

Lenticelrot research at Agroscope

Andreas Bühlmann
Agroscope

Lenticelrot meeting Wageningen 09/25

ETH zürich  Agroscope



Lubera
lustvoll gärtner

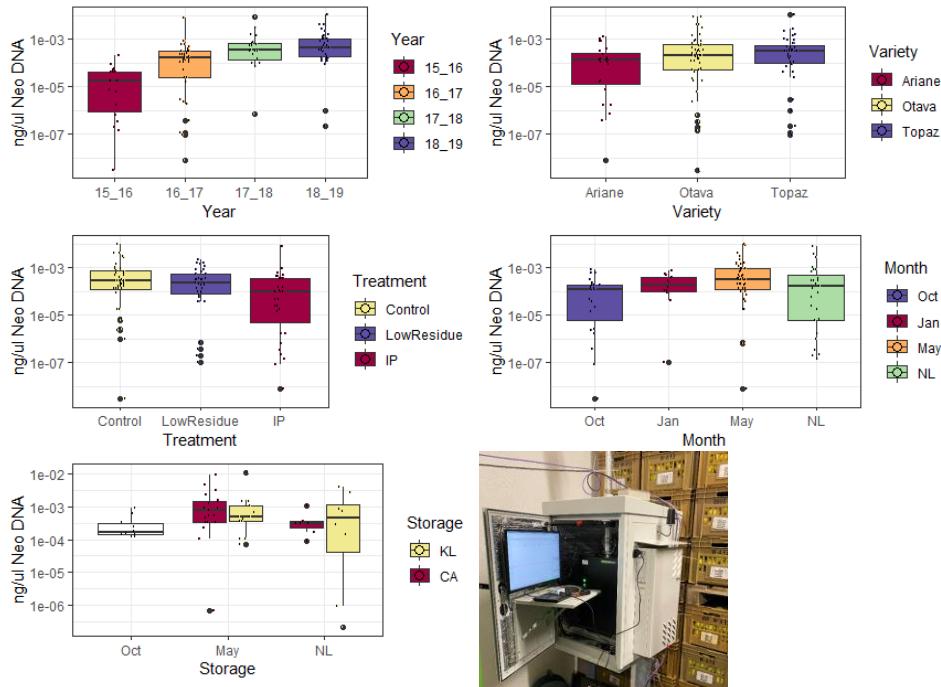
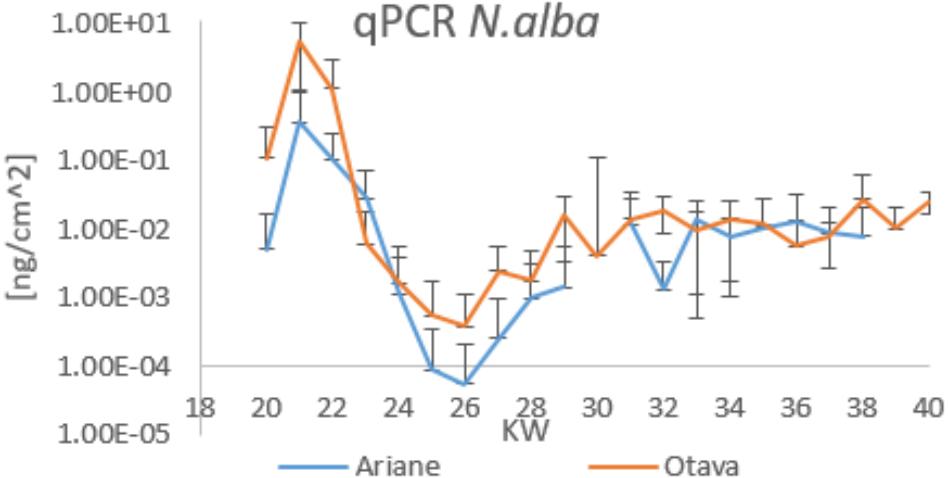
 Schweizerische Eidgenossenschaft
Confédération suisse
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Confederaziun svizra

Eidgenössisches Departement für
Wirtschaft, Bildung und Forschung WBF
Bundesamt für Landwirtschaft BLW

- Spore sampling/skin sampling/spoilage in field and storage
- Biocontrol
- Genome sequencing
- GWAS

Spores/ Spoilage

Spore sampling in field, skin sampling in storage



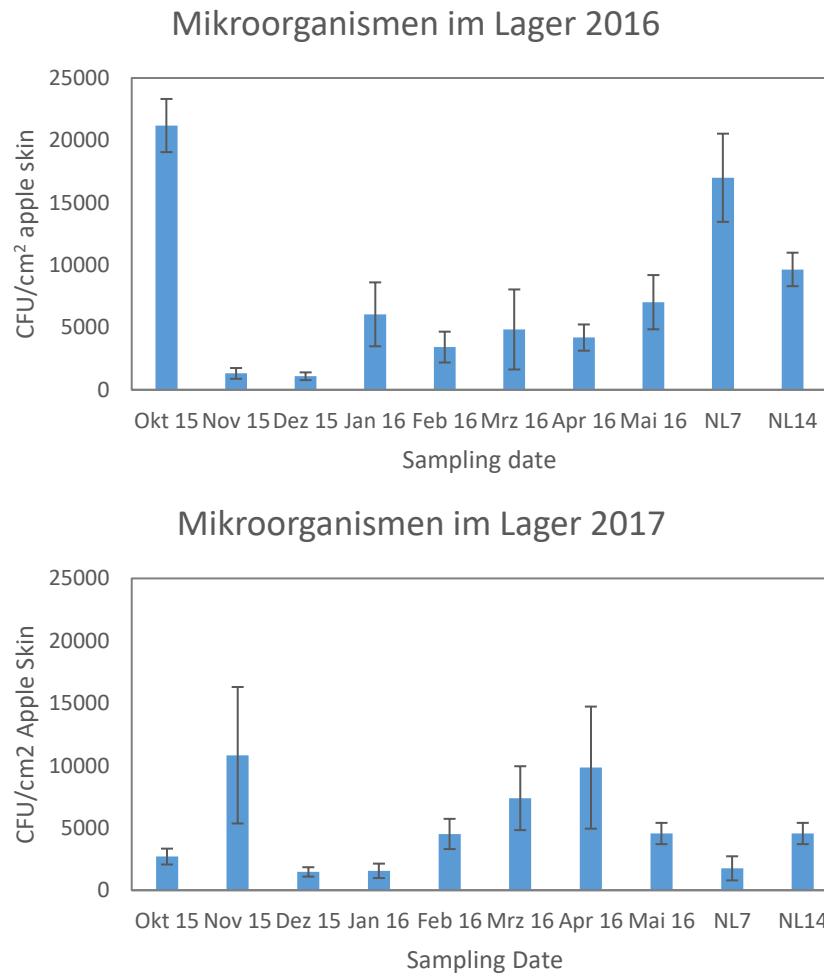
- Infection time point doable with qPCR
- Lots of work in sampling
- Analysis straightforward

Solution?

Gasser et al. 2025 MSc thesis, BOKU Wien

Microbiome in storage

Spores/ Spoilage



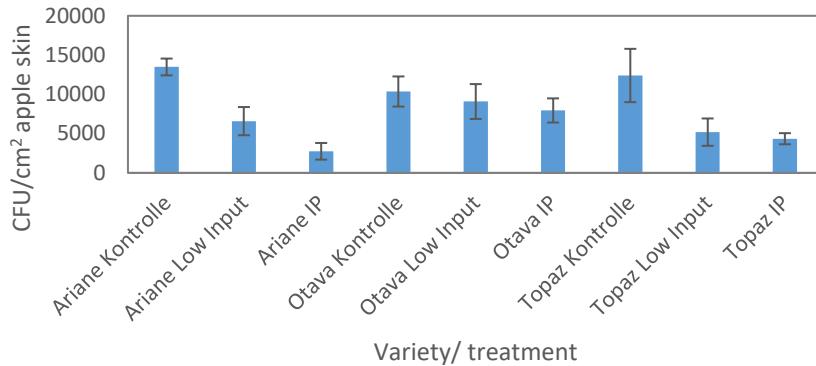
The microbiome changes

- During storage
- Between years

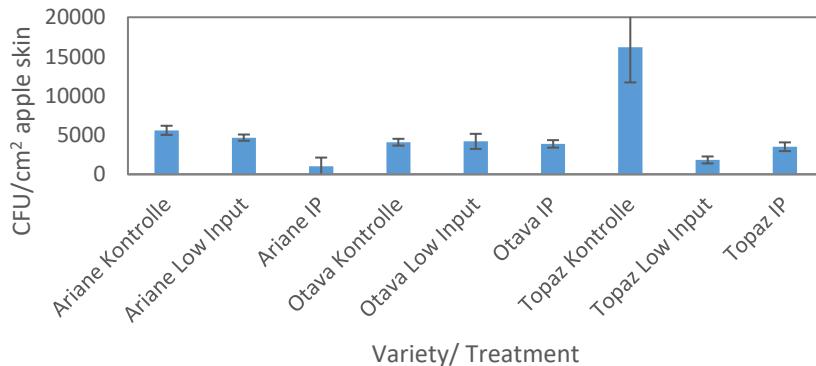
Microbiome in storage

Spores/ Spoilage

Mikroorganismen pro Sorte/Behandlung
2016



Mikroorganismen pro Sorte/Behandlung
2017



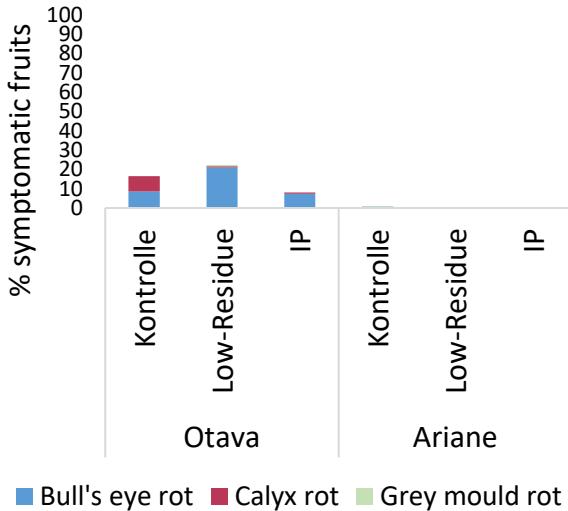
The microbiome shows

- Varietal differences
- Orchard management differences

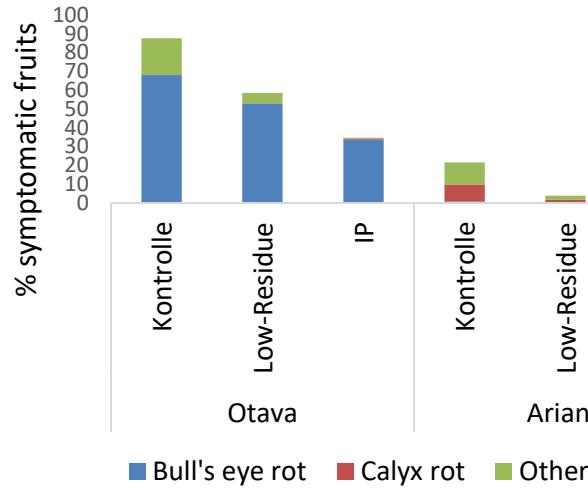
Metagenomics in storage

- Correlate metagenomics and disease scoring

Storage Diseases 2016



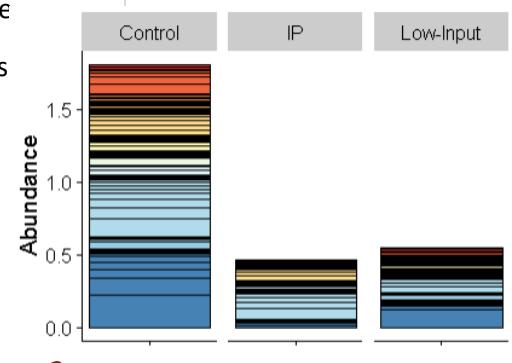
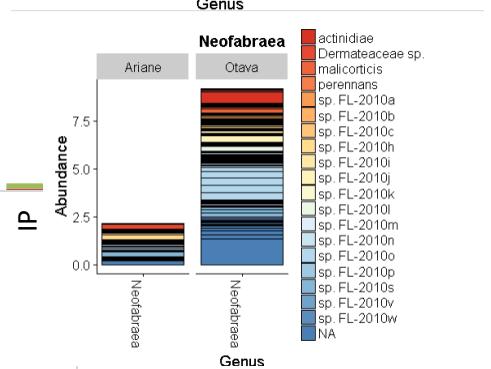
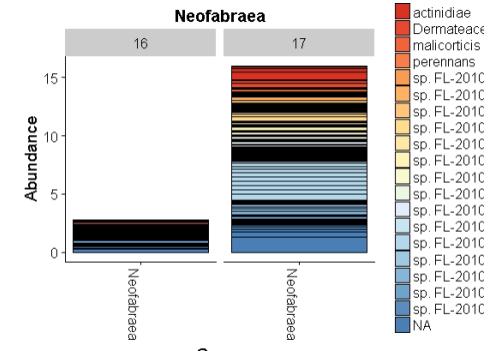
Storage Diseases 2017



Neofabraea DNA abundance correlates with disease severity over:
Years
Treatment
Variety

Spores/ Spoilage

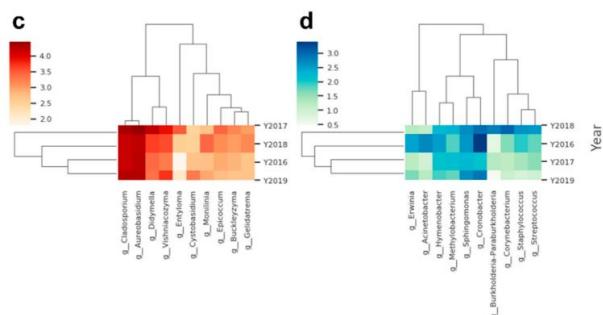
Neofabraea DNA



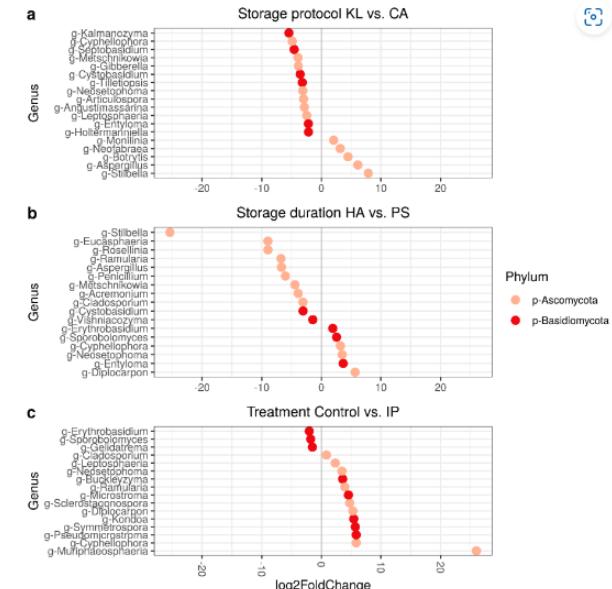
Metagenomics in storage



Fungal diversity controlled by
Storage method > Storage time > Year > Treatment > Cultivar



Core microbiome very similar to global core microbiome



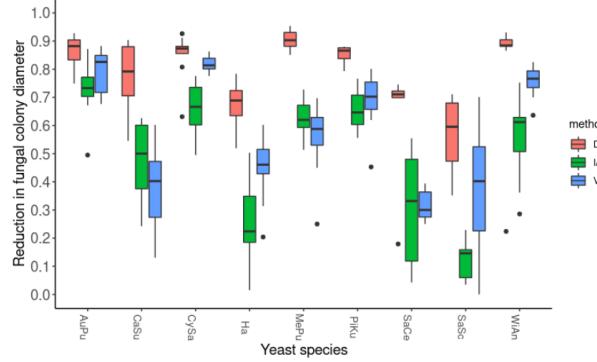
Identify key taxa for diseased vs healthy

Combine to design «synthetic» healthy microbiome > Good guys
Aureobasidium, Metschnikowia, Hanseniospora

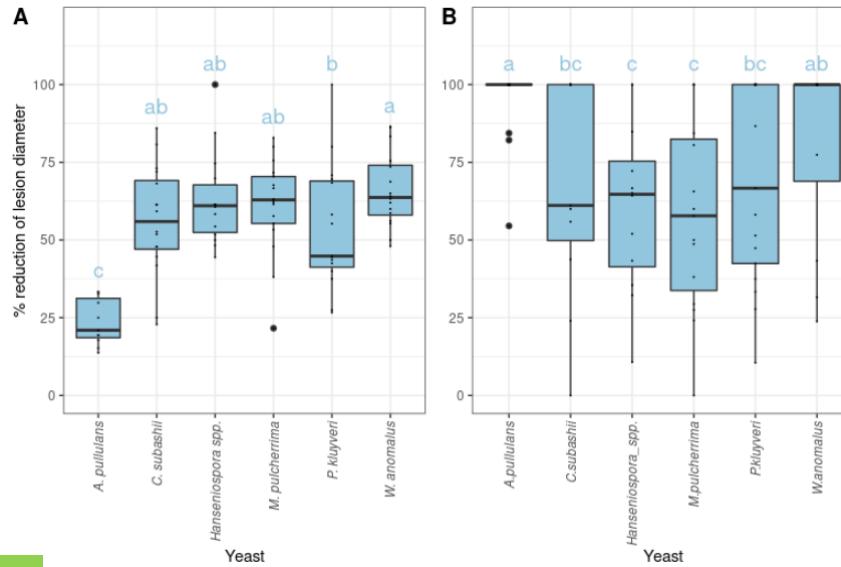
Dynamics of the Apple Fruit Microbiome after Harvest and Implications for Fruit Quality

Y Bösch, E Britt, ... A Bühlmann ... et al. 2021, - Microorganisms

Identify the good guys Biocontrol using taxa from microbiome data – *In vitro* trials



- Biocontrol works *in vitro*/ *in situ* with high efficacy
- Different modes of action
(Direct contact, Diffusible molecules, Volatiles,

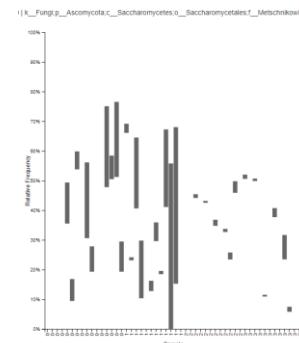
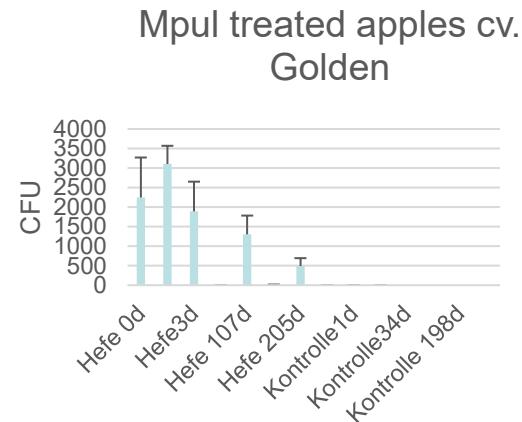
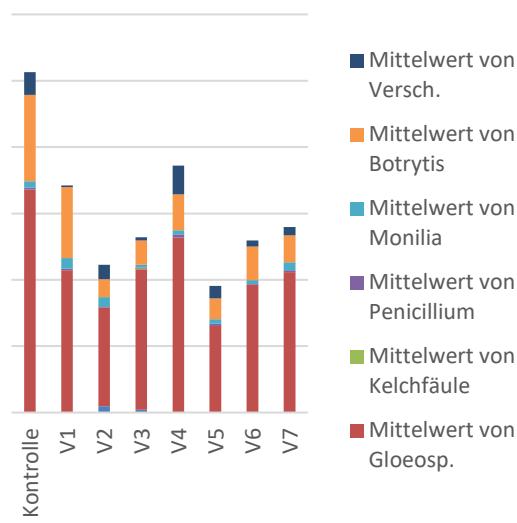


Biocontrol works *in situ*
3h and 24h before infection

Stability of Dry and Liquid *Metschnikowia pulcherrima* Formulations for
Biocontrol Applications against Apple Postharvest Diseases A. Bühlmann ...F.
Freimoser et al. 2022, - Horticulturae



Biocontrol treatment, reisolation, metagenomics



- Limited effects *in vivo*
- Optimisation to formulation that Mpul stays on fruit
- confirmed by culture and metagenomics

Characterize bad guys, identify nutritional needs

collaboration Uni Bozen/ Uni Bologna

4 species of *Neofabraea*

Sequencing on 2 PromethION chips

Illumina shotgun + RNA seq

Flye assembly – Pilon polishing



Sample	# contigs	Total size (Mbp)	coverage (x)	N50 contig length	read length cutoff
Na_ELi5	13	38.33	180	3903075	36148
Nk_FU64	13	38.29	300	3135548	50647
Nm_CBS 122030	16	50.14	465	4200967	70237
Np_CBS102869	20	44.15	470	3239928	67843

P. Vagabunda published- comparative genomics to do

Genome resource of *Phlyctema vagabunda* strain 19EL15, a pathogen of post-harvest bull's eye rot of apple, G. Amaral,... A. Bühlmann et al. 2025 Microbiol Res Ann

Projekt AZZ

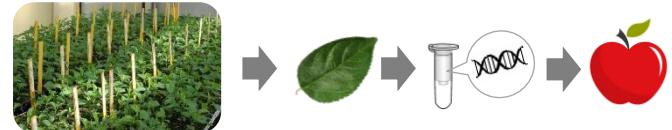
«Apfelzukunft dank Züchtung»

GWAS

Teilprojekt 1

Implementierung der genomischen Selektion für Fruchtqualitätseigenschaften in CH-Züchtungsprogramme

Charakterisierung des Zuchtmaterials und Implementierung molekularen Selektion im Zuchtpogramm von Lubera & Poma Culta



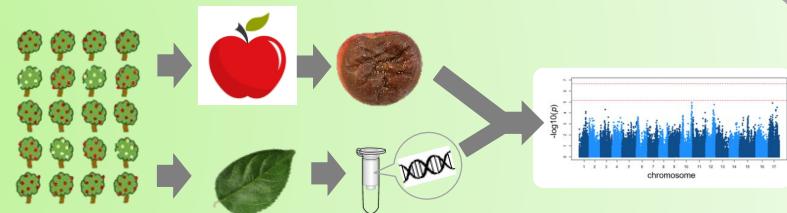
Teilprojekt 2

Kombination von «Fast Track» und genomischer Selektion für Fruchtqualitätseigenschaften



Teilprojekt 3

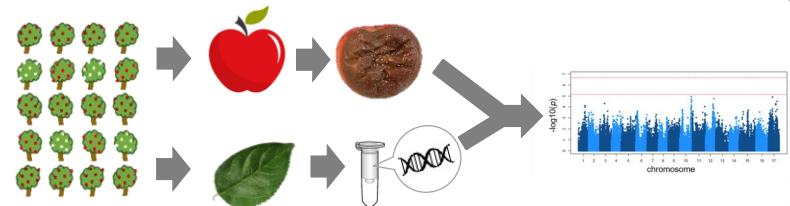
Neofabraea-Resistenz (Lentizellenfäulnis) Screening in Kombination mit genomweiter Assoziationsstudie (GWAS) zur Entwicklung von molekularer Marker



Andrea Knauf, Marius Hodel, Michaela Jung, Andreas Bühlmann

Teilprojekt 3

Neofabraea-Resistenz (Lentizellenfäulnis) Screening
in Kombination mit genomweiter Assoziationsstudie
(GWAS) zur Entwicklung von molekularer Marker



1) Inoculation protocol

T13: Protokoll zur Bestimmung der *Neofabraea*-Resistenz von Äpfeln ist entwickelt.

2) Phenotyping

T14/15: Phänotypisierung des Zuchtmaterials auf *Neofabraea*-Resistenz:
RefPop/ Zuchtmaterial

3) GWAS

T16 GWAS ist durchgeführt, mit Resistenz assoziierte Marker sind entwickelt.

Problem Infektiösität

- Neuer Stamm N.alba
- Kontrollen des Sporenstocks
- Wachstumskontrollen
- Regelmässige Erneuerung
- Aufbewahrung der Sporen bei 0-4°C

Soweit möglich gelöst



Problem Kontamination

GWAS

- Wisch-Dekontamination EtOH 70 %
- Parafilm
- Anpassung Luftfeuchtigkeit
- Desinfektion der Kisten



Soweit möglich gelöst

2 Phänotypisierung

- **Pro Jahr:**

- **REFPOP:** n = 233 Genotypen, davon 32 doppelt

- 1.325 Äpfel

- 6.625 Inokulationen

- **Stufe A (Agroscope):** n = 40 Genotypen

- 200 Äpfel

- 1000 Inokulationen

- ~ 10% Kontaminationsrate / „150 Äpfel“



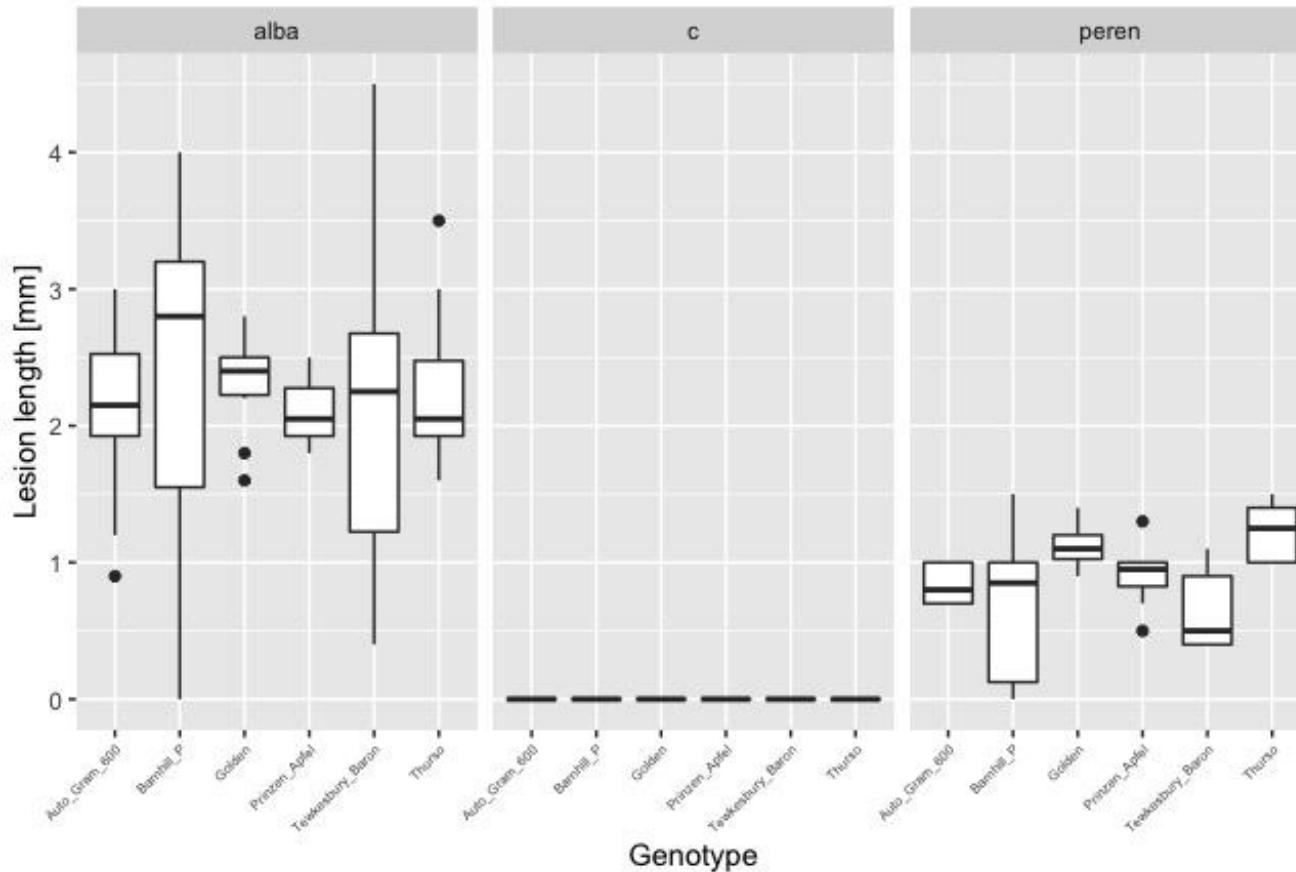
Lagerraum, 20°C, 70%ige
Luftfeuchtigkeit
Lagerung: 21 d

Ergebnisse

GWAS



Infektionsrate 98 %
Kontaminationen 10 %



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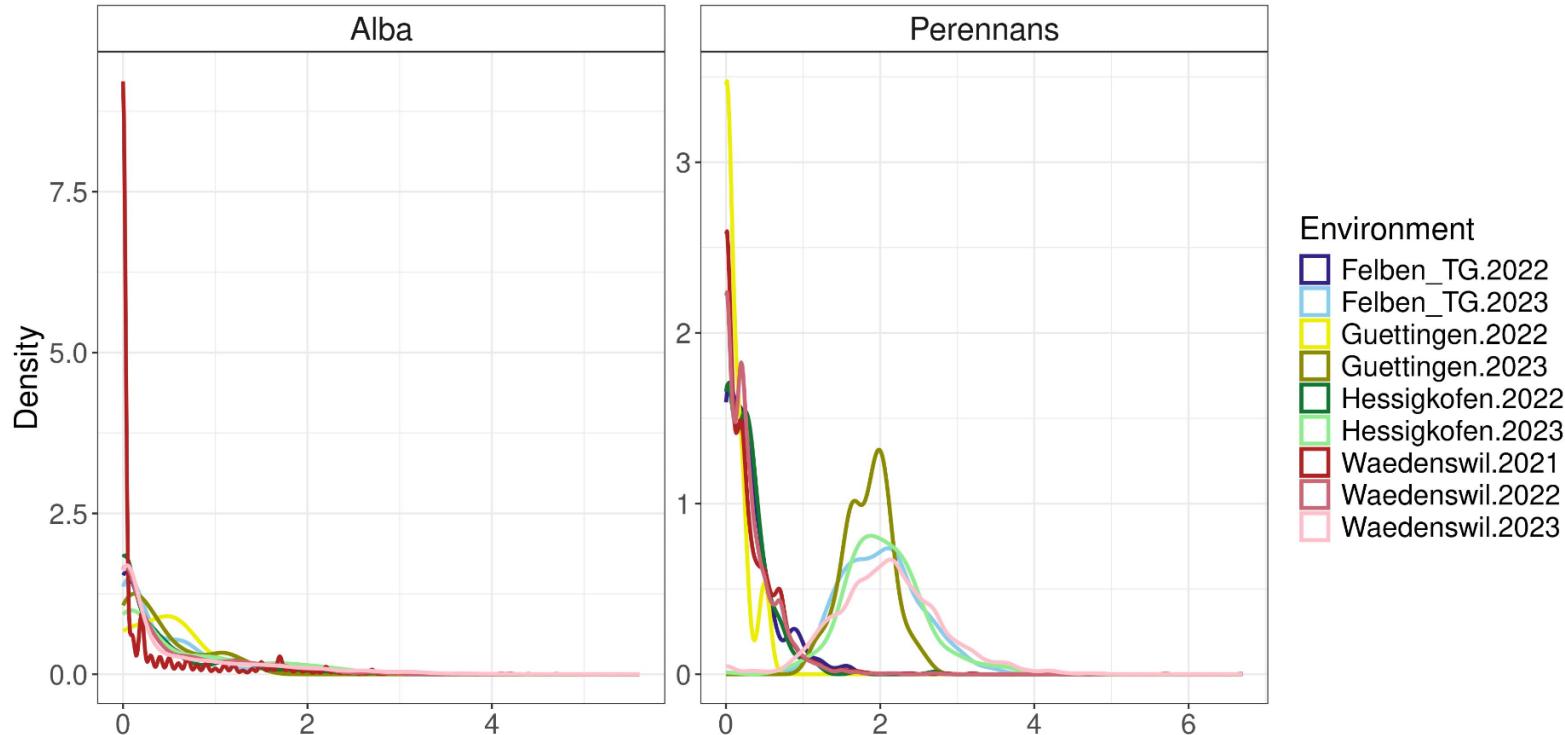


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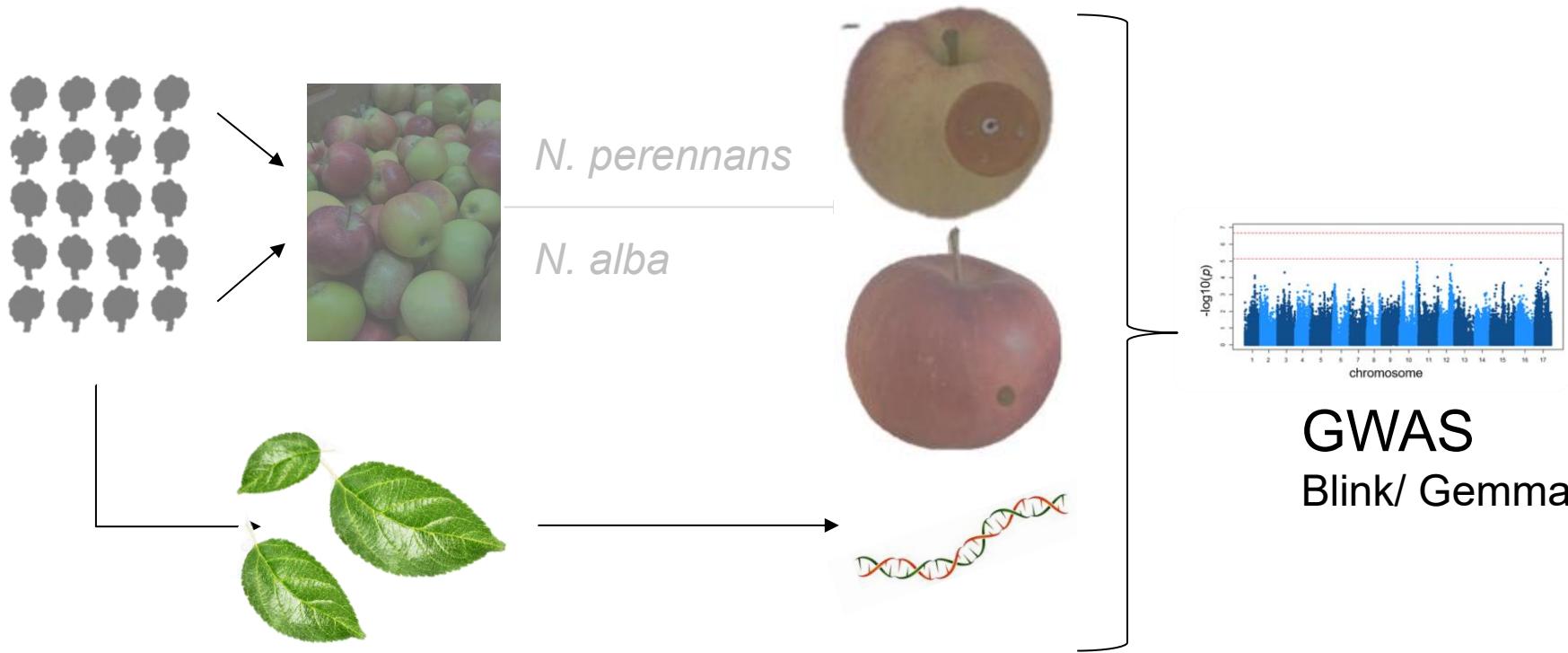
Ergebnisse Phänotypisierung

GWAS



3 GWAS

GWAS



Genotyping
by sequencing

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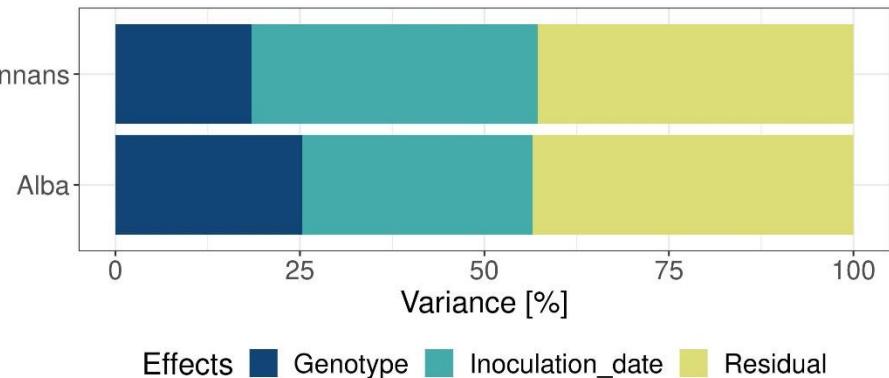


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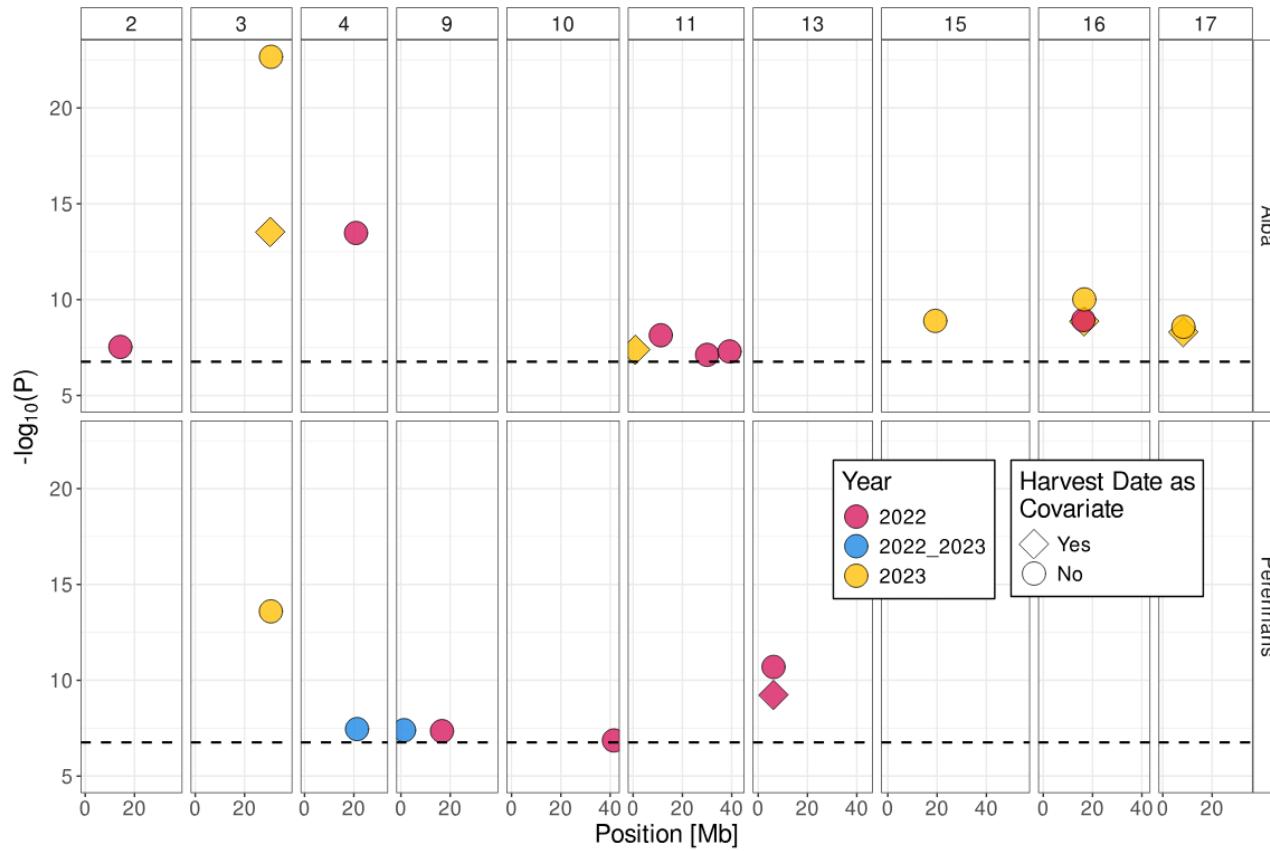
BLUPs – MLM I

- **Fixed effect:** Year_Location
- **Random effect:** Genotype & Inoculation date (trial effect)
- Inokulationsdatum hat grossen Effekt – kennen wir



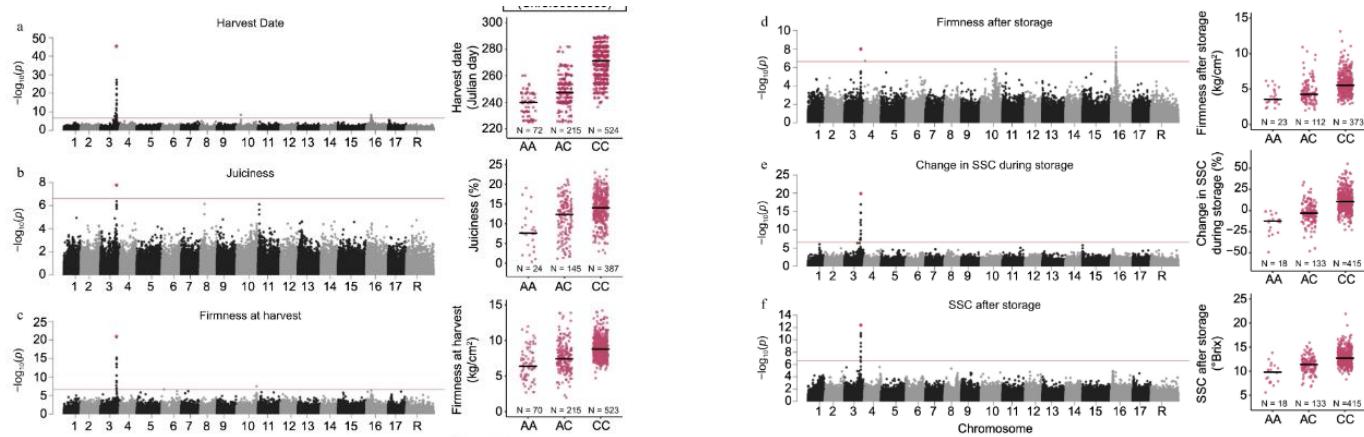
GWAS – full dataset

GWAS



- Wichtiger Locus auf Chr3, kleinere auf 4 und 16

Was ist auf Chr3



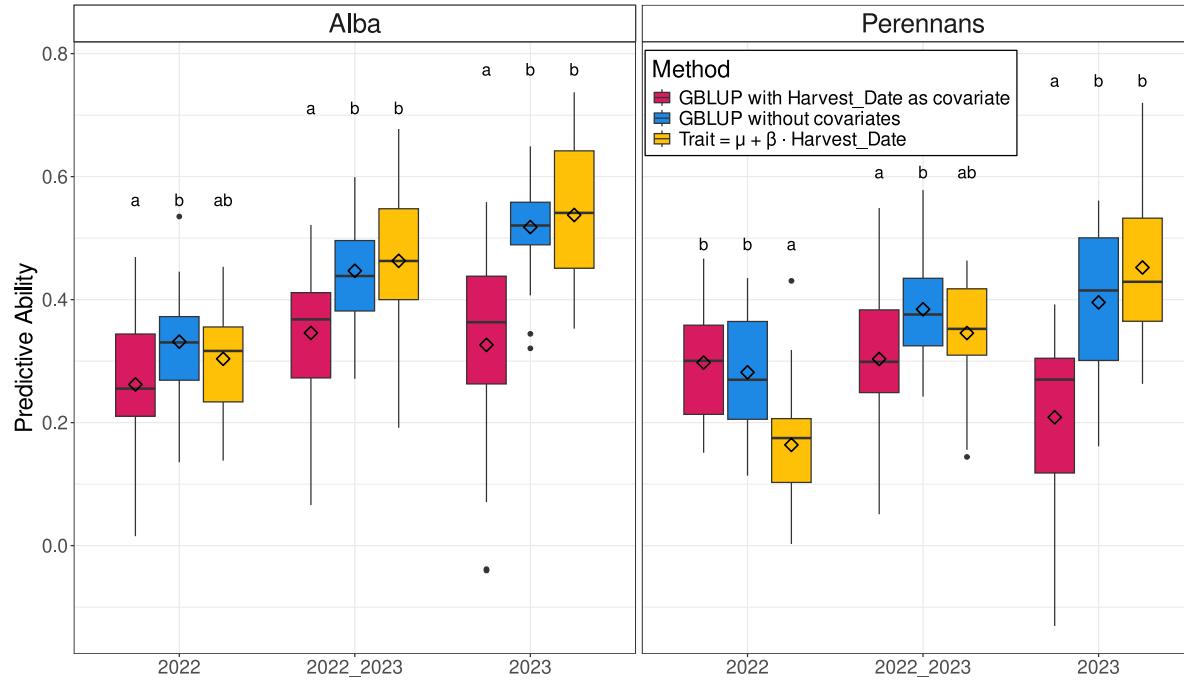
Chromosome	Class	Start	Stop	Annotation
Chr03	gene	30653663	30660855	Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein
Chr03	gene	30669574	30673758	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein
Chr03	gene	30676958	30677290	Protein of unknown function
Chr03	gene	30696191	30698216	NAC domain containing protein 2
Chr03	gene	30738599	30740479	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein

Region bekannt, Marker existiert, alle modernen Eltern haben «gutes» allel

Watts et al. 2023 Fruit research

[Large-scale apple GWAS reveals NAC18.1 as a master regulator of ripening traits \(maxapress.com\)](#)

Falls zu polygen für Marker, ist genomic selection eine Lösung



Modell mit nur Erntedatum ist gleich gut wie genomic selection

Summary

▪ Spores/ Spoilage

- Molekulare Markers for Lenticel rot difficult
- Limited problem since harvest date reasonably good predictor
- Robust early varieties unlikely
- Phenotyping our breeding program doable

Next steps

Spores/ Spoilage

- Sampling too labor intensive- automatic spore sampling and ID



Biocontrol

- Continue to optimize formulation
- Optimize application – cold fumigation

Genome sequencing

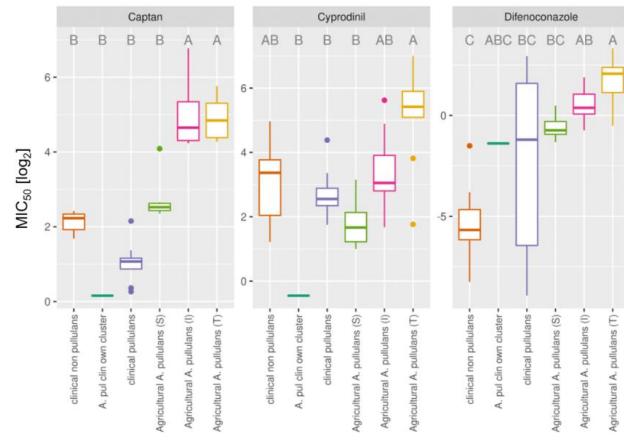
- Comparative genomics between species
- Diversity within *P. vagabunda*

GWAS

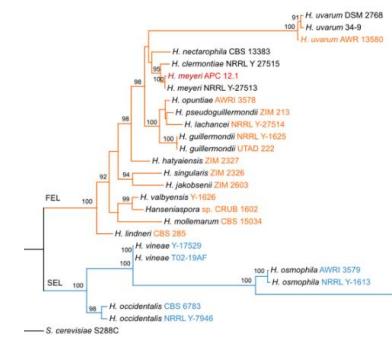
- 20 Genotypen WGS – check for NAC18.1 Locus – ETH/Gio
- NAC18.1 resequenzieren
- Chr4 und Chr16 loci charakterisieren
- Project RoBIS auf Birne– Masterarbeit für *Neofabraea kienholzii*

Characterize good guys, identify lifestyles, modes of action

Collaboration F. Freimoser, agroscope



Aureobasidium comparative genomics, fungicide resistance



Hanseniospora metabolic capabilities

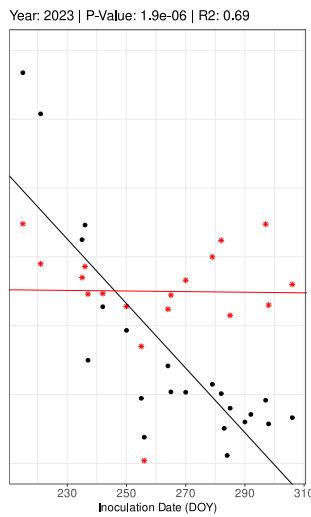
Clinical *Aureobasidium* Isolates Are More Fungicide Sensitive than Many Agricultural Isolates E. Magoye.... A. Bühlmann ... et al. 2023 Microbiol. Spectrum

Pantothenate Auxotrophy in a Naturally Occurring Biocontrol Yeast M. Rueda- Meija A. Bühlmann et al. 2023 Environm. Microbiol

Inokulationsdatum – versuch zu normalisieren

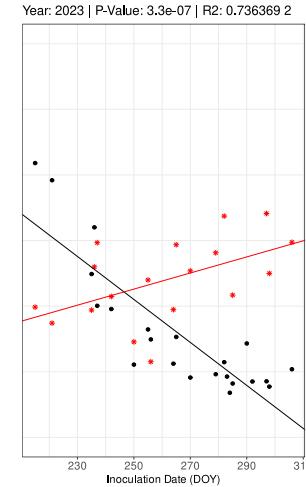
Mittlere
Läsionslänge pro
Inokulationsdatum

Golden Control
Genotypen



Mittlere Läsionslänge
korrigiert mit Golden
Kontrolle

Golden Control
Genotypen



Bringt nix weil Korrektur selber zu variabel ist
Lösung: als Covariate in die GWAS nehmen

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