

## **Complete Publication List (07/2022)**

(Articles submitted, Manuscripts on preprint servers, Articles, Book chapters, Other articles)

### **Key for Group Members only**

**Postdocs/Researchers**, **PhD Students**, **co-supervised PhD Students**, **Undergraduates**, **Technicians**

\*equal contribution

## **Articles**

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### **2022**

95. Vasileiadis S., Perruchon C., Scheer B., Adrian L., **Steinbach N.**, Trevisan M., Plaza-Bolaños P., Agüera A., **Chatzinotas A.**, Karpouzias G. D. Nutritional inter-dependencies and a carbazole-dioxygenase are key elements of a bacterial consortium relying on a Sphingomonas for the degradation of the fungicide thiabendazole. *Environmental Microbiology* DOI: 10.1111/1462-2920.16116
94. **You X.**, **Kallies R.**, Kühn I., Schmidt M., Harms H., **Chatzinotas A.**, Wick L.Y. (2022) Phage co-transport with hyphal-riding bacteria fuels bacterial invasion in a water-unsaturated microbial model system. *The ISME Journal* 16 (5), 1275-1283
93. **You X.**, **Kallies R.**, Hild, K., Hildebrandt, A., Harms, H., **Chatzinotas, A.**, Wick, L. Y. (2022). Transport of marine tracer phage particles in soil. *Science of The Total Environment*, 814, 152704.
92. **You X.**, Klose N., **Kallies R.**, Harms H., **Chatzinotas A.**, Wick L. Y. (2022). Mycelia-assisted isolation of non-host bacteria able to co-transport phages. *Viruses*, 14(2), 195.

### **2021**

91. Guerra, C. A., Bardgett, R. D., Caon, L., Crowther, T. W., Delgado-Baquerizo, M., (...), **Chatzinotas A.** (...), Eisenhauer, N. (2021). Tracking, targeting, and conserving soil biodiversity. *Science*, 371(6526), 239-241.
90. Cohen Y., Pasternak Z., Müller S., Hübschmann T., Schattenberg F., Sivakala K. K., Abed-Rabbo A., **Chatzinotas A.**, Jurkevitch E. Community and single cell analyses reveal complex predatory interactions between bacteria in high-diversity systems. *Nature Communications* 12, 5481
89. Voigt E., Rall B. C., **Chatzinotas A.**, Brose U., Rosenbaum B. (2021). Phage strategies facilitate bacterial coexistence under environmental variability. *PeerJ*, 9, e12194.
88. Liess M., Liebmann L., Vormeier P., Weisner O., Altenburger R., Borchardt D., Brack W., **Chatzinotas A.**, (...), Reemtsma, T. (2021). Pesticides are the dominant stressors for vulnerable insects in lowland streams. *Water Research*, 201, 117262.
87. Weitere M., Altenburger R., Anlanger C., Baborowski M., Bärlund I., Beckers L.-M., Borchardt D., Brack W., Brase L., Busch W., **Chatzinotas A.**, (...), **Kallies R.**, (...), Brauns A. (2021) Disentangling multiple chemical and non-chemical stressors in lotic ecosystems using a longitudinal approach. *Science of the Total Environment* 769: 144324.
86. **Hofmann P.**, Clark A., Hoffmann P., **Chatzinotas A.**, Harpole S., Susanne D. (2021) Beyond nitrogen: phosphorus - Estimating the minimum niche dimensionality for resource competition between phytoplankton, *Ecology Letters*, 24(4), 761-771.
85. Saraiva J. P., Worrlich A., **Karakoç C.**, **Kallies R.**, **Chatzinotas A.**, Centler F., Nunes da Rocha U. (2021). Mining synergistic microbial interactions: a roadmap on how to integrate multi-omics data. *Microorganisms*, 9(4), 840.

84. Saraiva J. P., Bartholomäus A., **Kallies R.**, Gomes M., Bicalho M., Kasmanas J. C., Vogt C., **Chatzinotas A.**, Stadler P., Dias O., Nunes da Rocha U. (2021). OrtSuite: from genomes to prediction of microbial interactions within targeted ecosystem processes. *Life science alliance*, 4(12).

## 2020

83. Guerra C.A., Heintz-Buschart A., Sikorski J., **Chatzinotas A.**, Guerrero-Ramírez N., Cesarz S., Beaumelle L., Rillig M.C., Maestre F.T., Delgado-Baquerizo M., Buscot F., Overmann J., Patoine G., Phillips H.R.P., Winter M., Wubet T., Küsel K., Bardgett R.D., Cameron E.K., Cowan D., Grebenc T., Marín C., Orgiazzi A., Singh B.K., Wall D.H., Eisenhauer N. (2020). Blind spots in global soil biodiversity and ecosystem function research. *Nature Communications* 11(1): 1-13

82. **Karakoç C.**, Clark A., **Chatzinotas A.** (2020). Diversity and coexistence are influenced by time-dependent species interactions in a predator-prey system. *Ecology Letters* 23(6): 983-993

81. **Cravo A.**, Schmeller D. S., **Chatzinotas A.**, Vredenburg V. T., Loyeau A. (2020). Environmental factors and host microbiomes shape host-pathogen dynamics. *Trends in Parasitology* 36 (7): 616-633

80. Risse-Buhl U., Anlanger C., **Chatzinotas A.**, Noss C., Lorke A., Weitere M. (2020). Near streambed flow shapes microbial guilds within and across trophic levels in fluvial biofilms. *Limnology and Oceanography* 65(10): 2261-2277

79. Banitz T., **Chatzinotas A.**, Worrlich A. (2020). Prospects for integrating disturbances, biodiversity and ecosystem functioning using microbial systems, *Frontiers in Ecology and Evolution* 8: 21

78. Weise H., Weise H., Auge H., Baessler C., Bärlund I., Bennett E.M., Berger U., Bohn F., Bonn A., Borchardt D., Brand F., **Chatzinotas A.**, Corstanje R., De Laender F., Dietrich P., Dunker S., Durka W., Fazey I., Groeneveld J., Guilbaud C.S.E., Harms H., Harpole S., Harris J., Jax K., Jeltsch F., Johst K., Joshi J., Klotz S., Kühn I., Kuhlicke C., Müller B., Radchuk V., Reuter H., Rinke K., Schmitt-Jansen M., Seppelt R., Singer A., Standish R.J., Thulke H.H., Tietjen B., Weitere M., Wirth C., Wolf C., Grimm V. (2020). Resilience trinity: safeguarding ecosystem functioning and services across different time horizons and decision contexts, *Oikos* 129: 445-456

## 2019

77. **Hofmann P.**, **Chatzinotas A.**, Harpole S., Susanne D. (2019). Phytoplankton trait topographies shift along temperature and stoichiometry gradients in a species-specific way. *Ecology* 100: e02875

76. **Ghanem N.**, Stanley C. E., Harms H., **Chatzinotas A.**, Wick L. Y. (2019). Mycelial effects on phage retention during transport in a microfluidic platform. *Environmental Science & Technology* 53: 11755-11763.

75. Sendek A. \*, **Karakoç C.\***, Wagg C., Domínguez-Begines J., Martucci de Couto G, van der Heijden M.G.A., Naz A.A., Lochner A., **Chatzinotas A.**, Klotz S., Gómez-Aparicio L., Eisenhauer N. (2019). Drought modulates interactions between arbuscular mycorrhizal fungal diversity and barley genotype diversity, *Scientific Reports* 9: 9650

74. **Kallies R.**, Hölzer M., Toscan R.B. , da Rocha U.N., **Anders J.**, Marz M., **Chatzinotas A.** (2019). Evaluation of sequencing library preparation protocols for viral metagenomic analysis from pristine aquifer groundwaters. *Viruses* 11: 484; doi:10.3390/v11060484

73. Wiczorek A.S., Schmidt O., **Chatzinotas A.**, von Bergen M., Gorissen A., Kolb S. (2019). Ecological functions of agricultural soil bacteria and microeukaryotes in chitin degradation: a case study, *Frontiers in Microbiology* 10:1293. doi: 10.3389/fmicb.2019.01293

72. **Kallies R.**, **Kiesel B.**, Schmidt M., **Ghanem N.**, Zopfi J., Hackermüller J., Harms H., Wick L.Y, **Chatzinotas A.** (2019). Complete genome sequence of Pseudoalteromonas phage vB\_PS-H6/1 that infects *Pseudoalteromonas* sp. strain H6. *Marine Genomics*, doi.org/10.1016/j.margen.2019.03.002

71. Cohen Y., Pasternak Z., **Johnke J.**, Abed-Rabbo A., Kushmaro A., **Chatzinotas A.**, Jurkevitch E. (2019). Bacteria and micro-eukaryotes are differentially segregated in sympatric wastewater microhabitats. *Environmental Microbiology* 21: 1757-1770

70. Said N., **Chatzinotas A.**, Schmidt M. (2019). Have an ion on it: The life-cycle of *Bdellovibrio bacteriovorus* viewed by Helium-Ion Microscopy. *Advanced Biosciences* 3: 1800250

## 2018

69. **Krohn S.**, Zeller K., Böhm S., **Chatzinotas A.**, Harms H., Hartmann J., **Heidtmann A.**, Herber A., Kaiser T., Treuheit M., Hoffmeister A., Berg T. & Hoffmeister A. (2018). Molecular quantification and differentiation of *Candida* species in biological specimens of patients with liver cirrhosis. *PLoS one*, 13(6), e0197319.

68. **Kuppardt A.**, Fester T., Härtig C., **Chatzinotas A.** (2018). Rhizosphere protists change metabolite profiles in *Zea mays*. *Frontiers in Microbiology* 9:857

67. Ye F., Ma M.-H., den Camp H. J. O., **Chatzinotas A.**, Li L., Lv M.-Q., Wu S.-J., Wang, Y. (2018). Different Recovery Processes of Soil Ammonia Oxidizers from Flooding Disturbance. *Microbial Ecology* 76: 1041-1052

66. **Ghanem N.**, Trost M., Sanchez Fontanet L., Harms H., **Chatzinotas A.**, Wick L. (2018). Changes of the Specific Infectivity of Tracer Phages during Transport in Porous Media, *Environmental Science & Technology* 52:3486-3492

65. **Karakoç C.**, Radchuk V., Harms H., **Chatzinotas A.** (2018). Interactions between predation and disturbances shape prey communities. *Scientific Reports* 8:2968

64. Schmeller D.S., Loyau A., Bao K., Brack W., **Chatzinotas A.**, De Vleeschouwer F., Friesen J., Gandois L., Hansson S.V., Haver M., Le Roux G., Shen J., Teisserenc R., Vredenburg V.T. (2018). People, pollution and pathogens - global change impacts in mountain freshwater ecosystems. *Science of the Total Environment* 622: 756-763

## 2017

63. **Narr A.**, Nawaz A., Wick L. Y., Harms, H., **Chatzinotas A.** (2017). Soil viral communities vary temporally and along a land use transect as revealed by virus-like particle counting and a modified community fingerprinting approach (fRAPD) *Frontiers in Microbiology* 8: 1975

62. **Johnke J.**, Baron M., Leeuw M., Kushmaro A., Jurkevitch E., Harms H., **Chatzinotas A.** (2017). A generalist protist predator enables coexistence in multitrophic predator-prey systems containing a phage and the bacterial predator *Bdellovibrio*. *Frontiers in Ecology and Evolution* 5:124

61. **Kallies R.**, **Kiesel B.**, Zopfi J., Wick L.Y., **Chatzinotas A.** (2017). Complete genome sequence of *Alteromonas* virus vB\_AspP-H4/4. *Genome Announcements* 5(43), e00914-17

60. Bock C., **Chatzinotas A.**, Boenigk J. (2017). Genetic diversity in chrysophytes: Comparison of different gene markers. *Fottea* 17(2): 209–221

59. **Johnke J.**, Boenigk J., Harms H., **Chatzinotas A.** (2017). Killing the killer: Predation between protists and predatory bacteria. *FEMS Microbiology Letters* 364 (9): fnx089

58. Geisen S., Mitchell E.A.D., Wilkinson D.M., Adl S., Bonkowski M., Brown M.W., Fiore-Donno A. M., Heger T.J., Jassey V.E.J., Krashevskaya V., Lahr D.J.G., Marcisz K., Mulot M., Payne R., Singer D., Anderson O.R., Charman D.J., Ekelund F., Griffiths B.S., Rønn R., Smirnov A., Bass D., Belbahri L., Berney C., Blandenier Q., **Chatzinotas A.**, Clarholm M., Dunthorn M., Feest A., Fernández L.D., Foissner W., Fournier B., Gentekaki E., Hajek M., Helder J., Jousset A., Koller R., Kumar S., La Terza A.,

Lamentowicz M., Mazei Y., Santos S.S., Seppey C.V.W., Spiegel F.W., Walochnik J., Winding A., Lara E. (2017). Soil protistology rebooted: 30 fundamental questions to start with. *Soil Biology and Biochemistry* 111: 94–103

57. **Karakoç C.**, Singer A., Johst K., Harms H., **Chatzinotas A.** (2017). Transient recovery dynamics of a predator-prey system under press and pulse disturbances. *BMC Ecology* 17: 13

56. Jousset A., Bienhold C., **Chatzinotas A.**, Gallien L., Gobet A., Kurm V., Küsel K., Rillig M.C., Rivett D.W., Salles J.F., van der Heijden M.G. (2017). Where less may be more: how the rare biosphere pulls ecosystems strings. *The ISME Journal* 11: 853–862

55. Perruchon C., **Chatzinotas A.**, Omirou M., Vasileiadis S., Karpouzias D.G. (2017). Isolation of a bacterial consortium able to degrade the fungicide thiabendazole: the key role of a *Sphingomonas* phylotype. *Applied Microbiology and Biotechnology* 101(9): 3881-3893

54. **Kallies R., Kiesel B.**, Schmidt M., Kacza J., **Ghanem N., Narr A.**, Zopfi J., Wick L.Y., Hackermüller J., Harms H., **Chatzinotas A.** (2017). Complete genome sequence of *Pseudoalteromonas* phage vB\_PspS-H40/1 (formerly H40/1) that infects *Pseudoalteromonas* sp. strain H40 and is used as biological tracer in hydrological transport studies. *Standards in Genomic Sciences* 12:20

## 2016

53. **Ghanem N., Kiesel B., Kallies R.**, Harms H., **Chatzinotas A.**, Wick L. (2016). Marine phages as tracers: effects of size, morphology, and physico-chemical surface properties on transport in a porous medium. *Environmental Science & Technology* 50: 12816–12824

52. Steinauer K., **Chatzinotas A.**, Eisenhauer N. (2016) Root exudate cocktails: the link between plant diversity and soil microorganisms. *Ecology and Evolution* 20: 7387-7396

51. Grossmann L., Beisser D., Bock C., **Chatzinotas A.**, Jensen M., Preisfeld A., Psenner R., Rahmann S., Wodniok S., Boenigk J. (2016). Trade-off between taxon diversity and functional diversity in European lake ecosystems. *Molecular Ecology* 23: 5876-5888

50. **Saleem M., Fetzer I.**, Harms H., **Chatzinotas A.** (2016). Trophic complexity in aqueous systems: Bacterial species richness and protistan predation regulate dissolved organic carbon and dissolved total nitrogen removal. *Proceedings of the Royal Society B: Biological Sciences* 283: 20152724

49. Chakravorty, S., Bhattacharya, S., **Chatzinotas, A.**, Chakraborty, W., Bhattacharya, D., Gachhui, R. (2016). Kombucha tea fermentation: Microbial and biochemical dynamics. *International Journal of Food Microbiology* 220: 63-72.

## 2015

48. **Fetzer I.**, Johst K., **Schäwe R.**, Banitz T., Harms H., **Chatzinotas A.** (2015). The extent of functional redundancy changes as species' roles shift in different environments. *Proceedings of the National Academy of Sciences of the USA* 112: 14888-14893 (**F1000Prime article recommendation**)

47. **Glaser K., Kuppardt A.**, Boenigk J, **Fetzer I.**, Harms H., **Chatzinotas A.** (2015). The influence of environmental factors on protistan microorganisms in grassland soils along a land-use gradient. *Science of the Total Environment* 537: 33-42

## 2014

46. **Giebler J.**, Wick L.Y., Harms H., **Chatzinotas A.** (2014). Evaluating T-RFLP protocols to sensitively analyze the genetic diversity and community changes of soil alkane degrading bacteria. *European Journal of Soil Biology* 65: 107-113
45. Lentendu G., Wubet T., **Chatzinotas A.**, Wilhelm C., Buscot F., Schlegel M. (2014). Effects of long term differential fertilization on eukaryotic microbial communities in an arable soil: a multiple barcoding approach. *Molecular Ecology* 23: 3341-3355 (**F1000Prime article recommendation**)
44. **Kuppardt A.**, Kleinstaub S., Vogt C., Lüders T., Harms H., **Chatzinotas A.** (2014). Phylogenetic and functional diversity within toluene-degrading, sulphate-reducing consortia enriched from a contaminated aquifer. *Microbial Ecology* 68:222-234
43. **Krohn S.**, Böhm S., Engelmann C., Hartmann J., Brodzinski A., **Chatzinotas A.**, Zeller K., Prywerek D., **Fetzer I.**, Berg T (2014). Application of qualitative and quantitative real-time PCR, direct sequencing and T-RFLP for the detection and identification of polymicrobial 16S rRNA genes in ascites. *Journal of Clinical Microbiology* 52: 1754-1757
42. **Johnke J.**, Cohen Y., de Leeuw M., Kushmaro A., Jurkevitch E., **Chatzinotas A.** (2014). Multiple micro-predators controlling bacterial communities in the environment. *Current Opinion in Biotechnology* 27:185–190
41. **Glaser K.**, **Kuppardt A.**, **Krohn S.**, **Heidtmann A.**, Harms H., **Chatzinotas A.** (2014). Primer pairs for the specific environmental detection and T-RFLP analysis of the ubiquitous flagellate taxa Chrysophyceae and Kinetoplastea. *Journal of Microbiological Methods* 100: 8-16
40. Allan E., Bossdorf O., Dormann C.F., Prati D., Gossner M., Blüthgen N., Barto K., Bellach M., Birkhofer K., Boch S., Böhm S., Börschig C., **Chatzinotas A.**, Christ S., Daniel R., Diekötter T., Fischer C., Friedl T., **Glaser K.**, Hallmann C., Hodac L., Hölzel N., Jung K., Klein A. M., Klaus V.H., Kleinebecker T., Krauss J., Lange M., Morris E.K., Müller J., Nacke H., Pašalić E., Rillig M.C., Rothenwöhrer C., Schall P., Scherber C., Schulze W., Socher S.A., Steckel J., Steffan-Dewenter I., Türke M., Weiner C.N., Werner M., Westphal C., Wolters V., Wubet T., Gockel S., Gorke M., Hemp A., Renner S.C., Schöning I., Pfeiffer S., König-Ries B., Buscot F., Linsenmair K.E., Schulze E.-D., Weisser W.W., Fischer M. (2014). Interannual variation in land-use intensity enhances grassland multidiversity. *Proceedings of the National Academy of Sciences of the USA* 111: 308-313

## 2013

39. **Chatzinotas A.**, Schellenberger S., **Glaser K.**, Kolb S. Assimilation of cellulose-derived carbon by microeukaryotes in oxic and anoxic slurries of an aerated soil. (2013). *Applied and Environmental Microbiology* 79: 5777-5781
38. **Saleem M.**, **Fetzer I.**, Harms H., **Chatzinotas A.** (2013). Diversity of protists and bacteria determines predation performance and stability. *The ISME Journal* 7: 1912-1921 (**F1000Prime article recommendation**)
37. **Giebler J.**, Wick L.Y., Schloter M., Harms H., **Chatzinotas A.** (2013). Evaluating the assignment of alkB T-RFs and sequence types to distinct bacterial taxa. *Applied and Environmental Microbiology* 79: 3129-3132

36. **Giebler J.**, Wick L.Y., **Chatzinotas A.**, Harms H. (2013). Alkane degrading bacteria at the soil-litter interface: Comparing isolates with T-RFLP based community profiles. *FEMS Microbiology Ecology* 86: 45-58

## 2012

35. **Saleem M.**, **Fetzer I.**, Dormann C., Harms H., **Chatzinotas A.** (2012). Predator richness increases the effect of prey diversity on prey yield. *Nature Communications* 3:1305

34. Schulz S., **Giebler J.**, **Chatzinotas A.**, Wick L.Y., **Fetzer I.**, Welzl G., Harms H., Schloter M. (2012). Plant litter and soil type drive abundance, activity and community structure of alkB harbouring microbes in different soil compartments. *The ISME Journal* 6:1763-74

33. Siegfried K., **Endes C.**, Khaled Bhuiyan A.F.M., **Kuppardt A.**, Mattusch J., van der Meer J.R., **Chatzinotas A.**, Harms H. (2012). Field testing of arsenic in groundwater samples of Bangladesh using a test kit based on lyophilized bioreporter bacteria. *Environmental Science and Technology* 46: 3281–3287

32. Furuno S., Remer R., **Chatzinotas A.**, Harms H., Wick L.Y. (2012). Use of mycelia as paths for the isolation of contaminant-degrading bacteria from soil. *Microbial Biotechnology* 5: 142-248

## 2011

31. **Schäwe R.**, **Fetzer I.**, **Tönniges A.**, Härtig C., Geyer W., Harms H., **Chatzinotas A.** (2011). Evaluation of FT-IR spectroscopy as a tool to quantify bacteria in binary mixed cultures. *Journal of Microbiological Methods* 86: 182-187

## 2010

30. **Kuppardt S.**, **Chatzinotas A.**, Kästner M. (2010). Development of a fatty acid and RNA stable isotope probing-based method for tracking protist grazing on bacteria in wastewater. *Applied and Environmental Microbiology* 76: 8222-8230

29. Findenig B., **Chatzinotas A.**, Boenigk J. (2010). Taxonomic and ecological characterization of stomatocysts of Spumella-like flagellates (Chrysophyceae). *Journal of Phycology* 46: 868–881

28. Foit K., **Chatzinotas A.**, Liess M. (2010). Short-term disturbance of a grazer has long-term effects on bacterial communities - Relevance of trophic interactions for recovery from pesticide effects. *Aquatic Toxicology* 99:205-211

27. **Kuppardt A.**, Vetterlein D., Harms H., **Chatzinotas A.** (2010). Visualisation of gradients in arsenic concentrations around individual roots of *Zea mays* L. using agar-immobilized bioreporter bacteria. *Plant and Soil* 329: 295-306

26. Herrmann S., Kleinstaub S., **Chatzinotas A.**, **Kuppardt S.**, Lueders T., Richnow H.-H., Vogt C. (2010). Functional characterisation of an anaerobic benzene-degrading enrichment culture by DNA stable isotope probing. *Environmental Microbiology* 12: 401-411 (*F1000Prime article recommendation*)

25. Jousset A., Lara E., Nikolausz M., Harms H., Chatzinotas A. (2010). Application of the denaturing gradient gel electrophoresis (DGGE) technique as an efficient diagnostic tool for ciliate communities in soil. *Science of the Total Environment* 408: 1221-1225

24. Bombach P., Chatzinotas A., Neu T., Kästner M., Lueders T., Vogt C. (2010). Enrichment and characterization of a sulphate-reducing toluene-degrading microbial consortium by combining in situ microcosms and stable isotope probing techniques. *FEMS Microbiology Ecology* 71: 237-246

## 2009

23. Wu Q. L.\*, Chatzinotas A.\*, Wang J., Boenigk J. (2009). Genetic diversity of eukaryotic plankton assemblages in eastern Tibetan lakes differing by their salinity and altitude. *Microbial Ecology* 58:569–581 (\*equal contribution)

22. Nikolausz M., Chatzinotas A., Tánksics A., Imfeld G., Kästner M. (2009). Evaluation of single-nucleotide primer extension for detection and typing of phylogenetic markers used for investigation of microbial communities. *Applied and Environmental Microbiology* 75: 2850-2860

21. Nikolausz M., Chatzinotas A., Tánksics A., Imfeld G., Kästner M. (2009). Single-nucleotide primer extension (SNUPE) method for the multiplex detection of various DNA sequences: from detection of point mutation to microbial ecology. *Biochemical Society Transactions* 37: 454-459

20. Kuppardt A., Chatzinotas A., Breuer U., van der Meer J. R., Harms H. (2009). Optimization of preservation conditions of As (III) bioreporter bacteria. *Applied Microbiology and Biotechnology* 82: 785-792

19. Fountoulakis M.S., Terzakis S., Chatzinotas A., Brix H., Kalogerakis N., Manios T. (2009). Pilot-scale comparison of constructed wetlands operated under high hydraulic loading rated and attached biofilm reactors for domestic wastewater treatment. *Science of the Total Environment* 407: 2996-3003

18. Pfandl K., Chatzinotas A., Dyal P., Boenigk J. (2009). SSU rRNA gene variation resolves population heterogeneity and ecophysiological differentiation within a morphospecies (Stramenopiles, Chrysophyceae). *Limnology and Oceanography* 54: 171-181

## 2008

17. Solé M., Chatzinotas A., Sridhar K.R., Harms H., Krauss G. (2008). Improved coverage of fungal diversity in polluted groundwaters by semi-nested PCR. *Science of the Total Environment* 406: 324-330

16. Wackwitz A., Harms H., Chatzinotas A., Breuer U., Vogne C., van der Meer J. R. (2008). Internal arsenite bioassay calibration using multiple bioreporter cell lines. *Microbial Biotechnology* 1: 149-157

15. Kleinstaub S., Müller F-D., Chatzinotas A., Wendt-Potthoff K., Harms H (2008). Diversity and in situ quantification of Acidobacteria Subdivision 1 in an acidic mining lake. *FEMS Microbiology Ecology* 63: 107-117.

14. Nikolausz M., Chatzinotas A., Palatinszky M., Imfeld G., Martinez P., Kästner M. (2008). A single nucleotide primer extension assay for the detection and typing of Dehalococcoides sequences. *Applied and Environmental Microbiology* 74: 300-304.

## 2007

13. **Lara E.**, Berney C., Harms H., **Chatzinotas A.** (2007). Cultivation-independent analysis reveals a shift in ciliate 18S rRNA gene diversity in a polycyclic aromatic hydrocarbon polluted soil. *FEMS Microbiology Ecology* 62: 365-373.
12. **Lara E.**, Berney C., Ekelund F., Harms H., **Chatzinotas A.** (2007). Molecular comparison of cultivable protozoa from a pristine and a polycyclic aromatic hydrocarbon polluted site. *Soil Biology and Biochemistry* 39: 139-148.

## 2006

11. Strüder-Kypke M.C., Wright A.-D. G., Foissner W., **Chatzinotas A.**, Lynn D. H. (2006). Molecular phylogeny of litostome ciliates (Ciliophora, Litostomatea) with emphasis on free-living haptorian genera. *Protist* 157: 261-278.
10. Boenigk J., Pfandl K., Garstecki T., Harms H., Novarino G., **Chatzinotas A.** (2006). Evidence for geographic isolation and signs of endemism within a protistan morphospecies. *Applied and Environmental Microbiology* 72: 5159-5164.
9. **Lara E.**, **Chatzinotas A.**, Simpson A. G. B. (2006). Andalucia (n. Gen.) - the deepest branch within jakobids (Jakobida; Excavata), based on morphological and molecular study of a new flagellate from soil. *Journal of Eukaryotic Microbiology* 53: 112-120.

## 1997-2005

8. Boenigk J., Pfandl K., Stadler P., **Chatzinotas A.** (2005). High diversity of the "Spumella-like" flagellates: An investigation based on the SSU rRNA gene sequences of isolates from habitats located in six different geographic regions. *Environmental Microbiology* 7: 685-697
7. **Gremion F.**, **Chatzinotas A.**, Kaufmann K., Sigler W. V., Harms H. (2004). Impacts of heavy metal contamination and phytoremediation on microbial communities and functions during a twelve months microcosm experiment. *FEMS Microbiology Ecology* 48:273-283.
6. **Gremion F.**, **Chatzinotas A.**, Harms H. (2003). Comparative 16S rDNA- and 16S rRNA sequence analysis indicates that Actinobacteria might be a dominating part of the metabolically active bacteria in heavy metal-contaminated bulk and rhizosphere soil. *Environmental Microbiology* 5: 896-907.
5. Pelz O., **Chatzinotas A.**, Zarda-Hess A., Abraham W. R., Zeyer J. (2001). Tracing toluene-assimilating sulfate-reducing bacteria using C-13-incorporation in fatty acids and whole-cell hybridization. *FEMS Microbiology Ecology* 38: 123-131
4. Pelz O., **Chatzinotas A.**, Andersen N., Bernasconi S. M., Hesse C., Abraham W. R., Zeyer J. (2001). Use of isotopic and molecular techniques to link toluene degradation in denitrifying aquifer microcosms to specific microbial populations. *Archives of Microbiology* 175: 270-281
3. Berchtold M., **Chatzinotas A.**, Schönhuber W., Brune A., Amann R., Hahn D., König H. (1999). Differential enumeration and in situ localization of microorganisms in the hindgut of the lower termite *Mastotermes darwiniensis* by hybridization with group-specific rRNA-targeted probes. *Archives of Microbiology* 172: 407-416.



2. **Chatzinotas A.**, Sandaa R-A., Schönhuber W., Amann R., Daae F. L., Torsvik V., Zeyer J., Hahn D. (1998). Analysis of broad-scale differences in microbial community composition of two pristine forest soils. *Systematic and Applied Microbiology* 21: 579-587.

1. Zarda B., Hahn D., **Chatzinotas A.**, Schönhuber W., Neef A., Amann R., Zeyer J. (1997). Analysis of bacterial community structure in bulk soil by in situ hybridization. *Archives of Microbiology* 168: 185-192.

### **Book chapters**

---

**Kuppardt-Kirmse A., Chatzinotas A.** (2020). Intraguild Predation: Predatory Networks at the Microbial Scale. *In: Jurkevitch E., Mitchell R. (eds.) The ecology of predation at the microscale (pp. 65-87).* Springer, Cham.

**Johnke J., Chatzinotas A.** (2015). Studying Protistan Communities in Hydrocarbon-Contaminated Environments. *In: T.J. McGenity et al. (eds.), Hydrocarbon and Lipid Microbiology Protocols, Springer Protocols Handbooks, DOI 10.1007/8623\_2015\_169, Springer-Verlag Berlin Heidelberg.*

**Chatzinotas A., Harms H.** (2003). Nachweismethoden für pathogene Mikroorganismen. *In: Pathogene Mikroorganismen im Grund- und Trinkwasser. A. Auckenthaler, P. Huggenberger (eds.). Birckhäuser Verlag, Basel, Schweiz.*

Hartmann A., **Chatzinotas A.**, Assmus B., Kirchhof G. (2001). Molecular microbial ecology studies of diazotrophic bacteria associated with non-legumes with spatial reference to endophytic diazotrophs. *In: Microbial Interactions in Agriculture and Forestry. Vol. II. N. S. Subba Roa, Y. R. Dommergues (eds.). Oxford & IBH Publishing Co., Pvt. Ltd., New Delhi, India.*

### **Other articles**

---

Wick L.Y., **Chatzinotas A.** (2019). Capacity of ecosystems to degrade anthropogenic chemicals. *In: Atlas of Ecosystem Services - Drivers, Risks, and Societal Responses.p. 179-182. In: Schröter, M., Bonn, A., Klotz, S., Seppelt, R., Baessler, C. (eds.). Springer International Publishing.*

Harms, H., Höhener P., **Chatzinotas A.** (2001). Veränderung mikrobieller Gemeinschaften in Böden während Zyklen von Kontamination und biotechnologischer Reinigung. *Bulletin BSA/VBB* 5.