

## Ion Torrent sequencing and pipeline assembly of the first genome sequence of a mesophilic syntrophic acetate oxidizing bacterium (SAOB)

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### Motivation and Objectives

Syntrophic acetate oxidising bacteria (SAOB) have been identified as key organisms for efficient biogas production from protein rich materials under moderate conditions. *Tepidanaerobacter acetatoxydans* strain Re1 is the first reported mesophilic SAOB which genome has been sequenced (Manzoor *et al.*, 2013). Growth experiments and genetic studies allocated *T. acetatoxydans* to the physiological group of homoacetogens producing acetate through the Wood-Ljungdahl pathway when growing heterotrophically (Manzoor *et al.*, 2013, Westernholm *et al.*, 2011). However, when growing in syntrophy with methanogens, SAOB reverse this pathway and oxidise acetate to hydrogen and carbon dioxide (Müller *et al.*, 2012, Hattori *et al.*, 2005, Schnürer *et al.*, 1997).

### Motivation and Objectives

Bioinformatics analysis might aid us to define general features being essential for maintaining a syntrophic lifestyle and to answer question concerning regulation, energy conservation and electron transfer mechanisms. This knowledge will enable us to further understand the mechanisms triggering SAO in different environments, to monitor the activities of known SAOB and to find new isolation strategies.

### Methods

The genome was sequenced by Ion Torrent PGM™ Systems and we assembled the genome by using a comparative pipelined approach by using MIRA3 for mapping and Newbler 2.8 for *de novo* assembly. The finished genome was annotated with the annotation tools provided by MaGe (Microbial Genome Annotation & Analysis Platform).

### Results and Discussion

Our comparative approach with mapping and *de novo* assembly contributed successfully for finishing the bacterial genomes with high accuracy and less PCR work. After complete genome assembly and annotation (Table 1), a first genome analysis confirmed the two *fhs* clusters identified by Müller *et al.* (Müller *et al.*, 2012) as well as the suggested operon structure including all genes encoding the Wood-Ljungdahl pathway with one exception: No format dehydrogenase has been identified underlying the observed inability of this organism to establish an autotrophic lifestyle (Müller *et al.*, 2012). ATP seems to be generated by substrate level phosphorylation exclusively because no complete FOF1-ATP synthase has been found. Further two V-type ATPase operons, a cluster encoding an Rnf complex and several hydrogenases clusters have been identified and might contribute to the energy conserving systems of the cell.

Table 1. Genomic features of SAOB Genome.

Strain	T. size (bp)	T. Protein coding genes	Avg. CDS Lgth.	Avg. Interg. Lgth.	Total rRNAs	Total tRNAs	Protein Coding Density	G+C %
TepRe1	2,759,867	2,524	917	136	6	52	86.92	38

## References

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