



13th Young Scientists Meeting Conference 2021

11th – 13th October
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- Abstracts -



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Greetings from the President

Dear Young Scientists,

Welcome to the 13th Young Scientists Meeting!

Two years ago during the 12th YSM, no one could have imagined the challenges we had to face in 2020/2021. This time required inconceivable efforts in our work and private life and meant new territory for all of us. The fact that we have successfully come through this extremely difficult time is also thanks to you.

Nevertheless, I hope that you spent this time as good as possible, and you were able to carry out your projects and research as far as possible. And I hope that you will now have an exciting YSM. Despite the Covid-19 pandemic and the online YSM, young scientists at JKI have a keen interest in exchanging ideas about plant science. This is reflected in the number of 59 registrations for the YSM.

It is very sad that this year's Young Scientists Meeting unfortunately cannot take place in Quedlinburg but it is also a challenge to conduct it for the first time as a video conference.

Plant scientists at JKI work on a wide range of topics. This year's keynote speakers will address three of these: fruit breeding (Prof. Dr. Henryk Flachowsky, head of the JKI Institute for Breeding Research on Fruit Crops), plant genetic resources (Prof. Dr. Andreas Börner, head of Resources Genetics and Reproduction at the IPK Gatersleben) and genome editing (Dr. Jochen Kumlehn, head of Plant Reproductive Biology at the IPK Gatersleben).

We also continue the tradition of offering a soft skill seminar at the end of the Young Scientist Meeting. This time it will focus on resilience and self-motivation in research work, in particular on what resilience is, how resilience strategies can be implemented in everyday scientific life and how self-motivation can be increased during PhD.

I wish all of you a successful and pleasant meeting both scientifically and socially as well as interesting and inspirational discussions.

Quedlinburg, October 2021



Prof. Dr. Frank Ordon

President of the JKI



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Poster

Characterization of entomopathogenic fungi as biocontrol agent for codling moth: insights into their variation in growing parameters

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Use of entomopathogenic fungi (EPF) as control agents for pest insect is a promising alternative to chemical pest control. As a resource of biodiversity, EPF function as natural antagonists of pest species. They can be found in different climatic zones and agroecosystems. The bilateral German-Brazilian project Bio-Entosource, therefore, aims to assess the biodiversity of EPF in two different climatic zones (Germany and Brazil) in apple, soybean and in eucalyptus. The main goal is to develop new microbial control strategies bilaterally for sustainable agriculture and forestry to promote the use of new efficient microbial-based insecticides.

The current study aimed to characterize the entomopathogenic fungi against the larvae of *Cydia pomonella*, a serious pest of perennial fruit industry in Germany. About 38 EPF have been isolated from organic apple orchard soil samples by using insect Bait-method. For molecular and morphological characterization, isolated EPF were identified by microscopic examination and genetic sequencing of the ITS region.

Initial screening based on the virulence against *C. pomonella* was performed by using standardized pathogenicity assay. 13 strains showed >80% mortality. Later, these 13 strains were tested for chitinase activity through agar-chitin plate assay and four potential strains showed higher (>1) chitinase activity. After these two primary experiments, four strains, JKI-BI-1496 (*Cordyceps* spp.), JKI-BI-2620 (*Beauveria* spp.), JKI-BI-2642 (*Beauveria* spp.) and JKI-BI-2647 (*Metarhizium* spp.) have been selected for further growing parameter analysis under laboratory conditions.

As the importance of environmental factors in the development of microbial-based insecticides is greatly increasing. Therefore, in next step, thermo-tolerance at 7 different temperature (5° C, 10° C, 15° C, 20° C, 25° C, 30° C, 35° C) and sunlight tolerance (four hours exposure) were evaluated simultaneously through germination rate analysis for these four strains. Additionally, various factors, such as spore count, optical density, wet and dry biomass measurement in four different media (malt peptone, malt peptone with 1% chitin, potato dextrose and potato dextrose with 1% chitin) were evaluated to observe the influence of media composition with four selected strains.

The results suggest that these four strains differ in virulence and growth factors at different environmental conditions. Therefore, the characterization of EPF will allow us to obtain potential strains, which can be needed for sustainable production of microbial-based insecticides.

Virus monitoring in grapevine genetic resources

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Virus infections in viticulture have a negative impact on the physiology of the vines. They cause losses in grape quality and yield and consequently economic losses.

For the maintenance of genetic resources in *ex situ* collections virus infections are an increasing threat, too. As there are no effective curative methods to eliminate viruses in the vineyard, their spread currently can only be limited by monitoring the disease based on laboratory tests and by replacing infected vines by healthy plants.

Virus detection is mostly based on ELISA (Enzyme-linked Immunosorbent Assay) or PCR (polymerase chain reaction) techniques, which are cost and time intensive. Non-invasive methods using sensors shall enable faster and a more cost-effective monitoring in the future.

Sensors such as hyperspectral sensors offer the possibilities to describe the plant physiology and monitor virus infections (Bendel et al. 2020). However, to set up the system reference methods such as PCR or ELISA are still necessary to establish the baselines for a sensor-based monitoring. Three RNA-viruses (Grapevine leaf roll associated virus- 1 and -3 (GLRaV-1 and GLRaV -3) and Grapevine Pinot Gris Virus (GPGV)) are of major importance in our investigation, which are detected by a reverse transcriptase reaction followed by multiplex-PCR.

At JKI Geilweilerhof genetic resources are organized in different thematic collections: e.g. table grapes, international *Vitis vinifera* cultivars, so called historical varieties and interspecific genotypes. Based on a previous study (Bendel et al. 2020), in a first step a targeted virus screening could be performed, to identify virus infected plants for future sensor analyses.

In the present investigation we considered (1) four varieties (Aligote, Dolcetto, Riesling and Regent) of the international cultivars and (2) 17 varieties from the *Vitis vinifera* collection. To establish a reference method, two PCR studies with wood samples from 150 grapevine plants and approx. 1000 PCR reactions were carried out.

Study 1 showed a virus infection rate of 23% of the plants and study 2 revealed an infection rate of close to 100%. Simple and multiple virus infections were observed. The 150 infected and non-infected plants are a very good training set for sensor validation analyses. For that purpose within the next weeks spectral sensor data will be recorded and tested for correlation with data obtained by the reference method.

Genome-wide association study of resistance to late blight based on JKI pre-breeding potato clones (*Solanum tuberosum*)

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Despite decades of research, late blight, caused by the oomycete *Phytophthora infestans*, still causes high yield losses in potato cultivation. Particularly organic farming suffers badly because *P. infestans* can be controlled by copper only. For this reason, JKI is running a long-termed pre-breeding programme with a focus on polygenic resistance, which we believe is the only sustainable approach to fight late blight in potato.

To locate the resistance of this valuable gene pool, 161 pre-breeding clones and 39 varieties were tested for their foliage blight reaction using a detached leaf assay and for tuber resistance using a tuber slice test. In parallel, DNA samples were genotyped using Genotyping by Sequencing (GBS).

The reference genome has been the *S. tuberosum* group 'Phureja' clone, which was sequenced in 2011. After filtering for minor allele frequency (5 %) and missing values (30 %), 28,055 SNPs were used for the genome-wide association study (GWAS).

First results show that QTL of this gene pool for foliage blight resistance are located on chromosomes 9 and 11 ($\log_{10}(p) > 5$). QTL for tuber blight resistance were identified on chromosome 11. In the following two project years, results will be confirmed by additional data.

Priming for enhanced defense as strategy to optimize crop resistance

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Priming is a physiological defense state of a plant, which can be divided into three different phases.

It starts with a naïve plant, which has not been in contact with a priming agent. The following “*priming* phase” is a reaction of the plant to the priming agent, usually very subtle however, changes in plant metabolites or transcriptome are possible. These changes are specific for different *priming* agents. Generally, it can be distinguished between “*priming* fingerprints” of plant growth promoting fungi, bacteria or chemical priming agents. Primed plants usually react faster and stronger to an upcoming challenge. In this “post-challenge phase” metabolomic and transcriptome changes lead to a higher resistance of the plants against the pathogen or/and biotic and abiotic stress.

Quorum-sensing (QS) molecules are produced to monitor the density of bacterial population(s). In plants, these molecules can trigger a primed state. Different QS molecules from different bacterial species are well known and used for plant protection. One of the best-studied group of QS molecules are the *N*-acyl homoserine lactones (AHL). Oxo-C14-HSL is one of the molecules of this group and is produced for example by the beneficial bacteria *Ensifer meliloti*.

Our research is focusing on the three-way interaction between *Hordeum vulgare*, *Blumeria graminis* and a priming agent. In our case, we investigate the different priming-triggering soil borne bacteria for example *E. meliloti* or *Bacillus* spp..

In the current second phase of the project, we apply previous findings from greenhouse experiments to the field. Therefore, we did screen the priming capability of different *Bacillus* spp. and *E. meliloti* in seven different genetically diverse spring barley lines. In upcoming experiments we intend to expand our research and carry out two field trials at different sides in Germany.

Furthermore, we aim at a deeper understanding of AHL-*Priming* in barley and answer some of the open questions like e.g.: How long does the priming effect last?

Reduced tillage, cover crops and organic amendments affect soil microbiota and improve soil health in Uruguayan vegetable farming systems

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Conventional tillage and mineral fertilization (CTMF) jeopardize soil health in conventional vegetable production systems. Using a field experiment established in Uruguay in 2012, we aimed to compare the soil restoration potential of organic fertilization (compost and poultry manure) combined with conventional tillage and cover crop incorporated into the soil (CTOF) or with reduced tillage and the use of cover crop as mulch (RTOF). In 2017, table beet was cultivated under CTMF, CTOF and RTOF, and yields, soil aggregate composition and nutrients, as well as soil and table beet rhizosphere microbiota (here: bacteria and archaea) were evaluated. Microbiota was studied by high-throughput sequencing of 16S rRNA gene fragments amplified from total community DNA. RTOF exhibited higher soil aggregation, soil organic C, nutrient availability and microbial alpha-diversity than CTMF, and became more similar to an adjacent natural undisturbed site. The soil microbiota was strongly shaped by the fertilization source which was conveyed to the rhizosphere and resulted in differentially abundant taxa. However, 229 amplicon sequencing variants were found to form the core table beet rhizosphere microbiota shared among managements. In conclusion, our study shows that after only 5 years of implementation, RTOF improves soil health under intensive vegetable farming systems

Aphid and virus resistance in potato

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Due to climate change and the restriction of pesticides, aphid populations are growing (Halle et al., 2010). As vectors for viruses, they have a huge impact on plant health. ADLATUS (Adding Layers of Protection to gain a resistant status against *M. chitwoodi*, PLRV, PVY & TRV) is a project consisted of five partners that wants to face the problematic of the tritrophic system consistent of the plant, viruses and their vectors (aphids and nematodes).

In the JKI-Quedlinburg genetic sources for aphid and virus resistances shall be detected. The focus is on *Myzus persicae* and its transmitted viruses Potato Virus Y (PVY, *Potyvirus*, *Potyviridae*) and Potato Leaf Roll Virus (PLRV, *Polerovirus*, *Luteoviridae*). In potatoes, *M. persicae* is described to transmit these viruses in the most efficient way (Halbert et al., 2003; Naga et al., 2020).

The plant material covers a dividing population created by Janine König and several wild accessions, proposed from the Gross Luesewitz Potato Collection of the IPK Genebank.

The phenotypic screening of the plant material with regard on aphid resistance will be done in a two-tier system. A video tracking system is the medium for the first tier of the screening. Afterwards the most interesting genotypes will be tested via a in the entomology common and more detailed technique (Electrical Penetration Graph, EPG).

The infection with the persistent PLRV-virus needs to be done via aphid-transmission, therefore the most efficient *M. persicae* biotype has to be selected from a total amount of 20. The infection with the PVY-virus occurs in a mechanical manner. The infection of the dividing population concentrates on the PVY-Wilga. Whereas the infection of the wild accessions will be done via grafting with five different PVY-strains in regard to find a total resistance.

Genotypic data of the dividing population will be generated via Illumina and its GGP Potato-24 12K Array. Resistance genes shall be detected and diagnostical markers shall be designed.

With our poster we would like to present first results of the establishment of the video tracking method with wild potatoes.

Prax-REDUCE - Implementation of urease in-hibitor formulation for ammonia mitigation in the cattle farming

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Too many ammonia emissions from agri-culture are still released into the environ-ment. 86% of ammonia emissions from German agriculture are caused by animal husbandry especially by manure manage-ment. To achieve German obligations un-der Directive (EU) 2016/2284 to reduce ammonia emissions, by 5% for any year from 2020 to 2029, by 29% from 2030, further measures are necessary.

One possibility could be the use of an ure-ase inhibitor (UI) to inhibit the conversion of urea to ammonia in the urine of ani-mals. The effectiveness was already demonstrated in the project REDUCE. Under practically relevant conditions in naturally ventilated dairy barns signifi-cant reductions of ammonia emissions by 40 to 60% were proven by regular apply-ing urease inhibitor (UI). Through the Project Prax-REDUCE, the UI usage shall be transferred and established in broad agricultural practice (dairy/cattle farm-ing).

Therefore, a feasible technique will be developed for automatically daily dos-age, mixing and application of the UI for formulation on the stable floor. Two con-cepts for the application technique will be pursued:

- (1) robotic manure scraper and
- (2) flexible hose drop system.

In addition to good application tech-niques, also a qualified proof of safe us-age must be provided.

This evidence based on exposure scenarios and exposure data obtained under stable conditions. Fluorometry is a methodical approach to measure those exposures. For this purpose, the fluorescent dye pyranine is sprayed as a tracer instead of the UI. Col-lectors such as filter paper, petri dishes and plastic strings can be used and placed in certain areas of the barn or on a cow model to collect exposures. In a first ap-proach, studies were performed to eval-uate the suitability of the different collec-tors to detect a wide range of exposure levels. Depending on the applied amount of pyranine, some of the collectors are more suitable than others to detect the exposures precise enough.

Filter papers proved to be suitable for high exposure levels as there is no drip-ping. However, due to the fact that the filter material has a certain amount of flu-orescence by itself, very small quantities of the applied fluorescent dye pyranine could not be detected properly. Plastic strings appeared to be more useful to de-tect small pyranine exposures.

For further method development, an im-provement of the lab analysis and systematic testing of further collectors is necessary.

Efficiency of *Sbm1* and *Sbm2* resistance against soil-borne furoviruses in wheat under specific climatic conditions

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Soil-borne wheat mosaic virus (SBWMV) and *Soil-borne cereal mosaic virus* (SBCMV) are important cereal viruses worldwide. Infections with these viruses result in approximately 40% yield loss. Two SBWMV strains (SBWMV-NY, SBWMV-N) are known and SBCMV is categorized into three main serotypes. Important cereals, including wheat, are host of these viruses. SBWMV and SBCMV are transmitted by the soil-borne plasmidiophorid *Polymyxa graminis* which infects the roots of cereals.

As soils contaminated by the virus remain infectious over many years, the only efficient control strategy is the growth of resistant cultivars. Until now, only two resistance genes, *Sbm1* and *Sbm2* are thought to confer translocation resistance to wheat, restricting SBWMV/SBCMV to the roots. The stability and the expression pattern of the *Sbm1/Sbm2* resistance genes as well as the effect of additional, yet unknown resistance genes remain unclear.

To better characterize SBCMV/SBWMV resistance with respect to stability and mode of action, 15 genotypes differing in the grade of resistance were sown in Elxleben, Heddesheim (Germany) and Vatan (France) where SBWMV-N (in Germany) and SBCMV, respectively, were previously identified. Four plants of each genotype were sampled, cut into three parts (leaves, stem, roots) and tested for the presence of the viruses with serological tools. The infection rates were very low in Heddesheim, but the analysis in Elxleben and Vatan showed that firstly, most of the upper parts (leaves or shoot) of the plants carrying *Sbm1* remained uninfected, secondly, *Sbm2* did not prevent at all the infection of the upper parts, thirdly, the infection rates of the roots of the cultivars expressing *Sbm1* and/or *Sbm2* were much lower compared to plants without *Sbm* gene, and lastly, the viral titer were lower in the plants carrying *Sbm1* compared to the other plants.

These data were complemented by experiments in soil from Elxleben conducted under controlled conditions, where inoculation took place under specific environmental settings (temperature, water, nutrients). The first serological analysis suggests that temperature is an important parameter for infection.

Altogether, our results suggest that firstly, *Sbm1* is not only a translocation resistance as previously described, secondly *Sbm2* is probably less efficient than *Sbm1* against SBWMV and SBCMV in wheat, and thirdly, the environmental conditions have a high impact on the infection rates of the viruses. Further transcriptomics studies are required to understand expression pattern of *Sbm1* and *Sbm2* and physiological processes impacted during infection by SBWMV and SBCMV.

Variability of drought stress responses among barley genotypes

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Drought is one of the most important factors for crop losses in agriculture. Drought stress is defined as an insufficient availability of water that is increased during higher temperatures (Matiu et al., 2017), which could lead to crop yield losses about 25-40 % (Daryanto et al., 2017). In addition, drought-stressed plants have an increased susceptibility to pathogens because of the reduced defense of the plant (Liu et al., 2016). Recently, plant strengthening agents and biostimulants based on organic and inorganic materials or microorganisms have been reported to enhance the health of plants and their tolerance to abiotic stress (du Jardin et al., 2020). For example, the extract of *Fallopia sachalinensis* (Milsana®) possesses a plant-strengthening and infection-reducing impact on *Blumeria graminis* (Konstantinidou-Doltsinis et al., 2017). Therefore, we aim to investigate the drought stress tolerance (JKI, Quedlinburg), reported here, and the resistance against *Blumeria graminis* infection (JKI, Darmstadt) in barley in response to the treatment of the plants with various biostimulants. First, we selected 50 contrasting genotypes from the Genobar collection (Pasam et al., 2012) by the relation of ear type, origin, known drought stress tolerance, and genetic diversity. These 50 genotypes were grown in the greenhouse under either drought stress or well-watered conditions in juvenile stages. The characterization of drought stress tolerant and susceptible genotypes is performed by a determined definition of drought stress parameters.

First regulatory mechanisms of water-limitation are stomatal closure and decreased photosynthetic activity to reduced transpiration (Ali et al., 2017). Also, physiological characteristics such as “stay-green” parameters (chlorophyll content and –fluorescence) are important for the determination of drought stress tolerance (Gepstein & Glick, 2013). Additionally, parameters like high water use efficiency (WUE) and high content of osmolytes indicate drought adaptation of barley genotypes. Quantitative parameters in late developmental stages are as well affected by early drought stress, usually leading to yield losses (Hafid et al., 1998). Therefore, we also determined yield traits like biomass, tiller number, grains/ear, thousand-grain weight, and grain yield/plant.

On our poster we will summarize the results from this drought stress experiment and discuss the differential responses among the 50 barley genotypes.

Based on these results, we selected ten contrasting genotypes for further examinations in greenhouse trials and under field conditions in rainout-shelter facilities. In these experiments, we will test the impact of plant strengthening agents and biostimulants on these ten selected genotypes in regard to their response on drought stress and infection with *Blumeria graminis*.

Assessment of climate change impact on wheat production in Germany using a multi-model-ensemble

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Process-based crop simulation models provide valuable information on potential crop production under future climate conditions. They further allow the development and evaluation of suitable adaptation strategies in crop management to address future risk factors like increased temperature and altered precipitation patterns. Thereby the use of a multi-model-ensemble approach in crop modelling can increase simulation robustness compared to single model outputs. The objective of this study is to simulate mid-century mean yield development and yield stability of winter wheat (*Triticum aestivum*) under different climate scenarios of RCP 2.6, RCP 4.5 and RCP 8.5 for important wheat production regions in Germany. We use the three wheat crop models CERES, CROPSIM and NWHEAT embedded in the Decision Support System for Agrotechnology Transfer (DSSAT). This enables depiction of the model-specific uncertainties in addition to the climate-related uncertainties allowing a more robust evaluation of potential future wheat yields.

In the first step, we conduct a cultivar specific calibration and validation of the three models building on a vast experimental data set of around 100 site-years, with 75 % of the data being used for model calibration and 25 % for model validation. Model calibration is executed to a similar extend for all models adjusting comparable types and number of coefficients to fitting observed and simulated phenology, growth and yield parameters. We then compare simulated yields in 2031-2061 with simulated yields in 1971-2000. We find significant differences between climate scenarios and between the three crop models. While for some scenarios all models show comparative yield trends, for some scenarios results differ between models. We demonstrate the potential and necessity of using multi-model ensembles both, with regard to climate change scenarios and crop models, especially when intended for policy advice.

Undersowing and intercropping for regulation of pest insects in white cabbage

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Horticultural crops are affected by a large number of different herbivorous insect species. Controlling those pests is becoming more and more difficult due to the increasingly smaller number of registered insecticides and development of resistance. Alternative measures for pest control are therefore gaining in importance.

Undersowing in vegetable crops can bring many advantages such as reduced erosion, heat protection and improved soil structure. In addition, phytosanitary advantages can be triggered: an undersowing strategy that is adapted to a specific cultivation system can reduce immigration and dispersal of pest insects by e.g. creating a physical barrier, hindering recognition of host plants by pests and promoting natural enemies.

Aim of the collaborative project “OptiUnder” is to develop an optimized undersowing system for white cabbage production. For this purpose, various plants are evaluated with regard to their potential effects on herbivorous insects.

In 2020, a randomized plot design was used as a set-up for a field trial investigating effects of a wheat undersowing alone, as well as combined with intercropping of the flowering plant *Lobularia maritima*.

Both systems were tested in white cabbage and compared to an untreated control and an insecticide control.

The results of this experiment are presented with regard to the abundance of pest insects, with focus on aphids and their natural enemies.

Results show that the influence of undersowing and intercropping is not consistent in the two common aphid species *Brevicoryne brassicae* and *Myzus persicae*. While both undersowing variants reduce numbers of *M. persicae*, the abundance of *B. brassicae* is only affected by insecticide application.

Intercropping with *L. maritima* results in a higher number of adult hoverfly visits. However, this effect is not reflected in numbers of hoverfly larvae on cabbage plants, which resembles the predatory developmental stage. This can possibly be traced back to rather small distances between plots of 2 m.

Furthermore, numbers and damage by cabbage flea beetles *Phyllotreta* spp. were strongly increased in plots with *L. maritima* intercropping. Therefore, integrating this plant species is not entirely suitable for production of cabbage and other Brassica crops.

Optimization of a protocol to embed *Hypericum perforatum* L. seeds

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St John's wort (*Hypericum perforatum*) is a widely known as medical plant for its biological properties. It has been cultivated and used for medical for thousands of years. *H. perforatum* is cultivated in a small area in Germany. Fungal infections are a major threat in cultivation of *H. perforatum* and can cause severe yield losses. One of the most important fungal pathogens is *Colletotrichum gloeosporioides*, which causes anthracnose. The fungus can be lethal for the plant by infecting the stem base. It spreads over splashing water between the plants. Investigations revealed that the fungus is a seed borne pathogen and infected seeds are an important inoculum source for first infections and for distributing the fungus. Previously studies showed that the fungus was localized in the seed coat. However, it is unclear that the fungus spreads into the embryo of the seeds. Therefore, localization of the fungus in the seeds is important to develop seed treatments to control the fungus as well as to prevent the early stages of plants infection. In this study, we optimized the protocol to embed *H. perforatum* seeds for preparation of cuttings with the microtome for their localization by light microscopy.

For the analysis, the seeds were embedded in resin (Technovit 7100). We found that, conventional embedding protocols are not suitable for small and hard *H. perforatum* seeds, because the embedding solution did not infiltrate the whole seed and many embryos of the seeds are lost after cutting with the microtome. The base of the adjustments was an embedding protocol for Melastomataceae seeds. We extended the time of fixation, infiltration of the embedding solution as well as added a step between fixation and dehydration. The steps were increased the porosity of the seed coat and rising the infiltration of the embedding solution into the seed. We incubated the embedded samples at 4 °C, resulting in an extension of the resin polymerization time. Our study shows that they are more successful in an increasing number of infected seeds from 10% to 40 %. The new embedding protocol was developed and optimized which can be improve for the studies on localization of pathogens in *H. perforatum* seeds. Currently, we work on our protocol for testing with other small and hard seeds.

Methodology and indices for the spatial evaluation of different planting patterns

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An optimized spatial planting pattern can help to minimize negative intraspecific competition for light, nutrients and water. Furthermore, the competitiveness against weeds can be increased and an improved microclimate may help reduce diseases. In addition to the conventional drill seeding technique, where the seeds are placed rather randomly within the row, there are now single grain seed drills, with more precise spacing within the row as well as prototypes of precision sowing machines, which enable an equidistant planting pattern.

So far, there is a lack of methods and criteria to assess and evaluate the spatial pattern of different sowing techniques in the field. Therefore, we developed a standardized and reproducible approach and respective indices.

The methods were developed and tested building on two field experiments. First, a winter wheat experiment conducted in Berlin-Dahlem testing conventional vs. equidistant sowing since 2018. Second, an experiment conducted in Dahnsdorf in Southwest Brandenburg, testing winter wheat and winter rye in conventional vs. single grain sowing since 2019. Photos of the planting pattern realized by different sowing techniques were taken just after emergence (BBCH 9) using a RGB-camera mounted on a standardized photo-frame (0,25m²). The photos were processed using the GIS-software ArcGIS, tagging each point of plant emergence. Using Voronoi partitioning the theoretical planting space was allocated as a polygon to each plant.

Following indices relevant for spatial evaluation were derived: (i) number of plants, (ii) mean space per plant, (iii) coefficient of variation of space per plant (CVSP), as well as (iv) mean polygon-circle-ratio (MPCR), i.e., mean roundness/compactness of polygons. CVSP describes the evenness of the single plants' spaces in the different planting patterns. MPCR describes the mean of the ratio of the area of the individual plants' polygons to a circle of equal edge length; it ranges theoretically between zero and one. These indices enable a comparison of actual vs. target state and in combination, they allow a comprehensive comparative evaluation of different planting patterns.

As the manual tagging of each plant's emergence is very laborious and hence has its limitations regarding large-scale applications in experimental and practical agronomic applications, we are currently working on an AI-assisted image-recognition approach for tagging plant emergence.

Precise Nitrogen – Increase nitrogen efficiency in crop production

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Nitrogen is considered the macronutrient that is most limiting for plant growth [1]. Due to this property, nitrogen is often distributed on farmers' farmland via synthetic fertilizers to achieve an optimized harvest. Since both over-fertilisation and under-fertilisation with nitrogen has negative consequences on the development and the final harvest and thus on the farmer's yield, fertilisation tailored to the individual crop is becoming increasingly important and desirable. The disadvantages of over- or under-fertilisation includes, for example, an increased susceptibility to diseases [2] or an increased risk of leaching into the environment.

In a global and national context, over-fertilisation with nitrogen fertilisers is a particular problem. Overall, since the 1960s, the global nitrogen use efficiency has fallen from approx. 68% to approx. 47% [3]. Thus today, half of the added nitrogen in the fertilizer is not converted into the plant product but would be lost in the environment.

In order to counteract the trend of non-plant and field-specific fertilization, a plant nitrogen estimation is to be carried out using modern remote sensing methods in order to give the farmer the possibility of site-specific fertilization.

Unlike traditional laboratory methods, remotely sensed plant analyses are non-destructive and can cover a vast area in a short time. A site-specific determination of the nutrient requirements of arable crops can lead to improved yields, lower fertilizer costs and a reduced risk of leaching into nature. Since the nutrient requirements of plants are strongly related to soil conditions, additional soil monitoring is useful.

In the project Precise Nitrogen, based on remote sensing data (mainly UAV and satellite) and a soil sensor network, strip trials are carried out on experimental fields in the Braunschweig area. In addition to fertilizer optimization, one of the main aims of the project is to make precision farming methods easily accessible to farmers and to optimize them through practical tips.

First interim results of the first year of the trial show problems with the soil sensory system and the implementation of the application maps. Initial evaluations of investigated fertilizer variants indicate the highest N efficiency with a combination of soil sensors and remote sensing data. A precise comparison of yields per fertilizers variant will allow further conclusions to be drawn once the harvest data is received.

In the trial year 2022, further in-situ measurements will be carried out to validate and optimize the remote sensing measurements.

A review on model-based development of drought-tolerant cereal ideotypes

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Climate models are predicting a spiraling trend in global mean temperatures and altered precipitation patterns. Consequently, production levels of staple foods are alarmingly dropping due to increased climate variations and recurring weather extremes such as heatwaves and drought spells.

To increase climate resilience of cereal production, it is crucial to understand the most affected processes in crop production and develop respective adaptation strategies. Crop modeling is a tool that allows investigating the genotype * environment * management interactions by simulating the plant-soil-atmosphere system. Crop models can simulate crop growth under future climatic conditions by performing *in silico* experiments. Climate change adaptation options can be investigated, including the design of novel genotypes better adapted to future climate, i.e., crop ideotypes.

An ideotype is a model plant defined on a set of crop and cultivar-specific parameters that control crop development and growth in different environments. These parameters describe morphological, physiological, and phenological traits; for an ideotype, they are combined to optimize crop performance in a particular biophysical environment and crop management situation for a specific end-use. Phenotyping and genotyping results constitute the base providing guidance to identify and optimize parameters of desirable ideotypes.

Phenotypic data is a result of screenings for physiological, morphological, and phenological traits contributing to drought tolerance and recovery. These results are used as an input to design a model build ideotype. Phenotypic experiments provide a base to define growth and yield parameters of ideotypes and plausible/optimal range of values.

Breeders use genomics to define the genetic composition, point out meaningful mutations, describe their functions in the expression of qualitative and quantitative traits, and clarify the links and interactions between target genotypes (G*G) and interactions between genotypes * environment. Genotyping creates a roadmap for future phenotyping and ideotyping.

To create genotypes adapted to future climates, we need to place emphasis on the variations caused by the interactions between genotypes and environments. The accurate representation of the target environments is crucial to have reliable results. That is reached by collaborations of breeders, agricultural engineers, and crop modelers, combining phenotyping, genotyping, and crop modeling tools.

In the present study, we highlight and discuss the basic operations required for designing and developing drought-tolerant cereals. We review recent scientific advancements and related challenges. We further explore the required linkages between these three operations and how they can be utilized to shape the crops of the future.

New approaches to the identification and selection for *Wheat dwarf virus* (WDV) tolerance in wheat (*Triticum aestivum*)

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Wheat dwarf virus (WDV) is an important pathogen in wheat and other cereals. In many European countries, e.g. Hungary, Spain and Germany, WDV causes high yield losses. WDV is transmitted by the leafhopper *Psammotettix alienus*. Symptoms of a WDV infection on wheat include chlorosis, dwarfing and streaking along with high yield loss. Due to climate change, the incidence of insect-transmitted viruses will become more important worldwide due to the extended survival time of the vector. The absence of insecticides efficient against *P. alienus* renders growing of WDV resistant/tolerant varieties the only effective way to control WDV. However, little is known about WDV resistance/tolerance sources.

The assessment of resistant lines is based on inoculation with virus bearing leafhoppers and subsequent phenotyping in gauze houses. Abiotic conditions, especially temperature, have a crucial influence on the success of the inoculation. In previous approaches, the inoculation of plants took place under semi-field conditions in gaze houses. Considerable fluctuations in the infection rates were observed and spontaneous infections could occur after warm winters. Furthermore, the stock of cicadas living in captivity had to be rebuilt after each infection, which delayed the screening process.

As a part of an actual project on marker-based selection for WDV tolerance in wheat, we have addressed this problem and developed an improved approach. In this methodology, plants are inoculated in small greenhouses and are subsequently planted out in the gaze houses. This gives the leafhoppers optimal environmental conditions for WDV transmission and WDV infection can develop under natural environmental conditions. In addition, the virus bearing leafhoppers can be removed from the plants after infection, so that a sustainable use of the animals is possible. The method thus allows more reliable phenotyping through a higher infection success and the testing of a larger number of genotypes in a shorter time.

Effect of timing and duration of combined heat and drought stress on oilseed rape (*Brassica napus* L.)

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Oilseed rape (*Brassica napus* L.) is a major global oil crop grown mainly under temperate climatic conditions. With increasing global edible oil demand and improving genetic yield, its production further expands to warmer climatic zones. Moreover, global climate change leads to an increasing incidence of heat and drought stress, which are critical limiting factors to plant growth and yield formation in oilseed rape, impeding its agronomic and economic performance.

A pot experiment was conducted in the experimental facilities at Julius Kühn-Institut in Kleinmachnow. The study aims at investigating the single and combined effects of heat and drought stress on crop morphology, physiology, and yield formation under consideration of timing and intensity of stress. Hence, four factors are tested in combination: heat stress at five levels as well as drought stress, treatment timing, and treatment duration with two levels each. We find that all experiment factors exerted significant effects on grain yield, with increasing heat and drought stress as well as longer duration leading to lower yields. We further find that stress during flowering showed lower yield effects than during seed filling stage. Finally we find that early stress, which mainly acts on the main branch, is compensated by increased formation of siliques, seeds and grain yield on the lower side branches. Analysis of seed size distribution and fatty acid composition provide deeper insights in the effects and mechanisms of combined heat and drought stress.

Anise – a new crop for Germany?!

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In Germany, more than 50% of the arable land is used for growing cereals like wheat, maize and barley. The resulting narrow crop rotation leads to an increasing disease pressure, resistance against plant protection products and an increase of harmful insects. Special measures have to be used to ensure high yields in the future. One important step is the widening of the crop rotation by growing crops of different plant families. This would impede a fast reproduction and spreading of pathogens.

A rarely seen plant family in German farming are Apiaceen, like fennel (*Foeniculum vulgare*), caraway (*Carum carvi*), carrots (*Daucus carota*) and anise (*Pimpinella anisum*). It is, like the others, a traditional medicinal plant in Europe. Today, most of the processed anise in Germany is imported from the Mediterranean region and East-Europe. The demand of anise in Germany is equivalent to 2500 ha.

Due to the climate change and the increasing drought periods, anise can be easier grown in Germany. It is adapted to a warm and dry climate. The sowing in spring enables the farmer to do a mechanic-weeding step, which is advantageous within an herbicide resistance management. Another aspect is the attractiveness of the flowering plants for all kinds of insects. The promotion of beneficial insects helps to decrease the amount of pest insects. Growing anise can be a reasonable tool of integrated plant protection and has beneficial environmental effects.

Since the German climate is quite different to the traditional growing regions of anise, suitable varieties have to be selected and an optimization of the cropping method is necessary. In 2021, several accessions of anise as well as populations from breeders and farmers are phenotyped at two locations (JKI Quedlinburg and University of Bonn) in the field. Additional to developmental and yield parameters the quantity and quality of the oil, as well as the taste is important. The fruits of anise are used as a spice and for medicinal purposes and have to fulfill defined quality standards.

Further, the optimization of the cropping technique is important to generate stable yields and a high quality product. Fast emergence of the plants is important to get a uniform and well-developing crop. The influence of the seeding time was tested in a field trial. Anise was sown from beginning of March until beginning of June. It could be seen that low temperatures in early spring but also drought in early summer slowed down the development. The influence of temperatures and seeding depth on the developmental speed and root growth will be investigated in further experiments.

After identifying advantageous genotypes, homozygous lines should be generated. These lines should be thoroughly phenotyped and be used later for creating synthetic populations. To be able to produce homozygous lines fast, a method for creating double-haploid genotypes should be established.

The aim of the projects is the optimization of the cropping method and breeding of adapted varieties to increase the cropping area of anise in Germany.

A new non-destructive process for the *Brachycera* identification via DNA Barcoding

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In a subproject (FKZ: 22019814) of the BMEL/FNR project “prospective risk management of biotic pests in forests to maintain sustainable forestry” the impact of helicopter-applied insecticides for flies (*Brachycera*) was examined. Several flies are known pine insect pest antagonists and therefore relevant non-target organisms. The maggots and adults of several families have parasitoid (e.g. Tachinidae) or predatory (e.g. Asilidae) modes of life.

Morphological identification of families and species is supplemented by DNA Barcoding, because of the high number of individuals and the limited taxonomical expertise. To accomplish maximum yield DNA templates, destructive DNA extraction is regularly performed and the cytochrome c oxidase subunit is amplified and sequenced. To preserve the morphology of individuals the performance of non- or semi-destructive DNA extraction is a requirement to enable a later morphological identification. The stability of the wing membrane can be challenging and pre-trials showed that the loss of pigments and dorsal thorax bristles take place with established non-destructive methods related to commercial kits.

We modified an established non-destructive DNA extraction from mycology avoiding usage of proteinase. With this method DNA can be isolated from flies of laboratory insect rearing, commercial insects rearing and parasitoids hatched from subfamily Enonominae (Lepidoptera, Geometridae) and subfamily Diprioninae (Hymenoptera, Diprionidae) cocoons without impairing morphological traits. The non-destructive DNA extraction shall prospectively be considered for field ecological examinations. The potential application spans from biodiversity research to analysis of insect pest antagonistic complexes to studies about insecticide impacts on *Brachycera*.

Characterization of genetic loci conferring grapevine black rot (*Guignardia bidwellii*) resistance

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Since years, the EU aims at a reduction of plant protection in viticulture. The reduction of copper, the only approved spray agent to control downy mildew in organic viticulture, is prescribed in the regulation. Breeding of fungus-resistant grapevine varieties by crossing of traditional susceptible *Vitis vinifera* cultivars with resistant American or Asian wild *Vitis* species is a crucial step towards the increase for a sustainable and environmentally friendly viticulture.

One important pathogen in viticulture is the hemibiotrophic ascomycete *Guignardia bidwellii* (according to the latest nomenclature recommendation named *Phyllosticta ampellicida*), which is the causal agent for black rot. Since the beginning of the 21st century, an increased incidence of the disease was reported from regions in Europe, like Germany, Switzerland, Austria, Luxembourg and Romania. Therefore, there is concern that the new bred mildew-resistant grapevine varieties, which are cultivated with reduced plant protection measurements, are prone to black rot infection.

The pathogen hibernates in fruit mummies. Throughout the year, several asexual infection cycles can lead to severe infection of green and expanding parts of the grapevine and can cause massive crop loss. Especially in areas with a warm and humid climate, the vineyards are at high risk of black rot infection.

In 2014, two black rot resistance conferring loci were identified in a V3125 (Schiava Grossa x Riesling) x 'Börner' crossing population. The resistance is inherited by 'Börner', an interspecific rootstock variety originating from hybridising two American wild *Vitis* species (*V. riparia* x *V. cinerea*). An extended population of the initial V3125 x 'Börner' population is available for fine mapping of the two reported quantitative trait loci (QTL) and finally the development of closely linked markers for marker-assisted selection in grapevine breeding.

The overall goal of this project is to characterize known resistance loci but also to identify new genetic resources for breeding of black rot resistant grapevines. Further characterization of their resistance mechanism (e.g. through microscopy studies) will elucidate, if they are useful for pyramidalisation of resistances in breeding programs.

Session 1

Using artificial intelligence for grapevine yield forecasts

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In viticulture yield is closely linked to the quality of the grapes/wine and determines the economic viability of a vineyard. In general terms: the higher the yield the lower the wine quality. Yield is therefore one of the most important parameters for wine production and needs to be in a good equilibrium with the production goals. Until now, yield estimation is usually done manually and is prone to errors. Yield is influenced by a various parameters like genotype, soil, weather, and vineyard management. Estimation errors in viticulture occur to be on average of +/- 30%. The goal of this study is to use artificial intelligence to improve yield forecasts in viticulture and grapevine breeding.

In a first step for a more accurate yield forecast system three main sources of data are taken into account by the artificial intelligence (AI): (1) long-term yield data, (2) environmental data (soil and weather) as well as (3) process management data. In a second step the AI is extended and further improved by sensor-based feature acquisition. For this purpose, yield-relevant characteristics are recorded directly in the vineyard in real time by the „PHENOboxx“ which is an Embedded-Vision-System. The most important characteristics include the quantification of shoots, bunches and the mass of dormant pruning wood as well as the nutrient and chlorophyll content of the leaves. The „PHENOboxx“ is placed on the „Phenoliner“, a converted grape harvester used for data collection and as a phenotyping platform for grapevine research. In addition, the soil in the corresponding plots is recorded by using the „Stenon“ sensor.

During data gathering and validation for step one first inconsistencies in recorded data have been found. The allocation of yield data to individual plots turned out to be very difficult, as this data were not recorded precisely enough for individual plots within the past 16 years. To overcome this issue, yields from one vinegrower from plots with the same variety were aggregated to obtain an adjusted yield per hectare. Existing weather data gathered from the weather station is also very heterogenous over the last 16 years, allocation to single plots is been done by distance to the weather station. Process management data is only available for certain plots.

It can be said that historic data must be screened very carefully before taken into the modeling process. So far, the AI can forecast yields up to 74% correct just by using the historic data without adding any sensor measures in the vineyard.

In the long run, sensor data acquisition will improve the AI and needs to be carried out casually during standard vineyard work on the tractor to improve yield forecasts and therefor quality management in viticulture.

White, black, or rather grey? Choosing color for the predictive model for human Puumala orthohantavirus infections driven by a common forest rodent

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The Puumala orthohantavirus (PUUV) is the most common hantavirus in Europe. It is transmitted to humans by infected bank voles, a common forest rodent that can cause significant damage to young trees. PUUV infection in humans can cause severe symptoms, such as kidney failure. Forestry works are particularly at risk. Monitoring the distribution of the virus both in the bank vole populations and in humans shows that it is present in several states of western and southern Germany. According to data from the Robert Koch Institute from 2010 to 2019, there have been >1000 reported human PUUV infections per year in 2010, 2012, 2017, and 2019, with a yearly incidence of 2.29, 2.94, 1.37, and 1.25, respectively. In 2021, there are already 813 reported infections (incidence 0.98, status 05-07-2021).

Weather parameters, such as temperature and precipitation, and the proportion of deciduous forest have been identified as strong predictors for human PUUV infections. The weather parameters are linked to the beech mast intensity of the following year, which determines the food availability and governs the growth of the bank vole populations. In turn, the deciduous forest is the natural habitat of the bank voles, and its proportion is a proxy for the probability of human-bank vole interaction.

Previous work in our group led to two distinct predictive models for human PUUV infections, for districts in northern and southern Germany, respectively, both based on Classification and Regression Trees (CART). These models are “white boxes”, meaning that their function can be directly inspected and analyzed. In autumn 2020, we started a project to improve these models.

During this talk, we will explore the predictors, by observing characteristic 2D and 3D plots. We will use these plots to interpret the results of white-box approaches. Next, we will discuss the potential of using “black-box” techniques, such as the random forest and the artificial neural networks, and present countermeasures to gain intuition in their internal operation; rendering them rather “grey”. The results can be used to improve prediction of outbreaks of disease and forest pest rodent dynamics alike. This is highly important to support strategies and decisions for the protection of plants and human health.

This project was commissioned by the German Environment Agency and funded by the Federal Ministry for the Environment, Nature Conservation and Nuclear Safety within the departmental research plan - research code 3720 48 401 0.

Investigations of fungi as potential cause of sea buckthorn dieback in Northern Germany

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Sea buckthorn, *Hippophae rhamnoides*, is a diecious, hard wooded shrub, which is grown in North-East Germany. The berries are characterized by high contents of vitamin c and antioxidants. Therefore, applications are pharmaceuticals, cosmetics and food products like juices or marmalades. Further, wild plants grown along the coastline of the Baltic Sea are of relevance for erosion protection and also form an important habitat and food source for various insects and animals. Since 2015, reports on the occurrence of sea buckthorn dieback, both in wild plants and plantations, have been accumulating, leading to serious ecological and economic consequences. Up to now, the cause of the plant death remains unexplained.

A joint project, HippRham, started in November 2020. It was established investigate the cause of sea buckthorn dieback and to develop practical control strategies. The project partners are Landesforschungsanstalt für Landwirtschaft und Fischerei Mecklenburg-Vorpommern (LFA), Landesamt für Landwirtschaft, Lebensmittelsicherheit und Fischerei Mecklenburg-Vorpommern (LALLF), and JKI/OW. Our focus will be on fungi in context of sea buckthorn dieback. In addition, phytoplasmas and viruses will also be subject of investigations. A culture-dependent isolation approach and a culture-independent sequencing approach will be used to study the fungal community. Later, inoculation experiments are planned. So far, a total of 185 fungi have been isolated from root and shoot material of different varieties and origins. ITS-PCR and Sanger-Sequencing will be applied for identification. In addition, a method for DNA extraction from sea buckthorn plants was established.

In prior work, total nucleic acids were extracted from leaf samples of symptomatic plants and analyzed by high-throughput sequencing (NextSeq). A total of 2 x 36,498,078 reads were generated and *de novo* assembly resulted in 120,723 contigs. Blast analyses of contigs gave hits to a mycovirus, botrytis cinerea mitovirus 2 (RdRp gene), and black currant leaf chlorosis associated virus (50 – 75 % identity). Next steps will be to determine the complete sequence of both potential viruses.

Using infection studies and molecular techniques to investigate differences in virulence of the agent causing dieback on ash trees (*Hymenoscyphus fraxineus*)

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The causal agent of ash dieback *Hymenoscyphus fraxineus* [synonym: *H. pseudoalbidus*, anamorph: *Chalara fraxinea*], is a non-native fungal pathogen from Asia that was first detected in 2002 in northern Germany. The main symptoms on the European ash (*Fraxinus excelsior*) include shoot dieback, as well as necrotic lesions on leaves, stems and root collars. These symptoms cause reduced tree vitality, reduced timber quality, and tree mortality. The pathogen is associated with significant economic and ecological damages, and it continues to threaten the survival of ash populations across Europe.

Further insights into disease development are necessary to improve disease management. As part of the FraxForFuture project, we will analyse virulence, infection properties and population structures of the pathogen using molecular techniques and infection studies. More specifically, we will determine whether virulence is connected with genetic structure, plant tissue material or geographic distribution using microsatellite analysis. We will use standardised protocols for inoculation and also develop new protocols for strain rejuvenation and ascospore suspensions to more closely replicate natural infection processes and disease development in saplings under greenhouse conditions.

We will also perform infection studies for our project partners to investigate the influence of viruses and fungal endophytes on the virulence of the pathogen and disease expression. It may be possible for naturally occurring antagonists to be used as a biological control of the pathogen.

Together with our project partners, we will also study the development of root collar necroses and contribute to the determination of their aetiology, as they are known to accelerate the decline of infected trees. Overall, the project will contribute further insights into the pathogen, which will facilitate the development of new and existing strategies for disease management in Germany.

What is the impact of different landscape factors on urban wild bee communities?

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The loss of natural and semi-natural habitats in our landscapes over the last decades is considered as a main driver for the decline of wild bee diversity and the associated pollination services. Therefore, it is important to develop measures to promote pollinators in anthropogenic environments.

Urban areas are often considered as bee refuges. However, knowledge about which habitat elements specifically determine wild bee diversity in cities and where supporting measures might be most effective is scarce. Therefore, we examined the urban wild bee community of the city of Braunschweig at 50 sites in 2019. At each site, a set of different coloured pan traps were set up for 24 h in April, June and August. A total of 1876 bees of 102 species were caught. The majority of the individuals was found in spring, while in early summer, the highest number of species was observed. Using this data set, different landscape factors affecting the bee community in the city were analysed.

Urban structure affected bee communities at different scales. On the one hand, bee species richness and abundance were related to impervious surface in a hump-shaped manner at a 100 m scale. On the other hand, species richness and abundance linearly increased with the proportion of allotment gardens at the 300 m scale.

Based on the resulting knowledge, supporting measures can be improved to increase attractiveness of urban areas for wild bees.

Session 2

Ripening detection in grapevine: development of a handheld NIR sensor

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The quality of wine is influenced by various factors e.g. cultivar, vineyard site, nutrition of plants, health status, and weather conditions. Sugar and acidity belong to the metabolic compounds, which are indicators for ripeness and harvesting grapes. The quality level is highly depending on the sugar converted into alcohol or remains as residual sugar determining the wine's sweetness. In order to obtain a balanced and tasty wine a certain amount of acids is required besides of aromatic compounds. While the sugar content increases steadily, acids decline as the berries start to ripen. Based on that, the winemaker is facing the challenge to determine the optimal harvest date.

To this aim a random sample of one hundred berries is taken in viticulture practice to measure sugar and acids in a squeezed sample, for example by using Fourier-Transform Infrared (FTIR) Spectroscopy. This sampling method is costly and time intensive and could be improved by implementing a non-destructive sensor measurement using Near-Infrared Reflectance (NIR) Spectroscopy (NIRS). This technique has previously been shown to be successful for many agricultural applications such as ingredient determination of oils, proteins and starch.

A small handheld device measuring diffuse reflection of the berries between 1350 nm and 2500 nm with a resolution of 16 nm was used (Si-Ware, USA). Sixteen individual berries of Riesling (*Vitis vinifera* L.) were sampled per vineyard and week over the whole ripening period, starting with *Véraison* (beginning of berry softening) until one week after harvest, to ensure a broad range of ingredient concentration. Physiological differences in ripening were taken into account by sampling berries from different fruit as well as cluster zones, and from shaded and unshaded bunches. Corresponding reference sugar (fructose, glucose) and acid (malic and tartaric acid) content were determined with high performance liquid chromatography (HPLC) coupled with refraction index and diode array detectors.

With this approach, in a first study we systematically investigated ripening progress of a whole vineyard, to develop a simple and time effective handheld sensor for viticulture practice. The sugars glucose and fructose could be individually predicted with an 87 % accuracy for each (RMSE_P: ± 7.59 g/l and ± 6.57 g/l, respectively). Simultaneously tartaric and malic acid could be predicted independently, with 89 % and 78 % accuracy (RMSE_P of ± 0.52 g/l and ± 1.89 g/l, respectively), with a better forecast for tartaric acid, which is predominant during harvest.

Marker-assisted selection for *Wheat dwarf virus* (WDV) tolerance in wheat (*Triticum aestivum*)

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Wheat dwarf virus (WDV) is an important pathogen in wheat and other cereals. In many European countries, e.g. Hungary, Spain and Germany, WDV causes high yield losses. WDV is transmitted by the leafhopper *Psammotettix alienus*. Symptoms of a WDV infection on wheat include chlorosis, dwarfing and streaking along with high yield loss. Due to climate change, the incidence of insect-transmitted viruses will become more important worldwide due to the extended survival time of the vector. The absence of insecticides efficient against *P. alienus* renders growing of WDV resistant/tolerant varieties the only effective way to control WDV.

However, little is known about WDV resistance/tolerance sources.

Based upon a previous project- in which wheat accessions were screened for WDV resistance/tolerance and quantitative trait loci (QTL) were identified by genome-wide association studies (GWAS), this project aims to use this tolerance in breeding. For this purpose, breeding partners produced single seed descent (SSD) and doubled haploid (DH) populations by crossing tolerant genotypes with susceptible varieties.

This material was phenotyped for WDV tolerance and agronomical traits and genotyped using the 25K Illumina Infinium Chip. Based on the obtained data the WDV tolerance will be mapped and molecular markers (KASP/CAPS) will be developed.

The identification of QTL for WDV resistance and the development of molecular markers are essential to replace the laborious and time-consuming resistance tests with WDV bearing leafhoppers. This will facilitate the integration of breeding for WDV resistance/tolerance into applied wheat breeding.

Mapping of the waxy bloom gene in ‘Black Jewel’ in a parental linkage map of ‘Black Jewel’ × ‘Glen Ample’ (*Rubus*) interspecific population

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Red raspberry, *Rubus idaeus* L., is an economically important temperate crop. Today's consumer prefer fruit produced without the use of chemical plant protection, which makes growing raspberries challenging. Breeding new cultivars with genetic resistance against pests and diseases could solve this issue. Mapping resistance genes is a good way to design markers and thus ease the otherwise lengthy breeding process.

Black raspberry (*Rubus occidentalis* L.), although of less economic importance, is closely related to the red raspberry. Their close relation makes their genetic information easily useable for both species. The current amount of genetic data available on both species eases the mapping of breeding relevant traits.

One such trait, controlled by gene B, is the amount and form of visible epicuticular wax on canes, called waxy bloom. This trait has been shown to influence resistance / susceptibility to several cane diseases in raspberry, but has not been fully studied in conjunction with other morphological traits. Gene H, which controls cane pubescence, was previously reported to be likely closely associated with gene B.

In this study, we used an interspecific population of *R. occidentalis* and *R. idaeus* segregating for waxy bloom to identify the de novo SNPs through tunable genotyping-by-sequencing. The linkage maps created for both species were then used to map the identified SNPs to the seven chromosomes of *Rubus*.

This study delivers new information on the location of gene B, which we mapped to chromosome 2 of *R. occidentalis*. The genetic map we created consists of 443 markers spanning 479.76 cM. Another important finding of this study is the poor transferability of *R. idaeus* SSRs to *R. occidentalis* and discrepancies in their locations on chromosomes compared to previous studies.

Illuminating SBWMV-host interaction – Subcellular localization and function of CP-RT during virus infection

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Soil-borne cereal viruses cause substantial crop losses and therefore represent an extensive threat for agriculture in Europe, Asia and America. The Furovirus *Soil-borne wheat mosaic virus* (SBWMV) infects several crop species like wheat, rye or barley and is transmitted by a soil-borne plasmodiophorid, called *Polymyxa graminis*. Resistances against Furovirus infections are barely described; in wheat, the *Sbm1* and *Sbm2* genes code for a translocation resistance, which restricts the infection to the plant roots. The viral movement protein (MP) and coat protein–readthrough (CP-RT) protein are believed to play a major role in infection of plant roots and the translocation of the virus into upper plant tissues.

We modified a SBWMV cDNA clone to express fluorescent CPRT fusion proteins (CP-RT:FP) to illuminate their subcellular localization and uncover the function of the CP-RT protein during SBWMV infection. The subcellular localization of the CP-RT:FP was compared with fluorescent markerproteins expressed in *Nicotiana benthamiana* mutants as well as wild-type plants, which were transiently transformed by *Agrobacterium*-infiltration prior to virus infection. Fluorescent infection sites were studied by confocal laser scanning microscopy.

Our results show that the CP-RT:FP co-localizes with the endoplasmic reticulum (ER) and forms dot-like structures along the ER, tightly associated with the ER membrane. Following this observation, we investigated the role of CP-RT for the plant secretory pathway, as this is a common route for virus spread in higher plants. This was done by leaf infiltration of Brefeldin A (BFA) in transiently transformed *N. benthamiana* leaves. BFA is a fungal toxin, which blocks the vesicle formation between ER and Golgi and thus leading to the emergence of distinctive hybrid compartments. Moreover, co-expression of CP-RT:FP with GTP-locked and GFP-tagged Sar1, a small GTPase which regulates COPII-Vesicle formation at the ER, revealed co-localization at dot-like structures, indicating that the ER-associated dot-like CP-RT:FP structures might represent sub-ER sites at which CP-RT accumulates during virus infection. We hope that this knowledge will provide new ideas and targets for the development of novel resistance strategies against soil-borne virus disease.

Session 3

Epidemiology and pathogenicity of *Sclerotinia sclerotiorum* in oilseed rape: Overview of SkleroPro project

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The cooperative project "ValiProg", which is headed by Central Institute for Decision Support Systems in Crop Protection (ZEPP), is concerned with the fundamental validation and new development of decision support systems in agriculture. Prediction models have to be checked and optimized regularly for actuality and accuracy. The goal of decision support system is the reduction of chemical pesticides, which can be realized by accurate forecasts. In the subproject "SkleroPro", the forecast model of *Sclerotinia sclerotiorum* in oilseed rape is revalidated and adapted to the changed conditions. The model specifically calculates the importance of the *S. sclerotiorum* treatment during oilseed rape flowering. The cost of fungicide application and expected yield losses are included in the calculation. The model is available on the website www.isip.de.

The pathogen *S. sclerotiorum* is a soil-borne fungus that can persist in the soil for several years by means of sclerotia (permanent bodies). As the sclerotia germinate, apothecia (fruiting bodies) are formed, which produce ascospores. These infect the petals of the oilseed rape crops. During flower senescence, the infected petals fall into the leaf axils where the fungus infects the plant under favourable weather conditions. The difficulty of the pathogen management lies in the delayed formation of symptoms. Once symptoms are visible, it is too late for control.

To revalidate and optimize the "SkleroPro" forecasting model, two trials were conducted at the Julius Kühn-Institute (JKI) in Braunschweig in 2020. To investigate the relationship between *Sclerotinia*-infestation and yield losses, the winter oilseed rape cv. Avatar was artificially inoculated with different amounts of fungal inoculums at flowering stage (BBCH 65). Disease incidence and severity was assessed at BBCH 81-83 and correlated with crop yields after harvest. Symptom severity was dependent on inoculum levels, plant moisture and air temperature. There was a significant difference in disease severity between the untreated control and inoculated plots. Moreover, the economic and biological control thresholds of the model were investigated in two further field trials. It was shown that a fungicide treatment was not economical in 2020. Furthermore, to improve risk assessment, sclerotia depots were established in autumn 2020. At four locations on JKI campus, 100 sclerotia were buried at 3-5 cm depth, which weekly have been assessed. The depots will remain for 3 years without soil cultivation. The germination rate of sclerotia will be determined per year. In addition, the effect of temperature, light intensity, and relative air and soil moisture on sclerotia germination will be studied under controlled conditions.

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Influence of temperature on the sensitivity of rapeseed varieties and genotypes to turnip yellows virus (TuYV) and animal pests (aphids)

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Rapeseed is an important, globally grown oil plant, used for food and technical applications. In recent years, turnip yellows virus (TuYV) turned out to be a serious threat to rapeseed production. The ban of neonicotinoids for seed treatment that were able to control insect pests in the past increases the risk of infection by TuYV and infection rates may also be affected by climate change. However, TuYV monitoring for the years 2015 until 2017 already revealed high infection rates in several parts of Germany. Furthermore, TuYV monitoring suggested the presence of virus isolates that may overcome TuYV resistance, a trait of several rapeseed cultivars. By using a collection of different virus isolates from different parts of Europe, this observation was confirmed by greenhouse infection experiments under controlled environmental conditions. In addition, it was shown in temperature tests that predicted climatic changes (temperature) have an influence on the resistance to TuYV. We identified differences within the TuYV genome sequence that might be relevant for the ability of specific isolates to overcome resistance. In combination with the ability of *Myzus persicae* clones to transmit TuYV with a high efficiency, as demonstrated by using feeding behaviour observation as well as infection assays, the spread of highly virulent virus isolates might increase pressure on future rapeseed production.

Analysis of an East Asian *Vitis* species to identify a new resistance to downy mildew

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Almost all European grapevine cultivars (*Vitis vinifera* L.) are susceptible to downy mildew, a serious grapevine disease caused by the biotrophic oomycete *Plasmopara viticola*. Outbreaks of the pathogen are prevented by regular fungicide treatments to avoid serious yield losses. However, synthetic or copper-based fungicides are known to be detrimental to human health and exhibit eco-toxicological effects. Therefore, the cultivation of resistant new grapevine varieties is one of the imperatives for a sustainable and environmental friendly viticulture.

A wide range of American but only a few East Asian *Vitis* species have been utilized as natural resistance donors for breeding of new resistant cultivars. Several QTLs for resistance to *P. viticola* (*Rpv*), mainly from North American species, have been mapped on various chromosomes. One major long term objective of grapevine breeding is to introgress and pyramidize these naturally occurring resistances of wild *Vitis* species into the *V. vinifera* genetic background to finally develop new varieties with a permanent and robust resistance. This procedure is facilitated by the development and application of molecular markers tightly linked to the resistance (marker-assisted selection; MAS).

To identify a new resistance to downy mildew an unexploited segregating bi-parental mapping population based on East Asian *Vitis* species was analyzed. The study follows a typical QTL mapping approach, explaining the statistically significant association between phenotype and uniformly distributed markers located on a genetic map, to identify the genomic regions responsible for resistance. A SSR marker-based initial framework map was generated that consists of 19 linkage groups with an average of 5.2 markers per chromosome. At the same time, artificial inoculation experiments were carried out to investigate the degree of resistance to *P. viticola* among the F1 individuals of the mapping cross. Automated photographic recordings were made of the treated leaf discs, and were manually scored for disease severity based on reversed 452 OIV scale. Since this manual rating is tedious, time consuming and obtained data is very subjective, a high throughput phenotyping system for downy mildew was developed on convolutional neural network (CNN) platform, to automatically evaluate the disease severity. Compared to the manual evaluation, the CNN efficiently identified and determined the percentage of area covered by downy mildew in the mapping population with an accuracy of 97%. The CNN performance was also validated on a second unrelated population. After the QTL mapping, future aims are the characterization of the resistance mechanism and determination of responsible candidate genes associated with the new resistance to downy mildew.

Vector monitoring on *Flavescence dorée*, *Xylella fastidiosa* and regulated non-quarantine pests in fruit crops and viticulture

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Quarantine pests (QPs) such as *Flavescence dorée* and *Xylella fastidiosa* are immense threats for fruit crops and viticulture. Globalization, tourism and climate change increase their distribution and the chance of their establishment in Germany. Additionally, regulated non-quarantine pests (RNQP) spread and affect the phytosanitary quality of planting material.

QP and RNQP phytoplasmas, bacteria and viruses are often distributed by plant-sucking insect vectors such as Auchenorrhyncha, scale insects and psyllids. Currently monitoring of QPs and RNQPs is mainly based on manual checking on symptoms and monitoring of vectors in orchards and vineyards. However, increasing risks for carryover lead to an increasing necessity for monitoring activities. Goal of this project is the development of a new effective and sensitive monitoring strategy based on the analysis of unsorted mass catches of plant-sucking insects from the field. For this, nucleic acids of both insects and pathogens need to be extracted from mass catches and analysed by next generation sequencing methods to identify both vectors and pathogens present in the field.

QPs and RNQPs have to be identified fast and effective to keep these important pests under control and prevent further spreading. Additionally, the generated data might help to investigate how QPs and RNQPs spread and/or to identify new vectors for important threats. To provide the results to researchers, plant protection services and farmers, an online platform will be set up.

Session 4

Acoustic insect detection for horticulture

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Digitalization holds the key to make plant protection and especially pest management more efficient and effective. To create a digital system, capable of assisting growers by advising on when and how to fight pests, the system must be able to assess the state of the pest population within the greenhouses. Therefore, there is a need to create digital pest detection sensors.

Many different methods, such as trap systems combined with optical or optoacoustic sensors for evaluation, have been proposed in the field of insect detection. However, none has yet fully solved the problem of digitally assessing the populations of pests in a greenhouse. While optical solutions offer many benefits, acoustic devices may end up being cheaper and less prone to problems like occlusion or varying light conditions. Microphones have successfully been used to detect pest infestations in grain storage as well as in different kinds of wooden plants.

One goal of this project is to investigate the feasibility of an acoustic insect detection system for use in pest management in greenhouses. Therefore, hardware has to be found that is sensitive enough to collect very low-level acoustic insect signals in a greenhouse environment and an algorithm has to be designed that is capable of recognizing different pests within these recordings. The first challenge can be solved by using highly sensitive measurement microphones, giving the system an acoustic perception far beyond human hearing. The second is a classic pattern recognition problem. Related problems, such as recognizing bird songs, have been very successfully solved by deep learning algorithms in the past years. To train such algorithms, big training data sets are necessary. For a highly specialized task, such as acoustic insect classification, adequate data sets are not yet available.

Consequently, as a first step, a data set has to be created. Using an anechoic box and a low noise microphone, a data set of high-quality recordings of the pests under investigation can be collected. By using this recording setup, the common problem of annotating the different sounds can be overcome, if only a single pest species is placed within the recording chamber and environmental noises are eliminated. Furthermore, a low-cost microphone array, consisting of six small microphones, shall simultaneously record a second data set.

Based on the data sets, a deep learning model will be trained to assess the general possibility of distinguishing relevant greenhouse pests by their sound and compare the low- and high-cost hardware performance. Plans for the final project stage include the setup of different microphones in a greenhouse, to compare their performance under real-world conditions. Finally, the developed sensor system will be validated against other solutions, such as digital camera equipped traps.

Phenology of core collection of apples in Dresden-Pillnitz

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Phenology is the branch of science that deals with the relationship between climate and biological phenomena. Plant phenological stages are sensitive to variations in climate. This also applies to apples cultivated in Germany and the rest of the world. Their phenology is subjected to fast-changing climates due to global warming. For example, the number of hot days in Germany (days with $T_{max} \geq 30^{\circ}\text{C}$) reached 18 – 20 in 2018, which is significantly higher than the national average (11.4 days). In addition, rising air temperature, intense climatic fluctuations, extreme weather events e.g. heavy precipitation, flash flood, heat waves, drought, etc. are bringing about shifts in the duration of individual seasons. Warmer winters are increasing the risk of frost damage to apple flowers. The earlier onset of spring has reportedly induced bud burst and precocity in apple plants. The growing season has elongated by 10 days (from 1988 to 2017) than the average 222 days (from 1951 to 1980) as well. Therefore, a comprehensive phenological record of apple trees can be useful to study the impacts of climate change in orchards in Germany. This study aims at observing changes in natural seasonal rhythms and associated time shifts in pheno-phases of the “core collection” of apple cultivars in Dresden-Pillnitz for three years (2018-2021). We used the BBCH (Biologische Bundesanstalt, Bundessortenamt und Chemische Industrie) scale for pome fruits to describe three principal growth stages e.g. inflorescence emergence, flowering etc. and twenty-five secondary stages e.g. bud burst, beginning of flowering, full flowering of these plants. We have developed groups of plants with contrasting flowering behavior e.g. plants showing early and late bud burst (BBCH stage 53), early full flowering, and late full flowering (BBCH stage 65), etc. Molecular characterization of selected candidate genes of these cultivars to identify SNPs and indels associated with flowering and dormancy traits is a major focus of the study.

The reasons for aggregated nesting and the nesting requirements of the ground-nesting bee *Andrena vaga* Panzer, 1799 (Hymenoptera: Andrenidae)

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Ground-nesting bees constitute 75 percent of the wild bee species in Germany, their cuckoo bees included. Although they are the most abundant functional group of wild bees, ground-nesting bees are less studied than cavity nesting bees that built their nests in wood or use pre-existing cavities.

Many ground-nesting bees nest gregariously, which means in aggregations of individual nests. The motives behind this behaviour are still indistinct, but five hypothesis should be reviewed: the saving of energy and time for building and provisioning of the brood cells (nest site fidelity), the reduction of parasitism risk, the distribution of key resources and a deficit of ideal nesting substrates.

Especially regarding nesting site characteristics ground-nesting bees depend on more knowledge is needed as further descriptions and details resulting from precise measurements are lacking. The importance of floral resource availability on bees has been studied extensively, whereas findings about their nesting requirements is often restricted to cavity-nesting bees. Information about nesting site preferences and tolerable ranges is crucial for wild bee conservation as well as for studies about the biology and ecology of bees.

The aim of this study is to review the introduced suppositions about the emergence of aggregations for the example of the ground-nesting bee *Andrena vaga* (Panzer 1799). For this, the portion of emerged females that build their own nest in their natal aggregation will be measured. In addition, the parasitism rate will be related to the size of the aggregation and the availability of food resources around the aggregations will be identified.

Further, the ideal characteristics of the nesting site and a range of tolerated conditions should be determined. Therefore, soil samples will be analysed regarding texture, water content, pH, organic material, salinity and the presence of heavy metals and pesticides. Additionally, both the soil and the surface temperature as well as the solar irradiation will be monitored. Site characteristics like the soil density, slope, exposition and vegetation cover will be surveyed. All parameters will be compared with the conditions on an un-colonised control.

Identification of interacting plant host factors from the Soil-borne wheat mosaic virus movement protein

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The soil-borne wheat mosaic virus (SBWMV) belongs to the genus Furovirus and infects cereal species. SBWMV is transmitted by the plasmodiophorid vector *Polymyxa graminis*, an obligate root parasite. In winter barley, no effective resistances against SBWMV or the vector are known. Therefore, to develop new resistance strategies against SBWMV, we investigate the molecular interaction between the virus and the host plant. Viral movement proteins (MP) are necessary for virus movement between cells and systemically. As a key factor in viral infection, we focus our investigation on the SBWMV MP. We use fluorescent protein-tagged MP to illuminate its localization to cellular compartments in the model host plant *Nicotiana benthamiana*. Using different established cellular markers, we found that SBWMV MP localizes to plasmodesmata (PD) in the plant cell, further confirming its function as MP and indicating a function of the protein at PD. By using co-immunoprecipitation experiments, we isolate MP-interacting plant proteins. Currently, we functionally characterize the MP-interacting plant proteins with respect to their subcellular localization and RNA-binding properties. The results will help us to understand the interaction between the virus and the host plant on a molecular level and lead to the identification of targets for new resistance strategies.

Session 5

MAGIC-RESIST: Identification and mapping of effective resistance genes to rust diseases and Fusarium head blight in the MAGIC WHEAT population WM-800

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Due to their high potential for damage and regular occurrence, phytopathogenic fungi like leaf rust, stripe rust and *Fusarium* ssp. belong to the most important pathogens of wheat. In particular, Fusarium head blight (FHB) is of great importance in cereal cultivation due to its ability to generate mycotoxins such as deoxynivalenol (DON) and thus reduce the quality of the crop. Aim of the MAGIC-RESIST project is to identify and map effective resistance genes in the multiparental wheat population WM-800, which consists of 800 lines and is based on the eight elite varieties Patras, Meister, Linus, JB Asano, Tobak, Bernstein, Safari and Julius by genome-wide association studies (GWAS). Field trials at two locations (Halle and Quedlinburg) that had previously been inoculated with spore material from the three pathogens were evaluated over several years. Due to drought stress situations, both rust pathogens occurred with different intensities in the tested environments. The traits are heritable and usable for genome wide association studies (GWAS). Due to the broad genetic variability of the parental lines, their resistance to rust, QTL for unknown leaf rust resistances could be detected using GWAS.

In order to validate the data on quantitative characteristics, such as resistance to FHB, grain samples were examined after the harvest with the aid of hyperspectral imaging methods, the DON content was determined using ELISA and related to the thousand grain mass and grain size. In this way, reliable parameters can be identified based on reflection values in specific wavelengths of the shortwave and infrared range, which establish a reliable connection with the resistance of the genotypes to FHB. By including plant morphological data such as plant height, grains per ear and flowering time, purely physiological resistance mechanisms can also be excluded. The rating of thousand grain mass, grain size, results of hyperspectral analyses and DON content will be used for GWAS. Because there are also great phenotypic differences in the parent lines for all recorded traits after Fusarium inoculation, previously unknown resistance QTLs are expected based on the DON data and the hyperspectral analyses. Using the WM-800 population and the QTL found can accelerate the breeding of varieties with an improved level of resistance to these diseases.

Treating apple replant disease with beneficial microbes: Effects of *Bacillus velezensis* FB01 and *Pseudomonas sp.* RU47 on the microbial community

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Apple replant disease (ARD) is a phenomenon occurring in apple production areas all over the world. Replanting apple on the same site leads to serious growth suppressions, a decline in yield and poor fruit quality. Even though ARD is a long-studied phenomenon and symptoms have been observed in apple-production areas worldwide, its etiology still remains unknown. However, actions to overcome ARD or at least reduce disease symptoms are urgently needed.

In the study presented, we aimed to test the common biocontrol agent *Bacillus velezensis* FB01 and the biostimulating strain *Pseudomonas sp.* RU47 as potential soil management strategies for ARD-affected soils. Both strains, FB01 and RU47 were tested in a greenhouse-trial where they were amended to ARD or healthy grass soil and planted with apple rootstock M26. Plants treated with sterile water served as control. Twenty-eight days after inoculation, samples from the microhabitats rhizoplane and bulk soil were harvested and analyzed by cultivation-dependent and –independent methods to gain knowledge about the establishment of the inoculants and their impact on the microbial community composition. The plant response was investigated three, 16 and 28 days after inoculation by measuring the regulation of selected ARD marker genes and the production of phytoalexins.

By selective plating of FB01 and RU47 on respective media, we showed that both strains had a good persistence in soil and rhizoplane as they were detectable in high abundance even four weeks after application. 16S rRNA-amplicon- and ITS-amplicon-sequencing of total community DNA extracted from both microhabitats showed that treating the plants resulted in shifts in the microbial community composition. The application of RU47 and FB01 had significant influence on alpha- and beta-diversity. For instance, treating plants with the beneficials lead to a clear increase of the species richness in bulk soil compared to untreated samples. Three days after inoculation, a significant short-term upregulation of the investigated ARD marker genes and only low amounts of phytoalexins were observed. After 16 and 28 days however, the abundance of these marker genes decreased to low levels.

With the results of this study, we hope to get one step closer to treat ARD in an environmentally friendly and sustainable way by the application of beneficial microorganisms.

Spot Farming – a new approach for a small-scale and sustainable plant production

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The climate change poses a challenge to agriculture: Changes in the annual temperature- and rainfall distribution, heat waves, and heavy precipitation events already have noticeable impacts. Furthermore, a constantly growing world population asks for a save food supply with a simultaneous social demand for a climate-friendly and sustainable agriculture, as well as the conservation of biodiversity. These challenges demand for an adoption of agricultural systems to accommodate for these changes.

One solution to deal with these challenges could be the Spot Farming approach, which is intensely investigated in the project „futurelab agriculture.“ In Spot Farming, the often heterogeneous field will be divided into several homogeneous fields (“spots“), based on their characteristics, e.g. soil properties, topography or risk of erosion. In these spots different crop rotations will be cultivated, adjusted to the location's characteristics. Alternative cropping systems will be applied, integrating variations in row distances and sowing pattern to optimally fulfil the plants' specific requirements. Additionally, ecological structural elements like flowering fields will be integrated on poorer spots to improve and conserve biological diversity. Because the generated spots will be small-scale, a management with modern, large-size agricultural technology will not be possible anymore. The integration of small autonomous field robots will provide new possibilities for a small-scale and site-adjusted management.

For some exemplary areas, located in different regions throughout Lower Saxony, Spot Farming management is in planning. Based on geodata, the spots are categorized into homogeneous zones. Different scenarios on varying data basis are being evaluated. The goal is to quantify the demands based on the input data in terms of abundance, resolution, and scaling: Which data is essential and which data can serve as additional information under preservation of practicability?

Furthermore, a theoretical Spot Farming cultivation is planned for the exemplary areas based on literature research, integrating alternative cropping systems, in which different crop rotations will be cultivated in the spots, adapted to the local soil properties and the incident radiation, depending on the area exposure. For erosion protection, permanent crops with soil cover will be grown in areas at risk. Moreover, ecological structural elements will be added to increase the biological diversity.

The Spot Farming approach will be a future tool to deal with the challenges of the climate change and a concept for more sustainable, resource-friendly, and small-scale agriculture.

Comparing different calibration strategies for the DSSAT-Nwheat model building on an extensive experimental data set for Germany

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Crop models are widely used in agronomic research. They can provide crucial information and decision support for crop management, crop breeding, climate change impact assessment and adaptation, as well as policy advice. Prior to model application, a crop model needs to be calibrated, i.e., crop coefficients are estimated by minimizing the error between observed and simulated crop growth and yield data. Neglecting model structural uncertainty, crop simulation accuracy relies entirely on model calibration if building on a robust experimental data set.

The calibration procedure is often conducted in an unstandardized and non-reproducible manner, with a substantial impact on the final coefficient setting. As a result, the same model and dataset may provide a broad range of model predictions from various users, depending on the crop modelers' experience and respective calibration procedure.

DSSAT-Nwheat is a freely available and globally employed crop model. However, Nwheat was rarely used in Germany. Hence, model calibration and validation are required prior to simulating the performance of specific German cultivars under German growth conditions.

We propose, execute, and comparatively assess six alternative calibration strategies. For this, we built on a vast cultivar-specific field experiment dataset of about 100 site-years per cultivar, which covers a wide range of growing conditions. We performed the calibration using the time-series estimator (TSE) for the DSSAT modeling system, allowing a coordinated calibration of multiple cultivar coefficients.

In combination with two calibration data sets (with yield component data vs. no yield component data), we applied three calibration strategies; we followed several coefficient combinations in strategies, reducing the error for different variables, taking into account the classical approach of initially calibrating phenology, then growth and finally grain yield.

Our study showed that TSE for model calibration, coupled with yield component data and strategy with giving weight to grain yield in each step, is a promising method for improving prediction capability in a reproducible way.

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