DATA NOTE

The 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 total 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× and 19.3× 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-producting 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.

Sequencing and quality control

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.

We then 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 filtered sequence data passed quality control.

Metagenome assembly and quality assessment

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 $9,796\,bp$. Table 4 summarizes our results.

Mapping, Picard-tools

We aligned the post-QC sequencing reads to the assembled contigs with bowtie2 [8], version 2.2.4, and used samtools [9], version 1.1, to convert SAM to BAM and thereafter sort the alignment file.

Gene prediction and annotation

We then used MetaProdigal [10], version 2.6.1, to predict $250,596$ protein-coding genes on the assembled contigs. Table 4 also includes these results.

TODO

We blasted all predicted genes against the KEGG database [11], release 72.0, using Protein-Protein BLAST [12], 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.

Relating the metagenome and the metatranscriptome

We counted aligned reads in predicted genes with BEDTools, version 2.22.0, [13]. Figure 2 shows metagenomic vs. metatranscriptomic coverage in RPKM units.

TODO

Availability

Data accession

The datasets supporting the results of this article are available in the [repository name] repository, [unique persistent identifier and hyperlink to datasets in http:// format]. Raw sequencing data was submitted to SRA and is available under accession BLA. Intermediate results for the review process are deposited in the project's GitHub repository [14].

TODO

Reproducibility

The complete workflow is organized in a single GNU Makefile and available on GitHub [14]. Starting from the raw read files, available from SRA and/or GigaDB, all data and results can be reproduced by a simple invocation of *make*. Excluding the KEGG analysis, which relies on a commercial license of the KEGG database, all steps are performed using free and open-source software. To further support reproducibility, all tools and dependencies are available in a single Docker container implementing the bioboxes assembly interface, version 0.8, from DockerHub.

TODO

Discussion

Potential use cases.

TODO

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. Possibly mention new data generated within the CSP? Tricky to phrase it without trashing this data set.

Identification of metaproteomic data out there (cite Vera, in preparation, and Magdeburg - Fabian).

Ultimate goal: process optimization by biological insights.

Competing interests
The authors declare that they have no competing interests.

Author's contributions
AB conveived 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 sampled stuff. AW and AA sequenced stuff. AP provided funding. ASch revised the paper. AScz conveived of many of the analyses and revised the paper. ASch and AScz jointly directed the project. All authors read and approved the final manuscript.

FIXME: Phrasing of middle authors' contributions

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ASch: Biogas Marker, Biogas Core

Acknowledge Stadtwerke?

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References

1. Weiland, P.: Biogas production: current state and perspectives. Appl. Microbiol. Biotechnol. **85**(4), 849–860 (2010). [DOI:10.1007/s00253-009-2246-7] [PubMed:19777226]
2. Bremges, A., Maus, I., Belmann, P., Eikmeyer, F., Winkler, A., Albersmeier, A., Pühler, A., Schlüter, A., Sczyrba, A.: Name of the GigaScience repository (2015). [DOI:foo/bar]
3. Jaenicke, S., Ander, C., Bekel, T., Bisdorf, R., Dröge, M., Gartemann, K.H., Jünemann, S., Kaiser, O., Krause, L., Tille, F., Zakrzewski, M., Pühler, A., Schlüter, A., Goesmann, A.: Comparative and joint analysis of two metagenomic datasets from a biogas fermenter obtained by 454-pyrosequencing. PLoS ONE **6**(1), 14519 (2011). [PubMed Central:PMC3027613] [DOI:10.1371/journal.pone.0014519] [PubMed:21297863]
4. Wirth, R., Kovács, E., Maróti, G., Bagi, Z., Rákhely, G., Kovács, K.L.: Characterization of a biogas-producing microbial community by short-read next generation DNA sequencing. Biotechnol Biofuels **5**, 41 (2012). [PubMed Central:PMC3395570] [DOI:10.1186/1754-6834-5-41] [PubMed:22673110]
5. Schlüter, A., Bekel, T., Diaz, N.N., Dondrup, M., Eichenlaub, R., Gartemann, K.H., Krahn, I., Krause, L., Krömeke, H., Kruse, O., Mussgnug, J.H., Neuweger, H., Niehaus, K., Pühler, A., Runte, K.J., Szczepanowski, R., Tauch, A., Tilker, A., Viehöver, P., Goesmann, A.: The metagenome of a biogas-producing microbial community of a production-scale biogas plant fermenter analysed by the 454-pyrosequencing technology. J. Biotechnol. **136**(1-2), 77–90 (2008). [DOI:10.1016/j.jbiotec.2008.05.008] [PubMed:18597880]
6. Bolger, A.M., Lohse, M., Usadel, B.: Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics **30**(15), 2114–2120 (2014). [PubMed Central:PMC4103590] [DOI:10.1093/bioinformatics/btu170] [PubMed:24695404]
7. Boisvert, S., Raymond, F., Godzaridis, E., Laviolette, F., Corbeil, J.: Ray Meta: scalable de novo metagenome assembly and profiling. Genome Biol. **13**(12), 122 (2012). [PubMed Central:PMC4056372] [DOI:10.1186/gb-2012-13-12-r122] [PubMed:23259615]
8. Langmead, B., Salzberg, S.L.: Fast gapped-read alignment with Bowtie 2. Nat. Methods **9**(4), 357–359 (2012). [PubMed Central:PMC3322381] [DOI:10.1038/nmeth.1923] [PubMed:22388286]
9. Li, H., Handsaker, B., Wysoker, A., Fennell, T., Ruan, J., Homer, N., Marth, G., Abecasis, G., Durbin, R.: The Sequence Alignment/Map format and SAMtools. Bioinformatics **25**(16), 2078–2079 (2009). [PubMed Central:PMC2723002] [DOI:10.1093/bioinformatics/btp352] [PubMed:19505943]
10. Hyatt, D., LoCascio, P.F., Hauser, L.J., Uberbacher, E.C.: Gene and translation initiation site prediction in metagenomic sequences. Bioinformatics **28**(17), 2223–2230 (2012). [DOI:10.1093/bioinformatics/bts429] [PubMed:22796954]
11. Kanehisa, M., Goto, S., Sato, Y., Kawashima, M., Furumichi, M., Tanabe, M.: Data, information, knowledge and principle: back to metabolism in KEGG. Nucleic Acids Res. **42**(Database issue), 199–205 (2014). [PubMed Central:PMC3965122] [DOI:10.1093/nar/gkt1076] [PubMed:24214961]
12. Camacho, C., Coulouris, G., Avagyan, V., Ma, N., Papadopoulos, J., Bealer, K., Madden, T.L.: BLAST+: architecture and applications. BMC Bioinformatics **10**, 421 (2009). [PubMed Central:PMC2803857] [DOI:10.1186/1471-2105-10-421] [PubMed:20003500]
13. Quinlan, A.R., Hall, I.M.: BEDTools: a flexible suite of utilities for comparing genomic features. Bioinformatics **26**(6), 841–842 (2010). [PubMed Central:PMC2832824] [DOI:10.1093/bioinformatics/btq033] [PubMed:20110278]
14. Bremges, A.: GitHub (2015). [https://github.com/abremges/2015-biogas-cebitec]

Figures

Tables

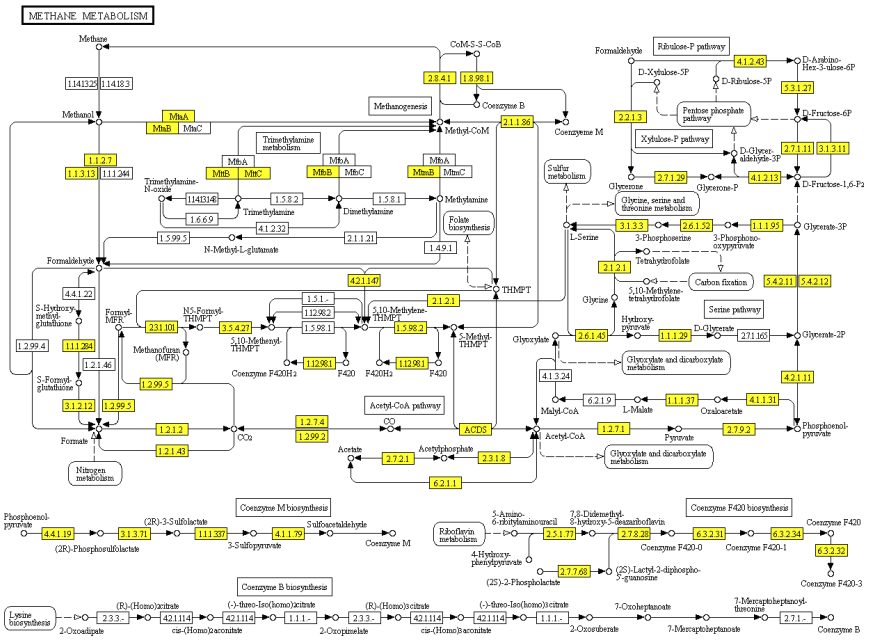

Figure 1 Methane metabolism pathway analysis. Genes reconstructed in our assembly, that are involved in the methane metabolism [PATH:map00680], are highlighted in yellow. Base pathway image copyrighted by Kanehisa Laboratories.

Nicer (?) alternative: 2 colors, metagenome and metatranscriptome!

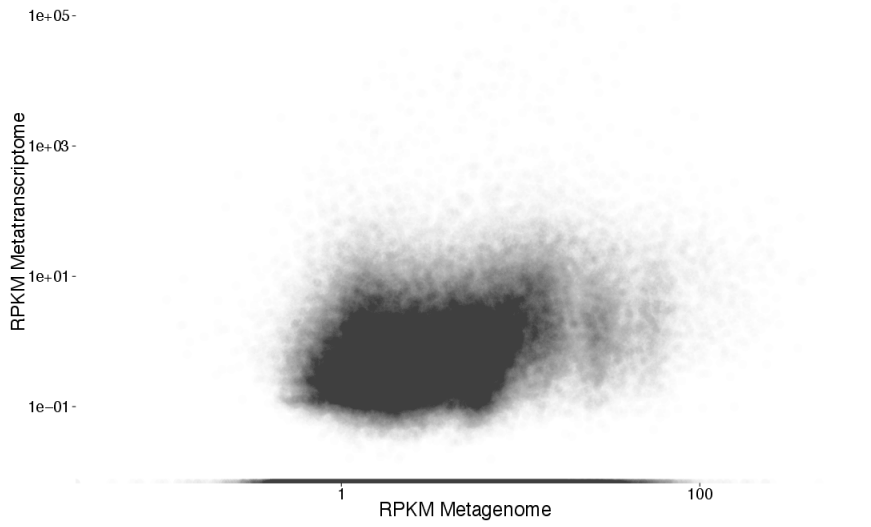

Figure 2 Relating the metagenome and metatranscriptome. Highlighted are genes involved in methanogenesis, color coded by pathway type: CO2 to methane [MD:M00567] green, methanol to methane [MD:M00356] red, and acetate to methane [MD:M00357] blue.

Table 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	$40\,^{\circ}\mathrm{C}$
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	$417.8\,l/kg\,oDM$

Table 2 Overview of the different sequencing libraries.

Library name	Library type	Insert size[1]	Cycles	Reads	Bases
GAIIx, Lane 6	RNA, TruSeq	202 ± 49	2×161	$78,752,308$	$12,679,121,588$
GAIIx, Lane 7	DNA, TruSeq	157 ± 19	2×161	$54,630,090$	$8,795,444,490$
GAIIx, Lane 8	DNA, TruSeq	298 ± 32	2×161	$74,547,252$	$12,002,107,572$
MiSeq, Run 1.1	DNA, Nextera	173 ± 53	2×155	$4,915,698$	$761,933,190$
MiSeq, Run 1.2	DNA, Nextera[2]	522 ± 88	2×155	$1,927,244$	$298,722,820$
MiSeq, Run 2.1	DNA, Nextera	249 ± 30	2×155	$3,840,850$	$573,901,713$
MiSeq, Run 2.2	DNA, Nextera[2]	525 ± 90	2×155	$4,114,304$	$614,787,564$

[1]Fragment sizes determined by Picardtools. [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.