In the Department of Biogeochemistry, research is focused on the microbial metabolism and its effect on biogeochemical matter cycles in soil, particularly on chemically well-defined processes e.g., the production and consumption of methane. The central research questions are: (1) which microbial taxa are responsible for a particular biogeochemical process, and (2) which is the genetic/physiological background for this structure-function relationship? The methodology includes chemical-analytical techniques, microsensors, application of stable and radioactive isotopes, isolation and physiological characterization of microorganisms and their metabolic function, and identification of microorganisms and their functional roles using cultivation-independent molecular-biological techniques, including metagenomic and metatranscriptomic approaches. Field experiments are combined with greenhouse studies and experiments under controlled laboratory conditions.

The Department of Biogeochemistry has been headed by Prof. Dr. Ralf Conrad (methanogenic degradation and the microbial metabolism of trace gases), Prof. Dr. Andreas Brune (microbial ecology of insect guts and microbial symbioses) and PD Dr. Werner Liesack (methanotrophic bacteria; environmental genomics and metagenomics) have been Research Group Leaders in the department. In March 2017 Ralf Conrad officially retired as Director of the Department of Biogeochemistry, and Andreas Brune and Werner Liesack became department-independent Research Group Leaders. They both have permanent positions and have a guaranteed budget (including personal) for their research. Ralf Conrad acted as provisional director of the Department from March till May 2017. With the beginning of June 2017 Prof. Dr. Tobias Erb started as new Director, and the Department of Biogeochemistry was replaced by the new Department of synthetic Biochemistry. The scientific achievements and collaborations of the Department of Biogeochemistry in 2016 and 2017 are found in the individual reports of A. Brune, R. Conrad, and W. Liesack. The plans of future research of the independent research groups of A. Brune and W. Liesack are also found in their respective reports.
METHANOCENIC DEGRADATION AND MICROBIAL METABOLISM OF TRACE GASES

We want to learn which groups of soil microorganisms are responsible for particular biogeochemical processes and to understand the reason why. For this purpose we investigate biogeochemical processes involved in the exchange of climatically relevant trace gases (CH₄, H₂) between soil and atmosphere. A particular focus is on processes in flooded rice fields, which we have used during the last thirty years as a model system for studying biogeochemistry and ecology of soil microbes.

Our experimental approach includes analytical chemical techniques and isotopic tracer studies (¹³C, ¹⁴C) for investigating the biogeochemical cycling of microbial substrates and effectors in soil. Another important experimental approach is the molecular characterization of rRNA genes and different protein-encoding genes for elucidating the composition of microbial communities, including transcript analysis and stable isotope probing (SIP) of DNA and RNA for the identification of metabolically active populations that incorporate ¹³C-labelled substrates.

Due to the retirement of Prof. Dr. Ralf Conrad in 2017, the size of the group decreased during the reporting period of 2016 and 2017. The former project groups of Dr. Martin Blaser and Dr. Guntars Martinson ended during the reporting period. The publications of M. Blaser (Bednarik et al., 2017; Blaser and Conrad, 2016; Breidenbach et al., 2016a; Breidenbach et al., 2017; Chaudhary et al., 2017; Freude and Blaser, 2016; Fu et al., 2017) and of G. Martinson (Brandt et al., 2017; Kanaparthi et al., 2017; Martinson et al., 2017; Suleiman et al., 2017) are included in the reference list.

The reference list also includes publications from former members of the department, which appeared in the reporting period; i.e., R. Angel (Angel et al., 2016), G. Braker (Behrendt et al., 2017; Brenzinger et al., 2017; Suleiman et al., 2017) and M. Dumont (Breidenbach et al., 2016b; Deng et al., 2016; Deng et al., 2017; Dumont, 2017; Yuan et al., 2017).

The research of the group of R. Conrad focused mainly on the biogeochemistry of methane formation in rice field soils and other anoxic environments. In addition, it contributed to several research projects of colleagues outside of the Max Planck Institute as documented by publications (Angel et al., 2016; Cai et al., 2016; Deng et al., 2017; Herrmann et al., 2017a; Herrmann et al., 2017b; Liu et al., 2016; Liu et al., 2017; Malghani et al., 2016; Vavilin et al., 2017; Wörner et al., 2016).

Effect of desiccation and flooding. We continued systematically investigating the effect of drying and rewetting on CH₄ production and methanogenic microbial communities using terrestrial systems differing in the extent of inundation. Some of these studies had already been initiated in the last reporting period. These included rice fields in the Philippines that were transformed into rotational fields shifting between flooded rice in the wet season and non-flooded maize in the dry season (Breidenbach et al., 2016a); rice fields in Thailand that were either flooded by irrigation or just by rain events (Reim et al., 2017); oxbow lakes in Amazonia that were almost permanently flooded (Ji et al., 2016). Newly initiated studies were on rice field and upland soil from the Sanjiang area in NE China, an
area which had been transformed from pristine wetlands into agricultural fields some 50 years ago (Hernandez et al., 2017). Another study concerned periodically flooded forest soils in the Cunia Reserve of Rondonia, Brazil (in preparation). Our studies showed that the structures of the methanogenic archaeal communities in the different soils were different. For example, diversity was maximal in paddy soils with regular change between flooded and dry conditions and was lower in soils that were either permanently flooded or dry during most of the time. Desiccation followed by rewetting almost generally resulted in an increase of the relative abundance of Methanosarcinaceae and Methanocellales or Methanobacteriales. The structures of the bacterial communities were comparatively less affected by drainage and reflooding, albeit there was a tendency that the relative abundance of endospore-forming Firmicutes was enhanced. In every case, methanogenic activity was preserved. However, activity either increased or decreased after reflooding. The reason for this different behavior is probably not a difference in the microbial community structures but in the chemical structure of the organic matter. This aspect deserves research.

Microbiology of carbon turnover. We investigated three aspects. (1) We previously found that root exudation and/or degradation of straw also affected the degradation of soil organic matter (the so-called priming effect). In order to differentiate whether the priming effect was caused by soil physicochemical or soil microbiological processes, sterile rice soil from China and from Uruguay was mutually inoculated with small amounts of the same or the other soil. The results showed that the priming effect, which was different in the two soils, was caused by the inoculums. Characterization of the microbial community structures of the two soils indicated that the difference in priming was due to specific microbial groups, Symbiobacter in particular (Yuan et al., 2017). (2) We hypothesized that hydrogenotrophic methanogenesis increases when the organic carbon source becomes less available for decomposition. We checked this hypothesis by incubating the soil repeatedly under methanogenic conditions. The results showed that the path of methane production indeed changed with decreasing availability of organic matter showing an increasing contribution of hydrogenotrophic methanogenesis. The community structure of the methanogenic archaeal and bacterial community and the network between individual microbial groups also changed (Ji et al., submitted). (3) Since propionate is next to H₂ and acetate the most important primary fermentation product, we were interested in which respect this compound can be used by competing methanogenic and sulfate-reducing communities, and which are the most important sulfate-reducing species involved in competition (Figure 1). We found that propionate is indeed an intermediate undergoing competing degradation and that Syntrophobacterae were the crucial bacterial species (Liu and Conrad, 2017). Interestingly we found that Syntrophobacterae were also the most important acetate-utilizing sulfate reducers in Italian rice fields soil (Liu et al., 2017a). This result was unexpected, since Syntrophobacterae, albeit known to be able to utilize acetate, had not been considered to be involved in acetate turnover in the environment.

Figure 1 | Hypothetical model of propionate degradation under sulfidogenic conditions in paddy soil (SOM: soil organic matter)
PUBLICATIONS


THESES

PhD theses:


TRANSFER OF KNOWLEDGE/CONTACTS TO THE BUSINESS WORLD

Nadicom, Gesellschaft für Angewandte Microbiology GmbH, Karlsruhe, Scientific Advisory Board.

DSM Nutritional Products, Basel, Research Collaboration.

EXTERNAL FUNDING

DFG Collaborative Research center (SFB) 987 "Response of methanogenic microbial communities to desiccation stress in flooded soils," 2012-2016, 158,000 €.

COMMITTEE WORK OUTSIDE MPIterMIC

DFG Fachkollegium 204 "Microbiology, virology and immunology," 2012-2016.

EDITORIAL BOARDS

Environmental Microbiology: Editorial Board.
Systematic and Applied Microbiology: Editorial Board.

INTERNATIONAL & NATIONAL COOPERATIONS WITH JOINT PUBLICATIONS, FUNDING OR PATENTS

Amnat Chidthaisong, King Mongkut University of Technology Thonburi, Bangkok, Thailand.

Markus Egert, Furtwangen Universität, Villingen-Schwenningen, Germany.
Ana Fernandez Scavino, Universidad de Republica, Montevideo, Uruguay.

Bo Fu, Jiangnan University, Wuxi, China.

Zhongjun Jia, Chinese Academy of Sciences, Nanjing, China.

Dheeraj Kanaparthi, Helmholtz Center, Munich.

Yongqin Liu, Academy of Sciences, Beijing, China.

Yahai Lu, Peking University, Beijing, China.

Michael Pester, University of Konstanz, Konstanz, Germany.

Alex Enrich Prast, Universidad Federal, Rio de Janeiro, Brasil.

Martin Rulik, Palacky University, Olomouc, Czech Republic.

Susan Trumbore, MPI for Biogeochemistry, Jena, Germany.

Vasily Vavilin, Russian Academy of Sciences, Moscow, Russia.

COOPERATIONS WITHIN THE INSTITUTE WITH JOINT PUBLICATIONS, FUNDING OR PATENT

None

INVITED LECTURES & ORGANISATION OF MEETINGS

Seminar, University of Konstanz, Feb 2016.

Int. Conference of the European Geophysical Union, Vienna, Austria, Apr 2016.

Seminar, University of Southampton, UK, May 2016.

Seminar, Linköping University, Sweden, June 2016.


Lecture and Seminar, Peking University, Beijing, China, Oct 2017.


Seminar, Jiangnan University, Wuxi, China, Oct 2017.

Seminar, University of Greifswald, Nov 2017.


SCIENTIFIC AWARDS & ELECTED MEMBERSHIPS IN 2016–2017

None
GROUP STRUCTURE (05/2017)

PI: Ralf Conrad
Postdoctoral fellows: Guntars Martinson, Pengfei Liu
Technical staff: Peter Claus, Melanie Klose, Bianca Pommerenke

CONTACT ADDRESS

Prof. Dr. Ralf Conrad
Max Planck Institute for Terrestrial Microbiology
Department of Biogeochemistry
Karl-von-Frisch Str. 10
35043 Marburg
Phone: +49-(0)6421 178-801
E-Mail: conrad@mpi-marburg.mpg.de

Figure 2 | Group of Ralf Conrad