2nd HEZagrar PhD Symposium

April 26, 2016

Proceedings

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Foreword by Prof. W. Windisch

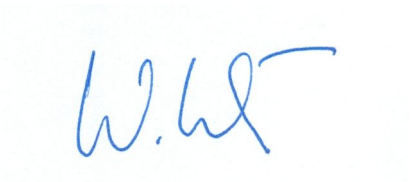
Director of the Hans Eisenmann-Center for Agricultural Sciences, TUM

Food security, global change, environmental protection, and, vice versa, sustainable generation of biomass for food, livestock feed, energy, as well as industrial purposes have been growing to big topics that will challenge the entire human society for the upcoming decades. Although well perceived among experts, the public awareness of these topics still seems to be underdeveloped. Even more, there is obviously a gap between the pictures of agriculture drawn in information media and hence also in the societal and political discussion, and the enormous potential of modern agricultural sciences to significantly address the abovementioned challenges. Underrating of agricultural sciences seems to originate at least in part from lacking public awareness of the broad portfolios of most modern tools from life sciences which are pointed at practical agricultural objects (e.g. soil, plants, livestock) in order to directly address applied questions. This systematic approach of combining fundamental life sciences with practical (on-farm) research in both directions (upward and reverse) is one of the big strengths of agricultural sciences that are experienced of the whole range of viewpoints (e.g. soil, plants, livestock, socio-economy, ecology, technique, etc.)

In this context, the campus Weihenstephan and the region around is very lucky to host three institutions dedicated to agricultural sciences from the applied to fundamental level: the chairs of the TUM School of Life Sciences Weihenstephan (WZW) forming the Hans Eisenmann Center for Agriculture Sciences (HEZ), the Bavarian State Research Center for Agriculture (LfL) and the Weihenstephan-Triesdorf University of Applied Sciences (HSWT). These institutions are successfully integrating their specific potential in order to achieve a critical mass of system-oriented agricultural research.

The HEZagrar PhD Symposium was initiated one year ago to support the process of integration. The great response and overwhelming feedback of participants encouraged us to put the HEZagrar PhD Symposium on a regular yearly basis. This year, the willingness to attend the symposium even increased. This again demonstrates the strong motivation to step jointly into novel directions of agricultural research and, in particular, the common spirit about modern agricultural sciences, and the great feeling to contribute to global challenges.

Weihenstephan im April 2016



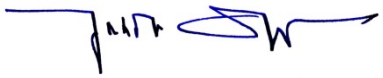
Foreword by J. Opperer

President of the Bavarian State Research Center for Agriculture (LfL)

In 2015 there was a good response to the first PhD Symposium. We had an active exchange between the different fields of agricultural science and the involved institutions in Freising. Many of the presented projects are joint ventures between the Technical University Munich (TUM) and the Bavarian State Research Center for Agriculture (LfL). This fits to our focuses on the fields of research, support and education. Regarding this, the cooperation is considered as a very important approach. It comprises the scientific exchange and the execution of joint projects.

For the involved PhD students results a good possibility to establish contact to other scientists and to start more effective collaboration. The joint mentoring of PhD students is of particular importance. Key aspects of the process are the scientific results as well as the generation of excellent junior academics. It allows the LfL an important access to improved methodical approaches and the university benefits from a strong link to the real concerns of a sustainable agriculture.

The LfL is therefore happy to actively participate in the **2nd HEZagrar PhD** Symposium. We wish this event every success and a promising future.



Program – April 26, 2016

9:00 **Welcome (Lecture Hall 17, Liesel-Beckmann-Str. 1)**

9:15 **T1:** **Manuel Geyer**
Improving fertility restoration and seed production efficiency in CMS hybrid wheat

9:30 **T2:** **Hanna Märkle**
Coevolution in action in host and parasite genomes – a theoretical approach

9:45 **P1 – P14:** "Elevator pitch" -> poster introductions (2 min each)

10:30 **Coffee break**(20 min)

10:50 **T3:** **Hind Sghyer**
Investigating the genetic structure and diversity of the barley pathogen Ramularia collo-cygni

11:05 **T4:** **Philipp Wree**
Economic evaluation of innovation in crop production using distance functions

11:20 **P15 – P28:** "Elevator pitch" -> poster introductions (2 min each)

12:00 **Poster-Session (HEZ, Liesel-Beckmann-Str. 2)**
13:00 **Lunch**

14:00 **T5:** **Maria de Vries**
Influence of tillage on carbon cycling genes in agricultural soils

14:15 **T6:** **Lydia Paetsch**
Waste additions to soils: Long-term organic carbon storage to mitigate climate change or just a flash in the pan?

14:30 **T7:** **Daniel Brugger**
Physiological adaption to subclinical zinc deficiency in the weaned piglet model

14:45 **T8:** **Maria Laparidou**
Analyzing early B-cell development in immunoglobulin heavy chain knockout chickens using retroviral gene transfer

15:00 **T9:** **Andrea Heinrich**
Sensor-based capturing of nesting behavior and laying performance in cage free housing systems of laying hens

15:15 **Coffee break** (- 15:45)

15:50 T10: Manfred Höld
Integrated Dairy Farming –
Energy from Photovoltaic and Biogas for supplying the dairy barn

16:05 T11: Veronika Dollhofer
Enhancement of biogas production from lignocellulosic biomass by the implementation of anaerobic fungi

16:20 T12: Magdalena Ochsenbauer
Development of a geodesign tool for analyzing, planning and evaluation of landscape connectivity in agroecological systems

16:35 Voting: "best poster"/"best pitch"/"best talk"

16:50 Conclusions and "Wrap up" with Beer & Brezn

Abstracts Talks

Physiological adaption to subclinical zinc deficiency in the weaned piglet model

Brugger, Daniel
TUM, Chair of Animal Nutrition

Introduction

An insufficient supply with the essential trace element zinc (Zn) is a common event. Most of the earlier studies investigated its effects in clinical Zn deficient individuals in which pathological events represent the endpoint of physiological counter regulation. However, in men and animals subclinical Zn deficiency most likely represents the most common phenotype regarding insufficient dietary Zn supply. To this day it is not well understood how the organism is sensing and communicating the Zn supply status on level of the complete system. Furthermore, it is not clear whether there is a direct connection between certain clinical symptoms and Zn homeostatic adaption or if they just represent indirect effects of secondary metabolic imbalance. Therefore, this doctoral project focused on the experimental modelling of subclinical Zn deficiency in the weaned piglet and the investigation of metabolic shifts arising thereof. The following research goals were targeted: 1) Development of an experimental approach that induces fine graded differences in Zn supply status ranging from subclinical deficiency to mild oversupply, 2) Investigation of homeostatic adjustments in response to varying alimentary Zn supply, 3) Investigation of the early metabolic shifts that lead to clinical Zn deficiency on a mid-term scale.

Material and Methods

The experimental approach was already published in detail[(1)]. In brief, 48 fully weaned piglets (50% male-castrated, 50% female, initial average life weight 8.6 ±1 kg) from six litters were fed a basal diet consisting mainly of corn and soybean meal (13 MJ ME/kg, 23.8% crude protein) for a period of 22d. The basal diet met all nutrient requirements of growing piglets[(2)] except for dietary Zn (native Zn content 28 mg/kg). During the first 14 acclimatization days, all animals were fed *ad libitum* the basal diet supplemented with 60 mg Zn/kg as $ZnSO_4$ x $7H_2O$ (SUPPLIER) to meet a total dietary Zn content of 88 mg/kg. During the last 8 experimental days animals were assigned to 8 dietary treatment groups with a balanced distribution of life weight, sex and litter mates. Each treatment group received the basal diet restrictively (450 g/animal *day^{-1}) but with varying Zn supply as $ZnSO_4$ x $7H_2O$: +0, +5, +10, +15, +20, +30, +40 and +60 mg/kg to reach total dietary Zn contents of 28, 34, 39, 43, 47, 58, 68 and 88 mg/kg. Titandioxide was added as indigestible marker (3 g/kg). After 8 experimental days animals were sacrificed without fasting through anaesthesia. Statistical analyses were performed with SAS 9.4 using two-way ANOVA (treatment, block), linear and broken-line regression analysis as well as average linkage cluster analysis.

Results and Discussion

A complete absence of clinical signs of Zn deficiency and, at the same time, fine-graded differences in Zn status parameters (e.g. apparently digested feed Zn, plasma Zn, plasma Zn binding capacity, plasma

alkaline phosphatase activity, liver Zn, liver Mt1a and Mt2b gene expression) indicated successful promotion of subclinical Zn deficiency in insufficiently Zn supplied groups. Moreover, broken-line response analysis of apparently digested feed Zn, liver Zn as well as liver Mt1a and Mt2b gene expression assessed the point of gross Zn requirement to lie at 58 mg Zn/kg under the present experimental conditions[(1)]. This is in line with the threshold published by the NRC[(2)] (60 mg/kg). Analysis of Zn contents in soft tissue revealed several response patterns which were not reported so far, which highlight a strict separation in Zn donating and Zn accepting organs under the terms of subclinical Zn deficiency. Average linkage clustering of tissue Zn distribution further confirmed these results by clear sub-clusters consisting of the groups receiving between 28 and 47 mg/kg and 58 to 88 mg/kg, respectively. Analysis of Zn transporter gene expression in jejunum, colon, liver and kidney revealed unique patterns of gene expression response to the dietary treatment as well as tissue specificity in piglets compared to already published data from laboratory animals and humans[(3)]. Furthermore, we found hints towards a change of the maximum absorption site from the small to the large intestine under the terms of subclinical Zn deficiency. Most interestingly, the response of ZnT7 in the kidney highlights the central role of this organ in the regulation of whole body Zn homeostasis. Analysing the response of pancreatic digestive enzyme activities relative to apparent crude nutrient digestibility revealed a decrease in digestive capacity after just eight days of subclinical Zn deficiency. Within the heart muscle, analysis of antioxidative parameters and stress responsive gene expression pointed towards a decrease in the ability to detoxify reactive oxygen species and a switch of the genetic program towards increased apoptosis in groups receiving minor amounts of supplemental Zn (<47 mg/kg).

Conclusions

The present doctoral project was successful in fulfilling its research goals. An experimental approach could be developed, which induced fine graded differences in Zn supply status ranging from subclinically Zn deficient to sufficiently/mild oversupplied groups. Furthermore, a deeper insight in the Zn homeostatic adjustments in the early phase of Zn deficiency has been gained. Most notably, we found evidence for loss of function regarding digestive and antioxidative capacity already in this early stage in the development of clinically manifest Zn deficiency. The practical consequence of this study is to urgently avoid even short periods of insufficient alimentary Zn supply in order to maintain animal productivity and welfare.

Literature

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Enhancement of biogas production from lignocellulosic biomass by the implementation of anaerobic fungi

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Abstract

The use of lignocellulosic residues and waste for renewable energy generation is a favorable strategy to mitigate greenhouse gas emissions and global warming. However, for economical bioenergy production, efficient hydrolysis of lignocellulosic biomass (LCB) is the issue to be solved before such substrates can be used in industrial pipelines. Anaerobic fungi are favorites for microbial hydrolytic pretreatment in biotechnological processes. They are able to disintegrate the plant material mechanically with their rhizoids growing into the fibers, bursting the lignin coat which protects cellulose and hemicelluloses from degradation. Concomitantly, they attack plant fibers with a multitude of hemicellulolytic and cellulolytic enzymes, catalyzing the conversion of the plant polysaccharides mainly to acids, ethanol, H2 and CO2. In our presentation we will give an overview about our progress in the development of an LCB pretreatment strategy involving anaerobic fungi and present possibilities for future applications.

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Improving fertility restoration and seed production efficiency in CMS hybrid wheat

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Introduction

Wheat (*Triticum aestivum* L.) is one of the three most produced staple crops in the world, and thus plays a critical role in global food security. Whereas hybrid breeding resulted in a large increase in grain yield in maize and rice, it was not shown in wheat production until now. Recent studies showed that hybrid wheat allows the exploitation of positive commercial heterosis for grain yield. Cytoplasmic male sterility (CMS) is one of the most discussed approaches to produce hybrid seeds and make use of this advantage. However, incomplete fertility restoration of the hybrids and the self-pollinating character of wheat are still major barriers associated with CMS hybrid wheat. Previous studies showed that the combination of different sources of fertility restoration in one restorer line leads to a superior restoration capacity. To facilitate this approach, we genetically mapped the highly effective restorer gene *Rf3*. In order to identify lines with increased pollen shed, we examined the anther extrusion of current wheat breeding material.

Material and Methods

Based on the CMS/maintainer line Sperber and the restorer line Primepi, we developed a mapping population comprising 198 BC_1 plants (CMS-Sperber/Primepi//Sperber). As a measure for fertility restoration, we determined the seed set of four bagged spikes for each individual. Using SSR (simple sequence repeat) markers, the restorer gene was mapped on the short arm of chromosome 1B. Individuals showing recombination between *Rf3* and the flanking marker loci *Xbarc128* and *Xwmc406* were subsequently genotyped with a proprietary 15k SNP (single nucleotide polymorphism) chip. SNP markers linked to *Rf3* were converted to CAPS (cleaved amplified polymorphic sequence) markers and validated by genotyping a diversity panel as well as a F_2 population derived from the cross between Sperber and the spelt wheat variety Holstenkorn. For the assessment of anther extrusion we determined the number of remaining anthers of 765 wheat lines ten days after the first anther extrusion was observed. Subsequently, 21 lines were selected and further examined for anther extrusion at four locations across Germany.

Results and Discussion

While the fertile plants of the mapping population showed a mean seed set of 1.58 seeds per spikelet, 46% of the progeny revealed no seed set, which implies a monogenic inheritance and a dominant gene action of the restorer gene in Primepi. *Rf3* was mapped between the marker loci *Xbarc128* and *Xwmc406* on chromosome 1BS. After we enriched the interjacent region with SNP markers, we identified three markers closely linked to *Rf3*. The two CAPS markers were also linked to *Rf3* in F_2.

Applying these markers to a diversity panel suggested diagnostic ability for one of them. The 21 lines tested for anther extrusion showed 0-3 extruded anthers per flower ($\bar{x}$ = 2.1; SD = 0.66). Genotype (G), environment (E), as well as G×E interaction had a significant effect on anther extrusion ($p < 0.01$). Two of the 21 lines showed an anther extrusion suitable for hybrid seed production.

Conclusions

The restoration capacity of Primepi and Holstenkorn is based on the dominant restorer gene *Rf3*, which was mapped on chromosome 1BS in both populations. The newly developed CAPS markers can be used for marker-assisted selection, thereby accelerating the development of restorer lines with superior restoration capacity. Wheat lines which revealed increased anther extrusion are an important resource to improve the efficiency of hybrid seed production.

Literature

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Sensor-based capturing of nesting behaviour and laying performance in cage free housing systems of laying hens

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Introduction

The Weihenstephan funnel nest box (FNB) and the high frequency group nest box (HFGN) are different RFID-based nest systems to detect individual hen data in floor housing systems [1, 2]. Individual laying performance can only be captured with the FNB [3]. Behaviour traits like nesting behaviour are not scored as performance traits [4], but they have an indirect influence on the economic success of egg production and can be recorded in both systems. Nowadays, breeders of layers have to include performance and behaviour traits into selection programs to improve the adaptability of layers to floor housing systems. Therefore, the HFGN is the preferred nest system in terms of behaviour data, because it is similar to commercial barns. However, the recording of hen specific laying performance has to be established also in family nests and is therefore the aim of this investigation. Two different approaches have been performed to detect the oviposition in family nests. First, the nesting behaviour of individual layers was evaluated in the FNB and HFGN and compared. The hypothesis was that if there is no difference in the nesting behaviour we would be able to detect oviposition of layers in family nests due to their behaviour in single nests. The second approach was based on the body weight change after an oviposition. With a weighing pop hole and a weighing perch the body weight of individual hens was recorded before and after each nest visit.

Material and Methods

All investigations were carried out at the experimental station Thalhausen of the Technische Universität München. Two flocks were tested in two barns, equipped with 72 FNBs or 16 HFGNs. In the first flock 313 LB and 548 LSL layers were mixed and divided into two groups each for one nest system. At an age of 46 weeks the groups of layers changed the nest systems. Data were recorded in total for nine laying periods (LP) in flock one. The second flock consisted of 855 LB hens. The layers were changed regarding the nest system at an age of 39 weeks and data were recorded for 10 LP. The selected behaviour traits for the comparison of the nest systems and strains were the number of nest visits and the duration of the nest visits. For the second approach 30 LB layers were housed in another barn with the weighing devices. Direct observations and video recordings were carried out for each, the weighing pop hole and the weighing perch on five consecutive days to observe nest visits with and without oviposition. The threshold for a nest visit with oviposition was set at a body weight difference of 40 g. All weighing data were analysed with 35 different algorithms and for the weighing perch with two different methods. The results were divided into four classes and with a confusion matrix different parameters of interest were captured.

Results and Discussion

Significant differences in both traits were observed but not with a clear connection to oviposition (Table **1**).

Table 1: Average medians of the behaviour traits per flock and group

Behaviour trait	Flock	Strain	Group 1		Group 2	
			FNB[1] ➡ HFGN[2]		HFGN ➡ FNB	
Number of nest visits [n][3]	1	LB[5]	25	31	29	30
		LSL[6]	30	37	35	30
	2	LB	28	25	29	29
Duration of a nest visit [min][4]	1	LB	21	20	21	23
		LSL	50	29	38	33
	2	LB	18	24	25	20

[1] FNB = funnel nest box, [2] HFGN = high frequency group nest box, [3] Average median of the sum of the numbers of nest visits per hen and laying period [n], [4] Average median of the duration of a nest visit per hen and day [min], [5] LB = Lohmann Brown, [6] LSL = Lohmann Selected Leghorn

For both weighing devices the best three results of data analysis were chosen. The weighing pop hole achieved up to 58 % sensitivity, 63 % specificity, 84 % negative predictive value (NPV) and 31 % positive predictive value (PPV). The further developed weighing perch reached up to 75 % sensitivity, 95 % specificity, 87 % NPV and 89 % PPV.

Conclusions

The postulated hypothesis had to be rejected. Therefore, it is not possible to determine the oviposition of an individual hen in the HFGN with nesting behaviour data. With the weighing perch it is possible to obtain information about the oviposition of an individual hen in cage free housing systems with family nest boxes, although higher accuracies should be reached to use data for breeding purposes.

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Integrated Dairy Farming - Energy from photovoltaic and biogas for supplying the dairy barn

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Using Energy from Photovoltaic on the roof of the dairy barn and Biogas from the slurry of the dairy cows for the electrical equipment in the dairy barn is the major task of the project. We will integrate these systems in the energy system of the dairy barn, so that we can use as much as possible of the self produced energy. Furthermore, the Energy Management System (EMS) should be able to supply the machines with electrical energy, when the sun is shining or Biogas can be used for producing energy. But when we use an EMS, the welfare of the cows must be guaranteed all the time.

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Analyzing early B cell development in immunoglobulin heavy chain knockout chickens using retroviral gene transfer

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There is not much known about early B cell development in birds. Deletion of the J segment of the immunoglobulin heavy chain in chickens leads to a block in post-bursal B cell development. Using retroviral gene transfer defined parts of the B cell receptor complex are reintroduced to further dissect B cell development in birds.

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Coevolution in action in host and parasite genomes – a theoretical approach

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Abstract

Understanding coevolution between hosts and their parasites and detecting the involved loci at the genomic level may help to improve crop disease management. In my project I focus on how signatures of ongoing coevolution between host and parasites should look like at the genomic level. Based on this knowledge I will develop a Bayesian method suited to infer loci under coevolution in host and parasite genomes.

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Acknowledgements

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Development of a geodesign tool for the analysis, planning and evaluation of landscape connectivity in agroecological systems

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Introduction

For several decades now the loss of structural diversity and of biodiversity has been observed as a result of anthropogenic factors such as urban sprawl and more intensive farming (1, 2). Natural preserved habitats are increasingly fragmentated due to human landuse e.g. agriculture, infrastructure, settlements and industry.

Nowadays there are a lot of publicly funded programmes for issues such as agroenvironmental measures or contract-based nature conservation programmes for minimising the negative impacts of intensive land use, especially for agricultural landscape. However, it is not enough to take areas out of use or to extensify areas at arbitrary places. These areas should rather be integrated in a 'basic ecological infrastructure' in the form of a network covering the entire (agricultural) landscape (1). The aim is therefore to optimise the allocation of protected sites, which could serve as stepping stones or ecological corridors improving the interconnectivity in the (agricultural) landscape. Because of the huge complexity of the agricultural system it is difficult for planners and decision makers to evaluate and to optimize their local efforts related to a global geographical context. Geo IT concepts and tools could help to anticipate and analyze the effects of planning in a virtual reality and furthermore, the effects could be evaluated comprehensively according to objective criteria (3, 4). The aim of the research project is the development of a spatial decision support system, which will enable immediate feedback at an early stage of planning regarding the impacts and implications of proposals.

Core Concepts

To support the decision process with the opportunity to plan iteratively, principal core concepts are required as shown in figure 1.

(1) Semantic modeling of the agricultural landscape as a network graph

One way to represent and analyse (agro-) ecological networks is the use of graph-theoretical methods. The great advantage over other possible ways of modelling functional connectivity is that graphs can easily be applied on a broad spatial scale (2). Generally, a graph consists of nodes and edges. In landscape graphs habitat patches are the nodes and edges representing functional connections between the nodes. The first challenge is the classification of the spatial base data and thematic data (environment, agriculture) as nodes and as edges. The second challenge is the classification of species to functional groups depending on their requirements and with similar behavior according to their locomotion. Determining factors which are relevant for categorizing the data and analyzing the

landscape connectivity are selected by literature review. Besides the graph model, features which are needed for evaluation are also mapped in a semantic data model.

(2) Coupling of semantic data model and analysis tools

The semantic data model and the graph model are linked with complex analytical tools for building up the network graph or for network analysis (5). In order to support automated decision-making it is necessary to evaluate the current state and alternative scenarios based on indicators, which are modelled and linked to spatial classes from the data and graph model using model weaving (5, 6).

(3) Planning with the concept of geodesign

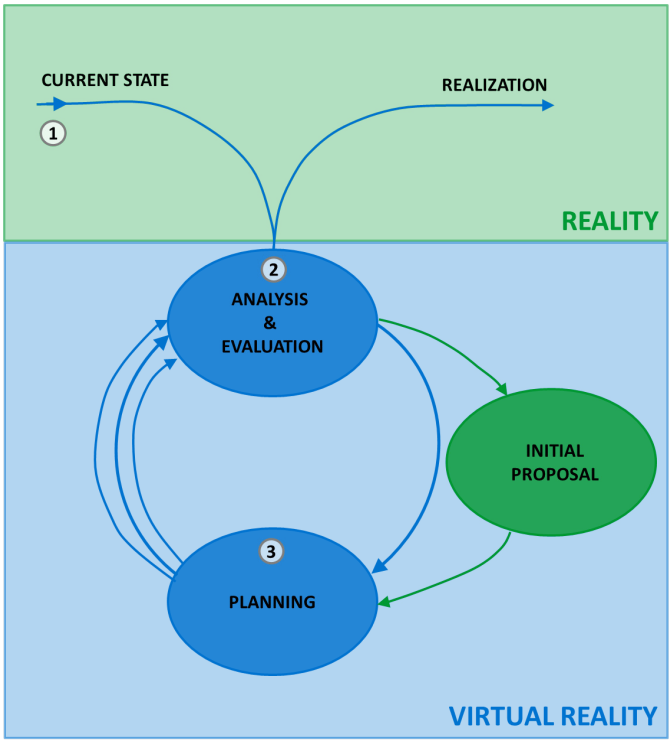

Figure 1: Framework for the design process

A well-designed, interactive user interface will assist the planning process by identifying and proposing the best locations for adding new elements to the network improving the connectivity. In the first iteration the user gets an initial proposal based on the analysis. The tool then supports inserting new spatial objects, like hedgerows or flowering areas representing the virtual execution of agroenvironmental measures. With the abstract concept of semantic modelling of planning actions it will be possible to predefine the effects of certain measurements, e.g. ecological value of an element, besides the location (7). Several scenarios could be designed and a concept of managing these different scenarios enables iterative analysis, evaluations and therefore comparisons against each other. The best scenario could then be chosen and turned into reality.

Outlook

Based on the ecological network analysis the main core concepts will be successively elaborated and intertwined. In collaboration with the department of agroecology (LfL) a prototypic implementation of the geodesign tool will be validated under real conditions.

Literature

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Waste additions to soils: Long-term organic carbon storage to mitigate climate change or just a flash in the pan?

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Abstract

Recycling of organic carbon originated from urban wastes can be a win-win-situation for agriculture and climate change mitigation. However, the fate of organic carbon in soil was still unknown. In our study we could show were (in what soil compartment/physical fraction) and how (in what chemical form) organic carbon is stored. With these results we can predict long-term carbon storage, an important tool to value these treatments.

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Investigating the genetic structure and diversity of the barley pathogen *Ramularia collo-cygni*

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Abstract

Ramularia collo-cygni (Rcc) is the biotic factor responsible for the disease Ramularia leaf spot (RLS) of barley (Hordeum vulgare). To address its genetic structure, the genome of Rcc (urug2 isolate) was de-novo sequenced and RNA-seq was performed. To evaluate the true genetic diversity of this fungus, whole genome sequencing of 19 Rcc isolates from multiple geographic locations and non-barley hosts was also performed. We hope by this approach to provide valuable insights in to the genetic diversity of this organism and to address how this diversity has influences on the evolution of the fungus. The understanding of the diversity is essential to identify sustainable control in Integrated Pest Management.

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Influence of tillage on carbon cycling genes in agricultural soils

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Abstract

Reduced tillage is a common practice in agriculture and reduces the release of sequestered carbon into the air by less soil cultivation compared to conventional tillage practices. In this study, the metagenomes of soil under either reduced or conventional tillage treatment have been compared to identify the major players and functions of the microbial community contributing to the differences in soil carbon content between tillage treatments. Our results show that signature microbial communities exist for both tillage treatments which differ between the soil layer above and below the depth of reduced tillage. These findings will help elucidate microbial pathways which regulate carbon fluxes in agricultural soil.

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Economic evaluation of innovations in crop production using distance functions

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Abstract

Compared to other major cash crops wheat yields increased on low scale in recent years. Based on GM technology researcher developed a wheat variety (HOSUT), which showed yield increasing potential of 28% compared to its conventional counterpart. For an economic assessment of that breeding innovation we use a stochastic distance functions approach to determine a shadow price for seeds with increased yield potential.

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Abstracts Poster

Analyzing gamma/delta T cell function in chicken by reverse genetics

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Abstract

The prevalence of ɣ/δ T-cells in chicken is as high as 50% of the peripheral blood lymphocytes. The particular functions of that T-cell population are still mostly unknown. Recently established methods of reverse genetics in chicken are used to deplete ɣ/δ T-cells in chickens, which can be used as model animals to uncover the functions of ɣ/δ T-cells in ɣ/δ T-cell high species subsequently.

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Generating genetically engineered chickens with inducible interferon expression

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Abstract

Interferons (IFN) are a highly diverse group of cytokines with multiple roles in chicken immunity. This study aims at establishing a transgenic animal model, in which IFN-lambda is not constitutively expressed but inducible after hatching, and thereby making it possible to illuminate the role of IFN-lambda in chickens' immune response.

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Tree species diversity, structure and natural regeneration in Tumbesian Dry Forests

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Introduction

Tropical dry forests are distributed on both sides of the ecuatorian line and cover approximately 1,048,700 km², from which 135,000 km² are localized in Ecuador and Peru forming the Tumbesian dry forests. Due to the climatic and topographic characteristics and suitable soils for agriculture, the areas of tropical dry forests are attractive for anthropogenic occupation, resulting in higher rates of intervention and destruction than in tropical wet forests. In the Tumbesian dry forests of southern Ecuador and northern Peru, the situation is the same: human settlement including conversion to agricultural land-use and grazing by goats and cows leads to forest degradation and deforestation in a unique ecosystem of high biodiversity and sustainable land-use concepts are needed in order to prevent further deforestation. However, little is known about the state and dynamics of the Tumbesian dry forest.

Methodology

The main goal of the study is to assess the impact of grazing on biodiversity and stand dynamics of Tumbesian dry forests. In a first step, the structure and tree species diversity have been evaluated on 72 inventory plots with a total area of 25,92 ha. The plots consider two major vegetation types (deciduous (0-700m asl) and semi-deciduous dry forests (200-1100m asl) and three levels of stand density (dense, semi-dense and sparse forests). Furthermore a part of the plots has been fenced against browsing to assess the impact of cattle and goats grazing on tree regeneration.

Results

The first results provide information about stand structure, tree species diversity (Shannon diversity and evenness indices) and regeneration for both forest types on a cluster level by comparison of the deciduous and semi-deciduous forest type:

Structure

The total number of trees (dbh >10cm) is generally slightly higher in the deciduous forest type. However, the higher number of individuals in the deciduous forest is limited to lower diameter classes and the semi-deciduous forest shows a slightly higher number of bigger trees, resulting

in almost equal basal areas for both forest types. Both types show negative exponential diameter structures. Mean and maximum tree height did not differ significantly between both types.

Tree species diversity

89 tree species have been identified in total within both forest types: 42 tree species are present in both forest types, 13 species are unique to the deciduous forest and 34 tree species have only been registered in the semi-deciduous forest. Species richness is lower within the deciduous forest where 55 tree species have been registered in total, compared to 76 tree species in the semi-deciduous forest. The Shannon diversity indices are also considerably lower in the deciduous forest, whereas the evenness indices show higher values compared to the deciduous forest.

Natural regeneration

2,300 individuals of natural regeneration have been registered in total on 1,152 m², resulting in 19,965 individuals per hectare. In general, the quantity of regeneration appears higher in the deciduous forest (mean 21,233 ind./ha vs. 18,698 ind./ha).

51 different tree species have been identified for 2,035 individuals, 32 species being present in the deciduous forest and 39 species in the semi-deciduous forest. In accordance to the mature trees, Shannon diversity indices are generally lower in the deciduous forest, but the difference is less pronounced. The evenness indices of tree regeneration are almost equal, indicating no differences regarding the regeneration between both forest types.

Conclusions

The deciduous and semi-deciduous Tumbesian dry forests do not show significant differences regarding their structure. However, species composition and richness of mature trees varies between both forest types. Tree regeneration numbers are high, but species richness is generally lower compared to the mature trees. The diversity indices of tree regeneration are almost equal between both forest types. However, the lower evenness index of mature trees in the semi-deciduous forest indicates a reduced presence of mature trees for several species.

In the next steps we will analyze the dynamics of natural regeneration over time by comparison of repeated inventories during the dry and the wet season. Data from open and fenced plots will serve for the assessment of grazing impacts of tree regeneration.

Specific amplification of bacterial communities in *Dactylis glomerata* plant samples

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Abstract

Plants promote tight interactions with microbes, which are essential for plant health, nutrient availability, growth promotion and disease suppression. Through secretion of specific chemoattractants, plants actively shape their microbiome. The composition of plant-associated bacterial communities can be affected by different factors like landuse intensity for example. High throughput sequencing will be used to unravel new insights to *Dactylis glomerat*a root associated microbiome in different landuse intensities.

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The role of the androgen receptor in avian sexual development

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Abstract

Androgens play a key role in male sexual development in most vertebrates. The aim of this study is to reveal the role of the androgen receptor during chicken embryogenesis and sexual development. Using a dTomato gene trapping construct the expression of the androgen receptor will be visualized in vivo during embryogenesis.

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Spatio-temporal variability of erosivity estimated from highly resolved and adjusted radar rain data (RADOLAN)[1]

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Abstract

Rainfall erosivity is the potential of rainfall to cause soil erosion. Regional mean annual erosivity factors are used for soil loss predictions of Agricultural Services. To update these widely used long-term factors, highly resolved radar rain data, obtained by the German Weather Service, are used. In a first step, a subset of the adjusted radar rain data was used to estimate the spatial and temporal variability of erosivity of two years in an area with high soil erosion risk. These results will be presented.

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Deregulation and Productivity – Empirical Evidence on Dairy Production

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In a well-functioning and free market, firms which cannot keep up with competitors are forced to reduce their market share or even cease their market participation, freeing the resources bound by their production activity and making them available for production by more productive firms. This process contributes to a more efficient production at the sector level (i.e. aggregate productivity). Market regulation, however, is suspected to hinder this resource flow by keeping firms with low productivity in the market. This suspicion can also be applied to the case of the EU milk quota system. We therefore investigate development of productivity and its relation to resource reallocation effects in the dairy sector in South-East Germany during the phase-out of the EU milk quota.

We make use of a dataset which is part of the European Farm Accountancy Data Network (FADN) and comprises Bavarian dairy farms. The data contain financial records and additional socio-economic variables providing information on e.g. the use of family labour, education of the farm manager, or physical input quantities. The dataset comprises a time span of 15 years (2000 to 2014).

Farm-level productivity is estimated by applying an endogeneity-robust proxy approach originally proposed by Olley and Pakes (1996) and modified by Levinsohn and Petrin (2003) and Wooldridge (2009). We compare the productivity estimates to other estimation approaches and an index analysis. Following Baily, Hulten and Campbell (1992) and Olley and Pakes (1996) we aggregate individual productivity levels to sector productivity as the output share weighted mean of the individual productivity levels. After aggregation we decompose sector productivity into unweighted mean productivity and a covariance term quantifying the allocation of production resources towards more productive farms.

We observe an increase in the covariance term coinciding with a period of rather volatile milk prices. Therefore, we hypothesize that reallocation of production resources are triggered by extreme prices possibly powered by market deregulation. We seek to find support for this hypothesis in a regression analysis linking the covariance term and price variability. However, we find only little support for our hypothesis in this analysis.

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Preferences in Sustainability Standard Design: Analysing Organizational Elements

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Abstract

Existing agricultural sustainability standards are hardly applied in Germany although there is public attention on sustainable farming and growing markets for sustainable food. Studies on organizational issues concerning sustainability standards are missing. We use the utility function to measure farmers preferences for attributes in standard design focusing on organizational elements like consulting, data transfer et cetera. These attributes will be evaluated in discrete choice experiments, which allow us to draw conclusions on the attribute importance and correlation to farmers` socio-demographic characteristics. Based on this information acceptable standards can be developed and target groups can be identified.

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Sustainability in the supply chain of ornamental plants

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Introduction

The market volume for ornamental plants in Germany was estimated to be 8.6 billion euros in retail prices with an average spending of 107 € per capita (Tröster 2015a). Nevertheless, intensive cultivation contributes to creating a significant environmental burden caused by input materials, energy and emissions (Stanghellini, Kempkes, & Knies, 2003). Working conditions in the industry, mostly in developing countries, have been also criticized (Riisgaard, 2009). Studies have shown that the demand from both consumers and retailers for sustainable ornamental crops is growing (Seuring & Müller, 2008; Wollaeger et al., 2015). Therefore, a method for assessing the sustainability of ornamental crops is needed. However, assessing the sustainability of the supply chain of ornamental crops is difficult because most studies address specific aspects of the supply chain or focus on a single product (Sahle & Potting, 2013; Soode et al., 2013). The aim of this study is to identify the most common supply chain for ornamental plants. The next steps will be to develop sustainability criteria and indicators for the identified supply chain.

Materials and Methods

Interviews were held with professionals from six ornamentals companies with the aim of identifying common processes in the supply chains. All interviews took place face-to-face at the IPM Essen (2016) using a semi-structured interview guide. The interviews were recorded and transcribed. Data was analyzed using Atlas.ti. Apart from the interviews, participants were also asked to fill in a table about the supply chain of plants from a list of the top-selling bedding and pot plants in Germany (Tröster, 2015b). Information about the propagation methods of these plants is presented in Table 1. The next step planned is to identify relevant sustainability criteria. This will involve extensive literature research and validation of the results with experts.

Results and Discussion

Table 1: Propagation methods of some bedding and pot plants sold in Germany.

	Propagation material	
Bedding plants	**Seeds**	**Cuttings**
Geranium	x	x
Viola	x	
Chrysanthemum	x	x
Petunia	x	x
Begonia	x	x
Primula	x	
Leucanthemum		x
Impatiens		x
Pot plants		
Poinsettia		x
Cyclamen	x	

The expert interviews showed that the majority of bedding plants, and some potted plants, go through similar steps in the supply chain. There are two main supply chains, which differ mainly in the propagation method. Plants are propagated either from seeds or cuttings (Figure 1). When cuttings are used as propagation material, the mother plants originate from elite plants in Europe. Each year, new mother plant seedlings are propagated from elite plants using in-vitro methods. The seedlings are then sent to Africa, mostly Kenya, Ethiopia or Uganda, where they are grown in accordance with strict

hygiene protocol to become the new generation of mother plants. Cuttings are harvested from the mother plants and transported via air back to Europe. The cuttings are cultivated by specialized growers for young plants. The rooted seedlings are often sold to other growers in Europe where they are grown typically to the end product. In the case of seeds as propagation material, seeds are mostly purchased from seed companies worldwide. Few breeders produce their own seeds. Germination takes place in germination chambers. The seedlings are grown in greenhouses to young plants. The young plants are marketed to other growers in Europe.

From the ten top-selling bedding plants in Germany (Tröster, 2015b), eight follow the supply chains identified (see Table 1). Viola and Primula are propagated only from seeds. Other plants such as Geranium, Chrysanthemum, Petunia and Begonia can be propagated from both seeds and cuttings. However, plants produced from cuttings are of better quality and therefore have higher market value. Pot plants that follow these supply chains are Poinsettia propagated from cuttings and Cyclamen propagated from seeds.

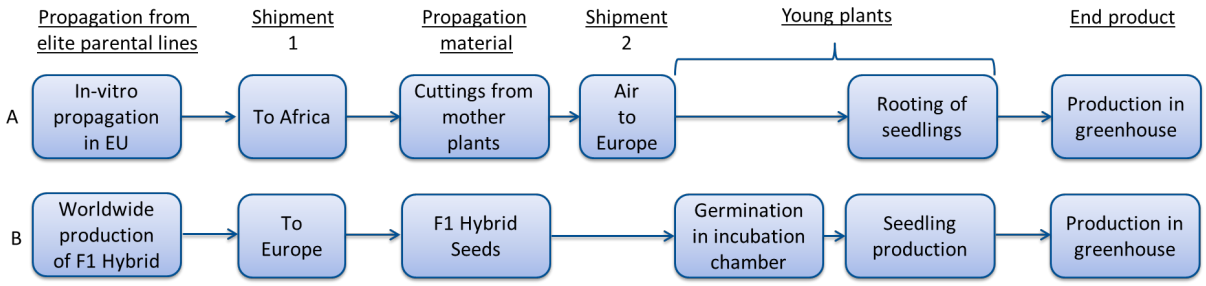

Figure 1: Supply chains identified. A: cuttings as propagation material. B: seeds as propagation material.

Conclusions

The results of this work are the characterization of typical supply chains for bedding plants in Germany. The supply chains for the majority of bedding plants and some pot plants contain similar steps. These data suggest that the sustainability of many ornamental plants can be assessed with a common set of criteria. Furthermore, it would be possible to perform a sustainability assessment of a variety of plants, because they share the same processes in the supply chain. Future goals are to develop a set of sustainability criteria and indicators to measure the sustainability of the identified supply chains.

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Assessing the efficiency of debarking harvesting heads

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Abstract

We are investigating together with the KWF and funded by the FNR, if and how debarking harvesting heads, which are already used in intense managed eucalyptus plantations (so called tree farms; Brazil/South Africa), can help to find solutions for German Forestry. In-stand debarking has the potential to maintain soil fertility, to reduce the spreading of pine bark beetles or lower the ash content of firewood. As the debarking heads were developed for a special purpose, it is necessary to investigate how they perform on Central European tree species to be able to estimate if those technical specifications are also suitable for local conditions. The task of the PHD is to develop an atomized system to measure debarking percentage and debarking quality throughout a laser and a photo-optical system directly in the stands

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Visual assessment of barley malt: An appropriate tool for *Fusarium* detection?

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Introduction

As in wheat the impact of *Fusarium* pathogens such as *F. culmorum*, *F. graminearum*, *F. avenaceum*, *F. tricinctum*, *F. langsethiae*, and *F. sporotrichioides* in barley is multifactorial. On the one hand, *Fusarium* pathogens cause substantial direct losses by reducing yield and thousand kernel weight. On the other hand, indirect losses arise from quality degradations such as mycotoxin contaminations, gushing, or altered solubility characteristics.
Quality control of the raw material is of major interest for malt production, because it has decisive influence on the quality of the end product beer. Up to now, almost no satisfactory and generally accepted method for the evaluation of malt quality is available for practice. The applied techniques base on visual screenings and therefore presuppose a direct connection between occurring symptomatology, actual infestation, and mycotoxin content.
For the visual assessment procedure according to the Mitteleuropäische Brautechnische Analysenkommission (MEBAK), called 'Handbonitur', the number of red kernels is determined in a representative subsample of 200g (approx. 4000 kernels) deriving from a whole malt batch. The exceedance of a defined limit (usually 5-7 kernels) can lead to reductions in price or to the rejection of the entire batch.

The validity, reliability, and sensitivity of this commonly used standard tool for predicting actual *Fusarium* contaminations in barley malt was evaluated in a cooperation project, combining professional competences of Phytopathology, Brewing and Beverage Technology, and Analytical Food Chemistry.

Material and Methods

To validate the informative value of the visual assessment according to MEBAK, a set (n=20 per year) of commercially produced malt samples, originating from different locations and years (2012-2014), was analyzed for the amount of colored kernels. In addition, the actual *Fusarium* contamination concerning DNA and mycotoxins was determined via qPCR and LC-MS/MS, respectively. Correlation analysis was carried out to reveal potential connections between symptomatology and de facto *Fusarium* infestation.
To detect the causal agents of symptomatology, color specific samples were created and as well analyzed for *Fusarium* contaminations. DNA and mycotoxin data of samples, exclusively consisting of red kernels, were compared to data of corresponding symptom-free control samples.
To verify the reliability and sensitivity of the visual assessment, a serial dilution experiment was conducted. Therefore, a distinct number (0, 5, 10, 20, or 40) of specific contaminated red kernels was added to pathogen-free tested barley malt. Created samples were tested for significant differences in *Fusarium* DNA and mycotoxin contamination.

Results and Discussion

The correlation analysis revealed positive connections between occurring symptomatology and *Fusarium* DNA. No such connections were found for symptoms and *Fusarium* mycotoxins. Thus, data indicate a certain informative value of the visual assessment to predict *Fusarium* DNA content in malt, but failed to validate mycotoxin contaminations.
The comparison of symptomatic and corresponding control samples showed strong differences. Contents of *Fusarium* DNA and associated mycotoxins were higher in malt samples consisting of red kernels than in samples without symptomatic kernels. *F. avenaceum* and *F. tricinctum* were found to be the main causal agents of red symptomatology. Species-specific DNA as well as associated primarily produced mycotoxins Enniatin B and B1, were most elevated. However, *Fusarium* DNA and mycotoxins of every tested species were also detected in symptom-free samples, suggesting latent *Fusarium* contaminations.
The serial dilution experiment revealed low sensitivity of the visual assessment for predicting *Fusarium* DNA and mycotoxin contamination. Significant differences in contents of *F. avenaceum* and *F. tricinctum* DNA as well as in contents of Enniatin B and B1 were only found for samples containing high numbers (10, 20, 40) of specific infected red kernels. These data put the relevance of the practically applied limits of 5-7 kernels to question.

Conclusions

The present study investigated the validity, reliability, and sensitivity of the visual assessment, a commonly used method for evaluating malt quality with regard to *Fusarium* infections. Results indicate a certain informative value of this method, but revealed a lack of reliability and sensitivity to display actual *Fusarium* contaminations.
Symptomatology of kernels can be perceived as indicator for *Fusarium* infestation, but does not exclusively represent *Fusarium* contamination. Consequently, for more accurate quality control in the malting and brewing industry the current study strongly suggest applying new methods for the detection of *Fusarium* contaminations.

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Establishing a near infrared spectroscopy (NIRS) system to control feed quality of soy cake on base of feed value assessments in-vitro and in-vivo (chicken studies)

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Introduction

Using locally produced feed is gaining more importance especially when regarding the protein sources and organic farming. A very valuable protein component for monogastric livestock is soy, due to its amino acid composition with high amounts of essential amino acids like lysine or methionine. But soybeans and products derived thereof contain significant amounts of antinutritive substances (e.g. trypsin inhibitors) and therefore, heat treatment is commonly used to reduce the activity of these substances to a minimum tolerable content (3). It was shown by Ahmed (2001) and NOPA (2003) that the intensity of the heat treatment has a significant influence on the feed's digestibility and therefore also on feed quality. Heat treatment may also impair feed quality through denaturation of feed protein, particularly when applied in excess. Therefore, heat treatment of soybeans and soy products like full fat soy cake or partly de-oiled soy cake needs to be optimized. The optimization of the heat treatment is the scope of the project, which is divided into four steps: Two different batches of soybeans will be first processed into partly de-oiled soy cake using different decentral processing plants and technologies. Thereafter, feed quality of the soy cake variants will be quantitatively assessed through laboratory analysis as well as in-vivo studies using growing chicken. Along with the processing of soybeans into soy cake near infrared spectra will be recorded. Finally all data will be used to calibrate a near infrared spectrometer (NIRS) for online process enhancement at decentral processing plants and hence for optimizing feed quality of soybean and soycake.

Material and Methods

Technical realization: At the beginning of the project the focus was put on the technical realization of different processing techniques for soybeans. Therefore two homogenous batches of soybeans (variety Sultana, conventional farming; variety Merlin, organic farming) were chosen due to their largest difference in trypsin inhibitor activity (TIA). Both batches were processed using the following different procedures:

- Thermal treatment: The raw, untreated soybean was slightly wetted and toasted (temperature 115 °C, duration 40 s). Following the thermal treatment the soybean was deoiled.

- Hydrothermal treatment: The raw, untreated soybean was treated with steam (temperature 103 °C, duration 40 min). Deoiling was done after the hydrothermal treatment.

- Pressure and thermal treatment: The raw untreated soybean was first deoiled. Afterwards is was treated with steam (temperature 102°C, duration 10 min) and extruded with an expander (temperature 130 °C, duration 1-5 s).

- Kilning and thermal treatment: The raw, untreated soybean was first treated with heat. During this process the revoked steam was circulated around the soybean (temperature 160 °C, duration 30 min). Then the soybean was deoiled.

Parameters chosen for laboratory analysis were activity of trypsin inhibitors, products of the Maillard reaction (ε- fructose lysine / free lysine), solubility in potassium hydroxide (KOH) and the Protein Dispersibility Index (PDI).

In-vivo assessment of feed value: The processed soybeans' suitability as animal feed will be tested in in-vivo studies with growing chicken. Therefore, growth performance experiments will be conducted. Both batches of soybeans, each divided and treated with 21 different intensities using the earlier explained processes will be fed to male broiler chicken. The trial will be repeated 6 times to secure statistical analysis. Furthermore, a positive control using commercially available soy meal will be integrated in the trial. The chicken will be fed ad libitum with a commercially available chicken starter (day 1 – 10), a grower (day 11 – 24) and a finisher diet (day 25 – 35) according to the nutritional needs of the birds. Grower and finisher diet will be fed using the differently treated partly deoiled soy cake. Parameters such as body weight, water usage, foot pad dermatitis, hypertrophy or hyperplasia of liver and pancreas will be raised during this trial.

Integration of technical processing and in-vivo assessment of feed value into a NIRS Calibration: During each step of the soybeans' processing into soycake a near infrared spectra (NIRS) was recorded. Those spectra will be combined with the results of the laboratory analyses and in-vivo studies, aiming at establishing a NIRS calibration using appropriate statistical methods (4). In order to receive a more valuable and robust calibration, a high number of NIR spectra needs to be recorded. Therefore, additionally different soybean and soy cake samples are collected at decentral processing plants from several steps during the treatment process. The last scope of the project is to implement a NIRS sensor system using the previously established calibration in order to be able to control the process of transferring soybeans into soycake and therefore optimizing feed quality.

Results

The processing of the two charges of soybeans using the four different methods resulted in proper degradation of the trypsin inhibitor. Insufficient, optimum, as well as excessive treatment could be verified in respective activities of the trypsin inhibitor in the different soybeans. A NIR spectrum could be taken for every different step during processing. The next steps in the project are to establish a test calibration and to start in-vivo growth performance trials with broiler chicken.

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Predicting natural regeneration in forest stands

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Introduction

Natural regeneration of forest stands is one of the key elements of modern forestry. Ungulate browsing often prevents the natural regeneration of forest stands. The project Biowild tries to examine the impact of ungulate browsing on the biodiversity. Part of the project investigates the effect of browsing on forest stand and the ability to regenerate such stands naturally. Therefore, suitable sites, where one can expect natural regeneration, have to be selected to conduct a comparative study between fenced and unfenced forest sites. With the comparison of the fenced areas against the areas without fence, one can determine the influence of ungulate browsing. The aim of the presented approach is the objective selection of suitable sites, where natural regeneration could be expected. A second goal was to determine the factors with influence the occurrence of natural regeneration.

Material and Methods

To fit a logistic model, which can predict the occurrence of natural regeneration, I used the data of the third federal forest inventory (Thünen-Institut 2012). Additionally, I used weather data from the German Weather Service and soil data available from the federal agency for geological science and resources. The final variables were selected to maximize the model fit and the forecast success. Fitting and testing was done with a separated subset of the data. The resulting model was used to forecast the occurrence of natural regeneration in five regions. Within the region forest inventory data was collected and georeferenced. A raster with lateral length of 200 x 200m was laid over each region. For every raster point the forest inventory data was used to calculate the probability of finding natural regeneration on the given point. I selected the 200 Points with the highest probability for further examination. To examine the impact of the different factors on the predicted probability, I used the Kruskal-Wallis test and the Dunn Test as post-hoc test.

Results and Discussion

The final model included ten variables (Slope, absolute Altitude, form of Property, diameter at breast height, tree height, tree age, number of stand layers, stand type, basal area and soil fabric). The le Cessie - van Houwelingen - Copas - Hosmer unweighted sum of squares test for global goodness rejected the H0 of no fit (Le Chessie und van Houwelingen

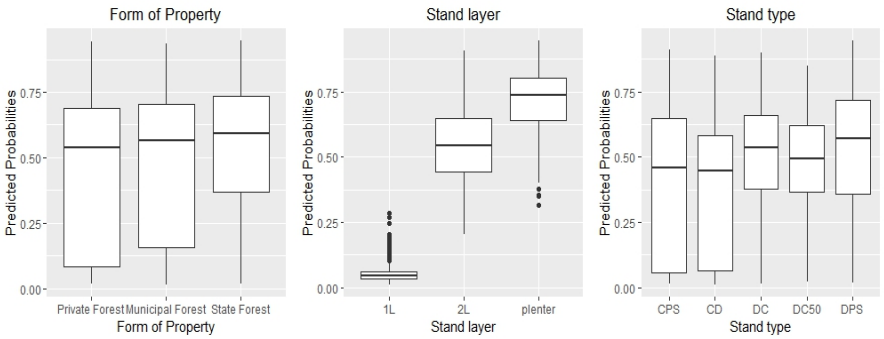

Figure 1

1991). The area under the receiver operator curve was 0,82. The overall correct specification was 72% and the correct specification of y=1 was 64%. The model was then used to predict the 200 points with the highest calculated probabilities. The main results of the examination of the group differences were shown in figure 1. All group differences were significant at least on a 1% level. The probability of occurrence of natural regeneration was higher in stands with two or more layers. It was also higher in state owned forests. When comparing the probabilities in dependence to the stand type, it becomes clear, that the highest probabilities were in deciduous pure stand (DPS) and in deciduous-coniferous mixed stands with leading hardwood trees (DC).

The good model fit allowed the prediction of the points with the highest probability of finding natural regeneration. The higher probabilities in the stands with two or more layers were as expected. One problem was the strong influence of the attribute form of property, because it resulted in survey points which were clustered in state forests. The higher probabilities in state owned forests were surprising, because it induced, that the hunting and sylvicultural management promotes natural regeneration. This is true, because the higher probabilities in state forests remained, after the probabilities were recalculated with a data set, where all cases got the attribute “state forest”.

Conclusions

It is possible to predict the occurrence of natural regeneration with a logistic model. The large database enabled me to select the most suitable variables for the model and produces a model with high fit and good predictive ability. The differences in stand type and stand layer were as expected. The difference between the predicted probabilities of the different forms of properties where surprising at first. Nevertheless, it appears to be logical, given the fact that state forests are usually managed with up-to-date silvicultural practices and hunting regimes.

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Soil Organic Carbon Stocks in Depositional Landscapes of Bavaria

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Abstract

Erosion leads to redistribution and accumulation of soil organic matter (SOM) within agricultural landscapes. These fluvic and colluvic deposits are characterized by a highly diverse vertical structure and can contain high amounts of soil organic carbon (SOC) over the whole soil profile. The aim of our study is to elucidate the spatial distribution of SOC stocks as well as its depth function and the role of these landscapes as a reservoir for SOM. Therefore we compare two representative sites in Bavaria composed of different parent materials (carbonate vs. granitic). We hypothesize that the soils associated with different depositional processes (fluvial vs. colluvial) differ in SOC contents and stocks, also because of different hydromorphic regimes in fluvic versus colluvic soil profiles.

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Investigations on the influence of disturbances in day to day housing routine on zoo-technical parameters of fattening pigs

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Introduction

Objective animal-associated indicators are the best measure to assess the quality of animal welfare (Veissier, Forkman 2008). Animal welfare assessment-protocols, however, mostly use indicators addressing housing conditions e. g. pen size, animals per pen, and other stable or management dependent factors (Averós et al. 2013). On the other hand, behaviour is directly linked to the animal but common techniques to observe animal behaviour are subjective because the rating value strongly depends on the person conducting the analysis (Dawkins 2004). Therefore finding new objective and easy-to-use indicators should be one of the most important aims in animal welfare research. The present study investigates on the usability of zoo-technical measures and feed-intake-behaviour as a new animal-associated welfare-indicator.

Material and Methods

A feeding trial with 96 fattening pigs was conducted to assess the influence of typical disturbances happening in the daily stable routine on performance parameters and feed-intake-behaviour. The animals (Pi x (GL x LW)) were distributed over eight pens according to litter, sex and weight. One automatic single-space-feeder was used per pen to record the time of visit and the amount of feed consumed per visit by each individual animal. The average starting age and weight was 74 days and 32 kg. Reaching 120 kg the animals were slaughtered consecutively.

To reduce nitrogen emissions three body weight depending feeding periods were designed. The grower diet I was fed from 30 kg to 60 kg, the grower diet II from 60 kg to 90 kg and the finisher diet from 90 kg until slaughtering. The feed represented a typical Bavarian composition of barley (40 %), wheat (39-46 %), soybean-meal (18-12 %) and mineral feed with supplemented amino acids (3-2 %) and contained 13.3 MJ (grower I) to 13.5 MJ (finisher) of metabolizable energy.

The experiment was built on four treatments each consisting of two pens. Three treatments simulated different kinds of short-term disturbances in day-to-day management procedures whereas the fourth was an undisturbed control. The interferences were simulated during the grower II period (weeks eight and ten) and the finisher period (week twelve). Treatment B was designed to show the influence of defects in the feeding technique (feed deprivation for 12 h and 24 h and restrictive feeding for 48 h). In group C we exchanged animals between the two pens (in week eight and twelve) and reduced the amount of available drinking water to the legal minimum (0.6 l/min) for 48 h (week ten). In treatment D the feed composition was varied (only cereals for 48 h in week eight, 100 % more mineral feed in week ten and initial-fattening-diet in week twelve) to simulate mistakes during feed preparation. The diets were changed in week six and week eleven which is the reason for the first two disturbances happening in the grower period II and the last in the finisher phase.

SAS 9.4 (SAS Institute, Cary, United States of America) was used for statistical analyses.

Results and Discussion

The mean values of the treatment groups' performance parameters are shown in Table 2. Six animals had to be excluded from the analyses due to diseases.

In the grower period II differences in daily weight gain and feed intake between the treatments and the control became visible indicating the treatment effect. The control gained on average 101 g/d more weight than the other three groups (932 g vs. 831 g). The daily feed intake followed the same trend. Treatment A fed nearly 150 g more per day than the other groups (2.24 kg/d vs. 2.10 kg/d). During the grower phase I the animal group B gained significantly less weight than the others (706 g/d vs. 766 g/d) because of tail biting.

Table 2: Average performance parameters over treatments

Treatment		A	B	C	D	Significance (p<0.05)
Animals	n	23	24	20	23	
Fattening period	d	103	104	104	105	0.96
			Bodyweight			
Beginning grower I period	kg	32	32	32	33	0.82
Beginning grower II period	kg	59	57	58	60	0.36
Beginning finisher period	kg	85	80	82	82	0.07
End of experiment	kg	114	111	113	114	0.48
			Daily weight gain			
Grower I	g	774[a]	706[b]	754[ab]	769[a]	**0.05**
Grower II	g	932[a]	821[b]	866[ab]	807[b]	**0.01**
Finisher	g	845	887	867	774	0.59
Overall	g	828	789	789	785	0.29
			Daily feed intake			
Grower I	kg	1.69	1.59	1.68	1.67	0.24
Grower II	kg	2.24[a]	2.02[b]	2.14[b]	2.15[ab]	**0.03**
Finisher	kg	2.47	2.40	2.30	2.40	0.33
Overall	kg	2.19	2.07	2.09	2.13	0.23

Thus the influence of short term disturbances was measurable within fattening periods meaning during the grower II phase. To analyse effects in grower phase I a follow-up-study already was conducted. Compensatory effects seemed to prohibit an influence on the animals' overall performance. Therefore zoo-technical performance is only able to detect disturbances within a limited period of time.

Conclusions

Our experiment showed that the zoo-technical performance data can reveal short-term influences on animal welfare but is quite insensitive. Future investigations on the influence of disturbing factors on feed intake behaviour are already in progress. Short term deviations are strongly visible in the feed-intake-patterns of the individual animal (data not shown). But statistical methodology has further to be established adequately analyse the data.

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In vivo phenotyping of the carcass-trait "backfat thickness" in mirror carps (*Cyprinus carpio*) by using ultrasound

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Introduction

In Germany, carp production has a long tradition and is still a part of the local culture. In 2013, 5.700 tons of carp were produced in Germany, most of them in the states Bavaria and Saxony. Several areas are protected under the European Quality Scheme called "PGI" – Protected Geographical Indication. This quality label requires that at least one stage of production, processing or preparation takes place in the respective area. In 2012 the "Aischgründer Karpfen" obtained said PGI-label. According to the product specifications the maximum allowed fat content of the fillet including the skin is 10%. The goal of this guideline is the consistent production of lean fish to achieve high customer acceptance.

A previous study of Oberle et al. (2015) has shown a high correlation between the fat content of the fish and its backfat layer thickness, measured at the split carcass. Although ultrasonic technology is a regular method for the determination of body composition in other species - such as pig or cattle - there are hardly any insights for fish.

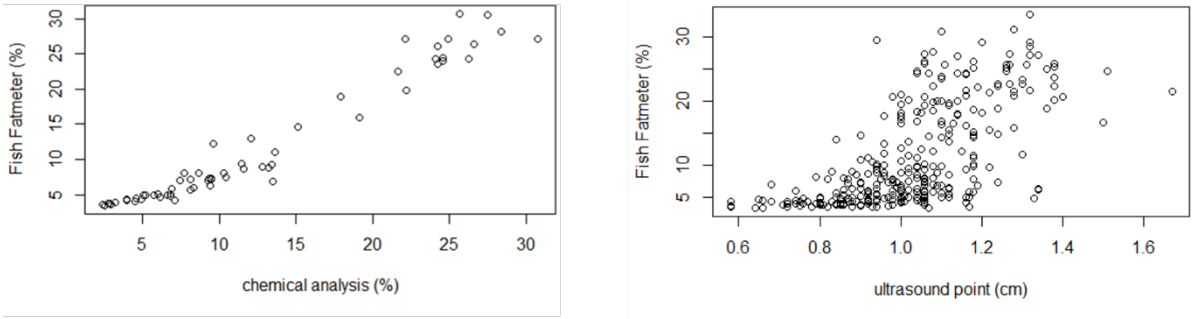
Material and Methods

307 live mirror carps (*Cyprinus carpio*) originating from six different ponds of the region around the „Aischgrund" were examined using a mobile ultrasound device (MircoMaxx, Fujifilm, Sonosite, Frankfurt am Main, Germany) combined with a 5MHZ Endolinear-probe. The non-sedated fish were put in narrow water-filled containers. Because of the water used as transmission medium, there was no direct contact between the fish and the probe needed. A sagittal image per fish was taken. This was used to measure the thickness of the backfat layer at a defined spot, close to the fish's head. Afterwards all carps were taken out of the water in order to measure the fat content using a Fish Fatmeter (Distell, Fauldhouse, Scotland, UK). This measurement is based on the microwave technology. The device was applied to the left side of the fish in four specific locations to digitally display the mean value of the four values. After the *in vivo* measurement 10 carps per pond were slaughtered and the left fillets including the skin were analysed chemically.

Results and Discussion

All data collected were inserted into Excel 2010 and analyzed using RStudio (Boston, US). First results generated an R^2 of 0.94 ($p <= 0.001$, n=61) looking at the single correlation between the fat content measured by the Fish Fatmeter and the fat content determined by chemical analysis. For further calculations the microwave technology was used as gold standard for the remaining fish that had not been chemically analyzed. Single correlation between the thickness of the backfat layer measured by ultrasound and the results provided by the Fish Fatmeter generated an R^2 of 0.41 ($p <= 0.001$, n=307).

Figure 1: Correlation between the fat content of live fish using the microwave technology (Fish Fatmeter) and the fat content of the fillet determined by chemical analysis (n = 61, R^2 = 0.94, p <= 0.001) and the correlation between the backfat thickness measured by ultrasound and the fat content measured by microwave technology (n = 307, R^2 = 0.41, p <= 0.001)



Conclusions

The Fish Fatmeter has proven to be a good method to predict the fat content in mirror carps. Regarding the ultrasound measurements, a moderate correlation could be generated using the Fish Fatmeter measurements as a gold standard. One reason could be the difficulty to take precise sectional images, as the living fish is constantly in motion.

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A non-stochastic portfolio model for optimizing the management of forest stands under risk

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Introduction

Forest stand simulation and the optimization of forest portfolios can be a powerful tool for forest managers and decision makers. Currently stochastic mean-variance optimization[1] is a frequently used optimization approach in forest studies. Either the economic return can be maximized or the risk, measured by the standard deviation, is minimized. This mean-variance optimization technique works if enough data are available: either field data or data generated through simulations such as a Monte-Carlo Simulation (MCS). The approach also assumes that future stand structure and economic performance, for example economic output, will be considered the same as the current structure and performance. A disadvantage of this method is that changes to initial parameters or missing data can lead to very different portfolio results. Therefore results cannot always be considered robust and can even be seen as manipulable. These reasons have promoted a search for a non-stochastic optimization approach that requires less data and can be considered robust.

Material and Methods

The non-stochastic optimization approach is formulated as follows[2]:

$$\boldsymbol{max\ E(Y_L) = \sum_{i \in L} y_i a_i}$$

The economic return ($E(Y_L)$), in this study the annuity per hectare, is maximized and formed by the sum of the products of the individual annuities (y_i) and their allocated land area (a_i). Values for land area a_i must sum up to 1 and cannot be negative. The different management options are the harvesting timings for Norway spruce (*Picea abies,* eight options) and European beech (*Fagus sylvatica,* nine options). These harvesting timings result in different age cohorts within the forest stands. To integrate uncertainties into the optimization process the annuities of each age cohort consider, among other things, fluctuating timber prices and natural disasters. Mean values were calculated using MCS. The standard deviations (s_i) of the single annuities were used to build the uncertainty sets for the non-stochastic approach. The size of each set depends on the multiplication factor ($m|1.0, 1.1, 1.2, \dots, 3.0$) for the standard deviation. As a result each age cohort has a maximum ($y_i + m * s_i$) and a minimum ($y_i - m * s_i$) value. The combination of all 17 age cohorts with their maximum and minimum values form the constraints (2^{17}) for the optimization and consequently the uncertainty sets.

Results and Discussion:

In general the economic results from the non-stochastic optimization are similar to those from the already established stochastic optimization. To compare both approaches, the annuities were calculated for similar risk levels. Data for the comparison are from Roessiger et al. (2011)[3]. The non-stochastic

robust portfolios resulted in economic losses between 0.22% and 11.32% below the efficiency frontier (see Figure 1). The composition of the portfolios from the different optimization approaches varied greatly. Non-stochastic portfolios were robust and included at least five age cohorts across high and low risk acceptance. Stochastic portfolios comprised a monoculture of spruce when risk acceptance was high, while an extremely low risk tolerance produced a portfolio of nine age cohorts with a share of 70% beech. This is clearly a result of the low standard deviation of European beech stands. However, economic performance vary much more across the different risk levels for stochastic portfolios: a range of 66€ between the lowest and the highest accepted risk compared to a variation of 42€ for the non-stochastic portfolios.

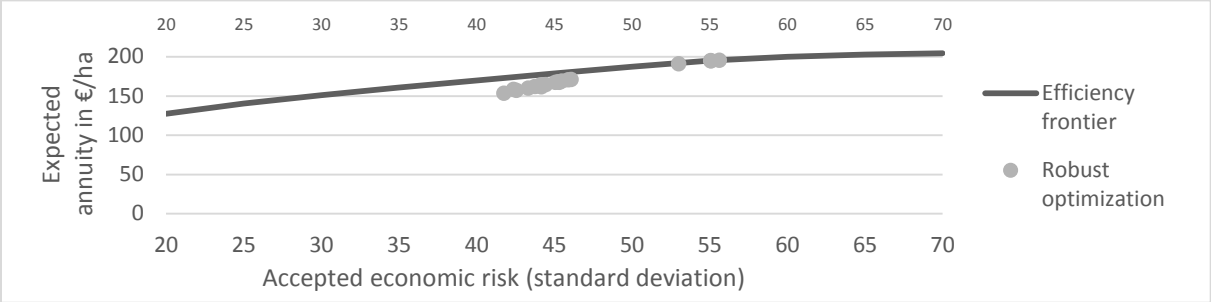

Figure 1: Economic comparison of the stochastic and the non-stochastic optimization. The difference in expected average annual payments for the same level of risk of both approaches is shown.

Conclusions

The economic losses of the non-stochastic portfolios are robust and, compared to the mean-variance portfolios, are acceptable. This new approach requires less data and no correlations or covariance between the single assets of the portfolio. Although the robust portfolios included at least five different age cohorts, the portfolios are not diverse in tree species because the age cohorts are all Norway spruce. Including tree species interactions within the optimization approach may prevent these monocultures and should be considered in future research.

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Effects of an automatic feeding system with dynamic feed delivery times on the feeding behaviour of dairy cows

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Introduction

Automatic Feeding Systems (AFS) gain in importance due to rising demands on animal welfare and performance-related feeding of cows [1]. These systems are offering the possibility to supply rations with a higher frequency [2]. The delivery of feed is described to have the greatest impact regarding stimulating dairy cows to feed [3, 4]. Several studies have focused on the effects of higher feeding frequencies on the behaviour of dairy cows. An increased feed delivery frequency leads to longer feeding times and a higher proportion of animals feeding at the feed bunk spread over 24 h [5, 6, 7]. But so far, under practical conditions, AFS are used with static settings for feeding times and frequencies without taking into account animal demands. Therefore, the objective of the study was to develop a method for feeding cows with an AFS at dynamic times concerning their behaviour and to analyse the effects of this feeding strategy on their patterns of feeding behaviour.

Animals, Materials and Methods

The studies were carried out in a commercial dairy farm in Bavaria. About 79 dairy cows housed in a freestall barn were milked with an AMS and fed by an AFS. The cows were subjected to each of two treatment periods, period 1 and period 2. During period 1, the cows were fed statically seven times per day. During period 2, the cows were fed dynamically seven times per day. These two treatment periods were conducted in winter 2014/15 and in summer 2015. Individual animal positioning data were collected by a Real Time Location System. Based on real-time processed positioning data regarding cows duration of stay at the feed bunk and periodically subjective evaluations of the percentage variation of amount of feed in the trough, decisions were made about starting time of the AFS feedings in predefined timeframes. The processed positioning data were used to determine feeding behaviour. Meal criteria were calculated according to the approach applied in previous studies [9, 10, 11] using the package “mixdist” in the open source software R. Depending on the type of distribution of the data, the Wilcoxon signed rank test or the t-test for paired samples was used for comparing the parameters between the treatment periods and the seasons ($p<0.05$).

Results and Discussion

Feedings in both treatment periods in winter and summer time led to similar proportions of animals at the feed bunk with maxima of about 70 – 80 % and showed a circadian pattern [11]. The presence of cows at the feed bunk increased directly following feed delivery, both in winter and summer periods 1 and 2, so that previous studies [3, 4] can be endorsed. This increase was just shifted according to the changes in feeding intervals during period 2. In winter time the total time per cow and day spent at the feed bunk was significantly shorter in period 2 (5.03 ± 1.21 h/d) than in period 1 (5.51 ± 1.35 h/d). In summer time a higher total time per cow and day at the feed bunk was observed when the AFS feeding times were performed dynamically (5.42 ± 1.53 h/d vs. 4.92 ± 1.38 h/d). The average total duration of meals per cow and day was also significantly higher in summer period 2 than in 1 (6.11 ± 1.68 h/d vs. 6.49 ± 1.79 h/d). But overall the daily total time a cow spent at the feed bunk was significantly higher in winter than in summer time. The proportion of utilized feeding places over 24 h was significantly lower in summer period 2 than in 1. Dynamic feed delivery times in winter and summer time increased the cows daily frequency of visits at the feed bunk as well as the number of meals per cow and day (winter: 7.72 ± 2.66 vs. 7.86 ± 2.00; summer: 6.85 ± 1.88 vs. 7.73 ± 2.74) by reducing the meal criteria (winter: 27.86 ± 26.68 min vs. 24.41 ± 19.02; summer: 39.74 ± 23.07 min vs. 32.63 ± 30.56 min). The tested dynamization of AFS feed delivery times resulted in longer daily total times and a higher frequency of single visits at the feed bunk as well as a longer summarized duration of meals per cows and day in summer period with high ambient temperatures despite a lower degree of utilization of the feeding places in the course of the day. This might indicate that cows distribute their visits at the feed bunk and their meals more evenly throughout the day with reduced competition during feeding when delivery times are controlled dynamically.

Conclusions

Based on current results, dynamization of feed delivery times according to cows duration of stay at the feed bunk may be beneficial for even distribution of feed bunk visits and meals throughout the day in the observed farm and in summer time. The present implementation of real-time processed positioning data is a possible approach for combining animal- and feed-related data of different sensor technologies to advance AFS for feeding cows according to their needs. In further investigations, precise measuring of amount and quality of feed in the trough as well as a dynamic adjustment of feeding frequencies and the delivered amount of feed should be tested.

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Consumer preferences for animal welfare standards in animal foods

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Abstract

This promotion examines different approaches to figure out the actual willingness to pay for products, which are produced in accordance with higher animal welfare standards. For finding out the willingness to pay we will do choice experiments and experimental auctions. Also, GfK data will be analyzed. Further we want to know, how consumers view the different players in the animal food production and in the food control and which actors are trustworthy.

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High-throughput phenotyping of yield formation of winter wheat under field conditions

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Introduction

The yield of winter wheat is required to be improved for meeting growing demand under increasingly unfavourable climatic conditions [1]. As a further constraint, increasing nitrogen use efficiency is becoming more and more important [2]. In recent years, wheat breeders have been able to benefit from the availability of genetic selection tools. Though, for maintaining necessary breeding progress, phenotyping under field conditions needs to be improved for enabling time-efficient scoring of relevant plant traits such as plant height, biomass accumulation, nitrogen uptake and yield parameters [3]. There is evidence that differences in the ability to translocate assimilates and nitrogen into the kernels during grain filling influence yield formation and grain protein concentration, respectively [4]. In order to investigate whether spectral high-throughput methods can be used for estimating plant traits and whether these traits are associated with translocation processes, a series of field experiments with wide genetic variation of winter genotypes is conducted in our study.

Material and Methods

A set of 400 double haploid breeding lines was grown at the field experimental station Dürnast in 2015. Additionally, hybrid wheat cultivars were compared to line cultivars under different nitrogen regimes (100, 160 and 220 kg/ha) for phenotyping of the traits of nitrogen use efficiency. During the main growing season in 2015, spectral measurements were conducted using both passive and active hyperspectral field spectrometer. Plant samples of selected genotypes were harvested at anthesis, milk ripe, and maturity, respectively, and separated into leaves, culms and spikes for determination of dry weight. Dry matter translocation (DMT) was calculated as the difference in dry weight of vegetative plant organs between anthesis and maturity. Spectral data was used for establishing PLSR-models for predicting plant traits.

Results and Discussion

All genotypes showed a reduction in leaf dry weight from anthesis to maturity, whereas stem dry weight increased until milk ripe. Dry weight of leaves increased stronger (by app. 20%) with an increase in nitrogen level from 160 kg/ha to 220 kg/ha compared to culms and spikes. DMT varied between 1500 and 3000 kg/ha and showed distinct differences among genotypes. However, no significant difference was found between nitrogen rates of 160 and 220 kg/ha and between the groups of hybrid and line

cultivars. These results suggest that wheat genotypes have different ability to remobilize assimilates during grain filling.

For most plant traits such as biomass accumulation, PLSR models with spectral data obtained at anthesis and milk ripe demonstrated the best correlations. Final grain yield could be estimated for an accuracy of 6 dt/ha with only one measurement at Zadoks stage 75. Thus, spectral phenotyping methods show the potential to identify the early crucial traits of wheat, which can assist plant breeders in selecting promising genotypes in the field.

Conclusion

Preliminary results indicate differences in DMT between wheat genotypes. However, the association with grain yield is dependent on growing conditions [4]. On the other hand, spectral sensing shows its potential to identify plant traits related to grain yield. Field experiments and measurements are carried out in a comparable way in 2016 for gaining further insight how plant traits can be linked to dry matter translocation and how these traits can be estimated using high-throughput phenotyping methods in the field. Nitrogen content will be determined using NIR spectroscopy in order to complement DMT data by nitrogen translocation.

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Land-Atmosphere Exchange of Greenhouse Gases in Bavarian Agricultural Landscapes

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Abstract

The terrestrial ecosystem stores a significant amount of the world's carbon in plants, animals, soils and microorganisms. Of these, soils and plants are the largest, and most rapidly fluctuating, stores. Vegetation drives the exchange of carbon between soils and the atmosphere via photosynthesis, decomposition and respiration. Nitrogen, as a major plant nutrient, is inextricably linked to the efficiency of these processes. Agricultural practices, such as tillage, increase the likelihood of erosion, in which soil is displaced during wind or rain events. The research objective is to quantify the fluxes of carbon and nitrogen between the land surface and the atmosphere at two distinctive watershed sites in Bavaria to determine the impacts of agricultural activities on the exchange of these elements.

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Body composition of Simmental cows and the relation of fat content to body condition parameters

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Introduction

The estimation of body fat reserves in cows has become an important part of dairy herd management. Commonly used methods to estimate fat reserves like body condition score (BCS) and backfat thickness (BFT) can only assess subcutaneous depots. The proportion of internal and subcutaneous depots, however, has been reported to differ significantly between breeds (1). Due to a lack of data the present study was conducted to determine the body composition of modern Simmental cows and to investigate the relation of BCS and BFT to whole body fat content.

Material and Methods

30 non-pregnant multiparous Simmental dairy cows, selected to cover a wide range of body condition, were slaughtered in order to measure whole body composition. Prior to slaughter BCS was assessed to the nearest 0.25 score (5-point system) and BFT was measured between the caudal quarter and fifth of the connection line between the dorsal part of tuber coxae and the centre of tuber ischia (2, modified) using a portable B-mode ultrasound scanner (Tringa Linear Vet, Esaote Europe BV, Maastricht, The Netherlands). During slaughter, the intestines, tail, right legs and the right halves of carcass, hide and head were divided into several parts which were weighed, minced and mixed. Samples were analysed for water, fat (ether extract), protein (DUMAS combustion method) and ash content, and results were summed up to determine whole body composition. Data were analysed using the REG and CORR procedures of SAS 9.2.

Results and Discussion

The cows varied widely in live weight and body composition (Table). The correlation of fat content (%) with BCS ($r = 0.84$, $p<0.0001$) was better than with BFT ($r = 0.65$, $p = 0.0001$). The equations obtained by linear regression analysis were as follows: fat (kg) = -106.1 +59.8 BCS ($R^2 = 0.71$, RMSE = 28.5 kg) and fat (kg) = 44.7 +5.2 BFT ($R^2 = 0.46$, RMSE = 39.0 kg). The estimated equivalent of 59.8 kg body fat for one unit change in BCS corresponds to previous findings in beef rather than dairy breeds (1). The BFT regression coefficient, indicating a change of 5.2 kg total fat related to a 1 mm change in BFT, matches the upper range of coefficients stated in literature (2).

Table: Live weight (LW), empty body weight (EBW), body condition score (BCS), backfat thickness (BFT) and analysed fractions of the empty body (n = 30)

	mean	SD	min	max		mean	SD	min	max
LW (kg)	742	101	416	869	Fat (%)	17.1	5.9	2.3	28.9
EBW (kg)	654	106	340	804	Protein (%)	18.6	1.0	16.4	20.9
BCS	3.73	0.74	1.75	5.00	Water (%)	59.7	4.7	50.7	71.7
BFT (mm)	13.8	6.8	4.5	34.2	Ash (%)	4.7	0.4	3.8	5.6

Conclusions

BCS is more accurate in estimating whole body fat content of mature Simmental dairy cows than BFT, despite its subjective character and the limitation of quarter point increments. However, further investigations should be conducted to clarify whether the chosen examination site is the most suitable for assessing BFT in Simmental cows. The relation of fat content to BCS and BFT indicates slight differences between Simmentals and pure dairy breeds. Furthermore, the analysed Simmental cows tend to be leaner than other breeds. Therefore caution should be taken when dairy breed related assumptions on body composition are applied to Simmental cows.

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MAGIC population in winter wheat: construction and genetic analysis of resistance to fungal diseases

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Introduction

Developing crops with durable resistance to biotrophic and necrotrophic pathogens is an ongoing process in plant breeding. In many cases long-lasting resistance is based on genetic factors with complex inheritance. Generally the genetic architecture of such traits is analyzed by quantitative trait locus (QTL) studies. Until now the majority of QTL mapped in plants are based either on bi-parental populations or association studies[1]. MAGIC (multiparent advanced generation intercross) populations feature larger allelic diversity as biparental crosses and there is no drawback of confounding population structure like in association panels[2]. In the present study an eight-parent MAGIC winter wheat population was constructed to provide a useful germplasm resource for the genetic analysis of resistance to fungal pathogens.

Material and Methods

Eight founder lines (A-H) of winter wheat were selected with respect to different breeding programs and phenotypic diversity for a range of traits (Table 1). Construction of the MAGIC population was based on five core stages: four two-way crosses (AxB, CxD, ExF and GxH), two four-way crosses (ABxCD and EFxGH), reciprocal eight-way cross (ABCDxEFGH), one eight-way intercross and selfing of the ABCDEFGH seeds via single seed descent to the F6 generation (Figure 1). The MAGIC population will be tested for seedling and adult plant resistance in glasshouse and field trials over several years. In QTL studies the genetic basis of resistance to powdery mildew (PM), leaf rust (LR), Septoria tritici blotch (STB) and tan spot (TS) will be analyzed.

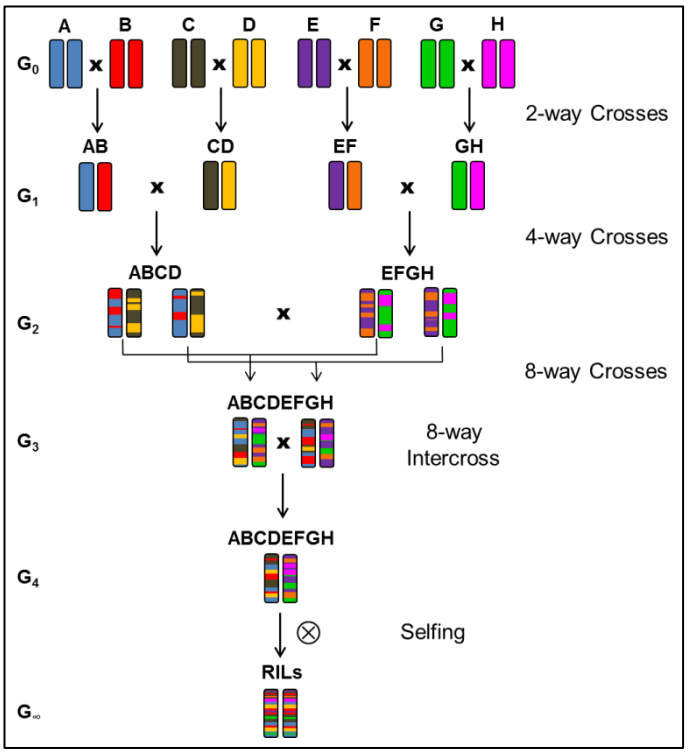

Figure 2: Crossing schema of eight-way MAGIC population

Table 1: Founder lines of the eight-parent winter wheat MAGIC population

Abbr.	Line	Breeding Program	Trait Attribute					
			Powdery mildew		Leaf Rust		S. tritici blotch	Tan spot
			SR [a]	FR [b]	SR [a]	FR [b]	FR [b]	FR [b]
A	Event	E	s	3	s	4	7	6
B	Format	A	s	5	r	5	4	5
C	BAYP4535	C	r	2	r	2	4	5
D	Potenzial	A	s	3	r	5	5	5
E	Ambition	C	r	2	s	5	4	6
F	Bussard	E	s	5	s	7	7	6
G	Firl3565	B	s	4	s	5	4	5
H	Julius	A	s	4	s	4	3	5

a = Seedling resistance (SR); b = Field resistance (FR)

s = susceptible, r = resistant; rating score: 1 (no disease) – 9 (severe disease)

Initial Results

First artificial inoculation experiments in the greenhouse suggested the segregation of two genes for seedling resistance to powdery mildew in the multi-parental population.

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$CD4^+$ T cell repertoire in JH-KO chickens during a humoral response

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Abstract

Chicken T cell biology has many parallels with those of mammals but chickens express a reduced repertoire of genes involved in the assembly of the TCR. Our understanding of T and B cell interactions in the chicken are limited. Using the JH KO birds, we can better understand the role of B cells in determining the repertoire and function of $CD4^+$ T cells during a humoral response.

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Characterisation of climate- and human-induced slope and meadow dynamics in Bavarian landscapes under Climate Change

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Introduction

Since the Neolithic Revolution the intensification of agriculture has been causing increased erosion in Bavarian landscapes. The correlated sediments often induce the formation of new colluvial and alluvial soils (WRB: Regic Anthrosol and Fluvisol i.a.). These soils are known to act as important reactors regarding climate-relevant greenhouse-gas balances in the atmosphere, as they are able to store considerable amounts of C- and N-compounds. Learning about the exact spatial extent and thickness of these soils in representative landscapes, but also about their geneses and processes is essential. It allows for a detailed quantification and understanding of the current and potential properties and characteristics of these soils in their role of greenhouse-gas reactors.

Two research locations were elected as representative Bavarian landscapes. They are composed of different lithologies and pedo-chemical environments: The Otter Cr. lies on crystalline structures at the southwestern foothills of the Bavarian Forest at the Donaurandbruch tectonic line next to Donaustauf (Lkr. Regensburg). Rottenbuch/Böbing is situated at the Ammer Rv. on the Würm-sediments and molasse bed-rocks of the Upper Bavarian pre-alpine forelands (Lkr. Weilheim-Schongau).

Material and Methods

Within the research areas, detailed local information on the pedosphere is gained by sounding and burrowing soil profiles. To learn about the spatial extent and thickness of these soil complexes of interest, a combination of geophysical methods along transects is applied in the field: Seismic refraction tomography (SRT) shows the travel times of seismic waves, and therefore, gives clear evidence of ground-layer compactnesses and densities. Electrical resistivity tomography (ERT) provides information on electrical resistivities of soils and thus, conclusions on water saturation and materials can be drawn. Ground penetrating radar (GPR) utilizes materials' distinct characteristics of reflecting or absorbing radar waves. Combining all these information is the basis for interpretations on spatial extents of colluvial-alluvial complexes and will be used as input numbers for GIS-based spatial soil models.

Results and Discussion

In general, the modelled geophysical data show great correlation with the local detailed information gained in the soil profiles and sounding cores. Thus, it is possible to bring these information into two dimensions. Repeating the geophysical measurements along geometric patterns allows for the interpolation into the third dimension. GIS-based models will be fed with these information. One additional major advantage of the applied geophysical methods is the vastly increased investigation depth with reliable information of up to 15 meter depth and more, depending on the nature of the present pedo- and upper-most lithosphere. One limitation is the relatively coarse data resolution compared to the excavated soil profiles or sounding cores. It is mostly not possible to see single soil horizons in the data gained from geophysics.

Conclusions and Outlook

So far, the combination of detailed local soil investigation and the extensive screening with geophysical ground prospection has shown satisfactory results. In a next step, the information has to be brought into the third dimension in order to model the spatial extent of colluvial-alluvial soil complexes in their respective landscapes. GIS-models will play a key role in order to achieve this goal.

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