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Julius-Kühn-Archiv

15th Young Scientists Meeting Conference 2023

15th – 17th November
in Dossenheim

- Abstracts -

Julius Kühn-Institut
Bundesforschungsinstitut für Kulturpflanzen

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Herausgeber / Editor
Julius Kühn-Institut, Bundesforschungsinstitut für Kulturpflanzen, Quedlinburg, Deutschland
Julius Kühn Institute, Federal Research Centre for Cultivated Plants, Quedlinburg, Germany

DOI 10.5073/20231012-100337-0
ISSN 2199-921X
ISBN 978-3-95547-135-4

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Session A

A question of the location: food and nesting resources are main drivers of urban wild bee community composition

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Land-use change is a major driver of biodiversity loss, whereby urbanisation represents one of the most profound types of land-use change. Therefore, environmental conditions characteristic for urban areas may act as strong environmental filters for wild bee communities. These filters might lead to a systematic loss of species and consequently to biotic homogenisation. Alternatively, different environmental conditions might enable diverse biological communities to exist within urban areas.

Here, wild bee community composition across 49 study sites in the city of Braunschweig, Lower Saxony, Germany was examined. The study sites covered a gradient from city centre to rural surrounding. Dissimilarities between wild bee communities were compared to community of flowering plants, nearby land use and soil characteristics as well as geographic distances using multiple matrix regression.

The sampled wild bee species represent 30% of the species known for Lower Saxony and included Red Listed species. The sampled communities differed markedly. Thereby, dissimilarity of the community of flowering plants had a significant positive effect on differences in wild bee community composition, as well as dissimilarity of nearby soil texture. In contrast, geographic distance between study sites, distance to the city centre, or dissimilarity of nearby land use had no effect. On average, 1/3 of the overall wild bee diversity of the city was detected at one sampling point (median true beta diversity: 3.309 compositional units).

These results show that cities provide suitable habitats for various wild bee communities. The composition of these communities are driven by the composition of essential food and nesting resources, i.e., flowering plants and nearby soil texture, rather than by dominant urban-specific environmental filters. In order to conserve and improve the resulting heterogenic set of urban wild bee species communities, it is important to preserve and create heterogeneous plant structures within cities.

Risk assessment innovation: Pioneering low-risk pesticides and dsRNA for sustainable agriculture

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Low-risk pesticides (LRP), including plant extracts, semiochemicals, and microbial pesticides, have gained global recognition as environmentally friendly alternatives to synthetic pesticides. Additionally, emerging microbial solutions and promising dsRNA pesticides are poised to revolutionize the market in the coming years. However, the absence of a dedicated risk assessment (RA) framework tailored to LRPs continues to impede their entry into the EU market, demanding immediate action.

Our research initiative, Risk Assessment Innovation for Low-Risk Pesticides (RATION), is committed to addressing this critical challenge through six work packages dealing with different LRPs. RATION's primary goal is to develop an innovative RA framework, complemented by essential methodological guidance, meticulously tailored to accommodate the unique characteristics of both established and emerging LRP solutions.

The Institute for Biosafety in Plant Biotechnology (SB/JKI) in Quedlinburg is leading the WP4 adressing dsRNA. WP4 is structured around two key components: hazard identification and characterization, alongside exposure assessment. Our initial efforts have centered on the Colorado Potato Beetle (CPB), a Coleoptera pest in Solanaceae crops, offering great promise as a target for dsRNA pesticides. We have successfully initiated CPB rearing under controlled conditions using Anabella potato plants.

Actin, a ubiquitously present and functionally diverse protein, was chosen as the target for designing dsRNA, given its conserved features across eukaryotic organisms. Employing innovative bioinformatics, we have identified unique, non-conserved regions in the actin sequence of CPB, a pivotal step in hazard identification. This choice facilitates the development of a "low-specific dsRNA" capable of targeting both CPB and specific non-target organisms (NTOs). We have designed a 297 bp dsRNA (dsact) based on previous research, initiating bioinformatics analyses across various NTOs. Furthermore, we have explored actin expression levels at different stages of CPB development.

In collaboration with Genolution, South Korea, we are in the process of scaling up dsRNA synthesis. Following the synthesis of small-layered double hydroxide (sLDH) nanoparticles, we have successfully formulated dsRNA carriers, demonstrating their ability to bind dsRNAs at varying ratios.

As we embark on this exciting journey, we anticipate making significant progress upon receiving dsact and commencing procedures and tools for assessing the safe use of dsRNA pesticides in plant protection practices. This research holds the promise of enhancing the sustainability and safety of agricultural practices, not only in the EU but also worldwide.

Derivation of crop traits using Sentinel-1 SAR data: A case study for winter wheat in northern Germany

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Accurate, area wide and frequent information on crop traits such as biomass and leaf area index can support decision making on improved, resource-efficient fertilizer application or management of pest infestations. However, conventional approaches such as ground surveys are time consuming and limited to field scale. These limitations are overcome by remote sensing technique by using Synthetic Aperture Radar (SAR), which can provide images almost independent from day light and weather conditions with high spatial resolution for large areas.

Two fields at the DEMMIN test site for 2021 and 2022 and one field close to the city of Braunschweig for 2022 in northern Germany were selected as study area. Here, we utilize openly accessible Sentinel-1 SAR data. The data for the analysis involves the Ground Range Detected (GRD) and the Single Look Complex (SLC) products of Sentinel-1, from which backscatter coefficients γ^0 (VV polarisation and VH polarisation), backscatter coefficient ratio (γ_VH^0/γ_VV^0), Dual Pol Radar Vegetation Index (DpRVI) were calculated. Additionally, the Surface Soil Moisture (SSM) product from Copernicus Global Land Service was deployed in this study. For deriving the target crop parameters, machine learning techniques (Partial Least Square regression (PLSR), Support Vector Regression (SVR), Random Forest (RF)) were applied. Therefore, the data was splited based on repeated k-fold cross validation method and as a result, 80% of data points were used for training and 20% for validating the model. Here, we used indicators such as Root Mean Square Error (RMSE) and coefficient of determination (R^2) for evaluating the model performance.

Among all extracted parameters, γ_VV^0, DpRVI and soil moisture were found to have more influence on LAI and biomass in all the models. Considering the model performance for LAI, the R^2 values of PLSR (0.39), SVR (0.49) and RF (0.69) and the RMSE values of PLSR (1.31), SVR (1.21) and RF (0.92), indicate that RF model outperforms the other models for retrieving crop traits of winter wheat. Likewise, the RF model yields a R^2 value of 0.90 for the biomass model outputs. The results as well as the accuracy achieved from the RF model demonstrate that it is generally feasible to derive information on the status and development of crop traits from Sentinel-1 SAR data. However, it is important to note that the specificity of Radar data prevent it from discerning within-field heterogeneities.

Potato breeding to investigate and establish an increased resistance to pectinolytic bacteria

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Pectinolytic bacteria of the species *Pectobacterium spp.* and *Dickeya ssp*. are responsible of blackleg and soft rot in the tubers and thus cause considerable damage. They can result in up to 50% reduced plant growth and thus cause a significant economic loss particularly while the heavy rain events or during rainy years. The only efficient control method at the moment is strict phytohygiene, especially when producing seed potatoes. In the »KUER« project, the problem of blackleg and soft rot will be addressed with focus on the identification of underlying resistance mechanisms. For this, high quality phenotyping methods will be established in order to separate factors that lead to the development of diseases. Specifically phenotyping and genotyping of blackleg and soft rot will be established after primary, secondary infections (with pectinolytic bacteria) as well as while the wound healing, which suggests an improvement in inoculation´s methods. The successfully developed phenotyping methods are then applied to a previously genotyped association panel from different genetic resources to increase the resistance again blacklegs and soft rot. The data obtained will be used to select genotypes for further breeding and for the development of specific molecular markers for marker-assisted selection.

The project is supported by funds of the Federal Ministry of Food and Agriculture (BMEL) based on a decision of the Parliament of the Federal Republic of Germany via the Federal Office for Agriculture and Food (BLE) under the innovation support programme.

Session B

Characterization of the VPg-region of BaYMV and BaMMV isolates in Germany and identification of resistance breaking features

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Barley yellow mosaic virus and Barley mild mosaic virus cause the yellowing disease in barley and lead to yield losses of 50% in infested fields. The soil-borne vector *Polymyxa graminis* transmits both viral species and forms resting spores containing infectious virus particles. Noteworthy, against *P. graminis* no environmentally or economically useful treatment is known. To avoid crop losses due to the two virus species, resistant barley cultivars are used by farmers. Interestingly, even by using cultivars carrying known resistance genes, plants, which show virus symptoms and are tested positive in ELISA for either one or both viruses can be found. We examine the VPg-region in the viral genome, which has been shown to be responsible for resistance breaking. By comparing virus-isolates from different fields and different barley cultivars, we explore the diversity and response to resistance genes of these virus isolates. We hope to find changes in the virus isolates characteristic for resistance breaking and want to use this information to further monitor the presence and spread of these resistant breaking virus isolates in fields in Germany.

Method developement in near-infrared spectroscopy as part of the monitoring of rye grain qualities

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The research work takes place as part of the climate protection project PRoKlima, which is dedicated to the potential of semi-dwarf rye to increase the climate protection performance of cereal rotations. The preliminary work is particularly relevant, in which they state that the cultivation of rye (*Secale cereale L.*) produces 20 percent less greenhouse gas emissions compared to wheat. This climate protection potential is of great importance with regard to the increased targets of the Climate Change Bill. In addition, modern breeding research has overcome the “classic” disadvantages of rye cultivation, such as a tendency to lodging and disease infestation. Despite these advances, cultivation area of rye is still significantly smaller compared to wheat (ratio of 1:5 according to DESTATIS). One reason could be the unsatisfatory fulfilment of the application-related requirements for grain quality.

To date, rye is used in animal feed in the form of mixed feed. The reason for this is the high content of arabinoxylans, which cause a high viscosity of the cereal pulp. This affects the digestion of nutrients and their absorption in the intestinal tract negatively, especially in monogastric animals, and consequently leads to reluctance by livestock farmers. In the baking industry, however, a high content of pentosans is crucial because they provide the necessary water-binding power in place of the missing gluten matrix. In addition, the high fiber content has a positive effect on human health and is therefore desired by consumers. This already shows that depending on the intended use the requirements for grain quality vary greatly. The aim of PRoKlima is to advance the development of rye varieties with tailored grain qualities to enable the broader utilisation of rye and therewith use its climate protectin potential.

In order to assess the grain quality, the content of quality-determining ingredients like water-soluble (WAX) and total arabinoxylans (AX), starch and protein are determined by appropriate chemical analysis. This analysis acts as a reference for a near-infrared spectroscopy (NIRS) method. This method can then be used to predict the content of the mentioned ingredients in new samples. Therefor one or more spectra of the sample are recorded and evaluated using calibration. This calibration is specific to the desired ingredient and usually the crop type. In the frame of PRoKlima, a robust multi-method for simultaneous prediction of WAX, AX, starch and protein in rye is to be established. For this aim, a data set of more than 400 rye samples was used, comprising 320 genotypes and at least two field replicates as well as four harvest years (2019-2022). The cultivation was carried out in various locations in different countries, such as Germany, Austria, Poland, Estonia and Canada. At first, the collected reference values must be assigned to the respective sample spectra. In the process of optimizing the calibrations, the corresponding spectral ranges, data pretreatments, outliers, etc. must be determined and adjusted for each parameter. Validation is used to test the predictive performance of the calibration, which is than assessed using various factors such as the *Residual Prediction Deviation* (RPD) and coefficient of determination.

From unwanted to wanted: Blending functional weed traits into weed distribution maps

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Sensing technologies like 3D cameras, multispectral imaging, and artificial intelligence are increasingly utilized in modern weed management to detect and classify weed species for site-specific weed management (SSWM). While weeds can compete with crops, they also offer valuable ecosystem services such as supporting pollinators and providing shelter for insects and animals. Knowing the morphological and functional traits of weed species in a field allows for the selection of SSWM methods that effectively reduce the competitiveness of specific weed species while supporting those with beneficial traits. Trait-based approaches have gained popularity in recent decades. However, the practical application of integrating and interpreting weed functional traits for SSWM remains a gap. This study aims to identify and evaluate weed functional traits related to both provisions of ecosystem services and crop competition to translate this knowledge into maps. A manual weed assessment was conducted in 2022 near Braunschweig (Germany) on a winter wheat field untreated with herbicides, with a grid of 40 sampling points (10 m x 6 m). Plant-specific functional traits relevant for the provision of ecosystem services and agro-ecosystem diversity (e.g. importance for insect families and species, birds, and duration of flowering) and crop competition (e.g. leaf dry matter content, leaf area per leaf dry matter, competition index, and plant height at the vegetative stage) were extracted from published datasets and combined into the two variables 'biodiversity' and 'competition'. Each variable was weighted for each grid point based on the occurrence and density of the occurring weed species. Afterwards, a spatial distribution map was created for each weed species and trait variable using an ordinary kriging interpolation technique. A PCA was performed for each pixel of the grids using the biodiversity and competition variables, allowing to consider the weed community as a whole. As a result, two maps were generated: one showing the areas in the field that provide biodiversity benefits, and the other showing the areas where there is high competition potential due to the present weed composition. The goal is not only to reduce the application of herbicides but also to make a statement about the extent of ecosystem service provided by the weed flora of an agricultural field.

Identification of apple cultivars robust to apple blotch disease

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Apple blotch disease is spreading rapidly in apple growing regions in Europe. It is caused by the fungus *Diplocarpon coronariae.* The fungus causes yield loss and reduces fruit quality due to the early leaf drop before fruit harvest. An effective approach to prevent damage from the disease is the cultivation of robust apple cultivars. This not only reduces the spread of the disease, but also reduces reliance on pesticides. Few studies have been carried out in a controlled laboratory environment on the susceptibility of traditional apple cultivars to the disease. In this study, 558 apple cultivars from the collection of the German Fruit Genebank (GFG) were evaluated for susceptibility to apple blotch. For the initial evaluation, the apple cultivars were tested in the laboratory using detached leaf assays. The results showed differences in susceptibility between traditional apple cultivars. The GFG collection includes also robust cultivars as they show reduced symptom development and delayed symptoms during the evaluation. To verify the results and to record the symptom of leaf drop, the cultivars were tested again in greenhouse trials. This second test confirmed differences in the development of the pathogen in the tested cultivars and showed variations in the time of leaf drop. These results provide information on robust apple cultivars that can be planted in cultivation with reduced fungicide use. This is an important step towards developing sustainable solutions to apple blotch disease in Europe.

Presentation topic: „Measures to reduce direct and indirect climate-impacting emissions caused by denitrification in agricultural soils"

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Gaseous emissions from denitrification (nitric oxide, NO, nitrous oxide, N_2O, and molecular nitrogen, N_2) cause significant nitrogen losses and contribute to climate change. Denitrification in soils is highly variable on temporal and spatial scale due to its controlling factors such as climate, soil properties and management. Because of its variability, denitrification is difficult to measure in field studies. Therefore, there is still a knowledge gap on mitigation measures of N losses from denitrification in soils. While most studies focused on ammonia- (NH_3) and N_2O-emissions due to their impact on climate change, N_2 emissions can account for a large proportion of the gaseous nitrogen losses. However, due to the high atmospheric background, the quantification of N_2 emissons from fertilisation is challenging. Within the project "Measures to reduce direct and indirect climate-relevant emissions from denitrification in agricultural soils (MinDen)", a field experiment was set up in Braunschweig to assess the impact of mineral and organic fertilisation in combination with different application techniques of the organic fertiliser on gaseous nitrogen losses from denitrification. ^{15}N labeled fertiliser and tracer solution was used to estimate nitrogen balance losses. The dominant and environmentally relevant nitrogen fluxes are determined by quantifying the amount of applied fertiliser, plant nitrogen uptake, soil mineral nitrogen content, in addition to NH_3-, N_2O- and N_2-emissions as well as nitrogen leaching. To account for a total nitrogen balance, the ^{15}N recovery rate not captured in soil and plant should equal to the amount of nitrogen lost in gaseous form (N_2O, N_2 and NH_3) or through nitrogen leaching. First results show that overall the N_2O emissions in Braunschweig are low, as expected, due to the sandy soil. The organic fertilised treatments had higher N_2O emissions than the mineral fertilised treatments, while the control treatment without fertilizer showed the lowest N_2O emissions. In addition, the mineral fertilizer resulted in higher nitrogen uptake in the maize plants compared with those under organic fertilization. The presentation aims to provide a brief overview of the project and to present preliminary findings on the impact of nitrogen fertilisation on gaseous N emissions, yield, and nitrogen uptake.

Investigation on apple blotch resistance of *Malus baccata* 'Jackii'

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The fungal pathogen *Diplocarpon coronariae* causes apple blotch and has spread massively in Europe in recent years. Typical symptoms of this disease are leaf chlorosis and premature defoliation, which can have a serious impact on the physiology of the tree, resulting in reduced vigor and decreased yields of apple trees. Especially in organic apple production and orchards with low chemical inputs, this disease leads to massive damage as there exist no resistant apple cultivars yet. The most promising and sustainable approach to control this disease is breeding cultivars that are highly tolerant or resistant to this disease. Screenings of the *Malus* germplasm collection from the Fruit Genebank of the Julius Kühn Institute showed that an accession from *Malus baccata* is resistant to *Diplocarpon coronariae*. In this study, *Malus baccata* 'Jackii' and two susceptible genotypes were artificially inoculated and evaluated for resistance to apple blotch with a detached leaf assay. The phenotypic evaluation revealed a significant difference between the genotypes in the number of necrotic spots and the diseased leaf area. Subsequently, the genotypes were inoculated after abrading the cuticle with silicon carbide and a higher amount of *Diplocarpon coronariae*-specific DNA was detectable with polymerase chain reaction in the susceptible cultivars compared to *Malus baccata* 'Jackii'. This indicates that the resistance mechanism of *Malus baccata* 'Jackii' is not restricted to the cuticle. Recently, also plants of the progeny 'Idared' × *Malus baccata* 'Jackii' were screened for resistance to apple blotch and the first results suggest that the resistance to this disease is heritable. With a genetic map available, the resistance genes can be studied in detail in the near future and molecular markers will be developed. This lays the foundation to increase the efficiency and to accelerate the breeding of new apple cultivars resistant to apple blotch.

Session C

Establishment of Biotechnologies in Oats and Lupins

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Oats are globally significant crop, providing essential nutrition for humans and livestock. They offer health benefits through their high levels of calcium, β-glucan soluble fiber and protein content. Oat seed is a healthy gluten-free substitute for those intolerant to gluten. Oat milk's popularity has surged due to multiple factors. It is a high-quality vegan substitute for dairy milk, offering sustainability by emitting fewer greenhouse gases. Additionally, oat milk caters to lactose-intolerant and dairy-allergic individuals. Harsh environmental conditions cause up to 50% of yield losses, necessitating the development of new oat varieties with improved adaptability and enhanced nutrition. Plant cell culture is necessary for classical and modern breeding. It enables genetic manipulation and precise genome editing for targeted changes at the cellular level.

Efforts to establish an oat regeneration system for development of new traits throughout classical and modern breeding techniques have been undertaken, utilizing different explant sources such as grains, split grains, mature embryos, and leaf bases to induce friable and embryogenic callus. The most successful multiplication of shoots, averaging 20 shoots per explant, was achieved from the embryogenic callus. This regeneration system has been implemented in commercial cultivar, contrasting with the prevailing literature that predominantly focuses on accessions exhibiting poor agronomic traits. Embryogenic callus has undergone Agrobacterium-mediated and bombardment transformation, leading to the emergence of visible green fluorescent protein (GFP) spots on the callus. Furthermore, the exploration of protoplast technology has opened doors to introduce DNA and proteins (including ribonucleoproteins) into plant cells and manipulate them at the single-cell level. Successful isolation of viable and healthy protoplasts has been accomplished, achieving a transformation efficiency more than 80% through PEG-based transfection. These cells have been subsequently cultured to develop micro colonies.

Lupins are cultivated for their protein, dietary fiber, minerals, essential fatty acids, and nitrogen-fixing capabilities. Alternative plant proteins provide numerous advantages, including improved health benefits, reduced environmental impact, enhanced animal welfare, food security, allergen accommodation, culinary diversity, and sustainability. Developing lupins with enhanced nutritional value can significantly impact their cultivation. Callus was induced from various explant sources, resulting in the emergence of somatic embryogenic structures derived from cotyledons and hypocotyls. Additionally, embryogenic callus was achieved from immature zygotic cotyledons, with multiple shoot initials and shoots formed from the embryo apex and shoot apical meristem, respectively. Viable protoplasts were isolated and transfected, exhibiting a transformation efficiency more than 50%. The protoplasts were further cultured to develop micro-callus.

Unravelling the tomato plant microbiome for consortia of microbial antagonists for *Phytophthora infestans*

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A joint project, funded by the DAAD between the Julius Kühn Institute, Institute for Biological Control, and the University of Embu, Kenya explores the microbiome of tomato plants for microbial antagonists that can be used to develop microbial consortia for application in tomato cultivation to manage a wide range of destructive pathogens. Firstly, culturable microorganisms from the rhizosphere and phyllosphere of healthy and diseased tomato plants are isolated, identified, and screened for potential antagonistic activity against one of the most destructive oomycete tomato pathogens, *Phytophthora infestans*. Afterward, consortia of the most promising microbial antagonists will be developed and tested for their efficacy in managing the detrimental disease-causing pathogens of tomatoes in the growth chamber and field trials.

Dilution plate microbial isolation technique using standard (nutrient agar and potato dextrose agar) and minimal (M9 and oatmeal agar) media under three different incubation temperatures (14 °C, 21 °C, and 28 °C) yielded 594 bacteria and 246 fungi from the rhizosphere and the phyllosphere of tomato plants. A total of 165 fungal isolates were subjected to confrontation assays with *P. infestans* after eliminating candidates unsuitable for commercial use, including non-spore formers, those growing at 37 °C or requiring special growth media. Confrontation assay results showed distinct inhibition zones in 66 isolates, indicating their potential as microbial antagonists. Intriguingly, ITS sequencing of DNA isolated from a subset of promising antagonists above revealed their closeness to diverse genera such as *Penicillium, Trichoderma, Cladosporium, Clonostachys, Paraphaeosphaeria, Ctenomyces*, and *Scytalidium*, including both commonly known antagonists but also some genera that have not been described as plant biocontrol agents before.

A similarly stepwise screening for bacterial isolates is underway. The subsequent phase of this study will focus on designing consortia of the most promising candidates considering different variables for further tests in ad planta trials in the growth room and semi-field conditions.

This project can contribute to reducing synthetic chemical pesticide usage through microbiome-based solutions with broad-spectrum effects, to which microbial antagonists can contribute significantly.

Beneficial microbes and catch crop amendments: Sustainable soil management options for Apple Replant Disease?

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Replanting apple at the same site leads to serious growth suppressions, a decline in yield and poor fruit quality. This phenomenon is called Apple Replant Disease (ARD) and occurs in apple production areas worldwide. Although ARD is studied since almost 100 years and many symptoms were described, the disease causing mechanism still remains unknown. However, the successful restoration of regular plant growth by soil disinfection clearly indicate biotic factors to cause ARD. Current disease management mainly depends on chemical soil fumigation, but actions to treat ARD with environmentally friendly approaches such as microbiome modulation and activation are urgently needed.

Here we report greenhouse trials in which we tested the potential of catch crop amendments or the application of beneficial microbes on ARD soils. We hypothesized that the modulation of the soil microbiome by inoculation of beneficial microbes or application of soil amendments can increase the resilience towards ARD. We developed practice-oriented application procedures for single or combined inoculation with beneficial bacteria and AMF as well as for the incorporation of Tagetes or a catch crop mixture. The inoculants *Pseudomonas* sp., *Bacillus atrophaeus*, *Rhizoglomus irregulare,* and *Funneliformis mosseae* were chosen based on their complementary functions, the niches they colonize and their potential to reduce the abundance of ARD-associated populations. Directly after inoculation, apple plantlets were grown in the differently treated soils and soil microbial activity was determined. After six weeks, plant growth, phytoalexin concentrations in the roots and the microbial communities were analyzed by *16S rRNA* gene and ITS amplicon sequencing in soil and rhizosphere DNA.

In soils with catch crop amendments, a high C-respiration was observed and dehydrogenase activity as well as root growth were significantly increased compared to plants in untreated ARD soil. Inoculation with AMF or the consortium and incorporation of Tagetes led to reduced phytoalexin concentrations compared to untreated ARD soil. Bacterial diversity was significantly higher in rhizospheres treated with the consortium compared to single inoculants, indicating that microbial consortia might exploit complementary or synergistic interactions. While in the rhizosphere of untreated apple plants, ARD-associated taxa like *Novosphingobium* and *Rhizobiaceae* were highly abundant, in the rhizosphere of plants grown in consortium or catch crop treated soils putative plant beneficials (e.g. *Bradyrhizobium* and *Pseudarthrobacter*) were predominant.

Our results suggest that the application of a consortium of beneficial bacteria and AMF as well as the incorporation of catch crops to the diseased soil are promising tools to treat ARD in the future in an environmentally friendly and sustainable way.

A novel *Laccaria bicolor* LysM1 effector is involved in fungal-fungal communication

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Ectomycorrhizal (EM) fungi such as *Laccaria bicolor* play an important role in different forest ecosystems. In contrast to arbuscular mycorrhiza, the EM is predominantly formed with woody plants and provides nutrients in exchange for photoassimilates from its host plants hence enhancing its tolerance to stress. While forming symbiosis with its hosts, *L. bicolor* also interacts with other host-associated fungi and encounters fungal competition for fixed carbon in the rhizosphere. The molecular signaling mechanisms involved in the interaction between *L. bicolor* and other fungi remain unknown to date. Important signaling compounds that might be involved in this communication are specific lipochitooligosaccharides (LCOs). Plant-fungi-interaction studies demonstrated that they are key components of symbiosis signaling with host plants but can also be perceived by *L. bicolor* itself leading to reduced growth of mycelium. The perception of LCOs is mediated by specific protein domains called LysM motifs that bind chitin molecules with very high affinity. These binding domains occur in plant- as well as in fungal proteins. Fungal effector proteins harboring LysM domains are mainly characterized for pathogens where they bind self-secreted chitin to prevent the triggering of plant defenses or protect hyphae from degradation by chitinases. The function of these effector proteins as well as their potential role in fungal-fungal communication in symbiotic EM fungi is so far completely unknown.

To understand the contribution of LysM effector to the EM lifestyle we screened through the genome of *L. bicolor* and identified three candidate genes with LysM domains. One of them, which we named LysM1 contains a signaling peptide crucial for its secretion out of the cell and two LysM domains. We compared expression levels of *L. bicolor* LysM1 (LbLysM1) when *L. bicolor* was co-cultured with other fungal species such as *Paxillus involutus*, another EM fungus that is seen as a direct competitor for host root tips and *Trichoderma harzianum* a mycoparasitic plant beneficial ascomycete. LbLysM1 expression increased when *L. bicolor* interacted with its potential competitor *P. involutus* but was not affected when *L. bicolor* interacted with the *T. harzianum*. As chitin is the backbone of LCOs, we hypothesized that LbLysM effectors might be involved in the LCO signaling cascade that is utilized by fungi during fungal-fungal communication. To test this hypothesis, we generated lblysm1 knockdown and overexpression lines and treated them with LCOs. As opposed to the wild type and LbLYSM1 overexpression lines, the mycelial growth and branching phenotypes of lblysm1 knockdown lines were not affected by LCO treatment, giving a hint that LbLysM1 might be crucial for LCO perception in *L. bicolor*. Furthermore, lblysm1 knockdown lines produced numerous pseudo-clamp connections suggesting that LysM1 might be essential for ensuring successful nuclear migration and hence stability of mycelial growth. Our findings compel us to propose that symbiotic EM LysM effectors such as LysM1 are involved in fungal-fungal communication, a very different role to that of pathogenic LysM effectors.

Session D

Assessing the carbon footprint of wine production in Germany to identify additional climate change mitigation potentials in viticulture

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The agricultural sector is responsible for approximately 10 - 12 % of the anthropogenic greenhouse gas (GHG) emissions and hence, contributes substantially to climate change. On global scale, the wine value chain emits about 0.3 % to anthropogenic GHG emissions. In countries with increased wine production and consumption, these rates might be even higher. Despite the fact that vineyards account for 0.6 % of Germany's total agricultural area, Germany as one of the top-ten global wine producers and top-five countries in wine consumption offers significant lever for GHG mitigation in the wine sector.

With regard to climate change, viticulture and the entire agricultural sector suffer from its negative effects. Especially extreme weather conditions, which are becoming more frequent, are challenging for viticulture. Therefore, the reduction of GHG emissions in viticulture in order to alleviate climate change is in the wine growers' own interest; but the knowledge about GHG mitigation potentials is scarce.

In the CaberNET project, we assess and investigate the carbon footprint of German wine production, to identify and evaluate factors to reduce its GHG emissions and to give practical recommendations to wine growers. Using life cycle analysis (LCA), we assess and quantify GHG emissions along the wine production chain and its four main phases, i.e., i) establishing of vineyards, ii) viticultural management, iii) vinificaion and iv) bottling. Regarding the LCA system boundary we apply a partial LCA stretching from cradle to fram gate, where distribution, consumption and recycling are not considered. To describe the status-quo of GHG emissions and to identify respective GHG mitigation potentials we consider 1 kg of grapes, 1 l of wine and a 0.75 l bottle of wine as functional units in the LCA. We use face-to-face interviews conducted virtually and in-person to collect data from about 100 wineries from important winegrowing regions in Germany. We collect fram data from the winemaking season 2022, entailing all information relevant to quanify all material- and energy flows in the farm specific production system.

We use econometric models, to investigate cause-effect relations in wine carbon footprints, considering demographic factors as well as farm-, region- and management specific factors, to identify respective GHG mitigation potentials. We further run Monte-Carlo-Simulations to consider and quantify various sources of uncertainty of wine carbon footprints.

Combined stressors in agriculture – Investigating more effects than honey bee colony development

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Agrochemicals (e.g. insecticides or fungicides) are applied to protect plants against pest insects or fungal infections. The use of fungicides in agriculture can affect pollinating insects and soil-living consumers like ants. The quality of plant-derived insects' nutrition and quantity thereof may also be impacted by agrochemicals through alterations of plants' microbial communities. Here, a field study was conducted to assess the impact of fungicide exposure and nutritional limitation on the honey bee *Apis mellifera* and the nectar microbiome of rapeseed, *Brassica napus*. Changes in nectar yeast community were not associated with fungicide exposure but might have resulted from seasonal and regional changes. The exposure lead to limited effects on honey bee population development. Young colonies exposed to combined stressors showed reduced development that was compensated within two month. On the individual level, detoxification measured by GST enzyme activity was significantly reduced during exposure to the fungicide. However, gene expression level of GST-D1 was not affected at the same time. When setting up honey bee colonies in spring, care should be taken to ensure sufficient food supply enabling resilience to agrochemical exposure.

RNAi_safe: The efficacy and potential impact of RNAi technology on target and non-target organisms in crop protection against aphids

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Agricultural ecosystems worldwide face an ongoing challenge from destructive pests. To address this issue, RNA interference (RNAi)-based technology, specifically external application of double-stranded RNA (dsRNA), holds promise as an emerging alternative to traditional chemical pesticides. RNAi is a highly efficient, naturally occurring process that can be tailored to target specific organisms and suppress specific genes. This customization allows for the reduction or elimination of unintended effects on non-target organisms and the environment.

RNAi-based biopesticides have demonstrated their effectiveness against pests like the pea aphid (*Acyrthosiphon pisum*) and the green peach aphid (*Myzus persicae*), which feed on phloem sap. These pests excrete gel saliva that forms a protective sheath around their mouthparts as they feed, ultimately damaging plants by depriving them of nutrients and transmitting viruses. Silencing the gene responsible for sheath formation, known as the structural sheath protein (*shp*), has been shown to hinder aphid growth, reproduction, and survival.

Our research project seeks to evaluate the potential of using dsRNA-spray applications as a means of controlling aphid infestations, while also investigating environmental exposure and the fate of dsRNA. Initially, we employed bioinformatics to identify target gene sequences that share high homology between the two pest species of interest, *A. pisum* and *M. persicae*. After aphids ingested dsRNA synthesized *in vitro* through an artificial diet, our analysis using quantitative polymerase chain reaction (qPCR) revealed a significant reduction in *shp* gene expression. Additionally, we identified suitable dsRNA sequences to silence other genes, broadening the applicability of this approach.

In the next phase of our project, we will focus on identifying potential routes of exposure and assessing the impact of applied dsRNA on non-target organisms such as honey bees, ladybugs, and other beneficial insects. Finally, we will assess the stability of the dsRNA spray at various temperatures to evaluate its effectiveness in different geographic regions and its resilience in the face of changing climatic conditions.

Development of molecular markers for fire blight resistance in pear (*Pyrus communis* L.)

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Pear is an important fruit crop species. Since most varieties grown commercially are highly susceptible to fire blight, a severe disease that is caused by the bacterium *Erwinia amylovora*, and appropriate control measures are scarce, the cultivation of pears remains challenging. The cultivation of varieties that are resistant to fire blight is considered as one of the most effective remedies against this disease. Therefore, resistance to fire blight is an important topic in pear breeding. In order to select for resistance at an early stage marker-assisted selection (MAS) is required. We report on the develompent on SSR-markers linked to fire blight resistance-loci of the pear variety ˈHarrow Sweetˈ, which will be used for MAS of pear seedlings.

Acknowledgements: The project FeuResBir is supported by funds of the Federal Ministry of Food and Agriculture (BMEL) based on a decision of the Parliament of the Federal Republic of Germany via the Federal Office of Agriculture and Food (BLE) under the innovation support programme.

Session E

Analysis of the relationship between landscape structure on the occurrence of peach aphid fly (*Myzus persicae)* in sugar beet fields

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Several insect infestations, some of which are vectors of viruses in sugar beet (*Beta vulgaris ssp. vulgaris L.*), can lead to large yield losses without appropriate control measures. The use of predictive models and decision support systems (DSS) can assist the farmers and their advisors on effective application of pest control measures and optimize their implementation.

The collaborative project "EntoProg" is developing DSS for the following insect pests: the Green Peach Aphid (*Myzus persicae*) and the Black Bean Aphid (*Aphis fabae*), as well as the Meadow Spittlebug (*Pentastiridius leporinus*). These aphids cause damage through sap-sucking feeding pattern, and former two also play a significant role as vectors of viral diseases. These pests are widespread, but their relative abundance varies from year to year and region to region.

Landscape structures act as sources and sinks for pests by serving as overwintering habitats or nesting/feeding sites thereby directly influencing the occurence and spread of pests in nearby agricultural fields. A habitat analysis was carried out to determine the effect of landscape features on pest populations. The data on pest occurences comes from regular field surveys in the form of trap captures and surveys of crops and soils carried out by the project partners. The Authorative Topographic-Cartographic Information System (ATKIS) and crop cover maps based on satellite images or the Integrated Administration and Control System (IACS/InVeKos) were used to describe the surrounding landscape in high resolution. The spatial ecology of the pests was examined in relation to environmental factors, behavioral responses, and the effects of spatial patterns. Percentual areas of and minimum distances to the different landscape classes in increasing buffer sizes of upto 10 km were analysed using machine learning methods such as random forests and mixed-effect models to identify areas/fields with high infestation risk.

The project is funded by the German Federal Ministry of Food and Agriculture (BMEL) based on a resolution of the German Bundestag. The project sponsor is the Federal Agency for Agriculture and Food (BLE). Funding reference: 2821ABS031.

Investigating the host plant selection of the brown marmorated stink bug *Halyomorpha halys* for developing a novel push-pull-kill strategy for organic fruit and vegetable production

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The Brown Marmorated Stink bug (BMSB) *Halyomorpha halys* (Stål) (Hemiptera: Pentatomidae) is an invasive and polyphagous pest insect. Over 200 different plants from several families are hosts for the bug native to Eastern Asia. The frequent occurrence in fruit and vegetable crops and feeding behaviour on the crops causes high economic losses for farmers in the newly invaded regions, especially for fruit growers. Because of the high robustness against several insecticides, only repeated applications or the use of broad-spectrum insecticides are currently effective for population control. In Germany, none of these insecticides are permitted against BMSB. Thus, a new pest management strategy against this plant-sucking insect is needed, especially for organic and integrated farming.

The aim of the joint project BIOBUG is to develop a new biotechnical plant protection strategy against BMSB in organic horticulture. It is based on a push-pull-kill system, where volatile attractants, repellents, and a biological insecticide or microbial antagonist will be encapsulated. This way, a selective, environmentally friendly, and cost-saving control method for BMSB will be developed.

To design such a strategy, it is important to understand the host plant recognition of the target insect. Specific scents are important for host plant selection and recognition by herbivorous insects. Colour can also contribute to attractiveness. For investigating this, field monitoring of the bugs on different crops was conducted. When high abundances of *H. halys* were observed with aggregation pheromone baited traps, plant volatiles were collected and colour spectra of fruit and leaves were measured. Subsequent analysis using thermodesorption, and gas chromatography coupled with mass spectrometry (GC-MS) gave an insight into the composition of the emitted volatiles and similarities of the VOC profile of the different hosts. Common compounds were tested using electroantennography and volatiles perceived by the test insects were determined.

Identifying common host plant volatiles that the bug can perceive, combined with specific visual cues, are the first steps in developing a potential attractant, that could then be used in an innovative capsule based attract-and-kill strategy. Here, I will present the first results of this chemical and spectral analyses and electroantennography with the BMSB.

The success of plant-beneficial microbial inoculants to boost plant growth is linked to bacterial community shifts at higher than lower taxonomic levels

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Soil microorganisms are key players of soil and plant health. Harnessing this potential for microbiome-based applications could contribute to reduce agrochemical inputs and therefore improve agricultural sustainability. One option to manage the microbiome is to externally add beneficial microorganisms by inoculation, which may restore crop productivity, promote plant growth or improve stress resilience. However, microbial inoculants often suffer from low or varying efficacy under field conditions. In order to better understand the underlying reasons we conducted a field inoculation experiment in two consecutive vegetation periods. The long-term field experiment in Bernburg/ Germany served as study site, which allows to compare the influence of different management practices (mould-board plough vs. cultivator tillage) as well as fertilization intensities (intensive fertilization including fungicides vs. reduced fertilization without fungicides) on inoculant performance. We drench-inoculated maize, grown in the differently managed soils, at two early plant developmental stages with a beneficial consortium (*Pseudomonas* sp., *Bacillus* sp. and *Trichoderma* sp.). Control plants received only water. Sampling was carried out five weeks after the second inoculation. Plating of the rhizosphere showed that the inoculants successfully colonized the roots independent of the year. Yet, their efficacy depended on the vegetation period. In 2020 with early drought, the inoculation significantly increased shoot biomass while this was not observed in 2021 with average rainfall. Also, the modulation effect on the indigenous rhizosphere microbiome (alpha- and beta-diversity) depended on the year as well as on the tillage practice. The integrative analysis of soil, plant and microbial data will allow to obtain further insights into inoculation-dependent root-microbiome interactions as well as the ecology of rhizosphere microbiome management under field conditions.

Studies on the identification of resistance to *Fusarium oxysporum* (Schlecht.) in different genetic backgrounds of *Asparagus officinalis* (L.) and its defense responds

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Fusarium oxysporum is a serious disease that causes root and crown rot in asparagus. Large asparagus growing areas in Europe are infected with it, resulting in yield and quality losses at harvest. It cannot be effectively controlled by cultural or plant protection methods. Therefore, breeding resistant cultivars is an important strategy for controlling *Fusarium oxysporum* in asparagus. The only resistance known in the literature is *Asparagus densiflorus*, a wild relative of garden asparagus. However, this has not yet been transferred into cultivars, making the identification of other resistant species important.

In the seedling test, several cultivars and wild species were tested for resistance to *Fusarium oxysporum* using two isolates of different virulence. The lines tested generally showed high levels of infestation, with *A. aethiopicus* showing no symptoms of infestation such as browning of roots or growth depression. This wild species was then examined for its defense response after infection with *Fusarium oxysporum*, *A. densiflorus*, and *A. officinalis* cv. Thielim were also tested for comparison. Like *A. densiflorus*, *A. aethiopicus* showed a hypersensitive reaction as a defense response, while A. officinalis cv. Thielim showed no such reactions. In *A. aethiopicus*, a new potential source of resistance to *Fusarium oxysporum* was identified.

The next step is to develop a greenhouse test to analyze resistance behavior at later plant stages. The goal is to determine if resistance in the seedling also occurs in the adult plant.

Natural products for control of powdery mildew on different barley genotypes

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Global warming is a major challenge for plant health and crop yield. Thereby, both drought stress itself and associated pathogens threaten harvests. Since chemical pesticides can pose a threat to the environment, their use is increasingly regulated, and more sustainable solutions are needed. Natural products can provide a remedy as they have the potential to promote plant growth and tolerance or resistance to diverse stresses. One of the main goals of the project MORGEN (Modelling of drought stress tolerance in barley using biological plant protection – the crop of tomorrow) is to find a sustainable way to reduce both powdery mildew infection and drought stress on barley. Twenty biostimulants, plant strengtheners and basic substances were screened for their effectiveness against *Blumeria graminis* f.sp*. hordei* on four different barley genotypes. Eleven products showed mildew reducing effects for at least one genotype. Two products were effective on all four genotypes. However, biotic and abiotic stressors do not occur separate from each other, but often simultaneously. Thus, to verify their potential, the most promising of the tested products were evaluated for their efficiency against powdery mildew under simultanious drought stress. In this way, promising products with genotype and drought stress independent efficiency were found. To adress the underlying mechanisms, gene expression (qPCR) analyses were conducted to identify regulatory pathways and the associated genes involved in the observed effects.

Fusarium diseases affecting pea cultivars across Europe: a characterization of virulence and resistance

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Pea (*Pisum sativum* L.) is one of the most cultivated leguminose plants. With a production that reached 12.4 million tons of dry peas in 2021, this crop is affected by several soil-borne pathogens. One of the major diseases is *Fusarium* wilt, caused by *Fusarium oxysporum* f. sp. *pisi*, which can cause high yield loses from 30 to 50% in pea. In this study, samples of infected pea roots were analysed from important growing areas in Europe, to determine which species were present on those sites. Single spore isolates were obtained from the samples, and initially, their morphology and growth rate in media was investigated. Next, species identification was performed by using PCR and morphological characteristics. Two single spore isolates of *F. oxysporum* were selected for virulence test on a Pea diversity set in greenhouse. Three pea cultivars and a resistant bearing expressing different resistance levels against *F. oxysporum* were tested using a sand-cornmeal mixture previously inoculated with one of the two single spore isolates. The results from these experiments provide important information on possible candidates for breeding programs with proven resistance to *F. oxysporum* and provide cultivars with high yield potential.

The project is supported by funds of the Federal Ministry of Food and Agriculture (BMEL) based on a decision of the Parliament of the Federal Republic of Germany via the Federal Office for Agriculture and Food (BLE) under the innovation support programme.

Session F

Proximity loggers to study spatial behaviour and contacts among small rodents in farming environments

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Small rodents are responsible for transfer of various pathogens to people and livestock and can cause considerable damage in farming. Frequent contacts between wild rodents and livestock favour pathogen transfer, which can lead to high economic losses. Understanding the movement patterns of small mammals on farms is therefore important to prevent damage and pathogen transfer. Miniaturised proximity loggers represent a newly developed tool for monitoring the spatial behaviour of wild rodents by using Bluetooth signal as indicator of close contacts between individuals. Differences in signal strength give information about the proximity among individuals and between individuals and specific spots on farms. By recording contact points between rodents and livestock feeding sites, the logger system gives also information about possible pathogen transmission routes. Our method study provide initial experience of the methodology in an agricultural setting as well as results of dry runs for testing and calibrating this technology in farming environments with animal husbandry. Such tests yield information about the effect of physical barriers that may interfere with Bluetooth signal and how the Bluetooth signal evolves in different habitat types on farms. The results will support developing the method further and contribute to apply a validated technique in the field.

This work was financially supported by the German Federal Ministry of Food and Agriculture (BMEL) through the Federal Office for Agriculture and Food (BLE), grant number 2821ERA22D. This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 862605 within the framework of Cofund ERA-Net ICRAD. This is a project RodentGate publication.

Development of a phenological model for winter rapeseed in Germany to predict flowering stages

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Phenological models offer valuable insights into crop growth and development, enabling timely and informed decisions for sustainable cultivation practices. Among the key agricultural crops in Germany, winter rapeseed (*Brassica napus*) holds a significant position. The incidence of diseases affecting winter rapeseed and the corresponding protective measures are linked to the phenological stages of the crop. Phenological models serve as the foundation for various pest and disease forecast models, facilitating the timely application of plant protection products. The current phenological model used in the *Sclerotinia sclerotiorum* risk forecast system (SkleroPro) hasn't been performing well in recent years. In response, this study focuses on recalibrating the existing model to enhance its accuracy. Additionally, a novel phenology model has been developed and tested. These efforts represent significant steps towards refining phenological modeling within the SkleroPro forecast system, ensuring more precise and reliable predictions of *Sclerotinia sclerotiorum* infection risk and suggesting a more accurate plant disease management to the farmers.

Since Sclerotinia stem rot is the main disease to consider during the flowering stages, the objective of this model is to accurately predict the flowering stages of winter rapeseed in Germany (specifically BBCH 55-69) with a target time difference of ideally +/- two days. We first enhanced two existing models through function modifications and parameter recalibration. Additionally, we developed a new temperature sum model that also considers the effect of photoperiod. The predictive accuracy of each model was rigorously evaluated using BBCH data collected from over 100 locations across Germany from 2020 to 2023. The observed BBCH data was provided by the Plant Protection Services (PSD) of the participating federal states and the Julius Kühn Institute, much of it collected as part of the field trials set up in the projects ValiProg and EntoProg.

Our best models are able to predict rapeseed flowering stages (BBCH 55-69) with an accuracy of +/- four days, starting simulation on February 1st, while disregarding sowing dates. Given this model's superior accuracy compared to existing models, it can be easily integrated into SkleroPro. This integration opens the door for further modifications to SkleroPro, with the potential to significantly enhance its accuracy in recommending appropriate management strategies against a possible Sclerotinia infection.

This study was carried out in the framework of the project "Computer-based prognoses and decision support systems in crop protection (ValiProg)" funded by the Federal Ministry of Food and Agriculture (BMEL) based on a resolution of the German Bundestag. The project executing agency is the Federal Agency for Agriculture and Food (BLE). Funding reference: 2819ABS101.

Strip cropping with oilseed rape and wheat – a strategy to enhance biodiversity in conventional agroecosystems?

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There is increasing awareness that modern agriculture needs to balance food production with environmental conservation. The adoption of diversified and wildlife-friendly farming systems is essential to achieve sustainable farmland biodiversity goals. Key drivers of farmland biodiversity include land use intensity, crop diversity, field size and edge density and the share of non-crop habitats in the surrounding landscape.

Our study focuses on assessing the potential of strip cropping with oilseed rape and wheat to enhance biodiversity and associated ecosystem services in commercial managed arable fields. Strip cropping is a farming system in which multiple crops are grown in adjacent strips on one field. It offers the prospect of maximising ecological benefits while maintaining high yields in agricultural production.
In 2022 and 2023, we assessed biodiversity on 16 conventionally managed farms in Lower Saxony and Saxony-Anhalt. We compared strip cropping fields, each consisting of seven alternating strips of 21 - 36 m wide, with nearby oilseed rape and wheat fields as reference. Field management practices within the strip cropping field were comparable to those in the reference fields on each farm. Using a combination of field surveys we evaluated the impact of strip cropping on various components of biodiversity, including birds, arable weeds and beneficial insects such as epigaeic arthropods and pollinators.

Our hypothesis was that strip cropping, with its increased crop diversity, edge density and habitat complexity, would promote greater biodiversity compared to *pure* arable fields.

First results suggest that strip cropping with oilseed rape and wheat enhances the number of farmland bird individuals and species. Moreover, the arable weed flora was more diverse in strip cropping fields compared to wheat fields. Natural predators of crop pests, such as carabids, also benefited from the increased crop diversity at field level through spill-over effects. Strip cropping fields with oilseed rape hosted more pollinators than wheat fields, possibly due to more pollen and nectar resources between crops.

However, the ecological benefits of strip cropping need to be weighted against the increased number of management operations and the lower crop yields near the crop boundaries in strip cropping fields due to edge effects.

Hence, strip cropping can serve as a diversification strategy to increase field edge density and crop diversity at field level, both of which are essential for integrating biodiversity conservation into conventional agriculture. However, the potential of strip cropping to enhance biodiversity depends on factors such as strip width, choice of crops and their combination.

Development of a rearing system for the potential biocontrol agent *Pemphredon lethifer* (*Hymenoptera*: *Crabronidae*)

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In vegetable and ornamental crops, biocontrol agents of aphids often leave leftovers such as droppings or aphid mummies, which are generally not accepted by retailers and consumers. Therefore, new methods for leftover-free biological control of aphids are necessary. A promising method is the use of digger wasps of the genus *Pemphredon* as biocontrol agents. Especially promising is the species *Pemphredon lethifer* (SHUCKARD 1837), as it is widespread in Central Europe. Females of *P. lethifer* collect and remove aphids completely from plants and transport them to their nests, to provide food for hatching larvae. Nests are dug into pithy twigs like *Sambucus* spp. or *Rubus* spp. However, until now, no rearing system of *P. lethifer* is established for research or commercial use. In order to develop a rearing system of *P. lethifer* for use as biocontrol agent, more details about its nesting preferences are needed. In this context, we evaluate which pith diameter and artificial tubes *P. lethifer* prefers for nesting.

In 2022, at seven and in 2023 at 20 study sites in Braunschweig, Germany and the surrounding area, three trap nests were installed per study site in accordance to nesting activity. Each trap nest consisted of 16 twigs of 30 cm length of *Sambucus* spp., with four different pith diameter categories ranging from 2.5 to 10.5 mm. Trap nests were checked weekly for signs of nesting. Twigs with a sign of nesting, were transferred to the laboratory and replaced with a new twig of the same category. Twigs with nests were stored in individual boxes. Adult wasps, which were present in the nests at time of collection, as well as wasps and parasitoids emerging from the nests later on, were measured and identified.

In a next step pith diameter preferences are studied in the laboratory. In this choice experiment a female and a male *P. lethifer* are placed together in a cage with twigs of defined pith diameters and nesting is documented. As soon as signs of nesting are visible, an additional twig of the same diameter category is offered.

Result of the described experiments as well as first results of additional experiments on artificial nesting materials are presented and discussed. The findings are crucial for development of a rearing system for *P. lethifer* for biological control in vegetable and ornamental crops.

Effect of soil restoration practices on the soil microbiota in Uruguayan vegetable and grain production systems

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Intensive agriculture affects soils worldwide leading to increasing soil degradation and loss of ecosystem functions. We hypothesized that soil restoration practices select beneficial soil and rhizosphere microbiota, preserve soil health and hence, increase plant biomass in contrast to conventional intensive agricultural practices.

Therefore, we evaluated two Uruguayan long-term field experiments (LTEs), where soil physicochemical properties, plant performance and soil and rhizosphere microbiota were studied. LTE1 allows to assess the soil restoration potential of organic fertilization (compost, poultry manure, cover crop) combined with conventional tillage (CTOF) or reduced tillage (RTOF) in a vegetable farming system. CTOF and RTOF were compared with conventional tillage combined with mineral fertilization (CTMF), and an adjacent undisturbed site (UND) was used as reference of healthy soil. LTE2 allows to assess the soil restoration potential of pasture-crop rotations in a grain cropping system. Short pasture-crop rotation (SR, two years grain crop cultivation alternating with two year of sown pastures) and long pasture-crop rotation (LR, two years grain crop cultivation alternating with four year of sown pastures) were compared with continuous grain crop rotation (CC), and an adjacent natural grassland (NG) was used as reference of healthy soil.

In LTE1, the fertilization source strongly shaped the soil and table beet rhizosphere microbiota. RTOF exhibited higher table beets yields than CTMF, also a significantly proportion of large soil aggregates (> 2 mm), soil organic C, nutrient availability and microbial alpha-diversity than CTMF and became more similar to UND. We propose that RTOF has the potential to restore and improve soil health under intensive vegetable farming systems mediated by soil and rhizosphere microbiota.

In LTE2, pasture-crop rotations increased soil aggregates >2 mm, soil N and decreased bulk density in comparison to CC and showed values similar to NG. High-throughput amplicon sequencing (16S rRNA gene/ITS2) showed that soil microbial communities, and rhizosphere bacterial/archaeal communities were shaped by rotations. Moreover, in spring, the two N-fixing bacteria Devosia and Microbacterium were positively correlated with oat aerial biomass and N content, and had a higher relative abundance in SR in comparison to CC. The selection of a beneficial soil and rhizosphere microbiota and the improvement of soil physicochemical properties lead to an increase of oat aerial biomass and N content in crop-pasture rotations in comparison to CC. In summer, the rotation effect on the microbial rhizosphere communities' was lost. Nevertheless, Microbacterium isolates were obtain by bacterial dilution plating from SR rhizospheres, which showed several in-vitro plant-beneficial traits. The majority of bacteria isolates were identified as *Bacillus* and *Pseudomonas* and isolates obtained from SR/LR showed several in-vitro plant-beneficial traits. In summary, our results suggest that pasture-crop rotations have the potential to improve soil health under grain cropping systems mediated by soil and rhizosphere microbiota.

A multiscale crop modeling framework can guide the prospective sustainability assessment

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Photosynthesis has garnered substantial scientific support for enhancing crop yields through precise targeting and exploiting natural variations using traditional plant breeding techniques. However, assessing the prospective impact of developing new cultivars presents significant challenges. These challenges primarily stem from the intricate nature of metabolism, resulting in a non-linear relationship between crop growth and resource utilization. Furthermore, accurately translating biochemical enhancements in photosynthesis to productivity on an agricultural systems scale adds another layer of complexity. These complexities emphasize the importance of conducting comprehensive assessments and exercising careful consideration when striving to optimize crop production and foresee the impacts of new crop varieties.

Multiscale crop modeling provides an opportunity to represent genetic, biochemical, and physiological traits that interface with various biological and technological scales of crop production. This approach closes data gaps and harnesses multisource data to capture complex interactions among genotype, environment, and management (G × E × M) in crop development, growth, and yield. Sustainability assessment can be accomplished by applying life cycle thinking, which is a comprehensive method utilizing life cycle assessment (LCA) to evaluate the economic, social, and environmental impacts of processes. It proves invaluable for gaining insights into designing new sustainable crops. Moreover, integrating multiscale crop modeling with LCA allows for a holistic examination of their effects on both crop productivity and ecosystem sustainability.

The objective of this study is to establish an integrated approach that combines multiscale crop modeling with prospective life cycle assessment (pLCA) to proactively evaluate the potential environmental and socioeconomic consequences of enhancing photosynthetic traits in maize. This framework involves incorporating a calibrated maize genotype into the process-based crop model (DSSAT) to simulate variables such as leaf area index (LAI) and specific leaf nitrogen (SLN). Subsequently, these variables will be integrated into the mechanistic model (DCaPS) to simulate daily canopy photosynthesis and biomass accumulation. To gain insights into the impact of rubisco activity on daily-accumulated biomass production, we will conduct a perturbation analysis on rubisco carboxilation activity, using the DCaPS. Following, the daily-accumulated biomass data will be reintegrated into DSSAT for allocation and computation of various crop attributes. The virtual genotype outputted from DSSAT, along with information on climate conditions and crop management practices, will be used to construct the life cycle inventory for the pLCA, facilitating a comprehensive prospective sustainability analysis.

This advanced framework will empower us to assess the impacts of photosynthesis-to-farm design within sustainable crop production systems. It will identify process bottlenecks and enable breeders to anticipate environmental, social, and economic considerations in the early stages of research and development.

Poster

Exploitation of plant genetic resources for sustainable sweetness of *Lupinus angustifolius* L.

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Narrow leafed lupin (NLL) (*L. angustifolius*) is a protein crop with a wide range of applications in feed and food industry. It is well adapted to light soils with poor groundwater conditions and can even improve soil quality with its ability to fix nitrogen with the help of nodule bacteria. However, its use is limited by the alkaloid content of the seeds (reference: 0.05% feed, 0.02% food). Due to the genetic bottleneck that has occurred during the selection of sweet NLL varieties in the 1930s, it is necessary to increase the genetic diversity in current breeding material. In order to overcome this bottleneck, a wide range of sweet and bitter varieties, gene-bank accessions, mutant-lines and landraces of different origins have been compiled. Potentially interesting results are expected from the mutant-lines, which previously showed low alkaloid content in several environments. In addition, they also did not test positive for the *iucundus* locus, which is widely distributed.

The main objective of this project is to develop environmentally stable NLL lines for high yield and low alkaloid content. To achieve this goal, (1) genome-wide association studies with alkaloid rich and poor varieties, (2) development of markers for performance of marker-assisted selection and linkage analysis, (3) genetic and functional characterization of alkaloid biosynthesis by transcription analysis (Frick et al. 2018), (4) genetic analysis with segregating populations and (5) pyramidization of gene variants for low alkaloid content will be conducted. Furthermore, the quantity and quality of alkaloids in leaves and pods will be measured by GC-MS and FID.

With potentially new sources of genes and mutations for low alkaloid content in so far unused plant genetic resources, we hope to improve future breeding programs and secure the application of NLL in the feed and food industry.

Boosting beneficial arthropods in nature protected areas to strengthen biological control – the project „Schutzhochzwei“

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In nature protected areas in Germany, the use of particular insecticidal pesticides, with risks for bees and other pollinators, is prohibited. Current discussions about extending these bans to other regions, such as Natura2000-areas, are causing farmers to fear lower crop yields and associated income losses. The project „Schutzhochzwei“ (funded by BfN – Federal Agency for Nature Conservation) will investigate whether the abandonment of these pesticides in combination with the consistent implementation of integrated pest management on cropland in nature protected areas, results in the promotion of beneficial arthropods and consequently in an increased natural pest control. Furthermore, additional actions for ecological enrichment will be elaborated to increase these target values.

Systems of pests and beneficial arthropods on cereal fields in nature protected areas, which are already affected by pesticide restrictions, are investigated. The beneficial arthropods present are monitored by the use of pantraps and sweep netting. The occurrence of aphids, the main pest in cereals, is assessed, as well as the presence of aphidophagous predators and of aphid mummies to determine parasitism. The beneficial arthropods of particular interest are hoverflies due to their important pest regulating role in arable crop systems. During further work process, specific interventions for the ecological upgrading of the fields and their surroundings, like flower strips and alternated hedgerow management will be developed and their effects examined. Positive results from this project may have the potential to reduce the concerns of affected farmers and further provide an indication of possible reduction of crop losses by avoiding insecticidal pesticides through the help of beneficial insects.

Variation in virulence behaviour and characterisation of field isolates of *Sclerotinia sclerotiorum* (Lib.) de Bary

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Sclerotinia stem rot (SSR), caused by *Sclerotinia sclerotiorum*, poses a significant threat to oilseed rape cultivation in Germany. Without disease management, *S. sclerotiorum* can lead to a substantial reduction in crop yield. To mitigate its impact, a combination of cultural management and fungicide application is necessary. The primary objective of this study was to assess the diversities in morphological characteristics and virulence within the population of *S. sclerotiorum*, which was collected from different geographic regions in Germany.

A total of 57 *S. sclerotiorum* isolates were gathered through a comprehensive *Sclerotinia*-monitoring initiative between 2020 and 2021. Various physiological and morphological assessments were conducted, including measurements of parameters like the mycelial growth index (MGI), mycelial compatibility grouping (MCG), and morphological characterization involving colony shape and colour. Additionally, the number and weight of sclerotia produced per isolate were determined. Furthermore, two distinct approaches were employed to evaluate the aggressiveness of the *S. sclerotiorum* isolates on specific genotypes of oilseed rape cultivars.

Among the examined *S. sclerotiorum* isolates, a high degree of phenotypic and pathogenic diversity was observed. The colony colours ranged from white to beige and even to brown (nearly black), while the growth patterns were categorized based on the appearance of the sclerotia. Four main patterns were observed, ranging from circular on the edge of the petridish to circular near the edge, and from two circles up to a non-circular distribution of the sclerotia, either with or without mycelial coverage.

Differences were observed among the isolates concerning the mean quantity of sclerotia per isolate. Furthermore, variations were identified among the isolates in terms of their pathogenic traits. Independent of the assessment method, the isolates were divided in the following categories: high aggressivity, moderate aggressivity, or low aggressivity. Differences were recognized in the reactions of different oilseed rape cultivars to various *S. sclerotiorum* isolates.

The outcomes of this investigation provides novel insights into the diversity of cultural attributes and levels of aggressiveness within the *S. sclerotiorum* population.

A project to identify and map scab and powdery mildew resistance genes in apple

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Apples are one of the most important fruits worldwide and the most important fruit species in Germany. However, the cultivation of this culture faces many different challenges. At the top of the list are apple scab (*Venturia inaequalis*) and powdery mildew (*Podosphaera leucotricha*). Both of these fungal pathogens are favored by climate change and are becoming increasingly important. To control these pathogens, up to 20 plant protection treatments are applied per season in commercial fruit production. The frequent use of fungicides leads to ecological issues and promotes the formation of fungicide-resistant races in these pathogens. An important approach for more sustainable apple production and less environmental damage is the cultivation of apple cultivars resistant to scab and powdery mildew. The aim of this project is to advance the breeding of new cultivars resistant to scab and powdery mildew by identifying and introducing new resistance genes. The objectives are to phenotype scab and powdery mildew at three different locations in Germany, to identify and map apple scab and powdery mildew resistances from genetic resources and *M. orientalis*, and to develop and validate KASP assays for powdery mildew and scab resistance genes.

Acknowledgements: The project is granted by the German Federal Office for Agriculture and Food.

Contamination of organic raw materials and recycled organic fertilizers with antibiotics

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Since the resources for mineral fertilizers are limited and the energy costs have recently risen considerably, there is an increasing interest in closing nutrient cycles and the recycling of nitrogen and phosphorus in secondary raw materials. Nutrient-rich waste materials can be used directly as a fertilizer or after processing. If other valuable ingredients such as organic carbon are in the product after processing, pollutants can be present as well. In the present work, contamination by antibiotics will be discussed. Antibiotics are used in large quantities to treat bacterial infections in humans but also in animals for food production. Resistant or even multi-resistant strains can occur in feces if antibiotics are regularly used in higher quantities. It was the aim of the study to show which recycled organic fertilizers contain a particularly high amount of antibiotics. Sewage sludge and composted sewage sludge, digestate with animal excrements, residues from food production and processed fertilizers such as ash products or struvite were studied. Exemplary, 14 antibiotics out of three classes were analyzed. Especially fluoroquinolones and tetracyclines are present at higher concentrations in fertilizers of animal origin. In processed fertilizers, the concentrations depend not only on the origin but also on the carbon content, since antibiotics can bind to organic matter.

The influence of infection with 16SrX phytoplasmas (e.g. apple proliferation, pear decline) on the development and behaviour of their vector insects (*Psyllidae*: *Cacopsylla* spp.)

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Several fruit tree diseases are caused by phytoplasmas (bacteria) of the 16SrX group. In apples and pears they cause leaf symptoms and dwarf fruits that are inedible and unmarketable. Another symptom in apples are the witches' brooms. In pears the bacteria also cause dieback of trees. Infection with '*Candidatus* Phytoplasma mali' (apple proliferation) or '*Ca*. P. pyri' (pear decline) is therefore very harmful to the plants and a major economic problem.

The bacteria are transmitted between the trees by the phloemsap sucking psyllids (Hemiptera: Psyllidae) belonging to the genus *Cacopsylla*. Much is known about the diseases and much is known about the interactions between plants and vectors. However, less is known about the impact of infection on the insect vector, especially on the fitness of the psyllids. Answering this question is the main goal of my study, which started in Februray 2023.

Several experiments are planned, two of which are already underway. To answer the question of whether infection affects the flight performance of the vector, adult *Cacopyslla pyri* are made to fly in a self-constructed flight mill. The animals were glued to a glass fibre that is connected to a needle attached to a magnet. This enables the animals to turn the glass fibre while flying. The animal can only fly in a circle and a laser counts the spins. The experiment is not yet completed, but the data already show that *Cacopsylla pyri* are generally not very motivated to fly for more than a few minutes.

In order to answer the question of which absolute sugar concentrations are preferred by the animals and in what ratio these must be to each other, a choice test with different nutrient solutions is currently underway. These consist of the sugars sorbitol and sucrose, which are the most abundant sugars in the phloem sap. It is also to be determined whether the preference differs between infected and non-infected animals. The experiment is not yet complete. What the data already show, however, is that male and female animals seem to prefer a ratio of about 1:3,5 between sucrose and sorbitol, regardless of infectious status.

It is also planned to determine the concentrations of lipids, proteins and sugars of the tested animals. It is assumed that infected psyllids may store different amounts of these compounds than uninfected ones, which should be evident in the data on flight behaviour and the food requirements needed.

Composition of fungi and oomycetes from specific peat substitute substrates

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In the current global concern about climate change, the protection of peatlands is becoming increasingly important, leading to a reduction in the use of peat in substrates for horticulture. As part of the project "Development and evaluation of peat-reduced production systems in horticulture (ToPGa)", the use of fiber nettle *(Urtica dioica* convar. *fibra)* as well as digestate (fermentation residue from biogas generator plants) as possible components of peat substitutes is investigated. The possible pre-contamination of the substrate components with fungi and oomycetes is considered to identify possible phytopathogenic species.

In this work, sample material was received and prepared from digestate, fiber nettle and peat-free commercially available substrates. For the isolation of fungi, two main methods were used: first, isolation via dilution series and second, by directly placing material on nutrient media. For the isolation of oomycetes, a bait test with rhododendron leaves was used. After isolation, DNA was extracted from the isolates, amplified on the ITS region, purified and sequenced. Lastly, the sequences were analyzed.

The partial results of the current work show a collection of 185 fungal isolates from the digestate, fiber nettle samples and commercial peat-free substrates. These isolates were successfully identified at the genus or species level. To date, only one oomycete was isolated.

After identification of mostly all isolates at species level, classification by lifestyle and thus determination of plant pathogens will proceed.

Development of a plant protection agent based on an isolate of the bacterial organism *Lysobacter enzymogenes*

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The project *OptiLyso* is a joint project between two public research institutes the Julius Kühn Institute (JKI) (Institute for Biological Control) and the Hochschule Geisenheim University (HGU) (Department of Crop Protection) and the companies e-nema GmbH and BioProtect GmbH. The aim is to develop a microbial plant protection agent based on a bacterial isolate of *Lysobacter enzymogenes* a well-known producer of lytic enzymes and secondary metabolites with high antibiotic/antimycotic activity. As part of the previous project *mikroPraep* an isolate exhibiting strong suppresive activity against different plant pathogenic oomycetes including *Phytophthora infestans*, *Pseudoperonospora cubensis*, and *Plasmopara viticola*, both in *in vitro* and *ad planta* experiments was identified.

The follow-up project *OptiLyso* focuses on the improvement of the bacterial plant-protecting agent by investigating and overcoming current challenges, such as sunlight stability and rain fastness. Therefore, stability and influence on efficacy of *L. enzymogenes* will be charachterized in *in vitro* - and *ad planta* assays with the pathosystem cucumber and *Ps. cubensis* using the weathering machine *ATLAS Suntest XXL+ FD* allowing for controlled exposure to drought, heat and irradiance. In parallel, the rain fastness of *L. enzymogenes* will be analyzed by the partners form HGU on *Pl. viticola* on grape using a rain simulator. Together with the industrial partners, appropriate additives will be developed and tested to enhance the stability of the product and to ensure high degrees of protection over time. Simultaneously the formulation's influence on the shelf life, anti-pathogenic activity/ disease suppressive activity and miscibility with common chemical-synthetic and microbial plant protection agents will be assessed in *in vitro*, greenhouse and field trials. Moreover, the integration into existing strategies and optimal time points of application will be investigated. In parallel, *L. enzymogenes* biology and responses to pathogens will further be analyzed.

The project and its output have a potential to contribute to a reduction in the usage of chemical-synthetic and copper-based fungicides and to broaden the spectrum of sustainable alternatives for farmers, thereby simultaneously ensuring food security and environmental protection.

Cryptostroma corticale, causal agent of sooty bark disease, and its taxonomic position within the genus *Biscogniauxia* (*Graphostromataceae*, *Xylariales*)

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Cryptostroma corticale is the causal agent of sooty bark disease and has led to the death of sycamores (*Acer pseudoplatanus*) in many regions in Germany and other European countries in the recent years, especially supported by dry and hot summers. *C. corticale* is an ascomycete, but no teleomorphic fruiting body is known so far.

In this project, we aim to classify *C. corticale* systematically. Initially *C. corticale* was described morphologically as monotypic genus, whereas recent findings show that *C. corticale* belongs to the genus *Biscogniauxia* (Graphostromataceae, Xylariales) due to its genetic similarities. However, important to mention, only one third of the whole family is sequenced so far (mainly limited to ITS) and almost all of the species are morphologically described based on their teleomorphic fruiting body.

For this reason, we try to generate sequences from the missing species to receive a full understanding of the taxonomic position of *C. corticale* and its family. Furthermore, there is hope to find the teleomorph of *C. corticale* within the not yet sequenced *Biscogniauxia* species.

Developing artificial model flowers for hoverfly monitoring

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Hoverflies are important pollinators and parts of them are efficient natural enemies of aphids, especially in arable crops. Hoverfly populations are threatened by habitat loss and agricultural intensification. Within the framework of the project MonViA (National Monitoring of Biodiversity in Agricultural Landscapes*), we currently develop, test and evaluate non-invasive methods which may be used in a long-term monitoring of hoverflies in the future. Adult Syrphidae are known to visit flowers frequently for nectar and pollen and can be easily observed here. Therefore, we are exploring the possibility to use artificial model flowers for a standardized observation of hoverflies regardless of flower availability. In greenhouse trials, we tested various flower traits, known to influence flower attractiveness to hoverflies, to create a final model flower combining the most attractive traits. Traits tested included flower colour, flower size, flower composition and arrangement/density, specific floral structures (e.g. fly catcher effect) and floral scent. First results indicate, that a fluorescent yellow colour is particularly attractive. Ultimately, such model flowers shall be used both by entomologists and by citizen scientists to observe and document hoverfly species in a standardized setting in the field. As the observation data from untrained citizen scientists can lack the higher resolution in insect identification, we also plan to collect eDNA samples from the model flowers to gain high quality data on flower visitor identity. Therefore, we are also testing different materials on their capability to retain eDNA, as well as the persistence of eDNA under certain environmental conditions. Based on the results from our laboratory experiments with three hoverfly species, further testing will be conducted in spring under field conditions, with broader range of target organisms and also the comparison of our artificial flowers to natural occurring ones (e.g. wild carrot). In a final step, citizen scientists will utilize the developed flowers in a preliminary survey under realistic field conditions.

*On behalf of the Federal Ministry of Food and Agriculture, a total of 12 specialist institutes of the Thuenen Institute and the Julius Kühn Institute as well as the Federal Office for Agriculture and Food are working together in the project MonViA (https://www.agrarmonitoring-monvia.de/en/).

Fine mapping and validation of highly effective, previously unexploited leaf and yellow rust resistances from wheat genetic resources

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Several rust-resistance genes for wheat have been identified and cloned in recent decades. Annual infections with leaf rust and yellow rust caused by *Puccinia triticina* and *Puccinia striiformis*, respectively, result in significant yield losses of up to 50% and quality losses. The integration of unused germplasm shows potential for breeding new cultivars with improved resistance genes. Therefore, identifying genotypes with new, previously unknown resistances is an important task to avoid epidemics caused by cereal rust and minimize yield losses in an environmentally friendly way. To achieve this, the main goal of the project Genebank is to transform the *ex-situ* wheat collection of the Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Gatersleben into a collection actively used in breeding. In the first two phases of the project, the Julius Kühn Institute (JKI) Quedlinburg has already tested about 9600 winter wheat and 2700 spring wheat accessions of the IPK Gatersleben ex-situ genebank in field and greenhouse tests for their resistance to defined highly aggressive races of yellow and leaf rust. Based on the phenotypic data obtained in combination with sequencing data, a GWAS identified yellow rust resistance QTL on nearly all wheat chromosomes as well as 194 leaf rust resistance-associated loci on chromosomes 1B, 4A, 4B, 6B and 6D, including resistance sources already used in elite material. Most of these resistances are active at the seedling stage. Moreover, some unknown resistances could be identified in adult plants in different field trials.

The third phase of the project aims to exploit resistances that have not yet been used in breeding. Using the Macrobot platform as a high-throughput phenotyping method, new resistance loci to yellow and leaf rust will be fine-mapped and validated using several races with different virulence patterns. Strategies for validating the resistance associations will be pursued, considering the size of the resistance-associated regions. The goal is to build a publicly accessible library of donors that are carriers of rare resistance loci to different races of powdery mildew, yellow rust and leaf rust. Furthermore, the genetic background will be analyzed, so that potential candidate genes will be detected.

Development of a standard trial for testing the agronomic efficiency of recycling-based P fertilisers

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The agronomic efficiency of fertilisers is largely dependent on substrate- and crop-related factors. Results from vegetation trials with different test designs are therefore often difficult to compare. For this reason, a standardised test procedure is needed, especially for testing new types of fertilisers.

In addition to standardising the test design, it is necessary to use a standardised growing medium. The substrate must be a) poor in the nutrient to be tested, b) reliably reproducible and c) designed in its properties to reflect the most important factors influencing plant availability of nutrients in agricultural soils ("'soil-like substrate'").

An artificial substrate mixture is presented, which is derived from a standardised formulation for ecotoxicological tests (EN ISO 11268), together with the associated test design. The standardised artificial substrate mixture developed consists of coarse quartz sand, the 3-layer clay mineral bentonite and bark humus or black peat as an organic component.

The developed substrate mixtures and test design were applied in a vegetation trial with *Lolium multiflorum*. The trial was conducted in 1.4 L pots with 2 kg substrate in a vegetation hall. During the 98-day trial period, three harvests were carried out to determine the plant availability of the different fertilisers at different times.

Struvite ($MgNH_4PO_4 \times 6\ H_2O$), a phosphorus (P) recycling fertiliser recovered during wastewater treatment, was used as a test fertiliser, while soft ground rock phosphate and triple superphosphate served as reference fertilisers. Both test and reference fertilisers were mixed into the substrate in ground form with 30 mg P/pot. As part of the basic fertilisation, all nutrients except P were provided to the plant in slight excess. Substrate and trial design proved to be feasible to demonstrate the expected fertilising effects of the tested products. However, P rate and basic fertiliser recommendation need further optimisation.

The series of trials will be continued with an upscaled container trial (1 m^3) with other (also dicotyledonous) crops, and a comparison of the JKI standard substrate with a purely mineral standard substrate (developed by HGoTECH GmbH Bonn) in Kick-Brauckmann pots (7 L).

Apple cultivars across the partners of the apple network within the German Fruit Genebank

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The German Fruit Genebank is a decentralized network, which focuses on the conservation and utilization of genetic resources of native fruit species. Within the German Fruit Genebank, 34 partners are cooperating across Germany under the coordination of the JKI - Institute for Breeding Research on Fruit Crops in Dresden-Pillnitz. To simplify the interaction between partners, each fruit species is represented by its own network. Here, the apple (*Malus* × *domestica*) network is the largest network as it is carrying the most cultivars. In the apple network, there are 16 partners such as governmental and educational institutions as well as plant nurseries. The network is managed by the Institute for Breeding Research on Fruit Crops in Dresden-Pillnitz. In recent projects, the cultivar collection of selected partners of the apple network have been assessed for trueness-to-type of their accessions. In the first step, at least two knowledgeable experts of the German Pomological Association characterized the accessions pomologically. In the second step, this approach was supported by a molecular characterization using a set of 17 simple sequence repeat markers and 8 reference genotypes recommended by the European Cooperative Programme for Plant Genetic Resources (ECPGR). The characterization of the apple cultivars gave rise to an overview of the abundance and diversity of apple cultivars in the German Fruit Genebank and the collections of the partners. Furthermore, an extensive database of molecular unique fingerprints per apple cultivar was built to use as a reference for future assessments of cultivar identity. The focus on the trueness-to-type of the apple cultivars highly elevates the quality of the German Fruit Genebank apple collection.

Use of artificial intelligence for grapevine yield forecast and sensor based screening of yield relevant characteristics within grapevine breeding research

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Yield in viticulture is closely linked to the quality of grapes and consequently determines economic profitability. In general, a higher yield leads to lower wine quality. Therefore, yield is one of the most important parameters for wine production and must be balanced. Yield is influenced by various parameters such as genotype, soil, weather, disease pressure, and vineyard management. Until now, yield estimation has usually been done manually, which is time-consuming and prone to errors. Estimation errors for yield average around 30%. The aim of this study is to utilize artificial intelligence (AI) to enhance yield forecasts in viticulture and grapevine breeding.

In order to generate a variety-specific yield forecast, the AI initially relies on two available data sources: (1) 10-year yield data (historical data) and (2) environmental data (soil and weather). However, during the collection and validation of the data, unexpected inconsistencies were discovered in the historical yield data when it became clear that yield data often were aggregated and not recorded for single vineyard plots. To overcome this fact, yield data of the same variety of a grower were combined to calculate an adjusted yield per hectare. However, this aggregation significantly reduced the size of the dataset. It has to be concluded that it is crucial to thoroughly review historical data before utilizing it in the AI modeling process. Nonetheless, the AI is already capable of achieving a yield prediction accuracy of 79.7%.

In order to optimize the accuracy of the prediction, the AI will be expanded in a second step to include (3) sensor data and (4) process management. With the "PHENOboxx", a multi-sensor system, yield-relevant features are recorded directly in the vineyard and evaluated with a specially trained AI. The most important characteristics include the number of shoots, the number of grapes and the amount of dormant winter pruning wood. Inorder to obtaind these data, the `PHENOboxx` is mounted on the `PHENOquad`, which is used for data acquisition and as a high-throughput phenotyping platform in grapevine breeding research. In first results of 690 evaluated images, the correlation in the images is r=0.963 between the values from the image evaluation AI and the manuelly counted reference data for the number of berries, an important yield parameter.

By including the process management as well as sensor data in the modeling process, we expect a significant improvement of the prediction accuracy.

SelWineQ: QTL analysis on a high-density genetic map based on fully informative haplophases for mapping wine quality traits

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The evaluation of new grapevine genotypes regarding their potential to produce high quality wines is the time limiting factor in the process of grapevine breeding. Young seedlings need three to four years on average to produce sufficient yield for micro-vinification (small-scale winemaking) and sensory evaluation. Hence, the development of quality-related markers that can be used in marker-assisted selection (MAS) as well as prediction models for this bottleneck trait, will tremendously enhance breeding efficiency. To achieve this goal, SelWineQ evaluates quality related aspects: (1) the genetic quality potential (irrespective of the environment), (2) the metabolic quality potential (genotype by environment interaction) of grapevine must, and (3) the wine quality (analytical and sensory properties).

A training set of a segregating white wine F1 population (150 F1 genotypes = POP150; `Calardis Musqué´ x `Villard Blanc´) was deeply phenotyped and genotyped. An improved high-density integrated genetic map consisting of highly informative haplotype-based markers (HBMs) form a genotyping by sequencing (GBS) approach was developed and used for QTL mapping of the collected phenotypic traits. We identified a major impact of the grapevine véraison locus *Ver1* regulating the onset of ripening on many important quality attributes of the population. Traits directly affected are sugar content, organic acid concentrations, pH value and important aroma compounds. For some of these constituents the *Ver1* locus shows the highest genetic impact in QTL analysis (i.e. tartaric acid, malic acid, pH) when véraison variation is not respected as covariate.

This makes véraison a central adjusting screw for the development of climate-adapted varieties with enhanced quality potential. Resulting grapes have balanced sugar and organic acids concentrations with no need of additional effort of adjustments during the vinification process (sugar enrichment/deacidification) under regular local growing conditions. Additionally, an optimal aroma characteristic has to be reached. Sensory evaluation indicated aroma compounds of the monoterpene group (in particular linalool and cis-rose oxide) to be of major importance for quality rating in this population. Beside of the strong influence of *Ver1*, additional important loci were detected indicating for candidate genes of the terpenoids biosynthetic pathway.

Applying genetic markers for the onset of ripening could therefore be a powerful tool in marker-assisted breeding (MAS) to develop climate-adapted varieties with high wine quality potential. Prior to that, these molecular markers will be validated for their applicability on broader genetic background. This knowledge will accelerate breeding for high quality and climate-adapted grapevine varieties with improved fungal disease resistances to be cultivated in a pesticide-reduced and sustainable viticulture.

Detection of *Puccinia pimpinellae* (anise rust) in *Pimpinella anisum* (anise)

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To promote domestic medicinal plant cultivation and to ensure product quality, the junior research group Medicinal Plants was established at the Julius Kühn Institute in 2020 (funded by FNR: 22002818). The focus of the research was, among other things, on the "expansion through optimisation of the cultivation of anise (*Pimpinella anisum*)" and the investigation of "fungal pathogens" that can currently be observed in the field and the associated problems. Within the framework of a broad-based monitoring of fungal pathogens over several years, massive infections with rust (*Puccinia pimpinellae*) were repeatedly observed. *P. pimpinellae* poses a great challenge for cultivation, as the infestation can lead to massive yield losses and a significant reduction in the quality of the harvested crop.

Infections with *P. pimpinellae* can be caused by spores present in the environment as well as by infected seeds. Interestingly, spore deposits were only found on stems, leaves and flowers shortly before the plants flowered. This observation raised the question of whether the plants were only infected at this time or whether the seedlings are already infected, the fungus latently colonises the plant and only switches to a pathogenic phase with vegetative and generative reproduction at the time of flowering.

To clarify this question, the organs of anise seedlings were to be checked for colonisation by *P. pimpinellae* at different times. Since the rust fungus is obligate biotroph and accordingly cannot be isolated, a culture-independent detection method was first verified by conventional PCR using genus-specific primers.

To investigate colonisation, seedlings were grown from infested seeds and harvested at two time points. Roots, hypocotyl, cotyledons and first leaves were analysed separately. It was found that *P. pimpinellae* could already be detected in early seedling stages. The results demonstrate that latently infected plants emerge from infected seeds and underline the need to use healthy seeds to prevent early infection of crops and minimise the spread of *P. pimpinellae*. To this end, seed batches could be routinely screened for the pathogen. In the case of contaminated seed, the pathogen concentration could be significantly reduced by different seed treatments. Initial trials on seed treatment have already been successfully carried out. The results still need to be confirmed in the future.

Phenotyping of sorghum for carbon sequestration under drought stress and optimum irrigation

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In Germany, climatic conditions with increasing drought stress and heat are expected in the future. Sorghum is a C4-plant that has great potential to add significant amount of organic carbon to the soil due to its large and deep root system. Therefore, increased cultivation of sorghum could increase the stock of organic carbon in the soil and thus contribute to climate change mitigation.

Sorghum is so far only cultivated on a very limited share of cropland in Germany, although its suitability and competitiveness with other crops like maize is expected to increase under future climate scenarios. Also, little is known about sorghum genotypes that are suitable for German climatic conditions.

In a complementary experimental set-up comprising field, greenhouse and laboratory, we screen 10 sorghum test hybrids in addition to commercial sorghum and maize cultivars used as references. In the field trial, we determine the potential for carbon sequestration by surveying the above-ground biomass (grain yield, straw yield, harvest index), the belowground biomass (root biomass, length and length density) up to a depth of 150 cm (using soil coring), as well as the shoot-root ratio. In addition to the phenological, morphological and agronomic parameters we carry out chemical analyzes of plant tissues (C and N contents). In a supplementary greenhouse experiment, sorghum and maize genotypes are also grown under drought stress and optimum water supply.

We assume that the different sorghum hybrids will vary greatly in their potential for biomass formation and carbon input into the soil under optimum irrigation and drought stress. Our results are expected to identify sorghum hybrids that are suitable for cultivation in German light soils susceptible to drought such as present in Braunschweig.

Influence of different CO_2 concentrations on the *Fusarium graminearum* ear infestation of different winter wheat cultivars

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The aim of the WheatFACE project is to clarify the influence of increasing CO_2 concentrations (e[CO_2]) on the development of different winter wheat cultivars and on the infection of different winter wheat cultivars with brown rust (*Puccinia recondita*) and ear fusarium (*Fusarium graminearum*). The project is a research network of the Julius Kühn Institute (JKI), in which the institutes "Crop and Soil Science", "Resistance Research and Stress Tolerance" and "Plant Protection in Field Crops and Grassland" are involved.

In this part of the project, the influence of e[CO_2] on the extent and intensity of infection of different winter wheat cultivars with *Fusarium graminearum* (*F. graminearum*) is investigated. *F. graminearum* is a necrotrophic fungus that causes *fusarium* head blight (FHB) in wheat, which leads to yield reductions and the formation of harmful mycotoxins such as deoxynivalenol (DON).

Field experiments at e[CO_2] are possible with the help of a Free Air Carbon Dioxide Enrichment (FACE) - facility. The ring-shaped FACE - facility surrounds the test plots and allows the CO_2 concentration to be increased to 600 ppm within the rings. This allows to investigate twelve different winter wheat varieties both under e[CO_2] and under control conditions at atmospheric CO_2 concentrations (a[CO_2]). At the growth stage BBCH 61-69, the wheat cultivars are artificially infected with *F. graminearum* by three rounds of spray inoculation with a conidial suspension of 3×10^4 conidia/ml. To assess the level of disease, the incidence and the severity of the infected ears are recorded at different times. Finally the FHB-index is calculated from this. The DON content of the crop is determined by ELISA and the *Fusarium*-DNA in the grains is quantified by PCR.

The 2021/2022 field trial showed differences in the FHB index between the varieties for both e[CO_2] and a[CO_2] conditions, which also corresponds to the classification of the varieties according to the German Descriptive Variety List of the Federal Plant Variety Office. The varieties KWS Donovan and Tobak showed an increased susceptibility at e[CO_2] compared to a[CO_2]. Further field trials will be conducted in 2022/2023 and 2023/2024.

Developing a FAIR framework for data quality analysis and data fitness for use of agrosystems research data

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In times of big data, dense, area-wide and high-resolution time series and an increasing number of *in situ* measurements, the FAIRness (findable, accessible, interoperable, and re-usable) of data becomes crucial. The data for analyses of various ecological and anthropogenic processes such as biodiversity assessments or the estimation of land losses, which provide the basis of political decisions, should also have a certain quality level. In common definitions, data quality is achieved by accuracy, consistency, reliability and completeness of data. However, these components differ according to data type and nature and, above all, according to the respective area of application and aim of data.

Within the framework of the FAIRAgro consortium, the various approaches to describing quality of agrosystems research data will be summarised and evaluated, as well as made applicable and available to the agronomic community. In the first preliminary studies, it has already become clear that information on data content such as "plausibility of content", "verified consistency of content" and "content completeness" are particularly relevant for the reuse of data. This content information is very application-specific and therefore difficult to comprehend and to generalise. In order to get an overview of the different application areas and the relevant properties defined by the user for a suitable quality description, the wants and needs of users will be identified in multiple surveys and workshops. The results of a broad literature research and initial experiences from use cases of the FAIRAgro consortium will also be included.

In addition to the interest in information on data content, "information on data pretreatment" is also considered as a relevant source of data quality. In addition to the assessment of general data quality, we are enhancing another new topic here. The Data Fitness For Use approach should be able to document different data applications and their resulting quality, the so called data performance, in different application areas. The aim of our work is to create a concept, which assesses quality information of different agrosystem research data and create long-term linkages between the information about the applied data performances and the data quality information.

In the presentation of our work, we show a first overview of how a (FAIR) framework for building a long-term concept for data quality analysis as well as for documenting the Data Fitness For Use approach can be structured. FAIRagro is the first project that implements such a comprehensive and detailed analysis of data quality of agrosystems research data.

Description and genetic mapping of black rot resistance in grapevine

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Breeding of fungus resistant cultivars has a long history. In the beginning of the 19th century, the introduction of various grapevine diseases from North America to Europe challenged European viticulture. Since none of the European high quality grapevines possess defense mechanisms against those diseases, the application of high amounts of pesticidies is necessary to maintain vineyards healthy. With the intended reduction of fungicide use, defined in the European Green Deal, the pressure is increasing on winegrowers to find a sustainable solution. One option is the cultivation of fungus resistant grapevine cultivars, which allow a fungicide reduction of up to 80%. Currently, breeding programs have focused on the two main dieseases of grapevine, downy and powdery mildew. But there is concern that diseases previously considered secondary, such as grapevine black rot (*Guignardia bidwellii*, anamorph: *Phyllosticta ampelicida*), may emerge and become relevant, through the intended reduction of fungicide use and the increase of acreage of new mildew-resistant grapevine cultivars. In fact, since the beginning of the 21st century, increased incidence of black rot has been reported from regions all over Europe. Therefore, the identification of resistances to black rot and their introgression in new varieties is now an important breeding goal.

To date, three resistance loci are known to confer resistance to black rot. Amongst them, *Rgb1* located on chromosome 14 is the most important one, due to its mediated resistance strength. This resistance locus (*Rgb1*) is currently validated in four cross populations screened for black rot resistance. In this study, the aim is to gain deeper insights into the genetic structure of *Rgb1*. Therefore existing genome sequences of the resistance donors are compiled and missing ones are generated via Oxford Nanopore. Comparison of chromosome 14 sequences might reveal candidate genes for black rot resistance.

The "Digital Information System Quarantine Pests" (DISQS): A central solution for surveys in Germany

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The surveys on the presence of Union quarantine pests are part of the early warning system of the European Union. Early detection of a pest introduction is the basis for successful eradication with reasonable effort. This can prevent establishment and further spread of the pests. The implementing regulation 2019/2072 lists 395 Union quarantine pests, which have to be surveyed through multi-year programs in the member states since 2020. These Union quarantine pests are species of bacteria, fungi, oomycetes, viruses, viroids, phytoplasmas, insects, mites, nematodes, mollusks and parasitic plants. The precise planning and digitalized documentation of the surveys is of great importance considering the large number of pests, which have to be surveyed by the plant protection services. Nevertheless, little information is available on many pests. The European Food Safety Authority (EFSA) is gradually developing so-called "Pest Survey Cards", which contain all scientific information that may be relevant for survey planning. These cards cannot be used directly for Germany, as they have to take into account the entire territory of the EU. Currently, Germany is experiencing at the federal and state level an enormous amount of redundant work on literature research as preperation of the surveys. In addition, the documentation and evaluation is mainly manual, as no central system is available to which all participants have access.

The project aims to create a digital and centralized solution for surveys of Union quarantine pests in Germany. On the one hand, the storage and processing of data for planning and, on the other hand, the flexible evaluation and presentation of the surveys will be accessible. This should enable the direct information retrieval for the planning. In the form of a database, information on the pests including their biology, countries of origin, routes of spread, diagnosis, factors relevant to the survey, etc. will be collected. In addition, the information in this database will be linked to the tool for collecting the survey data. This tool will greatly simplify the work of the state and federal agencies in collecting, evaluating and disseminating the data for a wide variety of purposes. This will also enable the development of clear evaluation modules of the survey data for Germany for the first time. The technical implementation is carried out by the project partner "Informationssystem Integrierte Pflanzenproduktion (ISIP) e.V. ", the joint advisory portal of the chambers of agriculture and the federal states.

Developing a set of qPCR biomarkers to analyse the reaction of apple plants to the apple replant disease

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Apple (*Malus x domestica* Borkh.) stands as Germany's most produced fruit, yet apple orchards and tree nurseries are increasingly grappling with the challenge of apple replant disease (ARD). ARD is a soil-borne disease that emerges through replanting, leading to substantial growth inhibition, decreased fruit quality, and reduced yields. Despite its significant economic impact, the underlying causes of this disease remain poorly elucidated, and sustainable countermeasures are yet to be developed. Apple plants exhibit heightened stress defense responses to ARD, with the nature and extent of this response varying across different soil types and genotypes. Transcriptomic analyses of apple plants cultivated in ARD-affected soil have revealed the upregulation of genes associated with biotic stress responses.

This research aims to identify potential genes suitable as biomarkers to indicate how apple plants respond to ARD. To achieve this, we have selected 90 candidate genes that have previously demonstrated differential expression in apple plants under ARD conditions. For 23 of these genes, new qPCR primers were designed and tested for their specificity and efficiency. The candidate genes will undergo validation by assessing their expression using qPCR with apple plants cultivated in 150 distinct ARD-affected soil samples collected from various locations in Germany, as part of the collaborative ORDIAmur project. Furthermore, we will investigate how various countermeasures, which have the potential to mitigate ARD, affect the expression of these candidate genes across different apple genotypes. The experimental protocol for the analysis of candidate gene expression will be refined to create a fast and cost-efficient biomarker-based method for measuring the severity of ARD in soils.

Impact of genotype-, environment- and management interactions on the factors cultivar resistance against fungal pathogens and weed suppression in winter wheat.

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Due to the increasing development of resistance in weeds, climate-related shift in pathogen infestation and the decreasing availability of plant protection product (PPP), the cultivation of winter wheat in Germany is facing major challenges. In order to achieve the goal of the European "Farm to Fork" strategy and to halve the use of plant protection products by 2030, the use of varietal traits and crop management strategies such as crop rotation and sowing time are becoming increasingly important. For example, a later sowing date can result in fewer weeds emerging in the crop or reduced infestation with pathogens such as *Oculimacula* sp. and *Zymospetoria tritici*. In a three-year field trial, the effect of different genotype x management combinations on yield, pathogen infestation and weed emergence is currently being investigated to answer the following trial questions:

Is it possible to reduce weed infestation by adjusting the sowing date (early/late) without significant yield losses of winter wheat?

Can competitive wheat varieties contribute to integrated weed control and which variety-specific traits are relevant?

Can higher levels of resistance in winter wheat varieties reduce the fungal pathogen infestation (*Fusarium*, *Septoria*, DTR...) also in the following crop, winter wheat?

The trial is set up in a multifactorial split plot design with the factors: previous crop, sowing time, variety and PPP intensity in four replicates. Six winter wheat varieties with different competitive strengths against weeds and different susceptibility to root and crown, and leaf and head diseases (e.g. *Fusarium*) were selected for the trial. In addition, maize (*Zea mays*) and broad bean (*Vicia faba*) were grown as preceding crops before winter wheat. To determine effects on weed emergence, the sowing time of winter wheat was varied (early vs. late).

In order to investigate the influence of contrasting locations (environments), the trials will be carried out at the three JKI trial locations Braunschweig, Quedlinburg and Groß Lüsewitz. In addition to assessing pathogen infestation and weeds (species and degree of cover), yield parameters (hectolitre weight, thousand grain weight and grain yield) are determined. In particular, variety-specific characteristics (e.g. leaf retention, tillering, height, degree of cover, biomass accumulation) that contribute to increased weed suppression/tolerance are recorded. In addition, the trials at each site are flown with a UAV and relevant vegetation parameters are calculated and analysed.

Plant traits influencing the response to elevated carbon dioxide in different winter wheat varieties

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Towards the end of the 21st century, global CO_2 concentrations are projected to reach 400 to 1140 parts per million, as indicated by emissions scenarios (Shared Socioeconomic Pathway - SSP). Given this steadily rising CO_2 concentration since the industrial revolution and the resulting climate changes, it is increasingly important to understand how wheat and its react to these future climate conditions. Winter wheat (*Triticum aestivum* L.) is a crucial crop for human nutrition, making it essential to sustain its productivity. Elevated CO_2 concentrations have the potential to boost yields and mitigate the adverse effects of climate change, such as drought and heat stress.

Within the WheatFACE project (Phenotypic and genetic determinants for adaptation of winter wheat to increasing CO_2 concentrations using leaf rust and ear fusarium resistance as examples.) we are investigating the response of various winter wheat cultivars under elevated CO_2 (e[CO_2] = 600 ppm) using a free air carbon dioxide enrichment (FACE) facility, as well as under ambient CO_2 (a[CO_2] ~ 420 ppm). Our objective is to discern plant traits that exert influence on the response to (e[CO_2]). This entails the examination of distinct source traits, including leaf area index (LAI) and the intercepted Photosynthetically Active Radiation (IPAR) as well as sink traits such as grain number and weight. Furthermore, we will analyze source-sink ratios, such as the flagleaf area-to-number of ears ratio, to elucidate their modulatory role in the e[CO_2] response. Importantly, these traits and ratios are also integral to our investigation of how e[CO_2] influences infection dynamics with leaf rust and ear fusarium and vice versa, which are both also components of our research project.

In 2023, we conducted a FACE trial with 12 genotypes, assessing phenological, morphological, physiological, and agronomical traits. Through analysis of the collected data, our goal is to pinpoint the traits that exhibit the most pronounced responses to e[CO_2], while also identifying key traits that may serve as predictive indicators of the response to e[CO_2] for other genotypes. Alongside the e[CO_2] factor, we are also investigating pathogen infection (leaf rust and ear fusarium) in our trials. Our objective is to understand how e[CO_2] alters infection and disease severity and how these changes affect yields and the other plant traits.

In 2024, we will continue the trials with our FACE-facility and the same varieties to investigate our findings further. Ultimately, we aim to identify varieties or traits that can capitalize on e[CO_2] concentrations without sacrificing quality and yield.

Trapping the bee and the baddie

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Ground-nesting bees constitute the vast majority of all wild bee species. Although they are the most abundant functional group of wild bees, ground-nesting bees are less studied than cavity nesting bees. The importance of floral resource availability on bees has been studied extensively, whereas findings about their nesting requirements are lacking.

For this, a standardized method to monitor ground-nesting bees is needed. Transect walks or pan traps often only record transitory foragers (“food tourists”), but not bees actually nesting. Emergence traps, collecting recently emerged individuals from the ground, could be used as a standardized method to monitor populations, which is missing so far. The bees collected with this method can be clearly assigned to a specific nesting site and it can be controlled that collected bees have not immigrated from other nesting sites. Thus, conclusions can be drawn e.g. regarding the quality of the nesting site. Therefore, these traps help gaining a better understanding of the biology and ecology of ground-nesting bee.

In our study, the grey-backed mining bee *Andrena vaga* is used as a model species as it is quite common, easily identifiable and forms large nest aggregations. This allows locating as many nesting sites as possible with the help of Citizen Science. 27 nest aggregations within the city of Braunschweig were selected for this study.

With the help of the emergence traps, the parasitism rate of three parasite species was analysed and compared between the aggregations. The aim was to detect differences between the parasite species regarding the influence of landscape characteristics, aggregation size and nesting site characteristics.

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