DATA NOTE

Deeply sequenced metagenome and metatranscriptome of a biogas-producing microbial community from an agricultural production-scale biogas plant

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Abstract

Background: The production of biogas takes place under anaerobic conditions and involves microbial decomposition of organic matter, with most participating microbes still considered unknown and non-cultivable. Accordingly, metagenome sequencing is currently the only possibility to obtain insights into community composition and the genetic repertoire.

Findings: Here, we report the first deeply sequenced metagenome and metatranscriptome of a complex biogas-producing microbial community from an agricultural production-scale biogas plant. We assembled the metagenome and reconstructed most genes involved in the methane metabolism, a key pathway involving methanogenesis populated by low-abundance archaea. This exemplary result indicates sufficient sequencing coverage for most downstream analyses.

Conclusions: Sequenced at least one order of magnitude deeper than previous studies, our metagenome data will enable novel insights into community composition and the genetic potential of important community members. Moreover, mapping of transcripts to reconstructed genome sequences will enable the identification of active metabolic pathways in target organisms.

Keywords: Biogas; Metagenome; Metatranscriptome; Sequencing; Assembly

Data description

Background

Production of biogas by means of anaerobic digestion of biomass is becoming increasingly important as biogas is regarded a clean, renewable and environmentally compatible energy source [1]. Moreover, generation of energy from biogas relies on a balanced carbon dioxide cycle.

The process of biogas production takes place under anaerobic conditions and involves microbial decomposition of organic matter, yielding methane as the main final product of the fermentation process. Complex consortia of microorganisms are responsible for biomass decomposition and biogas production. The majority of the participating microbes are still unknown, as is their influence on reactor performance. Since most of the organisms within biogas communities are non-cultivable by today's conventional microbiological techniques, sequencing of metagenomic to-

tal community DNA is currently the only way to obtain unbiased insights into community composition and the genetic potential of key community members.

Here, we report the first deeply sequenced metagenome of an agricultural production-scale biogas plant on the Illumina platform [2]. We sequenced $27.3\times$ and $19.3\times$ deeper, respectively, than previous studies relying on 454 [3] or SOLiD [4] sequencing. Metatranscriptomic sequencing of total community RNA complements the metagenome. Combined, these data will enable a deeper exploration of the biogas-producing microbial community, with the objective to develop rational strategies for process optimization.

Digester management and process characterization

The biogas plant, located in North Rhine Westphalia, Germany, features a mesophilic continuous wet fermentation technology and was designed for a capacity of $537\,kW_{el}$ combined heat and power (CHP) generation. The process comprises three digesters: a primary and secondary digester, where the main proportion of biogas is produced, and a storage tank, where the digestate is fermented thereafter.

The primary digester is fed hourly with a mixture of $72\,\%$ maize silage and $28\,\%$ liquid pig manure. The biogas and methane yields at the time of sampling were at 810.5 and 417.8 liters per kg organic dry matter ($l/kg\,oDM$), respectively. After a theoretical retention time of 55 days, the digestate is stored in the closed, non-heated final storage tank. Further metadata are summarized in Table 1.

Sampling and nucleic acid isolation

Samples from the primary digester of the aforementioned biogas plant were taken in November 2010. Prior to the sampling process, approximately $15\,L$ of the fermenter substrate were discarded before aliquots of $1\,L$ were transferred into clean gastight sampling vessels and transported directly to the laboratory.

Aliquots of $20\,g$ of the fermentation sample were used for total community DNA preparation as described previously [5]. A random-primed cDNA library was prepared by an external vendor (vertis Biotechnologie AG). Briefly, total RNA was first treated with $5'$-P dependent Terminator exonuclease (Epicentre) to enrich for full-length mRNA carrying $5'$ CAP or triphosphate structures. Then, first-strand cDNA was synthesized using a N6 random primer and M-MLV-RNase H reverse transcriptase, and second-strand cDNA synthesis was performed according to the Gubler-Hoffman protocol.

Metagenomic and metatranscriptomic sequencing

We sequenced one metatranscriptome and two metagenome shotgun libraries on Illumina's Genome Analyzer IIx system, applying the Paired-End DNA Sample Preparation Kit (Illumina Inc.) as described by the manufacturer and generating $2\times161\,bp$ paired-end reads. On Illumina's MiSeq system, we sequenced three further metagenome shotgun libraries, applying the Nextera DNA Sample Preparation Kit (Illumina Inc.) as described by the manufacturer and generating $2\times155\,bp$ paired-end reads. Our sequencing efforts, yielding 35 gigabases in total, are specified in Table 2.

Metagenome assembly and annotation

`KEGG`

Prior to assembly, we used Trimmomatic [6], version 0.32, for adapter removal and moderate quality trimming. After adapter clipping, using Trimmomatic's *Truseq2-PE* and *Nextera-PE* templates, we removed leading and trailing ambiguous or low quality bases (below Phred quality scores of 3). Table 3 summarizes the effect on sequencing depth, more than 25 gigabases of sequence data passed quality control.

We assembled the metagenome with Ray Meta [7], version 2.3.1, using a k-mer size of 31 and a minimum contig length of $1,000\,bp$. This resulted in a total assembly size of approximately 228 megabases in $54,489$ contigs, with an N50 value of $9,796\,bp$.

We then used MetaProdigal [8], version 2.6.1, to predict $250,596$ protein-coding genes on the assembled contigs. We blasted the protein sequences of all predicted genes against the KEGG database [9], release 72.0, using Protein-Protein BLAST [10], version 2.2.29+. Of the $250,596$ predicted genes, $191,766$ had a match in the KEGG database, using an Evalue cutoff of 10^{-6}. We determined the KEGG Orthology (KO) for each gene by mapping the top-scoring BLAST hit to its orthologous gene in KEGG, resulting in xxx genes with an assigned KEGG Orthology. Table 4 summarizes our results.

Relating the metagenome and the metatranscriptome

To illustrate potential use cases, we aligned the post-QC sequencing reads to the `RPKM` assembled contigs with bowtie2 [11], version 2.2.4, and used samtools [12], version 1.1, to convert SAM to BAM and thereafter sort each alignment file. We counted the number of reads within genes using BEDTools [13], version 2.22.0, and calculated the RPKM values for each gene as a crude measure for abundance (metagenome) or expression (metatranscriptome).

Figure 1 as a toy example, highlighting genes in some pathway.

Figure 2 shows metagenomic vs. metatranscriptomic coverage of predicted genes in RPKM units. We highlighted all genes involved in either of the three known types of methanogenic pathways. Going from CO2 to methane appears to be predominant, which is in agreement with the literature.

Availability

Data accession

The datasets supporting the results of this article are available in the European Nucleotide Archive (ENA) under study accession PRJEB8813.

Intermediate results for the review process are deposited in the project's GitHub repository [14], and will be uploaded to GigaDB [2] upon acceptance.

Reproducibility

The complete workflow is organized in a single GNU Makefile and available on GitHub [14]. Starting from the raw read files, all data and results can be reproduced by a simple invocation of *make*.

To further support reproducibility, we bundled all tools and dependencies into one Docker container available on DockerHub [15]. *docker run* executes the afore-mentioned Makefile inside the container.

Excluding the KEGG analysis, which relies on a commercial license of the KEGG database, all steps are performed using free and open-source software.

Discussion

[WRITE] ⌐ Potential use cases.

Metagenomic and metatranscriptomic profiling of the biogas-producing microbial community. Highlight, that methane metabolism pathway is widely covered, but still room for improvement, i.e. sequence deeper.

Identification of metaproteomic data out there [16].

Ultimate goal: process optimization by biological insights.

Author's contributions
AB conveied and performed all bioinformatic analyses and wrote the paper. IM investigated all metadata and drafted part of the data description. PB implemented the accompanying Docker container. FE collected the study material. AW and AA provided the sequencing service. AP acquired funding and revised the paper. ASch and AScz jointly directed the project and extensively revised the paper. All authors read and approved the final manuscript.
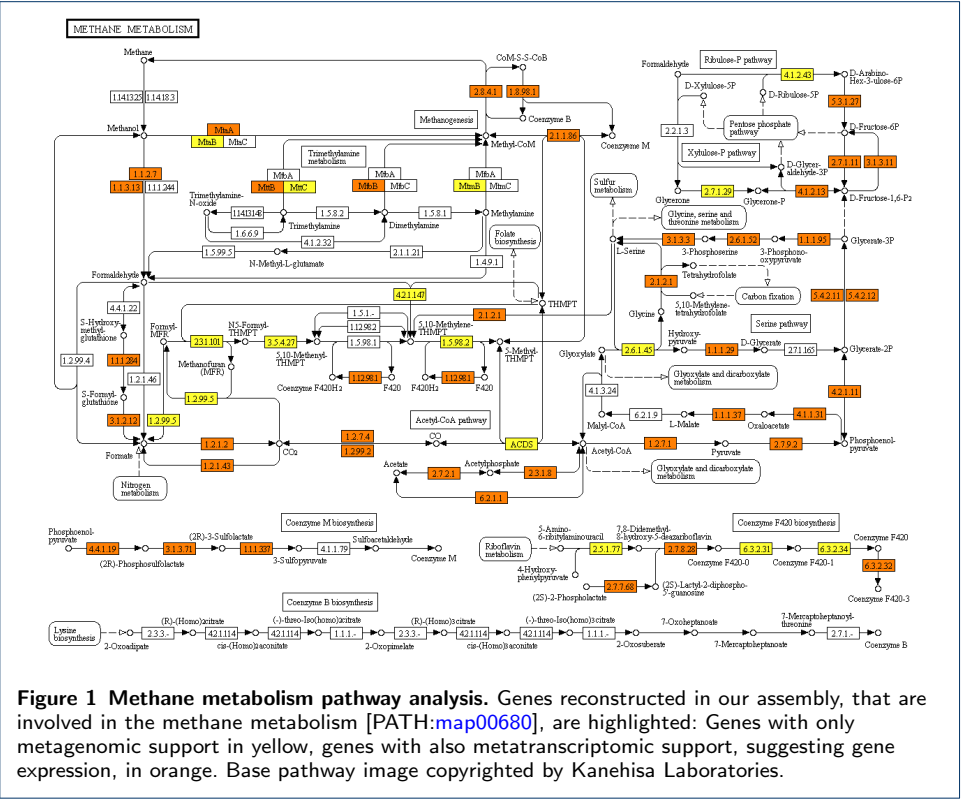
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Figures

Figure 1 Methane metabolism pathway analysis. Genes reconstructed in our assembly, that are involved in the methane metabolism [PATH:map00680], are highlighted: Genes with only metagenomic support in yellow, genes with also metatranscriptomic support, suggesting gene expression, in orange. Base pathway image copyrighted by Kanehisa Laboratories.

Tables

Table 1 Characteristics of the studied biogas plant. Primary digester, sampling date: Nov 15, 2010.

Process parameter	Sample
Net volume	$2041\,m^3$
Dimensions	$6.4\,m$ high, diameter of $21\,m$
Electrical capacity	$537\,kW_{el}$
pH	7.83
Temperature	$40\,^\circ C$
Conductivity	$22.10\,mS/cm$
Volative organic acids (VOA)	$5327\,mg/l$
Total inorganic carbon (TIC)	$14397\,mg/l$
VOA/TIC	0.37
Ammoniacal nitrogen	$2.93\,g/l$
Acetic acid	$863\,mg/l$
Propionic acid	$76\,mg/l$
Fed substrates	$72\,\%$ maize silage, $28\,\%$ pig manure
Organic load	$4.0\,kg\,oDM\,m^{-3}\,d^{-1}$
Retention time	$55\,d$
Biogas yield	$810.5\,l/kg\,oDM$
Methane yield	$417.8\,l/kg\,oDM$

Figure 2 Relating the metagenome and metatranscriptome. Highlighted are genes involved in methanogenesis, color coded by pathway type: CO2 to methane [MD:M00567] green, methanol to methane [MD:M00356] red, and acetate to methane [MD:M00357] blue.
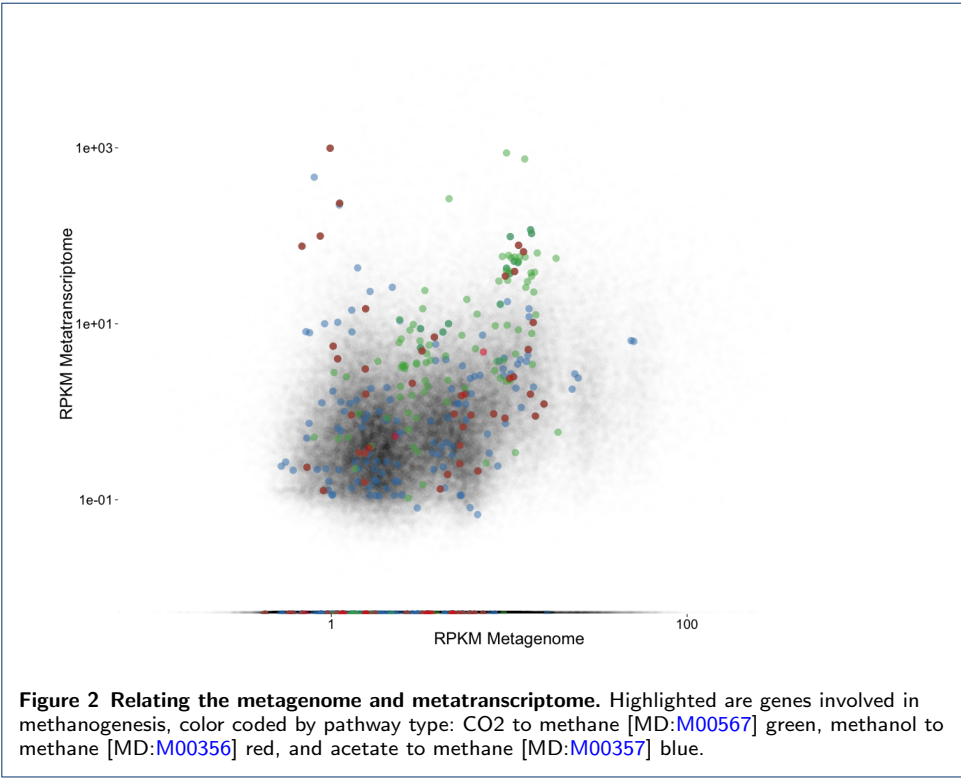
Table 2 Overview of the different sequencing libraries.

Accession	Library name	Library type	Insert size[1]	Cycles	Reads	Bases
ERS697694	GAIIx, Lane 6	RNA, TruSeq	202 ± 49	2×161	$78,752,308$	$12,679,121,588$
ERS697688	GAIIx, Lane 7	DNA, TruSeq	157 ± 19	2×161	$54,630,090$	$8,795,444,490$
ERS697689	GAIIx, Lane 8	DNA, TruSeq	298 ± 32	2×161	$74,547,252$	$12,002,107,572$
ERS697690	MiSeq, Run A1	DNA, Nextera	173 ± 53	2×155	$4,915,698$	$761,933,190$
ERS697691	MiSeq, Run A2	DNA, Nextera[2]	522 ± 88	2×155	$1,927,244$	$298,722,820$
ERS697692	MiSeq, Run B1	DNA, Nextera	249 ± 30	2×155	$3,840,850$	$573,901,713$
ERS697693	MiSeq, Run B2	DNA, Nextera[2]	525 ± 90	2×155	$4,114,304$	$614,787,564$

[1]Insert sizes determined with Picard tools. [2]This Nextera library was sequenced twice.

Table 3 Metagenomic and metatranscriptomic sequencing.

Library type	Reads, raw	post-QC	Bases, raw	post-QC
Metagenome (total)	$143,975,438$	$137,365,053$	$23,046,897,349$	$17,267,320,221$
Metatranscriptome	$78,752,308$	$73,165,986$	$12,679,121,588$	$8,455,809,264$

Table 4 Metagenome assembly statistics, minimum contig size of $1,000\,bp$.

Assembly metric	Our assembly
Total size	$228,382,457\,bp$
Number of contigs	$54,489$
N50 value	$9,796\,bp$
Largest contig	$333,979\,bp$
Predicted genes	$250,596$
of these, full-length	$172,372\,(69\,\%)$
Match in KEGG Genes (10)	$241,153$
Match in KEGG Genes (1e-3)	$200,214$
Match in KEGG Genes (1e-6)	$191,766$
Match in KEGG Genes (1e-9)	$184,251$
of these, assigned KO	xxx,xxx

KOs to be added asap, see above.