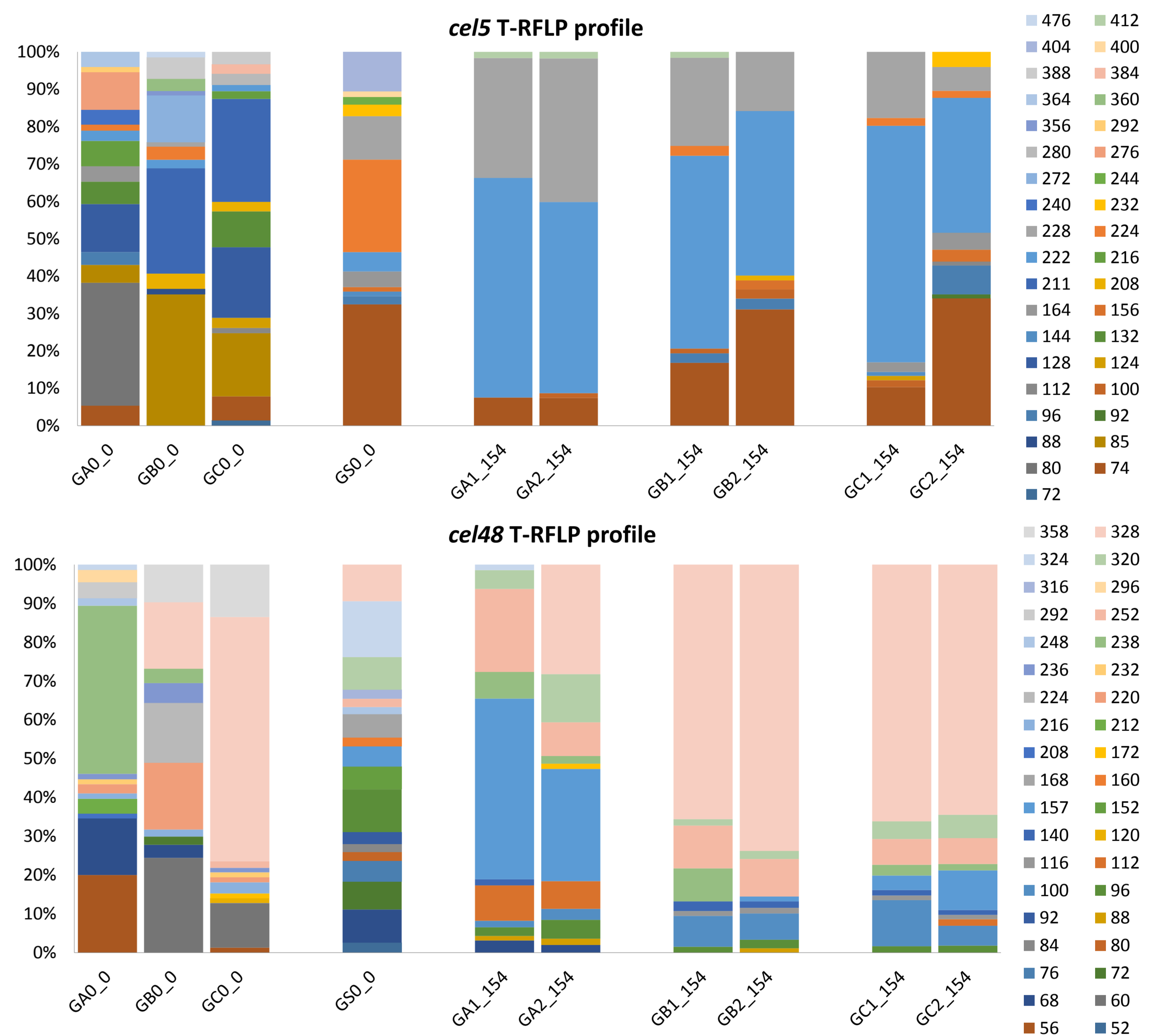


Fig 3. T-RFLP profile of cel5 and cel48 community after 0 and 154 days of operation with grass-manure (GS)

Results and discussions

The results revealed a difference between the digesters during start-up, with a slower degradation rate and methane formation when the processes were started with a high ammonia inoculum with a comparably lower initial microbial diversity. However after a few weeks of operation the processes all had equal performance and the initial different community structure were now unified (Fig 1 and 2). This result suggests that the substrate and operational parameters was more important than the inoculum source. Interestingly, even though the overall microbial community were shaped to a similar structure, differences were seen when targeting the cellulose degrading community specifically (Fig 3).