

Dr. CARL-ERIC WEGNER

PERSONAL DETAILS

OFFICE ADDRESS: Friedrich Schiller University
Institute for Biodiversity
Chair of Aquatic Geomicrobiology
Dornburger Str. 159, 07743 Jena, Germany

NAME: Carl-Eric Wegner
DATE OF BIRTH: September 4th 1986
NATIONALITY: German
E-MAIL: carl-eric.wegner@uni-jena.de
WEB: www.exploringmicrobes.science
FAMILY STATUS: married, two children

PROFESSIONAL EXPERIENCE

current	Project Group Leader / Assistant to the Chair <i>Institute for Biodiversity, Chair of Aquatic Geomicrobiology, Friedrich Schiller University Jena</i> Leading research projects dedicated to lanthanide-dependent C ₁ -metabolism, microbial carbon cycling, metal cycling, and multiomic analyses in groundwater, subsurface environments. Supervision of PhD, MSc and BSc students, teaching of microbiology, microbial ecology and bioinformatics classes/workshops.
2014-2016	PostDoc <i>Max Planck Institute for Terrestrial Microbiology, Department of Biogeochemistry, Marburg</i> Establishing research projects dedicated to microbial life in early-industrial soft coal slags, primarily using metagenomics. Providing bioinformatic support / developing pipelines for multiple metatranscriptomic/-genomic studies targeting carbon cycling in paddy soil. Co-supervision of a PhD student.
2011-2014	PhD student <i>Philipps University Marburg / Max Planck Institute for Terrestrial Microbiology, Marburg</i> Handling multiple projects relating to metatranscriptomic analysis in soil systems, especially paddy soil, with a focus on taxonomic and functional annotation of microbial key players in carbon-cycling. Establishment of wet-lab and bioinformatic workflows, supervision of BSc and MSc students.
2009-2011	Scientific assistant <i>Institute for Chemistry and Biology of the Marine Environment (ICBM) Carl von Ossietzky University Oldenburg</i> Contributing to different cultivation(-independent)-based projects by cultivation work, sequence analysis and hydrochemical analysis.

EDUCATION

10/2014	Doctorate , Dr. rer. nat. Max Planck Institute for Terrestrial Microbiology, Marburg (Germany) Phillips University Marburg (Germany) Grade: <i>1.0 (magna cum laude)</i> Thesis: Metatranscriptomic analyses of methanogenic plant polymer breakdown in paddy soil, Thesis supervisor: PD Dr. Werner Liesack
10/2011 - 10/2014	PhD student MPI Marburg, Dept. of Biogeochemistry (headed by Ralf Conrad), Liesack Lab
09/2011	Master of Science , M.Sc. Microbiology Max Planck Institute for Marine Microbiology, Bremen (Germany) Carl von Ossietzky University Oldenburg (Germany) Grade: <i>1.2 (excellent)</i> Thesis: Analysing gene expression changes in <i>Rhodopirellula baltica</i> upon utilising sulphated polysaccharides, Thesis supervisors: Prof. Dr. Frank-Oliver Glöckner (MPI Bremen), PD Dr. Thorsten Brinkoff (Carl von Ossietzky University Oldenburg)
03/2011 - 09/2011	Thesis work MPI Bremen, Dept. of Molecular Ecology (headed by Rudolf Amann), Glöckner Lab
10/2009 - 09/2011	MSc. student (Microbiology), Carl von Ossietzky University Oldenburg (Germany)
09/2009	Bachelor of Science , B.Sc. Applied Biology University of Applied Sciences Bonn-Rhein-Sieg, Bonn (Germany) Grade: <i>1.4 (excellent)</i>
08/2009	Bachelor of Science (honours) , B.Sc. (hons) Molecular Microbiology University of Aberdeen, Aberdeen (United Kingdom) Grade: <i>Upper Second Class</i> Thesis: The impact of chromatin remodelling on S-phase progression in <i>Saccharomyces cerevisiae</i> , Thesis supervisors: Dr. Anne Donaldson (University of Aberdeen), Prof. Dr. Annette Menke (University of Applied Sciences Bonn-Rhein-Sieg)
09/2006 - 08/2009	BSc. student (Applied Biology), University of Applied Sciences Bonn-Rhein-Sieg (Germany)
09/2008 - 08/2009	Bsc. (hons) student (Molecular Microbiology), University of Aberdeen

CAREER BREAK

01/2019 - 06/2019	parental leave
07/2021 - 12/2021	parental leave

AWARDS AND HONORS

2015	FEMS travel grant awardee
2011-2014	Scholarship holder of the International Max Planck Research School for Environmental, Cellular and Molecular Microbiology
2012, 2013	VAAM travel grant awardee
2011	Scholarship of the Carl von Ossietzky University, Oldenburg for excellent educational performance
2008	Scholarship of the German Academic Exchange Service for studies at the University of Aberdeen
2006	Award of the federal state of Northrhine Westphalia for exceptional volunteer service

FUNDING

- 2022-2025 Deutsche Forschungsgemeinschaft "Influence of lanthanides on (non-)methylophilic metabolism in Beijerinckia bacterium RH AL1"
granted as PI, WE6579/4-1, 252k €
- 2022-2026 Deutsche Forschungsgemeinschaft SFB 1127 "ChemBioSys" Project C04
"Metallophores as Mediators for Metal Cycling"
granted as Co-PI, 370k €
- 2020-2021 Deutsche Forschungsgemeinschaft "Microbial diversity ecosystem function relationships across environmental gradients" *total volume* **200k €**
granted as PI, WE 6579/2-1, 40k €
- 2020-2025 Federal state of Thuringia "Digitisation of life sciences"
as collaborator, in total 1.5M € for the whole consortium
- 2011-2014 International Max Planck Research School for Environmental, Cellular and Molecular Microbiology - scholarship
granted as PhD student, 42k €

ADMINISTRATIVE EXPERIENCE

- CRC 1127 "ChemBioSys" Metagenomics workshop (2023) - Convener & Organizer
- Faculty member Excellence Graduate School - Excellence Jena School for Microbial Communication at Friedrich Schiller University Jena (2022-)
- Appointment committees - Representative of academic mid-level faculty at Friedrich Schiller University Jena (2018-)
- CRC 1076 "AquaDiva" Metagenomics Workshop (2018) - Convener & Organizer
- Jena School for Microbial Communication (JSMC) Conference on microbial communication (MiCom) (2017) - Co-Convener
- PhD representatives MPI Marburg (2013-2014) - PhD students spokesperson
- Student member of the admission and examination board of the University of Oldenburg (2009-2011) - Student representative
- Member of the student body of the Microbiology study program, University of Oldenburg (2009-2011) - Member

OTHER QUALIFICATIONS

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| 2020 | Workshop <i>Project Management</i> |
| 2020 | Workshop <i>Career management for young researchers</i> |
| 2018 | Workshop <i>Pursuing a scientific career in Germany</i> |
| 2018 | Workshop <i>How to be a good supervisor</i> |
| 2018 | Workshop <i>Time management for young researchers</i> |
| 2017 | Certified operator <i>Illumina sequencing platforms (Illumina MiSeq)</i> |
| 2014 | Advanced training in accordance with § 15 GenTSV for group leaders |
| 2011 | Certified operator <i>Roche/454 sequencing platforms (Roche/454 GS Junior)</i> |
| 2008 | Certificate in <i>Good Clinical Practice</i> |

MEMBERSHIPS

2019-	EAG - European Association of Geochemistry
2016-	ASM - American Society of Microbiology
2016-	ISME - International Society of Microbial Ecology
2012-	FEMS - Federation of European Microbiology Societies
2012-	VAAM - German Society for Applied and General Microbiology

TEACHING

Friedrich Schiller University Jena

2019-	<p><i>Lecture:</i> Introductory Microbiology (BSc. Biogeosciences, BSc. Nutrition Science)</p> <p>Designing, preparing and giving of two hour long lectures as well as giving and correcting exams. This lecture is centered around basics in microbiology, prokaryotic metabolism, functional diversity, medical microbiology and biotechnology.</p>
2016-2020	<p><i>Lecture:</i> Microbial ecology From microbial diversity to ecosystem function (MSc. Microbiology, MSc. Evolution, Ecology, Systematics, MSc. Biogeosciences)</p> <p>Conceptualizing, preparing and giving of one hour long lectures as well as giving and correcting exams. The focus is on microbial ecology and how microbes contribute to ecosystem function.</p>
2016-2020	<p><i>Seminar:</i> From microbial diversity to ecosystem function (MSc. Microbiology, MSc. Evolution, Ecology, Systematics, MSc. Biogeosciences)</p> <p>Planning of the seminar based on recent literature about how microbes contribute to ecosystem function and biogeochemical cycling. Grading of student presentations.</p>
2016-	<p><i>Seminar:</i> Current research topics in Geomicrobiology (MSc. Microbiology, MSc. Biogeosciences)</p> <p>Conceptualizing of the seminar, the main interest is to give students an idea about methodic breadth in microbial ecology/geomicrobiology. Grading of student presentations.</p>
2017-	<p><i>Practical course:</i> Molecular microbial ecology (MSc. Microbiology, MSc. Biogeosciences)</p> <p>Design, teaching and supervision of one week of practical work that is aimed at giving the students a basic understanding of modern cultivation-independent techniques in microbial ecology (meta*omics), based on analysing pre-computed datasets. Grading and revision of student reports and presentations.</p>
2017-2019	<p><i>Practical course:</i> From microbial diversity to ecosystem function (MSc. Evolution, Ecology, Systematics)</p> <p>Planning and supervision of two-week long student projects that are aimed at isolating and characterizing representatives of microbial clades that have relevance for selected ecosystems. Grading and revision of student reports and presentations.</p>
2016-	<p><i>Practical course:</i> Introductory Microbiology (BSc. Biogeosciences, BSc. Nutrition Science)</p> <p>Supervision of practical work in introductory microbiology. The goal is that students get familiarized with microbiological techniques including sterile working and the basic morphological and physiological characterization of microbes.</p>

2011-2013 *Practical course: Microbial ecology* (MSc. Biology)
Guidance of practical work in microbial ecology. Students isolate target microbes based on isolation strategies designed by themselves with supervision.
Giving of short lectures, grading of student presentations and reports.

PUBLICATIONS

No. of publications:	36
No. of first/last authorships:	10
No. of book chapters:	2
h-Index:	18
i10-Index:	23
Citations:	1133
Average impact factor:	4.7
ORCID	0000-0001-7090-8717
Google Scholar	bit.ly/2uQmABm
Web of Science	ResearcherID U-9401-2019
Scopus	AuthorID 55565820600

Peer reviewer for: *Frontiers in Microbiology* (2017-), *Microbial Ecology* (2017-), *Molecular Ecology* (2017-), *Scientific Reports* (2017-), *Marine Genomics* (2017-), *Journal of Bacteriology* (2019-), *Microorganisms* (2019-), *Microbiome* (2019-), *iScience* (2020-), *Environmental Pollution* (2020-), *Environmental Microbiology (Reports)* (2020-), *ISME (Communications)* (2021-), *Nature (Communications)* (2022-)

Editorial board: *Frontiers in Microbiology* (2017-)

LIST OF PUBLICATIONS

Φ = shared authorship, Ψ = corresponding author

2024

37. **CE Wegner**^Ψ. 2024. Lanthanide utilization in the family Beijerinckiaceae in "Lanthanides in Enzymology and Microbiology" (ed. A Tani, T Nakagawa, R Mitsui). *Elsevier*.

2023

36. L Gorniak, JA Bechwar, M Westermann, F Steiniger, **CE Wegner**^Ψ. 2023. Different lanthanide elements induce strong gene expression changes in a lanthanide-accumulating methylotroph. *Microbiology Spectrum (in press)*.

35. **CE Wegner**, R Stahl, I Velsko, A Hübner, Z Fagernäs, C Warinner, R Lehmann, T Ritschel, KU Totsche, K Küsel. 2023. A glimpse of the paleome in endolithic microbial communities. *Microbiome* 11: 210. <https://doi.org/10.1186/s40168-023-01647-2>

2021

34. Q Li, RE Cooper, **CE Wegner**, S Lu, Kirsten Küsel. 2021. Draft Genome Sequences of *Acidithrix* sp. Strain C25 and *Acidocella* sp. Strain C78, acidophiles isolated from iron-rich pelagic aggregates (iron snow). *Microbiology Resource Announcements* 10: e00102-21. <https://doi.org/10.1128/MRA.00102-21>

33. Q Li, RE Cooper, **CE Wegner**, M Taubert, N Jehmlich, M von Bergen, K Küsel. 2021. Insights into autotrophic activities and carbon flow in iron-rich pelagic aggregates (iron snow). *Microorganisms* 9: 1368. <https://doi.org/10.3390/microorganisms9071368>

32. X Wu, P Liu, **CE Wegner**, Y Luo, K-Q Xiao, Z Cui, F Zhang, W Liesack, J Peng. 2021. Deciphering microbial mechanism underlying soil organic carbon storage in a wheat maize rotation system. *Science of The Total Environment* 788: 147798. <https://doi.org/10.1016/j.scitotenv.2021.147798>

31. **CE Wegner**^Ψ, M Westermann, F Steiniger, L Gorniak, R Budhreja, L Adrian, K Küsel. 2021. Extracellular and intracellular lanthanide accumulation in the methylotroph Beijerinckiaceae bacterium RH AL1. *Applied and Environmental Microbiology* 87: e0314420. <https://doi.org/10.1128/aem.03144-20>

30. RE Cooper, **CE Wegner**, K Küsel. 2021. Draft Genome Sequence of *Pseudomonas* sp. Strain FEN, Isolated from the Fe- and Organic Matter-Rich Schlöppnerbrunnen Fen. *Microbiology Resource Announcements* 10: e01017-20. <https://doi.org/10.1128/mra.01017-20>

2020

29. RE Cooper, **CE Wegner**, S Kügler, RX Poulin, N Ueberschaar, JD Wurlitzer, T Wichard, G Pohner, K Küsel. 2020. Iron is not everything: unexpected complex metabolic responses between iron-cycling microorganisms. *ISME Journal* 14: 2675-2690. <https://doi.org/10.1038/s41396-020-0718-z>

28. Q Li, RE Cooper, **CE Wegner**, K Küsel. 2020. Molecular mechanisms underpinning aggregation in *Acidiphilium* sp. C61 isolated from iron-rich pelagic aggregates. *Microorganisms* 8: 314. <https://doi.org/10.3390/microorganisms8030314>

27. RE Cooper, **CE Wegner**, S McAllister, O Shevchenko, C Chan, K Küsel. 2020. Draft Genome Sequence of *Sideroxydans* sp. CL21, an Fe(II)-Oxidizing Bacterium. *Microbiology Resource Announcements* 9: e01444-19. <https://doi.org/10.1128/MRA.01444-19>

26. **CE Wegner**^ψ, L Gorniak, S Riedel, M Westermann, K Küsel. 2020. Lanthanide-Dependent Methylo-trophs of the Family Beijerinckiaceae: Physiological and Genomic Insights. *Applied and Environmental Microbiology* 86: e01830-19. <https://doi.org/10.1128/aem.01830-19>

25. P Geesink, **CE Wegner**, AJ Probst, M Herrmann, HT Dam, AK Kastner, K Küsel. 2020. Genome-inferred spatio- temporal resolution of an uncultivated Roizmanbacterium reveals its ecological preferences in groundwater. *Environmental Microbiology* 22: 726-737. <https://doi.org/10.1111/1462-2920.14865>

24. A Heintz-Buschart, C Guerra, I Djukic, S Cesarz, A Chatzninotas, G Patoime, J Sikorski, F Buscot, K Küsel, **CE Wegner**, N Eisenhauer. 2020. Microbial diversity-ecosystem function relationships across environmental gradients. *Research Ideas and Outcomes* 6: e52217. <https://doi.org/10.3897/rio.6.e52217>

2019

23. M Herrmann, **CE Wegner**, M Taubert, P Geesink, K Lehmann, L Yan, R Lehmann, KU Totsche, K Küsel. Predominance of Cand. Patescibacteria in groundwater is caused by their preferential mobilization from soils and flourishing under oligotrophic conditions. *Frontiers in Microbiology* 10: 1407. <https://doi.org/10.3389/fmicb.2019.01407>

22. RZ Abdallah, **CE Wegner**, W Liesack. 2019. Community transcriptomics reveals drainage effects on paddy soil microbiome across all three domains of life. *Soil Biology and Biochemistry* 132: 131-142. <https://doi.org/10.1016/j.soilbio.2019.01.023>

21. **CE Wegner**, M Gaspar, P Geesink, M Herrmann, M Marz, K Küsel. 2019. Biogeochemical Regimes in Shallow Aquifers Reflect the Metabolic Coupling of the Elements Nitrogen, Sulfur, and Carbon. *Applied and Environmental Microbiology* 85: e02346-18. <https://doi.org/10.1128/aem.02346-18>

20. S Kügler, RE Cooper, **CE Wegner**, JF Mohr, T Wichard, K Küsel. 2019. Iron-organic matter complexes accelerate microbial iron cycling in an iron-rich fen. *Science of the Total Environment* 646: 972-988. <https://doi.org/10.1016/j.scitotenv.2018.07.258>

2018

19. J Peng, **CE Wegner**, Q Bei, P Lie, W Liesack. 2018. Metatranscriptomics reveals a differential temperature effect on the structural and functional organization of the anaerobic food web in rice field soil. *Microbiome* 6: 169. <https://doi.org/10.1186/s40168-018-0546-9>

18. AA Ivanova, **CE Wegner**, Y Kim, W Liesack, SN Dedysh. 2018. Metatranscriptomics reveals the hydrolytic potential of peat-inhabiting Planctomycetes. *Antonie van Leeuwenhoek* 111: 801-809. <https://doi.org/10.1007/s10482-017-0973-9>

2017

17. **CE Wegner**, W Liesack. 2017. Unexpected Dominance of Elusive Acidobacteria in Early Industrial Soft Coal Slags. *Frontiers in Microbiology* 8: 1023. <https://doi.org/10.3389/fmicb.2017.01023>

16. T Wagner, **CE Wegner**, J Kahnt, U Ermler, S Shima. 2017. Phylogenetic and structural comparisons of the three types of methyl-coenzyme M reductase from Methanococcales and Methanobacteriales. *Journal of Bacteriology* 199: e00197-17. <https://doi.org/10.1128/jb.00197-17>

15. RE Cooper, K Eusterhues, **CE Wegner**, KU Totsche, K Küsel. 2017. Ferrihydrite-associated organic matter (OM) stimulates reduction by *Shewanella oneidensis* MR-1 and a complex microbial consortia.

Biogeosciences 14: 5171-5188. <https://doi.org/10.5194/bg-14-5171-2017>

14. J Peng, **CE Wegner**, W Liesack. 2017. Short-term exposure of paddy soil microbial communities to salt stress triggers different transcriptional responses of key taxonomic groups. *Frontiers in Microbiology* 8: 400. <https://doi.org/10.3389/fmicb.2017.00400>

2016

13. AA Ivanova, **CE Wegner**, Y Kim, W Liesack, SN Dedysh. 2016. Identification of microbial populations driving biopolymer degradation in acidic peatlands by metatranscriptomic analysis. *Molecular Ecology* 25: 4818-4835. <https://doi.org/10.1111/mec.13806>

12. M Tollot, D Assmann, C Becker J Altmüller, JY Dutheill, **CE Wegner**, et al.. 2016. The WOPR protein Ros1 is a master regulator of sporogenesis and late effector gene expression in the maize pathogen *Ustilago maydis*. *PLoS Pathogens* 12: e1005697. <https://doi.org/10.1371/journal.ppat.1005697>

11. **CE Wegner**, W Liesack. 2016. Microbial community dynamics during the early stages of plant polymer breakdown in paddy soil. *Environmental Microbiology* 18: 2825-2842. <https://doi.org/10.1111/1462-2920.12815>

2015

10. X Wu, T Ge, W Wang, H Yuan, **CE Wegner**, Z Zhu, AS Whiteley, J Wu. 2015. Cropping systems modulate the rate and magnitude of soil microbial autotrophic CO₂ fixation in soil. *Frontiers in Microbiology* 6: 379. <https://doi.org/10.3389/fmicb.2015.00379>

9. LC Andresen, G Moser, R Seibert, C Guillet, L Grünhage, TW Donath, A Otte, M Hemfler, F Achilles, **CE Wegner**, W Liesack, C Müller. 2015. Permanent managed grassland at future climate change: is there a connection between GHG emission and composition of plant and microbial communities?. *Procedia Environmental Sciences* 29: 156-157. <https://doi.org/10.1016/j.proenv.2015.07.237>

2014

8. IY Oshkin, **CE Wegner**, C Lüke, MV Glagolev, IV Filippov, NV Pimenov, et al.. 2014. Gammaproteobacterial methanotrophs dominate cold methane seeps in floodplains of West Siberian rivers. *Applied and Environmental Microbiology* 80: 5944-5954. <https://doi.org/10.1128/aem.01539-14>

7. M Richter, T Richter-Heitmann, A Klindworth, **CE Wegner**, CS Frank, J Harder, FO Glöckner. 2014. Permanent draft genomes of the three *Rhodopirellula baltica* strains SH28, SWK14 and WH47. *Marine Genomics* 13: 13-14. <https://doi.org/10.1016/j.margen.2013.11.004>

6. A Klindworth, M Richter, T Richter-Heitmann, **CE Wegner**, CS Frank, J Harder, FO Glöckner. 2014. Permanent draft genome of *Rhodopirellula rubra* SWK7. *Marine Genomics* 13: 11-12. <https://doi.org/10.1016/j.margen.2013.11.005>

5. **CE Wegner**, M Richter, T Richter-Heitmann, A Klindworth, CS Frank, J Harder, FO Glöckner. 2014. Permanent draft genome of *Rhodopirellula sallentina* SM41. *Marine Genomics* 13: 17-18. <https://doi.org/10.1016/j.margen.2013.11.002>

4. M Richter, T Richter-Heitmann, A Klindworth, **CE Wegner**, CS Frank, J Harder, FO Glöckner. 2014. Permanent draft genomes of the *Rhodopirellula maiorica* strain SM1. *Marine Genomics* 13: 19-20. <https://doi.org/10.1016/j.margen.2013.11.001>

3. T Richter-Heitmann, M Richter, A Klindworth, **CE Wegner**, CS Frank, J Harder, FO Glöckner. 2014. Permanent draft genomes of the two *Rhodopirellula europaea* strains 6C and SH398T. *Marine Genomics* 13: 15-16. <https://doi.org/10.1016/j.margen.2013.11.003>

2. Y Kim, **CE Wegner**, W Liesack. 2014. Soil Metatranscriptomics in "Omics in Soil Science" (ed. P Nannipieri, G Pietramellara, G Renella). *Caister Academic Press*. <https://doi.org/10.21775/9781908230584>

2013

1. **CE Wegner**^Φ, T Richter-Heitmann, A Klindworth, C Klockow, M Richter, T Achstetter et al.. 2013. Expression of sulfatases in *Rhodopirellula baltica* and the diversity of sulfatases in the genus *Rhodopirellula*. *Marine Genomics* 9: 51-61. <https://doi.org/10.1016/j.margen.2012.12.001>