



Tracking fungal plant pathogens using biological soil monitoring data

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Agroscope

Molecular Ecology

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Fungal pathogen monitoring

- Typically, disease outbreaks are reported after symptoms occur

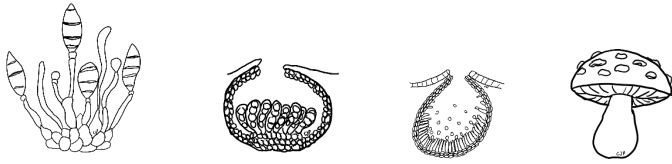


Pavlov et al. 2020

How can we obtain more information about soil-borne diseases before they occur?

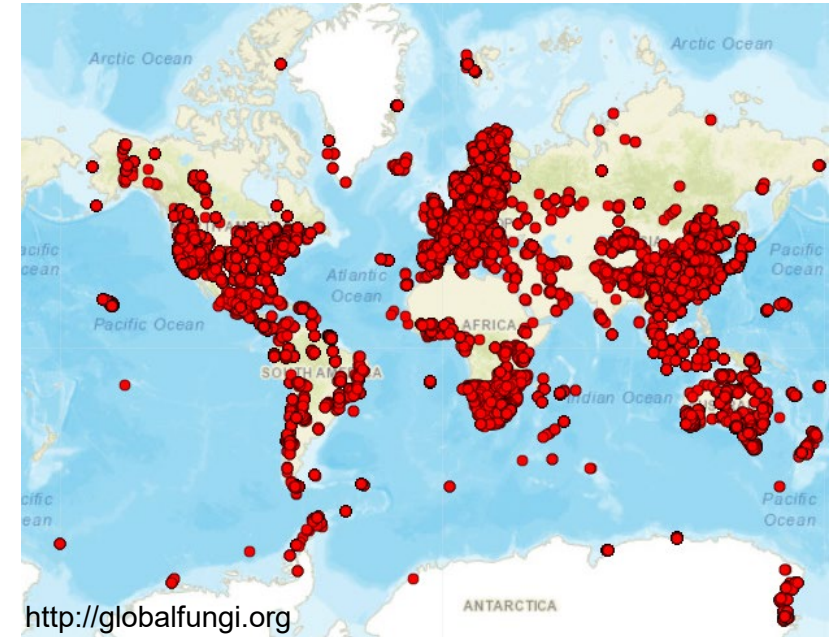
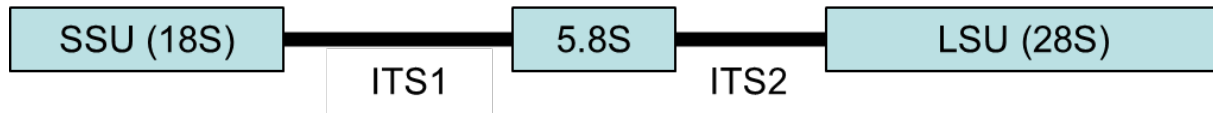


Pathogen tracking with DNA sequencing



- An increasing number of studies generate high throughput sequencing data through targeting fungal-specific DNA regions
 - Obtain large, relatively inexpensive datasets about microbial communities

Internal transcribed spacer regions (ITS)
to target fungal DNA

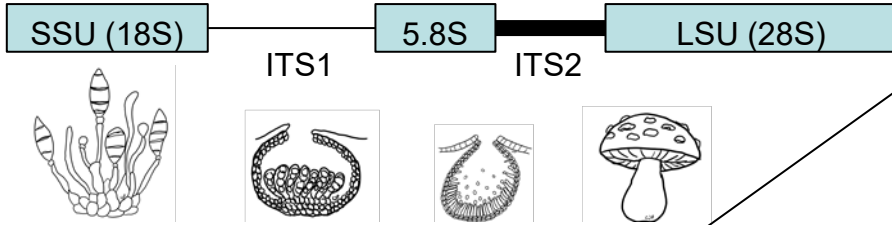


Widely used approach to study
fungal diversity

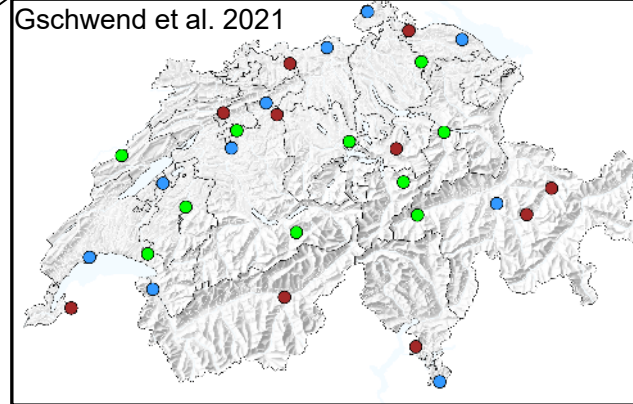


Pathogen tracking with DNA sequencing

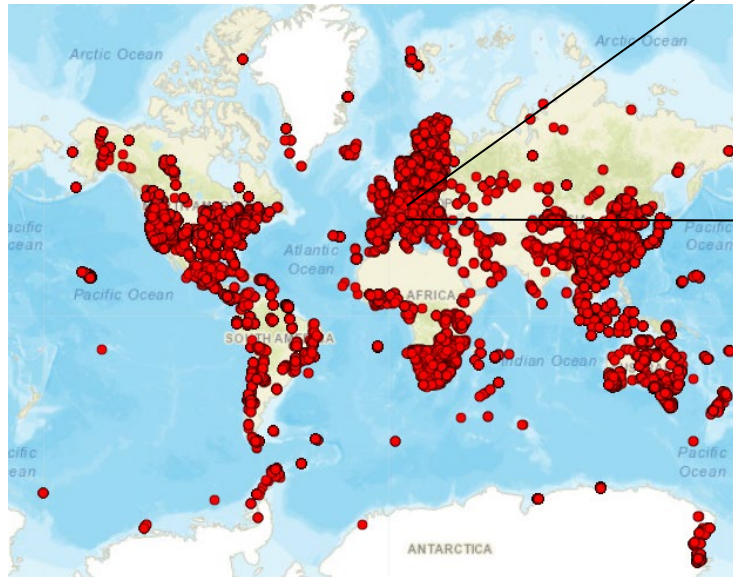
ITS fungal target region



Swiss Soil Monitoring Network (NABO):



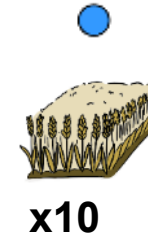
Long-term soil monitoring, including chemical, physical and biological properties



NABO dataset from 2012-2016



Permanent grassland



Arable land



Forests

Land use type of sampling sites



Main research questions:

How can we utilize the tremendous amounts of data to better understand soil pathogen communities in Switzerland?



















- Are temporal and spatial trends evident?
- Can we assess abiotic and biotic factors that influence pathogen communities?
- Can we obtain information about disease outbreaks from soil pathogen communities?





Soil-borne pathogens

- Conducted literature search for soil-borne pathogenic genera affecting arable land, grassland and forests
- Investigated sequence variants from focal taxa and explored their presence according to:
 - Temporal variation
 - Geographic differences
 - Abiotic and biotic factors

Pathogenic taxa	Land use type	Disease
▪ <i>Armillaria spp</i>		Root rot
▪ <i>Cylindrocarpon spp</i>		Black foot/damping-off
▪ <i>Fusarium oxysporum</i>	 	Wilt
▪ <i>Gaeumannomyces spp</i>	 	Take-all
▪ <i>Heterobasidion spp.</i>		Root rot
▪ <i>Paraphoma spp.</i>	 	Crown and root rot
▪ <i>Rhizoctonia spp.</i>	 	Root rot, damping-off
▪ <i>Thielaviopsis spp.</i>		Black root rot
▪ <i>Sclerotinia spp.</i>	  	Blights and rots
▪ <i>Verticillium spp.</i>	  	Wilt



Which factors are associated with the focal pathogenic taxa?

Each pathogenic taxa was converted into a categorical variable (presence/absence) to evaluate its relationship with the following categorical and quantitative variables:

- Meteorological conditions
- Microbial measurements (Biomass, basal respiration)
- Soil properties (Sand, Silt, Loam, pH)
- Site-specific properties (Land use type, altitude, longitude, latitude, site-specificity)





Conclusions

- Datasets of microbial communities yield information on pathogen presence and diversity that are otherwise difficult to observe
- Ultimately could help with disease detection and prevention
- Abiotic and biotic factors drive presence of different genera (ex. land use type, site, precipitation, temperature)



Next steps and open questions

- We can form new hypotheses based on observations, for example:
 - Does disease occurrence and severity correspond to sequence variants?
 - Are some of the sequences from non-pathogenic variants?
 - Can we predict disease outbreaks from soil monitoring samples?
- Oomycete pathogen presence using monitoring samples



Agroscope, H. Forrer



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Thank you for your attention:



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