

MINISTERIUM
FÜR EIN
LEBENSWERTES
ÖSTERREICH

HBLAuBA KLOSTERNEUBURG
WEIN- UND OBSTBAU

MIKROBIELLE VIELFALT IM BODEN DES HERBIZID - FREILANDVERSUCHES

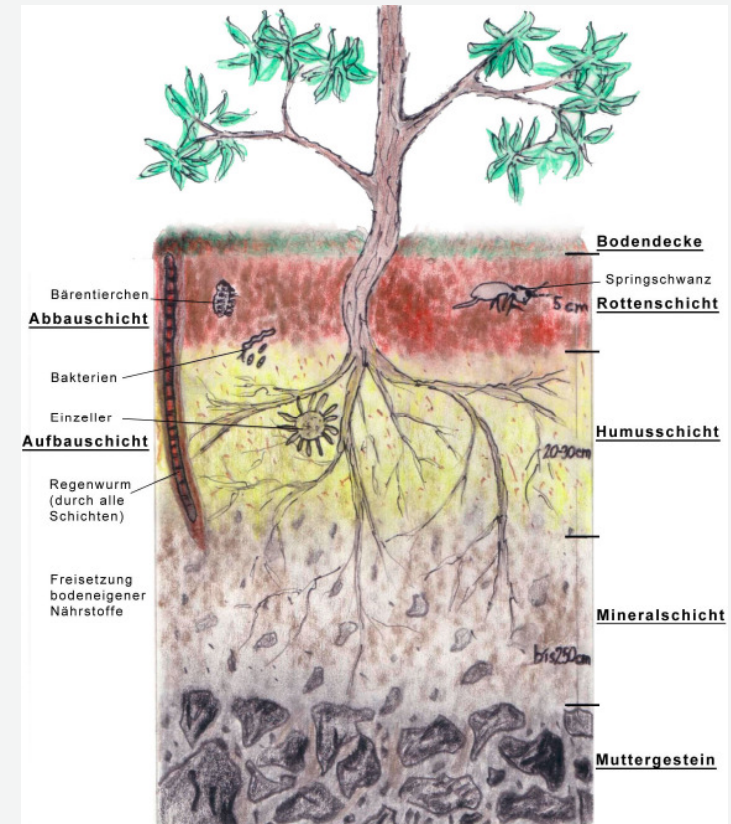
Karin Mandl, Clemens Cantelmo, Edith Gruber,
Florian Faber, Barbara Friedrich, Johann Zaller



WELCHE KEIME BEFINDEN SICH IM BODEN

- Mycorrhiza
- Pilze
- Trichoderma
- Hefen
- Bakterien
- Saprophyten
- Biocontrolagenten
- Pathogene im Boden
- Vektoren: Regenwürmer und Insekten

(Quelle: Angelo Huber, Land OÖ)

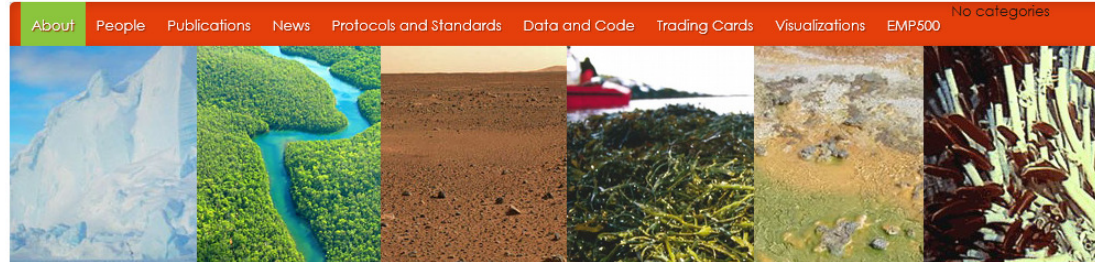


BEEINFLUSSUNG DER KEIMFLORA

- Feuchtigkeit des Bodens durch Regen
- Tiere wie Säugetiere, Vögel, Regenwürmer, Insekten, Wühlmäuse
- Sonnenstrahlung
- Wärme des Bodens, chemische Zusammensetzung des Bodens
- Bearbeitung des Bodens – mechanisch –chemisch
- Begrünung

Nachteil die Bodenflora ist immer eine Momentaufnahme





The Earth Microbiome Project is a systematic attempt to characterize global microbial taxonomic and functional diversity for the benefit of the planet and humankind.

The Earth Microbiome Project (EMP) is a massively collaborative effort to characterize microbial life on this planet. We use DNA sequencing and mass spectrometry of crowd-sourced samples to understand patterns in microbial ecology across the biomes and habitats of our planet. The EMP is a comprehensive example of open science, leveraging a collaborative network of 500+ investigators, supporting pre-publication data sharing, and crowdsourcing data analysis to enable universal principles to be explored. The standardized collection, curation, and analysis are enabling a robust interpretation of ecological trends.

The Vision: Constructing the Microbial Map for Planet Earth

The EMP was founded in 2010 as a massive crowd-sourced effort to analyze microbial communities across the globe. The general premise was to examine microbial communities from their own perspective. Hence we proposed to characterize the Earth by environmental parameter space into different biomes and then explore these using samples drawn from researchers across the globe. We set out to analyze 200,000 samples from these communities using amplicon sequencing, metagenomics, and metabolomics to produce a global Gene Atlas describing protein space, environmental metabolic models for each biome, approximately 500,000 reconstructed microbial genomes, a global metabolic model, and a data-analysis portal for visualization of processed information.

Data and Code

Data

EMP observation tables, metadata, and results are available on the [Qiita EMP Portal](#) and on our [FTP site](#).

Search

EMP samples and other samples in the [Qiita database](#) can be searched by observation data and sample metadata using [Redbiom](#).

Code

EMP-related code, analyses, and issues are on our [GitHub repository](#).

From Vineyard Soil to Wine Fermentation: Microbiome Approximations to Explain the “terroir” Concept

Ignacio Belda^{1,2}, Iratxe Zarraindia^{3,4}, Matthew Perisin¹, Antonio Palacios^{1,5} and
Alberto Acedo^{1*}*



<https://wineseq.com/#home>

**Soil Microbiome
im Weingarten**



Glyphosate-Induced Specific and Widespread Perturbations in the Metabolome of Soil *Pseudomonas* Species

Ludmilla Aristilde^{1,2,3*}, Michael L. Reed¹, Rebecca A. Wilkes¹, Tracy Youngster²,
Matthew A. Kukurugya¹, Valerie Katz¹ and Clayton R. S. Sasaki¹

 **frontiers**
in Environmental Science

ORIGINAL RESEARCH
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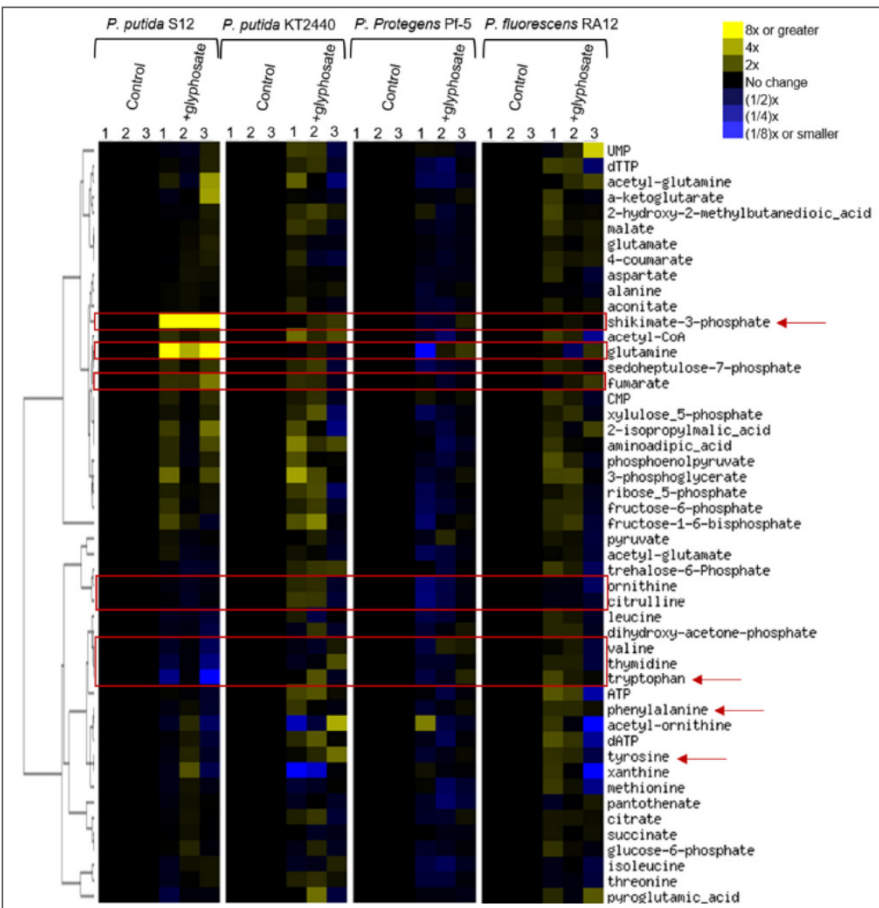


FIGURE 3 | Fingerprinting of the cellular metabolome of *P. putida* S12, *P. putida* KT2440, *P. protegens* Pf-5, *P. fluorescens* RA12. Unsupervised hierarchical clustering of metabolite levels in succinate-grown cells in the absence (control) and presence of 0.5 mM glyphosate (+glyphosate). Columns 1, 2, and 3 represent data from independent biological replicates. The red rectangular boxes highlight metabolite levels in the metabolome that were disrupted in the presence of glyphosate. The red arrows indicate metabolites that are present in the shikimate pathway.

VERWENDETE HERBIZIDE

- Herbizide
 - Roundup Power Flex® - Wirkstoff: Glyphosat
 - Katana® - Wirkstoff: Flazasulfuron
 - Basta® - Wirkstoff: Glufosinat -Ammonium



<https://www.unkrautvernichter-shop.de/Katana-200-g.html>



<https://www.unkrautvernichter-shop.de/Basta-5-Liter.html>



<https://www.samen-schwarzenberger.at/shop/de/pflanzenschutz-totalherbizid/668-round-up-powerflex.html>

VERSUCHSFELD

Weingarten in Klosterneuburg (Rothäcker XV)
Rigosol –Boden über Lehm mit Flyschschichten
Rebsorte fünfjähriger Grüner Veltliner mit Spalierhaltung



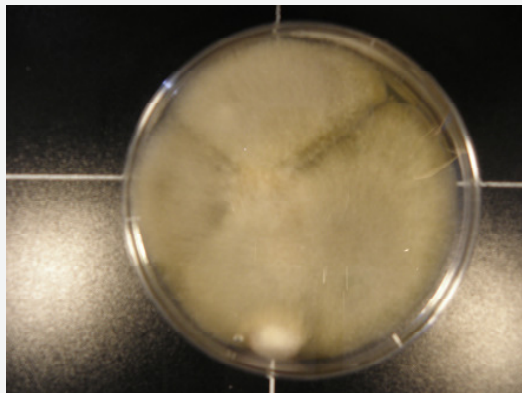
BODENPROBENNAHME

- Bodenproben wurden genommen in 10- 20cm Tiefe im Ausmaß von 5x5x10cm
- 400g Boden wurden der Firma Eurofins zur Durchführung von Next Generation Sequencing übergeben
- 1g Boden für Schimmelpilzanalyse

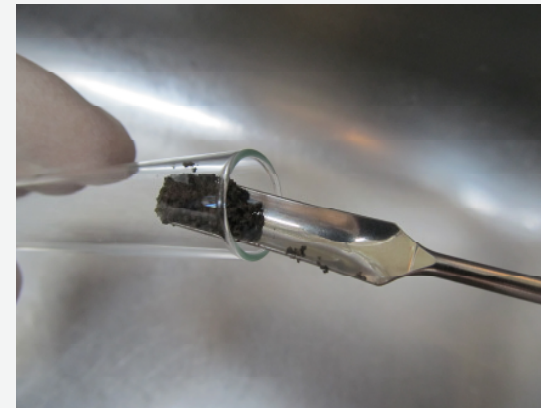
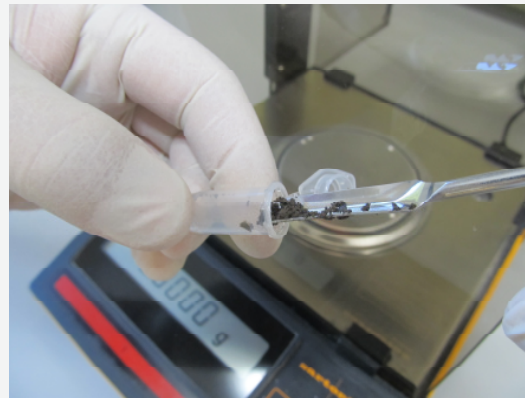


AUFARBEITUNG IM LABOR

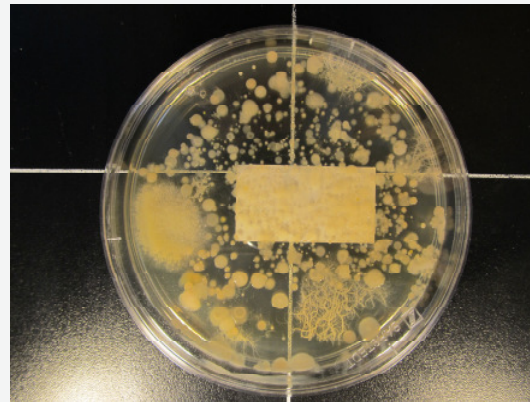
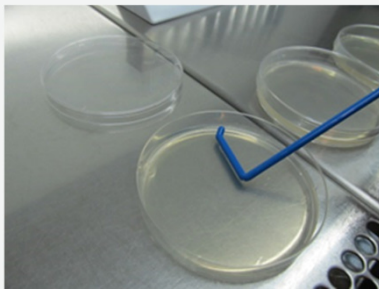
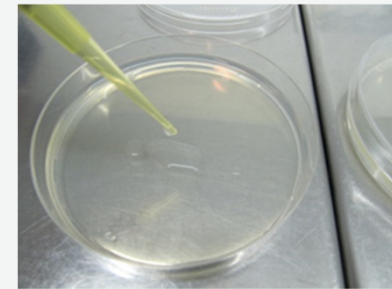
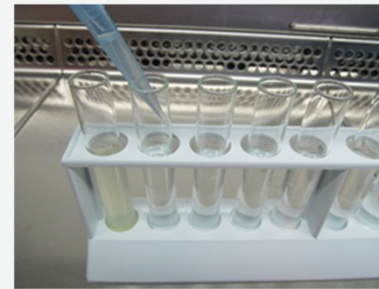
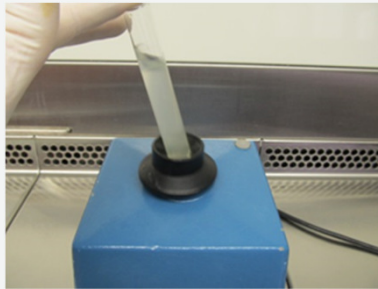
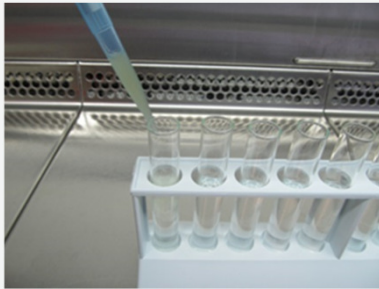
1. Schimmelpilze
2. Bakterien



PROBENEINWAAGE FÜR DIE SCHIMMELPILZANALYSE

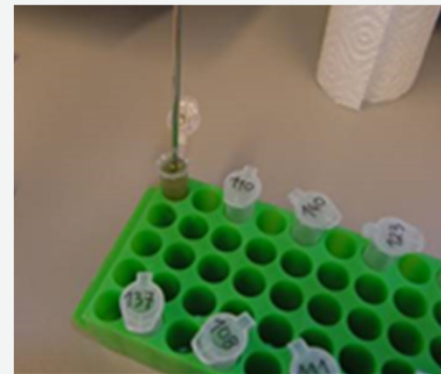
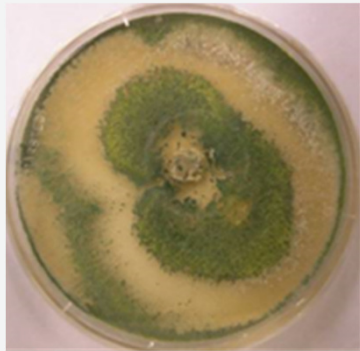


AUSPLATTIEREN UND AUSZÄHLEN



Verwendeter Agar
Wallerstein Nutrient Agar
Malzextrakt Agar

DNA REINIGUNG



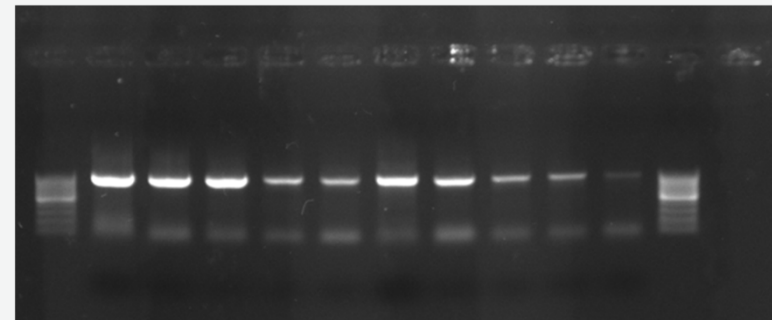
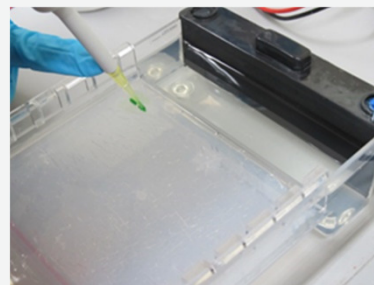
PCR



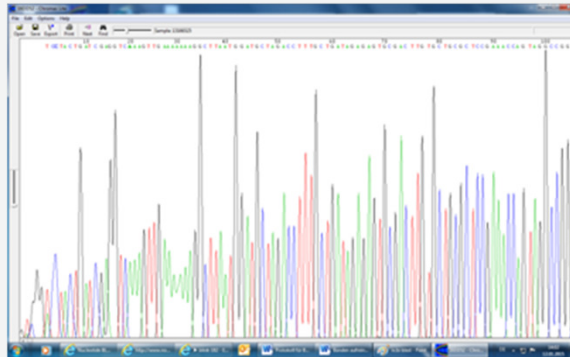
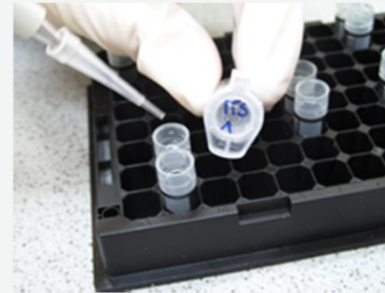
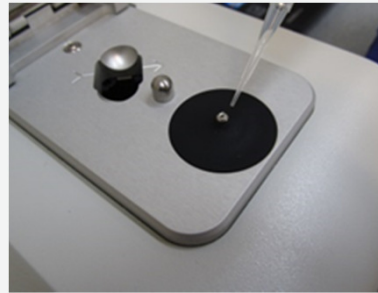
Primer ITS1
Primer ITS4



x 1		x 30	
1,5µL	Primer fw	45µL	Primer fw
1,5µL	Primer rev	45 µL	Primer rev
0,5µL	Taq	15µL	Taq
27,5µL	ddH2O	825µL	ddH2O
7µL	dNTP's	210µL	dNTP's
5µL	10xP	150µL	10xP
5µL	Dna - Probe	5µL	Dna - Probe

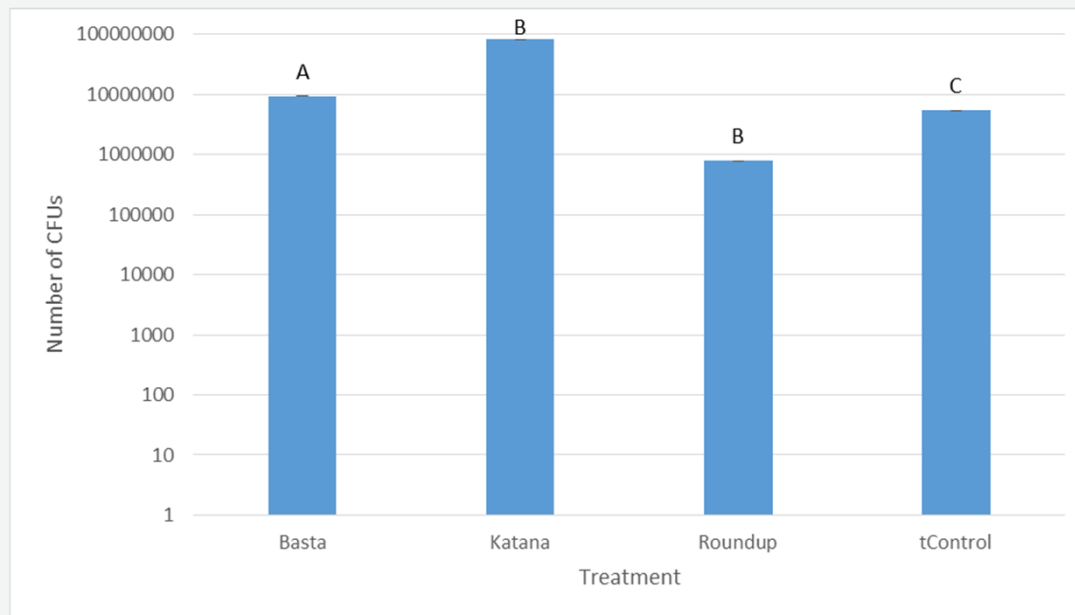


SEQUENZIERVORBEREITUNGEN



Accession	Length	Score	E-value	Identical
AB011011.1	100	100	1e-100	100%
AB011012.1	100	100	1e-100	100%
AB011013.1	100	100	1e-100	100%
AB011014.1	100	100	1e-100	100%
AB011015.1	100	100	1e-100	100%
AB011016.1	100	100	1e-100	100%
AB011017.1	100	100	1e-100	100%
AB011018.1	100	100	1e-100	100%
AB011019.1	100	100	1e-100	100%
AB011020.1	100	100	1e-100	100%

GESAMTKEIMZAHL



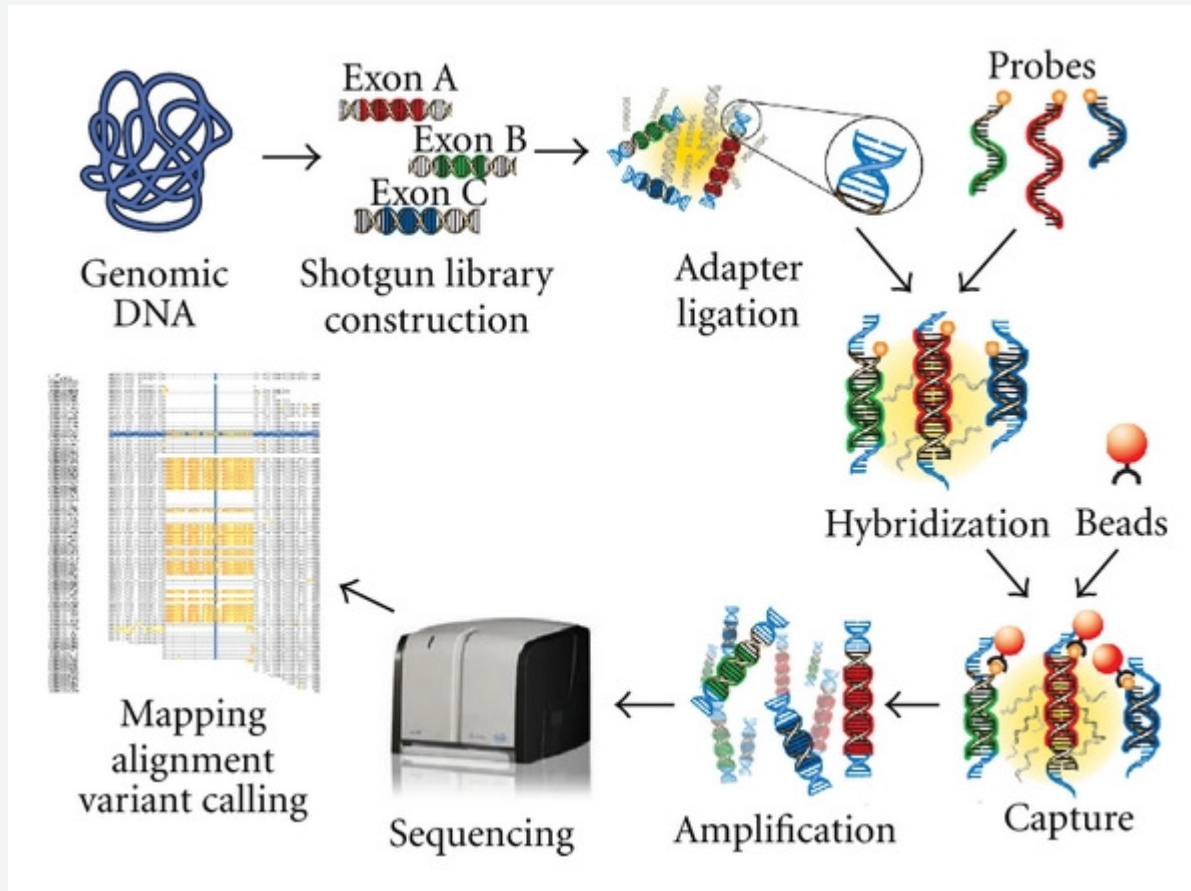
Gesamtkeimzahl mit
signifikanten Unterschieden
(Tukey's HSD, $p < 0.05$).

NEXT GENERATION SEQUENCING

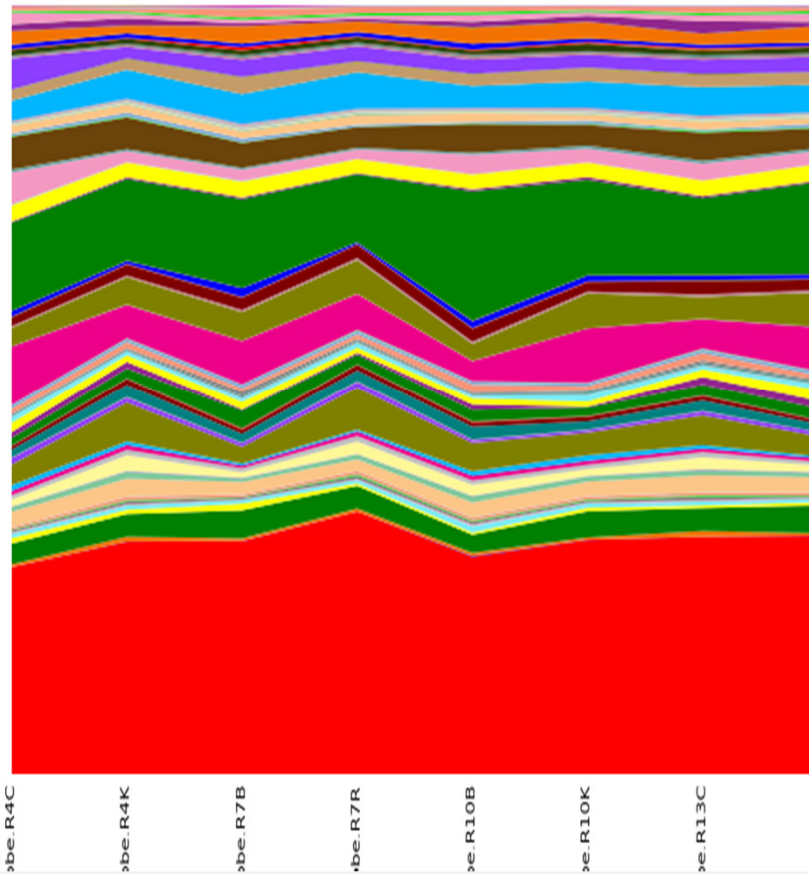
- 400g Erdprobe
- DNA Reinigung
- Codierung der Proben, Primer V3 Region, 16S Region
- Massensequenzierung mit Illumina Gerät
- Abgleich mit der NCBI Datenbank



NGS



Ordnungen



DATENMENGE

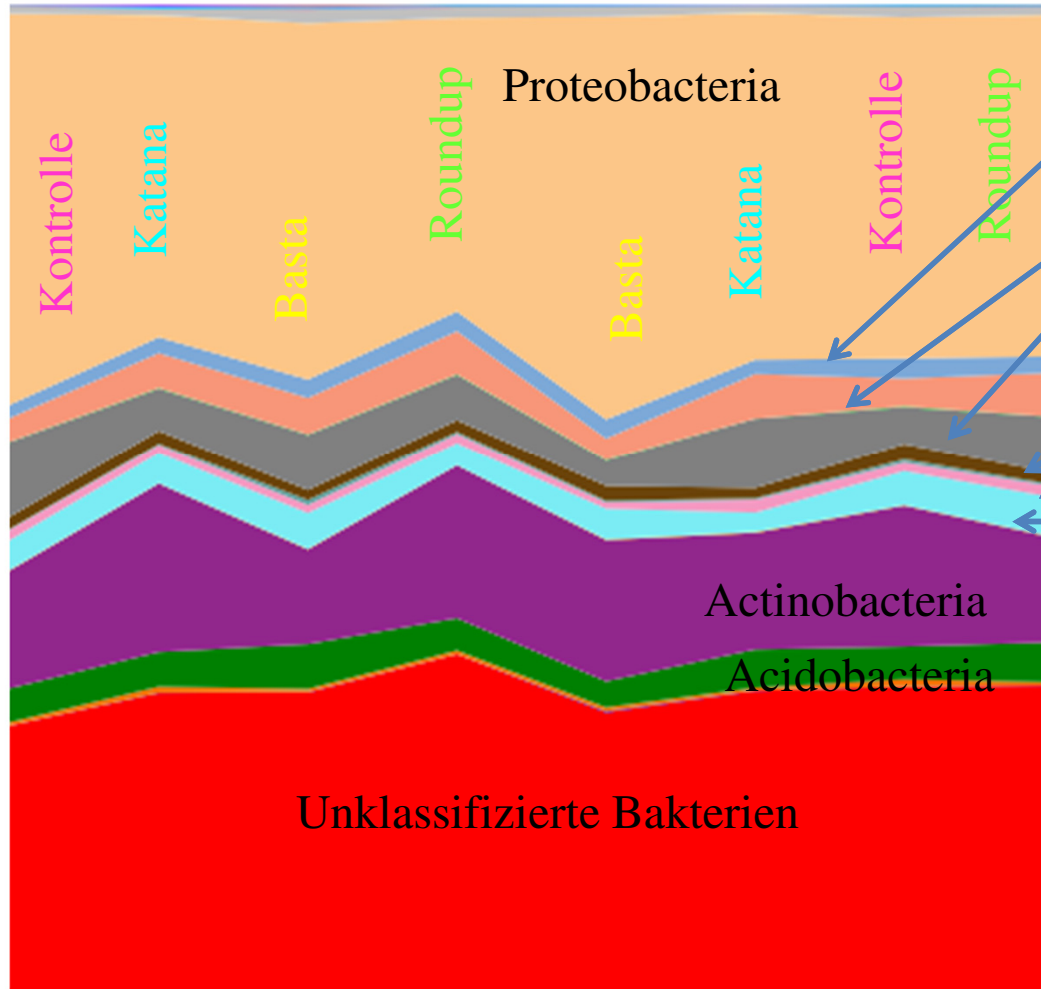


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- Unclassified;Other;Other;Other
- k_Archaea;p_Thaumarchaeota;c_o_Nitrosopumilales
- k_Bacteria;p_c_o_
- k_Bacteria;p_Acidobacteria;c_Acidobacteria;o_Acidobacteriales
- k_Bacteria;p_Acidobacteria;c_Holophagae;o_Holophagales
- k_Bacteria;p_Acidobacteria;c_Solibacteres;o_Solibacteriales
- k_Bacteria;p_Actinobacteria;c_Acidimicrobia;o_Acidimicrobiales
- k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_
- k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Acidothermales
- k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Catenulisporales
- k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Corynebacteriales
- k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Frankiales
- k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Geodermatophilales
- k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Kineosporiales
- k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales
- k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micromonosporales
- k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Nakamurellales
- k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Propionibacteriales
- k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Pseudonocardiales
- k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Streptomyces
- k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Streptosporangiales
- k_Bacteria;p_Actinobacteria;c_Nitrospirales;o_Euzebyales
- k_Bacteria;p_Actinobacteria;c_Rubrobacteria;o_Gaiellales
- k_Bacteria;p_Actinobacteria;c_Rubrobacteria;o_Rubrobacteriales
- k_Bacteria;p_Actinobacteria;c_Thermoleophilia;o_
- k_Bacteria;p_Actinobacteria;c_Thermoleophilia;o_Solirubrobacteriales
- k_Bacteria;p_Actinobacteria;c_Thermoleophilia;o_Thermoleophilales
- k_Bacteria;p_Armatimonadetes;c_Armatimonadiales;o_Armatimonadales
- k_Bacteria;p_Armatimonadetes;c_Fimbrimonadia;o_Fimbrimonadales
- k_Bacteria;p_Bacteroidetes;c_o_
- k_Bacteria;p_Bacteroidetes;c_o_Bacteroidetes Order II. Incertae sedis
- k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales
- k_Bacteria;p_Bacteroidetes;c_Cytophagia;o_Cytophagales
- k_Bacteria;p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales
- k_Bacteria;p_Bacteroidetes;c_Sphingobacteriia;o_Sphingobacteriales
- k_Bacteria;p_Chloroflexi;c_Anaerolineae;o_Anaerolineales
- k_Bacteria;p_Chloroflexi;c_Caldilineae;o_Caldilineales
- k_Bacteria;p_Chloroflexi;c_Chloroflexia;o_Chloroflexiales
- k_Bacteria;p_Chloroflexi;c_Thermomicrobia;o_Sphaerobacteriales
- k_Bacteria;p_Cyanobacteria;c_o_Nostocales
- k_Bacteria;p_Firmicutes;c_o_

k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales
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k_Eukaryota;p_Streptophyta;c_o_
k_Eukaryota;p_Streptophyta;c_o_Solanales
k_Eukaryota;p_Streptophyta;c_Bryopsida;o_Pottiales

Stammebene



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Planctomycetes

Nitrospirae

Gemmatimonadetes

Firmicutes

Chloroflexi

Bacteroidetes

- Unclassified;Other
- k_Archaea;p_Thaumarchaeota
- k_Bacteria;p_
- k_Bacteria;p_Acidobacteria
- k_Bacteria;p_Actinobacteria
- k_Bacteria;p_Armatimonadetes
- k_Bacteria;p_Bacteroidetes
- k_Bacteria;p_Chloroflexi
- k_Bacteria;p_Cyanobacteria
- k_Bacteria;p_Firmicutes
- k_Bacteria;p_Gemmatimonadetes
- k_Bacteria;p_Ignavibacteriae
- k_Bacteria;p_Nitrospirae
- k_Bacteria;p_Planctomycetes
- k_Bacteria;p_Proteobacteria
- k_Bacteria;p_Synergistetes
- k_Bacteria;p_Tenericutes
- k_Bacteria;p_Thermodesulfobacteria
- k_Bacteria;p_Verrucomicrobia
- k_Eukaryota;p_Bacillariophyta
- k_Eukaryota;p_Chlorophyta
- k_Eukaryota;p_Euglenida
- k_Eukaryota;p_Eustigmatophyceae
- k_Eukaryota;p_Streptophyta

ZUSAMMENFASSUNG

- Mittels NGS konnte kein signifikanter Unterschied zwischen Bakterien festgestellt werden
- Variation der Vielfalt zwischen den Herbiziden Katana® und Roundup® war ersichtlich. Katana® hatte eine höhere Keimzahl als die Flächen mit Roundup® Behandlung
- Mucor fehlte bei Round up® Behandlung (Wachstum der Pflanze unterbunden). Bei Katana® war Mucor erhöht (es kommt zum Absterben der Pflanzen)

KOOPERATIONEN DANKSAGUNGEN



- **Universität für Bodenkultur, Institut für Zoologie**
 - Clemens Cantelmo
 - Edith Gruber
 - Johann Zaller
- **Bundesamt für Wein- und Obstbau**
 - Florian Faber
 - Barbara Friedrich

AUSBLICK MIKROBIOLOGISCHE ERGEBNISSE 2017 VOM BLUTUNGSSAFT ZUR NÄCHSTEN HEFETAGUNG IM JAHRE 2018



BACHELORARBEIT PAUL PALLUA

**HERZLICHEN DANK FÜR
IHRE AUFMERKSAMKEIT**



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LAU BAU KLÖSTERNEUBURG
IN- UND OBSTBAU