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ABSTRACTS

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Key Lectures

Phenotyping Field Crops for Assessment of Growth Status

Cheng, Tao[1]; Zheng, Hengbiao[1]; Li, Dong[1]; Jia, Min[1]; Lu, Jingshan[1]; Guo, Tai[1]; Yan, Yan[1]; Yao, Xia[1]; Tian, Yongchao[1]; Ni, Jun[1]; Zhu, Yan[1]; Cao, Weixing[1]

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In recent years, smart agriculture has been considered by the central government report as one of the key strategies for renovating China's agriculture and rural development. How to use smart agriculture technologies to improve crop production becomes increasingly urgent for the country's food security, resource utilization and environmental protection policies. Crop phenotyping technologies could be used to provide valuable information on growth status, so as to optimize the management of nitrogen fertilizers, irrigations and pesticides in precision cultivation, and to select target genetic resources more efficiently and accurately in precision breeding. In this presentation we will showcase the recent progress on phenotyping of field crops (wheat and rice) for assessing growth status in the context of precision cultivation and breeding at the NETCIA. Extensive remotely sensed data were collected at ground, unmanned aerial vehicle (UAV) and satellite platforms from leaves or grains in the laboratory to multi-level canopies in the field. The technologies for phenotyping the field crops included laboratory/field reflectance spectroscopy, multispectral/hyperspectral imaging, solar-induced chlorophyll fluorescence, and LiDAR scanning. They were used to address the challenges in understanding the mechanism underlying the spectroscopic estimation of growth or nutrition indicators and grain quality, developing new multispectral or hyperspectral analytical methods, and exploring new ways to better monitor canopy structural and morphological parameters. In particular, we have made significant progress in automatic retrieval of leaf chlorophyll content, improved estimation of biomass and nutrition status with UAV imagery, and unique characterization of biomass, plant height and tiller number from LiDAR-derived metrics. At the end, we will use several examples to introduce the applications of phenotyping technologies in agricultural parks for extension purposes.

Key Lecture: Technology

Robotics and Vision for Precision Agriculture

Prof. Dr. Chris McCool

University of Bonn, Germany

Abstract

This presentation will overview some of the advances in robotic vision that have underpinned the development of agricultural robots such as AgBot II (for broadacre weed management) and Harvey (automated sweet pepper harvesting). The talk will discuss adaptations of the FasteRCNN approach of object detection for quality estimation as well outlining methods to derive efficient deep convolutional neural network (DCNN) approaches that can be deployed on resource-limited robotic platforms.

Biography

Chris McCool is a Professor at the University of Bonn within the Faculty of Agriculture and leads the Agricultural Robotics group. He received his PhD with the Speech, Audio, Image and Video Technologies (SAIVT) group at QUT in 2007. He worked as a post-doctoral researcher at the Idiap Research Institute (Switzerland) developing state-of-the-art face recognition techniques capable of running on mobile phones. He then returned to Australia to join NICTA in an initiative for Environmental Computer Vision. In 2014, he re-joined QUT where he worked on Agricultural Robotics and was a key member in the development of two agricultural robots AgBot II and Harvey. He has a particular interest in applied image classification, computer vision, pattern recognition and their application to robots and autonomous systems that can use this information to take action in challenging environments such as agriculture.

Key Lecture: Impact

How will phenotyping technologies contribute to future agriculture?

Malcolm Hawkesford

Rothamsted Research (BBSRC), Harpenden, United Kingdom

There is considerable global investment in research on automated plant and crop phenotyping technologies, with a trend to the development of in-field solutions. The key driver is crop improvement and diverse applications are envisioned to aid multiple sectors in the agricultural industry. An example in current usage is NDVI-related technology for precision nutrient application, yield prediction and measurement. Examples in the pipeline include automated precision fruit picking technologies, crop disease detection and treatment, and weed detection/elimination in the field. Furthermore, application in the breeding sector is a huge opportunity. At the technical level, developments in sensor technology, platforms for deployment and in software solutions for data extraction still remain a major focus for research. However, in parallel, crop scientists are already deploying applications in crop improvement programmes. Some examples to be presented are part of the UK Designing Future Wheat programme which focusses on exploiting novel wheat diversity and dissecting key traits associated with yield, sustainability, abiotic and biotic stress. Such programmes for crop improvement require large trials to be undertaken in the field, with assessment of performance from sowing to final harvest. In this kind of research there is a requirement for high throughput and automated technology to enable high temporal and spatial resolution to aid complex trait analysis. Whilst substantial progress has been made on research applications, the challenge is to extend the use of such phenotyping technology to the commercial agricultural sector, including breeders and farmers, to aid in crop production. For such implementation, key issues of practicality and automation issues and particularly financial costs need to be considered in relation to the promised benefits.

Session 1: Abiotic stress tolerance

Oral Presentation

35020: Functional Phenotyping Platform for Evaluating Yield-Related Quantitative Traits in a Dynamic Environment

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Many of the early components of a plant’s response to biotic and abiotic stress are related to modifications in plant water relations and, therefore, can be used as characteristic markers at a very early stage of the stress. Here, we reveal a simple, yet effective experimental platform that is based on a gravimetric system combined with a unique irrigation-drainage system and soil and atmospheric probes. This system enables tight control on multiple soil water/salinity scenarios while continuously monitoring in a quantitative manner the soil–plant–atmosphere water relations. The system monitors simultaneously numerous plants for a variety of biotic and abiotic stresses at high resolution. Five Quantitative Physiological Traits (QPT) are determined concurrently: 1) whole-plant transpiration rate; 2) daily/periodically increase in plant biomass; 3) canopy conductance; 4) whole-plant water-use efficiency (WUE); and 5) Root influx. These QPTs are measured for single plants in an array, over time periods ranging from minutes to the entire growing season, under normal, stress and recovery conditions at different phonological stages. A supplemental algorithm that integrates these traits enables to calculate additional important QPTs ; the root-to-shoot water flux ratios and whole-plant relative water content (RWC). Use of this experimental platform for the comparative physiological characterization of several crop cultivars has revealed several plant stress-response strategies that we have classified according to their relative “conservative” (isohydric-like) or “risk-taking” (anisohydric-like) character. We describe a “calculated risk-taking” trait that can be used as a marker for the selection of abiotic stress tolerance and resilient plants.

35036: High-throughput Phenotyping of wheat for water use efficiency-based donor identification

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Phenotype- genotype gap, has been bridged with the Phenomics, the next generation phenotyping (NGP). Under climate change scenario with uneven distribution of rains, water has become a rare entity. Therefore, judicious water use for crop production has become essential. so, Phenomics facility can play a role in phenotype the existing germplasm for water use efficiency in high through put manner. In Plant phenomics facility, large number of wheat genotypes were phenotype precisely in order to identify donors with high water use efficiency. With recommended packages of practices under recommended climatic conditions, wheat plants were grown in pot. Plants were subject to drought stress (soil moisture content up to 8% as per the soil properties) after anthesis as after reproductive stage, wheat suffers major impact of drought while leads to severe yield losses, while 18% soil moisture content was maintained in control plants. With automated weighing and water stations every day each pot was weighed to record pot weight and watered. At regular interval images were taken from different sensors i.e infra-red(IR)- to record canopy temperature of plants, fluorescence (PS2)- florescence camera was used to record the photosystem –II efficiency of the whole plant canopy, RGB -to record plant height at different stages along with the change in plant area over the whole life cycle which enable us to record change in plant growth over the complete life cycle. Based on the data recorded the wheat donors were identified for high water used efficiency under drought stress.

35180: High-throughput phenotyping for abiotic stress tolerance in a controlled environment - lessons learned over the past 10 years

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High-throughput phenotyping (HTP) using automation and latest sensor technology is an incredibly powerful tool to study the abiotic stress response of plants, and to undertake forward genetic studies. However, HTP is no plug-and-play system and requires optimisation and a good understanding of the capability and limitations of the technology used. When the Adelaide node of the Australian Plant Phenomics Facility opened its doors nearly 10 years ago, it was one of the first large scale phenotyping facilities in the public sector. Along the way, we found some of the answers to the important questions, often through trial and error. Some of those questions were basic, others a lot more complex. How do you set up pot experiments and ensure adequate watering in non-draining pots? Which imaging system is best suited to measure your traits of interest? Which parameters extracted from the images are of highest value? How do you analyse growth curves and use growth data in quantitative genetic studies? This presentation will share some of the mistakes made and lessons learned along the way to highlight the potential of HTP in understanding the genetics of abiotic stress tolerance. It will present results and insight from many collaborations over the years - too many to name in the author list.

35834: Accessing wheat competitiveness traits from high-throughput field observations of the borders of microplots

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During plant breeding process, genotype performances are assessed through successive steps. In the early stages, trials are conducted using small microplots with one to four rows width. For the final stages, genotypes are characterized under conditions mimicking the plain field ones with wider microplots to minimize the border effects. The variability of microplot width during the selection process induce biases in the genotype scoring depending on genotypic competitiveness. Further, describing the genotypic response to plant competition is required to model the plant plasticity and the impact of the sowing pattern and weed infestation. This study aims at proposing traits that describe plant competitiveness. It is based on experiments conducted in three locations with contrasted pedo-climatic conditions: Toulouse in France, Nanjing in China and Adelaide in Australia. similar experimental designs were followed: five genotypes under two contrasted sowing densities with microplots of various width, from a single row up to seven rows. In situ destructive measurements including total above ground biomass, Green Area Index (GAI), number of tillers/ears, mean tiller above ground biomass, chlorophyll content, have been achieved at the end of tillering and beginning of flowering over individual rows. At maturity. Total biomass, yield and yield components were also measured over individual rows. In addition, high throughput measurements were acquired every 150°C.day from sowing to harvest with emphasis on the green fraction from RGB high resolution imagery and detailed canopy structure from LiDAR. Results show a strong and early response of plants to the row competition, with some significant variability between genotypes. Observation based on high throughput techniques demonstrate that competitiveness could be accessed by observing the borders effect in regular wide microplots.

Poster

34840: Chlorophyll fluorescence (OJIP test) as a tool to screen cucumber genotype in response to different light intensities under cold stress

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Early cultivation of cucumber plants is usually restricted due to its sensitivity to low temperature conditions. Discovering fast and high throughout methods for cold tolerance assessments is substantial for screening of cucumber populations. Here we used polyphasic fluorescence transient (OJIP transient) to analyse low temperature (4 ºC) damage to electron transport chain in the photosynthetic apparatus of a collection of native Iranian cucumber accessions under different light intensities (0, 300 and 600 µmol m-2 s-1). Comparative analysis revealed a significant interaction between light intensity, cold stress and genotypes in biophysical parameters of photosynthesis, including fluorescence parameters, energy fluxes per QA– reduced PSII reaction center (RC), performance index (PI) and quantum yield. Cold and light stress influenced on biophysical parameters of photosynthetic in all 15 genotypes however, the effect was both genotype- and stress-specific. Using cluster analysis, genotypes categorized into 3 cluster including sensitive, semi-sensitive and tolerant genotypes. The tolerant cluster characterized with the highest quantum yield of the primary photochemistry (Fv/Fm), Maximum efficiency of the water diffusion reaction on the donor side of PSII (Fv/F0), the probability that a trapped exciton proceed an electron through electron transfer chain (ETC) beyond QA- (ψ0), quantum yield of energy dissipation (ϕD0), performance index per absorbed light (PIABS), trapped energy flux per reaction center (TR0/RC) and electron transport flux per reaction center (ET0/RC) while quantum yield of primary photochemical reactions (ϕPAV), light absorbance flux for PSII antenna Chl per reaction center (ABS/RC) and quantum yield of energy dissipation (DI0/RC) was lowest in genotypes categorized in first cluster. Data obtained from this experiment revealed that light stress influences photosynthetic aperture of plants more severely than cold stress and the nega.

35162: Phenotyping of wheat genetic resources under long-term drought stress

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An efficient exploitation of genetic resources collected in genebanks is limited by insufficient phenotypic data, including information on the stress tolerance. Therefore, we focus on assessment of the methods and tools for rapid evaluation of the traits associated with drought tolerance. In our previous program, we have created a collection of 25 diverse winter wheat genotypes selected from accessions of Slovak Genebank at NAFC-RIPP Piestany, Slovakia, which greatly covers a diversity of leaf traits, especially chlorophyll content, leaf thickness and leaf area. To examine the links between leaf traits and drought stress responses, we performed the phenotyping experiment using a whole collection of 25 wheat genotypes. Plants were grown in pots outdoors and in a growth phase of stem elongation, a half of the plants were exposed to long-term moderate water deficit by limiting water supply. The growth responses to drought were assessed by measurements of chlorophyll content (SPAD), chlorophyll fluorescence, leaf temperature (IR thermal imaging) and VNIR hyperspectral records were performed in 3-4 days interval to assess the effect of drought stress on photosynthetic apparatus. The measurements were followed by the analyses of aboveground biomass and grain yield. We observed a high diversity in the level of reduction of the leaf area, leaf chlorophyll content, spectral reflectance and parameters derived from fast chlorophyll fluorescence records indicating unequal effects of drought on the photosynthetic apparatus of diverse wheat genotypes. Moreover, we identified a close relationship between the changes of leaf traits and leaf optical properties measured by the hyperspectral reflectance records. Our results indicated that the parameters based on spectral reflectance and chlorophyll fluorescence techniques can be useful to assess the drought tolerance of the genotypes. The study was supported by the national grants VEGA-1-0831-17, APVV SK-FR-2017-0007 and APVV-18-465.

35178: High-throughput image-based phenotyping of wheat germplasm

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Understanding the interaction of the plant with the environment is essential for the advancement of basic plant science and its translation into breeding strategies. High-throughput plant phenotyping based on analysis of image data collected from different optical sensors has recently emerged as a new frontiers field for crop improvement and plant breeding. The Slovak PlantScreen Phenotyping Unit (SPPU) was used to investigate of growth, geometrical responses as well as functional physiology in 35 wheat genotypes. The methodologies for multi-sensor phenomics data collection of wheat plants and image analysis were tested and verified using high-throughput PlantScreenTM phenotyping platform with multi-sensor imaging facilities for FLUO, RGB, VNIR and SWIR imaging. We analysed dynamic properties of phenotypic trait realized during plant ontogeny. Plant architecture and geometrical traits (plant height, plant area) were correlated with yield forming components. Analysis of colour images revealed that leaf greenness corelates with foliar chlorophyll content and allows to calculate the index of senescence. VNIR and SWIR reflectance analysis reveals a different ability of wheat genotypes to synthesize leaf pigments (chlorophyll, carotenoids and anthocyanins) over growth time. Higher capacity of drought tolerance in wheat genotypes under water shortage was manifested by maintenance of photochemical PSII efficiency, higher NPQ and less reduction of growth rate. The analysis contributed to our knowledge of the phenotype formation structural and functional traits in wheat genotypes differing in drought tolerance, growth rate during ontogeny and grain yield. The study is supported by APVV-18-0465, APVV-15-0562, VEGA-1/0831/17, VEGA-1/0589/19.

35242: Characterization of the phenotypic and genomic diversity in sorghum: traits and genetic components involved in the adaptation to abiotic stress conditions

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Recently, sorghum has emerged as an alternative to maize as bioenergy crop in Central Europe due to its high biomass potential and tolerance to many biotic and abiotic stresses. Since Central European temperate climates may have a negative effect on sorghum growth, breeders are working on finding better adapted genotypes. A diversity set consisting of 194 biomass sorghum lines were fingerprinted with a 90k single nucleotide polymorphism (SNP) array and subjected to extensive phenotyping comprising field trials and controlled environment experiments. As well as, genome wide association studies (GWAS) were conducted to identify candidate quantitative trait loci (QTL). When sorghum genotypes were growth at high and low available-phosphorus (P) three different root system architecture (RSA) types were detected: (1) a small root system, (2) a compact and bushy rooting type and (3) an exploratory root system. GWAS revealed significant QTL (p < 2.9x10-6) on chromosomes SBI-02, SBI-03, SBI-05 and SBI-09. Furthermore, two hotspots controlling root-system development on chromosomes SBI-02 and SBI-03 were detected using co-localization of significant and suggestive (p < 5.7x10-5) marker-trait associations for several traits. On the other hand, when sorghum genotypes were grown at optimal and low temperatures and seedling vigor information combined with genetic data using GWAS, it was found a promising genomic regions including a putative hotspot for temperature-mediated seedling emergence and survival on SBI-06, which was previously identified in a bi-parental population and verified by means of GWAS in the present study. The results of this study will contribute to enlighten the root-system adaptation to P scarcity and the regulation of early-phase cold stress response in sorghum. As well as, it will benefit the development of molecular markers for tailor-designed breeding of biomass lines better adapted to temperate climates.

35251: Plants of N. tabacum with the Δ12-acyl-lipid desaturase gene of cyanobacteria after exposure to ultraviolet radiation

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The study of plant adaptation to abiotic stresses is quite relevant now. Increasing the percentage of unsaturated fatty acids in the composition of membrane lipids increases the viscosity of the membranes, increases their plasticity, which reduces mechanical damage after frost, osmotic stress and ultraviolet radiation. Desaturases are enzymes that promote the formation of double bonds in fatty acids and thereby convert them from saturated to unsaturated fatty acids. The tobacco plants of N. tabacum expressing the hybrid gene Δ12-acyl-lipid desaturase of cyanobacteria Synechocystis sp. PCC 6803 (desA) used. Wild-type and N. tabacum plants containing and expressing the gfp:licBM3 bifunctional reporter gene were used as controls. These plants were previously tested for resistance to frost and osmotic stress and showed better adaptation to the stimulus compared to controls. Indicators of superoxide dismutase enzyme activity, malondialdehyde accumulation, and reporter gene protein activity were investigated after UV exposure at total spectrum doses. The experimental plants were found to have a lower MDA accumulation and increased SOD activity compared to the control plants. The activity level of the protein of the reporter gene increased after the action of ultraviolet radiation.

35262: Leaf tip, a digital signature for counting total no of leaves and detecting water-stress phenotypes of the rice plant

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No of leaves tips are an essential agro-morphological trait. It can be used for counting the total numbers of leaves of a plant, especially for field crops like rice, wheat in image-based High-Throughput Plant Phenotyping (HTTP). Counting the total number of leaves of a plant is an important aspect and bottleneck for traditional phenotyping compared to image-based phenotyping. To count the total no of leaves in a plant, we have used a hypothesis that - the total no of leaves tips is equal to the total number of leaves. We also further categorized the plant leaves tips into three categories – 1. fully green leaf tip, 2. fully yellow leaf tip, and 3. partially green-yellow leaf tip. These three categories and the total number of leaf count of a plant can be a basis for understanding the associated water-stress condition of plants, phenotypes. We took RGB images of rice plant genotypes for study. We have applied YoloV3 for leaves tips detection, which is a popularly used algorithm for object detection for images as well as video. In our current work, we also applied R-CNN and Faster R-CNN for a comparative study.

35265: The use of transcriptomic data and protein interaction networks in determining genotype - phenotype interactions of MSC19 cucumber somaclonal mutant

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Somaclonal variability (SV) is a phenomenon causing the plants regenerated from in vitro culture to have phenotypes altered in relation to the material the culture was started from. Despite the phenomenon is long known, its exact molecular basis are still undetermined and are subject for this research. In this work, MSC19 (Mosaic Syndrome of Cucumber) cucumber somaclonal mutant was taken as a model for the study. It was obtained by passing material from highly inbred line "Borszczagowski", denounced B10, through in vitro culture. It is characterised by a distinct phenotype: impaired growth, decreased fertility, floral deformations and the presence of two types of sectors on the leaves: chlorotic and "zucchini-like". To determine the molecular basis of this phenotype, RNA-seq analysis was performed and the results were compared to the data from B10 (reference) line. Basing upon discovered differentially expressed genes (DEGs), protein interaction network (STRING) was created, later followed by Gene Onthology (GO) annotation, DEG promoter regions analysis and chromosome map construction. The experiment elucidated that MSC19 phenotype is caused by disturbances in transcription processes, programmed cell death regulation, meristem identity maintenance and metal ion and pectin management disruptions were found to be the major suspects for causing the distinct image of MSC19 phenotype. DEGs were not located evenly across all chromosomes, which suggests sort of directional changes rather than random ones in response to the in vitro culture process. DEGs' promoter regions showed presence of motifs associated with cell cycle regulation, light and stress stimuli response and meristem control, partially supporting conclusions drawn from the protein network. Expression of DEGs marked out to be of special importance for the phenotype was confirmed by qRT-PCR in 90% (9/10 investigated genes). This work was supported by grant no. NCN 2013/11/B/NZ/00814.

35645: Phenotypic Characterization by Imaging of Tomato Carotenoid Pathway Mutants under Abiotic Stress Conditions

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We are currently screening Red Setter tomato TILLING mutant collection (LycoTill Tomato mutant DB www.agrobios.it/tilling) for variations in their response to abiotic stress, in particular drought and salt stress. In this study the characterization of mutants of the carotenoid metabolic pathway is presented. As carotenoid metabolites are precursors of the stress related hormone abscisic acid (ABA) and that ABA is implicated in abiotic stress, four mutants of the metabolic pathway were chosen for analysis under stress. The control and salt treated plants were irrigated daily to 80% soil water capacity, saline stress being set at 5g/L Nacl (85.5 mmol/L), while drought stress plants were irrigated daily to 40% soil water capacity. Significant phenotypic difference between wild type Red Setter and the mutants subjected to abiotic stress were revealed with digital biovolume, height, and compactness. Under drought stress mutant mutant-D accumulated the least digital biomass, mutant mutant-A was affect but in a less severe manner while no significant differences were observed under salt stress. Drought stress again was important in revealing inter line differences, mutant mutant-B was the tallest line both unstressed and drought stressed, mutant mutant-A showed similar height to the mutant-B mutant but this difference was reduced under drought stress. These height differences were also observed under salt stress but in a reduced manner. Compactness of plants from a top view image, in these experiments used as a proxy to plant turgor, displayed a lot of variability but mutant mutant-A stood out in its ability to sustain a low compactness, hence avoid loss of turgor, under both drought and salt stress conditions. This work demonstrates the application of digital imaging phenomics in characterizing the stress response of mutants from a TILLING tomato mutant collection to the abiotic stresses of saline irrigation and drought.

35853: The role of magnesium salts in germination and growth of Cucumis sativus L.

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Biometric root analysis showed the stimulating effect of the nutrients regardless of the time of watering. Compared to the control, the increase in hypocotyl length was inhibited in the presence of magnesium ions and sulphates (Table 1). The highest growth of stems was observed in plants watered with nutrients supplemented with magnesium salts throughout the experiment. The petiole growth in length was stimulated by all modifications of Kottke media. Fresh mass values, regardless of the type of medium and the time of its use, were higher in relation to the mass values from the control sample (Table 2). Only the fresh mass of hypocotyls watered throughout the experiment with magnesium salts was lower compared to the control. An increase in the dry matter value was demonstrated for all cucumber organs analysed. The percentage of water content was the lowest for the roots and first leaves compared to the control. The positive effect of magnesium sulphate is most likely due to the presence of sulphur. This chemical element maintains normal physiological parameters that directly affect plant growth and development (Dobermann et al. 1998; Thomas et al. 2003; Hitsuda et al. 2005). The compounds of this element play key roles in many cellular processes (Dubuis et al. 2005). Sulfur is involved in the formation of proteins, carbohydrates, fats, in photosynthesis and in the synthesis of chlorophyll and lignin (Hell, Rennenberg 1998). The positive effect of magnesium carbonate on plants can be due to the optimal pH of the soil, in which magnesium was easily absorbed. Slightly acidic soils have the best magnesium content. The content of available forms of magnesium decreases on very acidic and alkaline soils (Tao et al. 2019).

35909: Quantitative genomic analysis of spectral traits from UAV-based multispectral images reveal loci for senescence in bread wheat

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Understanding about plant senescence can benefit to develop reliance cultivar for drought and heat stress. Using unmanned aerial vehicle based non-destructive remote sensing facility, five light spectrum bands (Blue, Green, Red, Red-edge and Nir) based spectral traits (s-traits) were extracted from 198 wheat double haploid (DH) lines. Experiment was conducted at two locations for two years using randomize complete block design (RCBD) with three replications to minimize the error probability. S-traits can be used to monitor senescence process in time-series manner while ground truth data was also measured to validate the UAV-based data set. High heritability and significant variations of these s-traits were observed among the DH lines across the growing environments. Thirty DH lines showed long senescence period and high grain yield, that could be considered function stay-green genotypes. A genome-wide quantitative traits loci (QTL) study of s-traits and ground normalized different vegetation index identified 60 loci, some are known QTL for stay-green and drought resistance. Forty loci were identified using s-traits and of these 20 loci were co-localized with previously reported stay-green, drought resistant related trait loci. Whereas, remaining 20 QTL also showed high phenotypic variations ranged from 10 to 15% for the s-traits at critical senescence period (early to late grain filling stages). These QTL could be the novel and identified due to the integration of UAV based S-traits and quantitative genomic analysis. QTL analysis established a network to understand the hub s-traits and hub loci for senescence rate. Our study provides a promising novel approach for the genetic dissection and discovery of QTL underlying for the senescence in wheat.

35949: Phenotypic plasticity and quantitative trait loci controlling root anatomical traits in rice under drought

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Drought is a major constraint to rice production in rainfed areas across Asia. Root anatomical traits have been shown to influence the adaptation of rice under drought conditions. Here we investigated phenotypic variation and plasticity in root anatomical traits and performed Quantitative Trait Loci (QTL) analysis on 135 Chromosome Segment Substitution Lines and KDML105. Plants were grown under flooded and drought conditions in two field locations (denoted URRC and RGD) in Thailand. Mean xylem area and theoretical hydraulic conductance significantly increased under drought conditions in both locations. Cortical aerenchyma area was significantly reduced by >5% in URRC but increased >30% in RGD. Differences in root responses and plasticity in distinct locations are likely to reflect the impact of environmental factors, particularly soil type. A total of sixteen QTL were identified. The phenotypic variation explained by individual QTL ranged from >6% for xylem area to 50% for theoretical hydraulic conductance. Many loci were either adjacent or in genes known as regulators of root development and hormone signaling. These QTL could be used in marker-assisted selection for root anatomical traits.

Session 2: Affordable phenotyping

Oral Presentations

36564: Automation and robotics for high-throughput phenotyping and precision horticulture: how to make it affordable?

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Automation, robotics, novel sensors and AI offer plant scientists, breeders and growers powerful tools to gather growth data to understand and optimize plant performance and productivity. Continuously new sensors, tools and solutions are launched by companies and novel approaches are presented in publication by academia, these tools are used for phenotyping and horticultural production. The purchasing costs of these technologies range from low/ affordable to sky-high and expensive. Next to that requirements to make use of these tools vary widely too; from expert programming skills to user-friendly, easy-to-use interfaces. Decisions which sensors/ software combinations fit with a targeted application are challenging. Several EU-projects and public-private partnership are exploring the benefits of these tools in an applied end-use setting and ideas, developments and results will be discussed. This cross-disciplinary interaction brings together different domains and these new connections are a catalyst for novel technological developments.

35215: Functional phenomics of crop physiology using affordable and open source phenotyping platforms

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The technologies behind high-throughput phenotyping are transforming crop physiology, but the generation of new knowledge about how crops can be optimized is limited by the lack of a conceptual framework. Functional phenomics delivers a next-generation plant physiology framework using phenotyping, physiology, multivariate statistics, and simulation modeling to generate and test new hypotheses about how plant traits integrate to influence crop performance. However, many of the exciting phenotyping platforms that have transformed plant science are expensive which limits their use by a majority of laboratories and ultimately hinders the ability of functional phenomics to impact plant science and plant breeding. Therefore, affordable phenotyping platforms backed by open source software and open hardware plans are needed. Here, several low cost but robust phenotyping platforms are described for both shoot and root phenotyping that are all driven by an imaging software designed for general use in plant phenotyping. Imager uses machine vision cameras, and has several features that make it optimized for plant phenotyping: a simple GUI, saving settings, controlling multiple cameras, live view, and use of a barcode scanner to trigger imaging while saving file names with the identification. Wheat populations are phenotyped during heat stress using a front-facing imaging booth and during drought using an overhead gantry. A backlit imaging system is used for evaluation of root crowns excavated from the field. Finally, a system is described that simultaneously images both shoots and roots of plants grown on blue filter paper in a semi-hydroponics system. Time series and multivariate data analysis are used to increase understanding of plant physiology, while the use of populations allows genetic analysis. Affordable plant phenotyping will be an important driver of the success of phenomics over the next decade.

35235: An Integrated Solution for High-throughput Estimation of Canopy Cover in Crop and Forest Fields Using UAV RGB Imagery

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UAV-based high-throughput determination of canopy cover is limited by mixed pixel effect in crop scenarios and by understory confusion in forest scenarios. For crop fields, although image segmentation techniques offer effective tools for proximal sensing imagery, they yield unreliable crop canopy cover (CCC) estimates for close-range sensing imagery. Few efforts were taken to address mixed pixel problem due to the non-quantitative signal output of RGB camera. For forest fields, overstory architectures, understory confusion and illumination variation obstacle the accurate estimation of tree canopy cover (TCC). Machine learning introduces a powerful tool for separating overstory and understory plants but with a trade-off of computation time and labelling work. We propose an integrated solution to resolve these problems then estimate canopy cover. (1) CCC estimation using Gaussian mixture model. The hue histogram of vegetation covered surface can be modelled by a Gaussian mixture model. A half-Gaussian fitting method minimizing the mixed pixel effect is developed to determine the image threshold. The method goes around the mixed pixels and infers threshold using only pure pixels. (2) CCC estimation using color mixture analysis. We used pixel decomposition in a color feature instead of spectral bands. We made full use of UAV flexibility to determine endmembers from UAV images. Endmembers are considered as random variables following Gaussian function. We estimate vegetation abundance based on Bayesian's theorem. (3) TCC estimation through incorporating UAV SfM point cloud and deep learning method. We propose a workflow to automatically determine those identifiable overstory superpixels and understory superpixels, through incorporating 3D height information and 2D superpixel-wise information. A simple convolutional neural network model is trained based on the labelled superpixels then classify uncertain superpixels and finally output canopy cover from an orthophoto.

35252: Revealing the relationship between biomass, sugar content and image-based phenotyping in beetroot

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Beetroot is the main raw material of sugaring industry in the Northern China. The beetroot type with different genotypes has great differences, and it directly affects the yield and sugar content of beet. The traditional classification of beetroot type relies heavily on human visual sense, the heavy workload and relatively large error make it difficult to meet the requirements of high-throughput beet GWAS analysis. In recent years, the development of image-based 3D reconstruction technology provides an opportunity for high-throughput phenotyping analysis. So the aim of this study is to reveal the relationship between biomass, sugar content and phenotypes by quantifying morphological structure of beetroot. Beetroots with 207 genotypes were selected as experimental materials. Multi-view images were obtained by moving mobile phone around beetroot. Three-dimensional point clouds were reconstructed from images. Beetroot height, diameter of each height and convex volume were extracted from denoising point clouds to characterize root morphology structure. According to the ratio of max-diameter to height (RMDH), max-diameter position (MDP) and expansion coefficient, beetroot type was classified into three categories: near-circular, wedge-shape, ellipsoidal. Finally, we analyzed the relationship between biomass, sugar content and beetroot type with cluster analysis. Our analysis demonstrates that ellipsoidal beetroot has a higher sugar content than wedge-shape beetroot, and near-circular beetroot has the lowest sugar content but the largest biomass than the others. The results provide basis for GWAS and breeding analysis in future research of beet.

Poster

34808: Predicting lodging using sensing technologies to enhance selection in sorghum breeding trials

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Global food production needs to increase by more than 60% from 2015 to 2050 to meet the projected demand. At the same time, yield advances have slowed at both a production, as well as, a genetic improvement level. To ensure further progress, a better understanding of the traits that lead to greater yield potential and better adaptation to challenging climatic conditions is needed, which is a major priority in the Australian sorghum pre-breeding program. However, monitoring and capturing physiological and phenological traits within large breeding trials is time consuming and costly, especially when data has to be collated across various environments. For example, the current method for estimating characteristics like plant and head counts, lodging and stay-green involves manually counting plants, heads, tiller numbers, as well as visually scoring lodging and stay-green across thousands of plots. The advent of sensing technologies, however, has provided avenues to develop tools to assess such traits efficiently and cost-effectively. This study outlines the application and ability of proximal sensing technologies to enhance plant-breeding research outcomes. Specifically, we describe the design of a high-throughput (HTP) software pipeline to capture, manipulate and analyse “BIG DATA” collated from proximal sensors on-board two phenotyping platforms. We discuss preliminary results from the use of high-resolution spatial characterisation of time-sequence data, obtained from multi-spectral sensors and reconstructed point-cloud data. Application of such an approach across breeding fields offers the potential to more accurately and cost effectively monitor number of plants, heads, height, stay-green and lodging responses among genotypes. The deployment of these new technologies into breeding programs will enable more rapid genetic gain and hence faster delivery of adapted commercial hybrids with improved yield in target environments.

35034: Identification of Maize Varieties Based on 3D Canopy Phenotype and LDA Method

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Phenotypic identification is an important aspect of phenotypic research which has become a hot spot in the post-genomic era. The identification of plant varieties mainly focused on fruit and seed by acquiring the image, texture, spectrum and other phenotypic information of them. These phenotypic characteristics may achieve a high recognition rate, but poor interpretability of the results, and most results are unnecessary for breeders. In this paper, the classification of varieties based on three-dimensional (3D) morphological features in phytomer scale was realized, and the significance of classification results in guiding breeding was analyzed. Firstly, we obtained the spatial coordinate points of maize. Then, through the selection and calculation of 3D characteristics, we obtained 14 3D morphological features of maize shoot in phytomer scale. The stepwise linear discriminant analysis (LDA) and Cross-validation was used for statistical classification based on these features. By comparing the classification of different phytomers, the optimal phytomer and features for identification was found and the classification of different varieties was realized. By analyzing the data of phytomers classification in different environments, the similarities and differences of 3D phenotypes of different maize varieties can be realized. In this study, 3D morphological features were used to classify maize varieties for the first time, and the classification results were used for phenotypic analysis. This method is more useful for breeders.

35143: LITERAL: a portable and cost effective phenotyping system

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LITERAL is a new hand held phenotyping system. It addresses the need for a flexible, low cost imaging device with high productivity for the monitoring of small plots in field trials or to sample farmers' fields. In practice, it integrates three high resolution RGB cameras and, as an option, a multispectral camera. This set of sensors offers a wide range of sensing configurations to fit the different crops specificities along their growing cycle. All the sensors are connected to an acquisition box that triggers the cameras, stores data and communicates with a tablet PC that allows the definition of measurements' scenarios through a user-friendly graphical interface. The measurement scenario describes the configuration of each sensor, the trial plan and the number of measures within each plot. This allows a handy use in the field and ensures the right referencing of each recorded image with associated metadata. A single battery powers all the cameras and the acquisition box, ensuring a one day of use autonomy. LITERAL has been used on several crops in 2019. The most common sensing configuration consists of placing the multispectral and the two RGB cameras in vertical viewing direction with a slight shift ensuring a stereoscopic setup. The third RGB camera can be placed with another viewing angle, typically 45°. The recorded images have been processed in the case of wheat crops to estimate (1) the crop's height using depth map generation from stereoscopic images, (2) the green cover fraction from image classification algorithm, (3) the leaf area index using a simple radiative transfer model, (4) the number of ears using deep learning technics. The high resolution and the multispectral images offer a large number of other applications to be developed, like chlorophyll content estimation or diseases detection.

35214: "Affordable high-throughput processing of multi-scale images to phenotypic data"

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Currently, it is possible to use softwares/tools to produce 3D point cloud and related output to be used for extracting phenotypic data from a set of images. However, this process is time-consuming and requires user input. Here we propose a pipeline that can automate this process through scripting commands. 3D reconstruction software can be automatically controlled by API, and parameters can be passed that will ensure an accurate result. The pipeline can process multiple image sets when executed, so large populations of plants can be efficiently analyzed. The input of the pipeline is an image set or group of image sets, and the output is 3D point cloud and related output such as DEM/orthophoto, as well as phenotypic data such as canopy cover, morphological traits etc. The system is affordable because the hardware is a standard RGB camera that can be handheld over plant pots, or mounted to UAV. Any PC can run the software and pipeline. The softwares are Agisoft Metashape and python/Matlab, which also can be acquired easily . The pipeline is affordable high-throughput because many pots can be quickly photographed with an RGB camera, and the pipeline can handle multiple image sets. In this study, 200 pots were photographed in under 3 hours (6 plants per image set, 34 image sets) and automatically generated pointcloud, DEM/orthophoto for each image set by the pipeline. Each DEM/orthophoto is then used to create CSV containing phenotypic data. This is a scalable solution that can enable researchers to get detailed measurement data with reduced labor and capital costs.

35245: Filed crop phenotyping by UAV remote sensing

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Field Phenotyping is becoming a focus research, attracting extensive attentions from crop genetics, breeding and plant biology.The accurate and rapid acquisition of phenotypic information of plants or cells in different environments is helpful for exploring the inheritance and expression patterns of the genome to determine the association of genomic and phenotypic information to increase the crop yield. Unmanned aerial vehicle remote sensing platforms (UAV-RSPs) equipped with different sensors have recently become an important approach for fast and non-destructive high throughput phenotyping and have the advantage of flexible and convenient operation, on-demand access to data and high spatial resolution. In this presentation, the latest results on filed crop phenotyping in our team will be introduced.(1) UAV platform and sensor development for crop phenotyping: Self-developed hyperspectral imaging sensor was only 900 gram with 2 nm spectral resolution which is suitable for mini-UAV. Now high quality of hyperspectral data and and high density of point cloud data can be acquired using this platform. CropSense was developed for crop health diagnosis in different growing stages.(2) Structural and morphological traits extraction: plant height extraction method was developed by using spatial Kriging interpolation, and its dynamic curve was selected as a new trait to support patterns clustering.And the leaf area and its vercital distribution extraction method was developed. (3) Physiological traits extraction including chlorophyll content, biomass and yield etc. Structural and spectral information provided by UAV remote sensing in combination with machine learning to estimate maize biomass. (4) Crop stress resistance traits extraction(pest,disease and crop lodging etc.): we introduce a comprehensive methodology to extract lodging features relying on statistical methods to screen several potential feature factors.

35264: NDVI vs SPAD-chlorophyll, comparative assessment for leaf nitrogen, total nitrogen uptake and grain yield in direct seeded rice

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Site specific nitrogen (N) management requires special consideration in direct seeded rice due to general recommendations followed as for transplanted rice. The present study compared the comparative performance of ground based two optical sensors greenseeker (Trimble, Germany) vs SPAD-chlorophyll meter (Minolta-Japan) for assessing leaf N, total uptake and grain yield along with their association under variable N supply rates (0, 80, 120 and 160 kg ha-1) applied in two or three splits in direct seeded rice. The NDVI indices at booting ($R^2 = 0.63^{***}$) and heading ($R^2 = 0.58^{***}$) stages showed strong positive relationship with leaf N contents at physiological maturity as compared to SPAD-chlorophyll values with relatively week association ($R^2=0.30^{**}$; $R^2=0.37^{**}$). However, the association of SPAD-chlorophyll values at both stages was strong with total N uptake ($R^2 = 0.47^{***}$; $R^2 = 0.62^{***}$) and grain yield ($R^2=0.39^{**}$; $R^2 =0.56^{***}$) than NDVI with relatively weak association ($R^2 = 0.47^{***}$; $R^2 = 0.40^{***}$) for both traits. Association of grain yield with total N uptake and grain yield ($R^2=0.56^{***}$, $R^2=0.55^{***}$), of total N uptake with sufficient index ($R^2 = 0.56^{***}$). This indicates that NDVI can be good predictor of leaf N concentration rather than SPAD-chlorophyll with poor association. However can be used to predict grain yield and total N uptake at maturity. Further, crop achieves the optimal plant N concentration during active tillering period to support growth when applied in two-splits at basal and anthesis. Improved yield was attributed to reduced spikelets sterility (24.15-29.33%), improved filled kernels (22.08-23.75%) and productive tillers per unit area (21.03-31.08%). Nonetheless, N application during this period may be reduced to save costs for additional inputs using 120 or 160 kg N ha-1. In crux, NDVI using greenseeker can be promising sensor to predict plant N status and optimize N supply accordingly as low cost phenotyping tools.

35940: Quantitative genomic analysis of spectral traits from UAV-based multispectral images reveal loci for senescence in bread wheat

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Understanding about plant senescence can benefit to develop reliance cultivar for drought and heat stress. Using unmanned aerial vehicle based non-destructive remote sensing facility, five light spectrum bands (Blue, Green, Red, Red-edge and Nir) based spectral traits (s-traits) were extracted from 198 wheat double haploid (DH) lines. Experiment was conducted at two locations for two years using randomize complete block design (RCBD) with three replications to minimize the error probability. S-traits can be used to monitor senescence process in time-series manner while ground truth data was also measured to validate the UAV-based data set. High heritability and significant variations of these s-traits were observed among the DH lines across the growing environments. Thirty DH lines showed long senescence period and high grain yield, that could be considered function stay-green genotypes. A genome-wide quantitative traits loci (QTL) study of s-traits and ground normalized different vegetation index identified 60 loci, some are known QTL for stay-green and drought resistance. Forty loci were identified using s-traits and of these 20 loci were co-localized with previously reported stay-green, drought resistant related trait loci. Whereas, remaining 20 QTL also showed high phenotypic variations ranged from 10 to 15% for the s-traits at critical senescence period (early to late grain filling stages). These QTL could be the novel and identified due to the integration of UAV based S-traits and quantitative genomic analysis. QTL analysis established a network to understand the hub s-traits and hub loci for senescence rate. Our study provides a promising novel approach for the genetic dissection and discovery of QTL underlying for the senescence in wheat.

Session 3: Biotic stress resistance

Oral Presentation

34747: The application of a deep learning approach for quantitative disease phenotyping in UAV images.

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Plant disease is estimated to cause a 13% reduction in global crop production. In order to breed for improved crop varieties with improved disease resistance, accurate measures of disease symptoms are required. Traditional visual assessments of disease incidence and severity are time consuming and prone to human error. Conventional image analysis can help to improve accuracy and throughput, but requires consistent image conditions that are difficult to achieve in the field. The advent of deep learning algorithms has helped to overcome these challenges through training a network that recognizes features of interest across a diverse range of field environments. Convolutional neural networks (CNN) have been used to classify images for the presence/absence of one or more diseases. We previously trained a CNN to classify images containing symptoms of Northern leaf blight—a serious disease of maize—in images of field-grown maize plants. We have extending this approach by applying instance segmentation using the Mask R-CNN framework to identify individual disease lesions in UAV images. This enables the number of disease lesions, area of each lesion and total lesion area to be quantified in each image. This data, combined with image geo-tags has allowed us to accurately assess NLB disease incidence at high spatial resolution throughout the maize growing season.

35201: Phenotyping of quantitative disease resistance

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Plants with quantitative resistance (QR) to pests and pathogens have the potential to provide a robust, durable and sustainable route for protecting crops against biotic stresses. Exploitation of QR requires accurate and reproducible measurements of disease and symptom development. The Wolfson Centre for Disease Phenomics at the University of Sheffield uses combinations of established phenotyping platforms (multispectral and chlorophyll fluorescence imaging) and novel methodologies to quantify plant responses to above and below ground diseases under controlled environmental conditions. Informative disease indices are extracted from the datasets that allow quantification of disease and symptom development, when these symptoms first appear and the rate at which they develop. This presentation examines how disease phenotyping can be used to measure QR in cereals, brassicas and horticultural crops in response to both foliar and root diseases. In these examples, differences in QR has been achieved by genetic approaches, chemical treatments that prime the plant immune system or by facilitating the development of disease suppressive soils.

35870: Combination of high-throughput multispectral and deep cell physiological phenotyping of barley resistances against fungal pathogens in controlled environments

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The external phenotype is determined by the sum of the complex interaction of metabolic pathways and intracellular regulatory networks that is reflected in an internal, biochemical phenotype. These various scales of dynamic responses need to be considered and genotyping and image based phenotyping must be linked to the physiology at the cellular and tissue level (1). The pathogen response of barley genotypes differing in their resistance to two fungal pathogens, the obligate biotroph Blumeria graminis and the necrotroph Drechslera teres, causal agents of powdery mildew and net blotch, were characterized in the high-throughput PhenoLab using multispectral imaging. The pathogenesis and mlo/Mla gene-based Blumeria resistances were identified by analysis of the multispectral reflectance patterns. Support Vector Machine for data mining approach from machine learning could validated the resistance types fully automatically. Thereby it was possible to relate spatial and temporal dynamics of changes in certain wavelength bands to specific resistance types. The non-invasive phenotyping was complemented by metabolic fingerprinting via the determination of activity signatures of key enzymes of carbohydrate and antioxidative metabolism, phytohormone profiles and determination of specific defense marker genes. The different resistance mechanisms could be related to distinct temporal dynamics of physiological responses. This study is a proof-of-concept study to show the potential of a holistic phenomics approach to complement non-invasive imaging by deep physiological phenotyping and creates the basis for an automatic spectral characterization of crop resistance phenotyping in a high-throughput facility with mechanistic verification at the cellular level. (1) D. Großkinsky, J. Svensgaard, S. Christensen, T. Roitsch (2015) Plant phenomics and the need for physiological phenotyping across scales to narrow the genotype-to-phenotype knowledge gap. J Expt Bot 66. 5429

Poster

35258: Study of synthetic spring wheat on the root system

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One of the biggest problem of agriculture ecology of republic is find new ways of wheat drought resistance by global warming. Have new perspectives, when use germplasm of wild relatives, it helps to achieve high drought tolerance. Original way of drought of wheat is attraction of wild types, which have natural sustainability to ecology stress by depending of natural selection, in particular to act of positive temperature, lack of moisture in the end leads to drought tolerance. Environment made high adaptability of wild kinsmen of wheats to drought tolerance. For finding ways to solve problem with drought have: 1) lines of wheat-alien hybrids of spring wheat like «bridge» and another object of breeding; 2) types of T.dicoccum, T. militina, T.timopheevi and T.kiharae; 3) spring wheat varieties T.eastivum, field experiment in KazSRIA&PG, Kazakhstan; CIMMYT-Turkey. Most of the powerful root system with maximum degree of analyzed features is genotype 6625x T.timopheevi; Kazakhstan 10 x T.zhykovskyi, 6625x T.timopheevi and wild types of T.militana and T.kiharae. Different of roots of T.militina are maximum lengths, area of root system, big diameter, counts of ending. Different roots of T.kihare are also length, area and reified system. Kazakhstanskaya 10 x T.zhykovskyi, 6625x T.timopheevi, they don't have different thing only in diameter, they are very thin. Roots of genotype of Kazakhstan x 10 T.zhykovskyi and 6625x T.dicoccum have difference in thickness of roots, area, and a lot of fresh roots. Genotype roots of Kazakhstan 10x T.zhykovskyi have different on each aspect, besides diameter and counts of endings. Number 6625 near by origin by lines of 6625 T.timopheevi (n) was different only in 4 aspects, not reaching maximum of length, medium diameter, counts of endings, and a lot of fresh roots. It mean, maximum developing root system characterize : 6625x T.timopheevi (n); 6625 x T.timopheevi-3 and Kazakhstan 10 x T.zhykovskyi and two spicies T.militinae и T.kiharae.

Session 4: Data management

Oral Presentations

32002: High-Throughput Phenotyping of Cowpea Seeds Using Multispectral imaging

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The aim of this work was to utilize both computer vision and multispectral imaging systems supported with multivariate analysis for high-throughput phenotyping of cowpea (Vigna unguiculata) seeds. The computer-vision system was used for automatic inspecting of seeds during imbibition and germination and the spectral fingerprints of every single cowpea seeds were extracted from multispectral images. Spectral data were processed by using linear discriminant analysis (LDA) for classifying the seeds into different categories according to ageing, viability, seedling condition and speed of germination. The obtained results indicated that the discrimination models provided good accuracy in distinguishing 'Aged' and 'Non-aged' seeds with an overall correct classification (OCC) of 97.51, 96.76 and 97%, 'Germinated' and 'Non-Germinated' seeds with OCC of 81.80, 79.05 and 81.0%, 'Early germinated', 'Medium germinated' and 'Dead' seeds with OCC of 77.21, 74.93 and 68.00% in training, cross-validation and independent validation data sets, respectively. The results demonstrated the capability of the multispectral imaging system in rapid categorization of individual cowpea seeds to different classes. Thus; this stat-of-the art multispectral imaging method associated with chemometric analysis in classifying seeds could be a valuable tool for on-line classification protocols in cost-effective real-time sorting and grading processes as it provides not only morphological and physical features but also chemical information for the seeds being examined.

34726: Unlocking the potential of plant phenotyping data using PIPPA

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While digital phenotyping claimed its central role in many plant research projects, phenotypic data is being produced at high speed and at high quantity. High-throughput phenotyping platforms continuously generate plant images with several modalities. Nowadays, the same system can acquire RGB, thermal infrared, fluorescence and hyperspectral images and stores both environmental and weighing and irrigation data. The next hurdle is to be able to properly manage the high amount of raw and derived data. At VIB we developed PIPPA as a central database and web interface with image and data visualization and analysis functionality. Several automated WIWAM phenotyping platforms, ranging from an XY table for controlled irrigation and imaging of Arabidopsis to more crop-oriented systems, have been integrated with PIPPA. The interface allows scientists to setup and analyse their own experiments, while keeping all data together in a structured database. The database takes care of the data management and integration, linking images, metadata, environmental data, and image analysis and measurement results. As the software package is developed as a web interface, the tool is available on every computer within the department. Pre-processing of images, such as cropping, can be automated and image analysis is performed by starting a task on the server or computer cluster, for fast processing. The analysis framework is designed to support the integration of external image analysis scripts. Furthermore, environmental measurements, weighing and irrigation output, the experimental design, and image analysis results can all be graphically visualized within PIPPA, bringing the plant phenotyping results to your fingertips. Current and future developments focus on the interoperability of image processing tools and the public accessibility of raw phenotypic data to enable community based 'big data' analysis initiatives.

35043: Implementation of FAIR Data Principles in Plant Phenomics

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Plant phenomics produces heterogeneous datasets from multiple sources that are taking into account spatial and temporal dimensions. These datasets characterize objects such as plants, organs, phenotyping facilities, associated environments and their interactions. An important challenge for Information Systems is the structuring of all these data by implementing FAIR principles (Findable, Accessible, Interoperable and Reusable). This challenge is one of the priorities of EMPHASIS European Infrastructure for Multi-Scale Plant Phenomic. Here we present methods and tools dedicated to data management developed in Phenome (French project), EMPHASIS and EPPN2020 (European Projects). These methods implement FAIR principles for various species and categories of installations (field, greenhouse). We describe a non-ambiguous identification system and naming convention for all objects, traits and variables in experiments and establish their relations via ontologies and semantic resources. We also describe the formalization of events such as plant management, anomalies and a standardized management of annotations associated to objects so they can be easily retrieved. We illustrate these methods and tools with the PHIS Information System, an ontology-driven architecture for integrating and managing data from multiple experiments and platforms. PHIS, creates relationships between objects and enriches data sets with knowledge and metadata. It allows data integration into other systems, e.g. modelling platforms or external databases. The proposed methods and tools are generic and flexible. They can be adapted for various phenomic infrastructures and deal with technological evolution.

35924: MAPEO: a drone based phenotyping platform for plant breeders

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Farmers in many crop producing region face more and more challenges in the coming years including aggravating drought climate and increasing scarcity of water usage due to irrigation extension. as well as the potential loss caused by plant disease such as fungi-related pests. Technological approaches evaluating of seed resistance quality or the efficiency of bio-chemical product actions, by quantifying crop structural and functional properties (plant phenotyping) in outdoor environments, is still in its infancy. Drone-based remote sensing technology can provide, at field scale, such accurate agrometrics (agronomic traits) on basis of which the seed selection process is made. The technology has been described in the literature for many crops and traits with generally high accuracies in comparison to field based methods. However, the practical implementation into the experimental fields of plant breeders or public research facilities has been limited to demonstrations and publicly funded research programs. The step towards fully exploiting the potential of drone based phenotyping requires (i) the simplification of data acquisition and data handling ,(ii) data analytics which are focussed to extract relevant agrometrics on micro-plot level and (iii) the integration within day-to-day workflows. Over the past 2 years, we have collaborated with plant breeders and public research facilities to develop MAPEO, a drone image processing platform dedicated to experimental fields. Plant height for wheat and corn plots, diseases in sugar beets and wheat trials, plant emergence for potatoes and spinach are just a few traits for which image analytics were provided and which resulted in agrometrics which reaches or even surpassed field based measurements. Technologies like MAPEO are there to help make plant breeders to fully adopt and integrate drones into their day to day lives.

Poster

35913: How to deal with multiple dataset for vegetation/background semantic segmentation?

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Images play a vital role in crop phenotyping. Pixel-wise classification (into vegetation/background) or semantic segmentation is a critical step in the computation of several canopy state variables. With the development of automated imaging phenotyping platforms, there is an urgent need for the conception of unsupervised methodologies. The current state of the art algorithms are based on convolutional neural networks. Those networks are often trained on a particular dataset. Results and performances of the models will be then suggestive of the characteristics of the training dataset. In field conditions, the dataset is often limited to specific conditions: they include a limited number of varieties, crop development stages, illumination conditions, sensor properties and acquisition conditions/ configurations. This is especially the case for the task of segmentation because of the tedious and expensive labor of pixel-level annotation. Open science, public datasets and collaborations between institute for data sharing have opened now the possibility of the construction of large datasets. Thanks to those initiatives, it is now possible to have access to huge diverse datasets. In the specific case of vegetation vs background classification, every dataset can add valuable information in the training process of the model and can contribute to improving the accuracy for a target dataset. This study aims at providing the best performances and robustness on a target dataset. In other terms, we provide strategies to train a model for a specific phenotyping platform. We investigate the impact of the specific attributes of the training datasets on the testing ones. The datasets used in this study were collected from diverse acquisition campaigns. Results show the importance of dataset diversity compared to that of the size of the dataset. Finally, few methods and perspective on which datasets or groups of images should be annotated and used for training are proposed.

Session 5: Image analysis

Oral Presentations

35017: Deep Learning Techniques for the Segmentation of 3D CT Plant Root Images.

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Plant phenomic analysis techniques — procedures to evaluate observable plant characteristics — are a crucial part of any approach to achieving desirable agronomic and biological traits. Traditional phenotyping techniques have been done manually by researchers, and plant features have been measured through time consuming efforts that are prone to errors and inaccuracies. Recently, plant studies have scaled up to thousands of plants, and phenotyping efforts need to scale up as well. Advances in sensor technologies have paved the way for faster and more efficient phenotyping, and new methods have been adapted from other scientific disciplines such as high-resolution X-Ray three-dimensional (3D) computed tomography (CT). A crucial step in the analysis of CT data for plant phenotyping is the segmentation of root systems: the deteremination of whether a particular voxel in the space is classified as "root" or "non-root". Unlike roots in transparent mediums, roots in organic soils, i.e., non-transparent mediums, are particularly difficult to segment from other materials (water, air, stones, debris, etc.) as root and non-root voxels have overlapping CT values. Here, we discuss a deep learning approach for the segmentation of 3D CT plant images that addresses the challenge of non-destructive root segmentation in high-throughput plant imaging systems. Our proposed solution is primarily implemented using the MapReduce model, and deployed on a computational cluster that segments CT images by processing subvolumes taken from the original CT volume. Our existing segmentation algorithms are designed to work on full volumes processed on single machines, and we expand them to work in a cluster environment by leveraging the work of multiple machines in parallel. We show initial results of our solution by analyzing several different types of plants (Casava, Potato, Bean, Maize), and discuss the challenges in developing a model for training data sets.

35071: A unified framework for image-based plant phenotyping under controlled growth environment: From image acquisition to phenotype interpretation

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Up to date, various plant phenotyping platforms have been established to automatically acquire arrays of plant images under controlled growth environment. If an image analysis pipeline, which can precisely quantify the complex phenotype of plants, were equipped to such platforms, it will provide plant scientists a novel research workflow that can unveil high-level features of gene functions and plant physiological responses which had been hard to analyze or even been overlooked by manual analysis. This presentation introduces a work towards combining controlled image acquisition platform and deep-learning-based feature extractions on the RIKEN Integrated Plant Phenotyping System (RIPPS). Using this platform, we grew various Arabidopsis genotypes constituting of mutants which gene(s) involved in circadian rhythms are dysfunctioned. We acquired abt. 10,000 top-view images in total, which were taken in a 3-hour interval at a duration of 3 weeks. With such images as a dataset, we newly developed and trained four neural networks to estimate plant features, including plant segmentation, leaf blade instance segmentation, leaf number estimation, as well as detection and temporal tracking of leaf tips. Based on the features, we extracted 15 morphological descriptors. Using our framework, we confirmed the clear difference among the characteristics of mutants, over the descriptors such as the width and length of leaves extracted based on instance segmentation. Also, the visualization via dimensional reduction of various descriptors formed unique clusters representing different genotype and growth conditions, intending that the multivariate analysis based on our framework can make the scientists to quantify and understand the effect of perturbation of gene and environmental condition on plant growth.

35122: RootNav 2.0: Machine Learning based Automatic Plant Phenotyping.

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This talk presents a new image analysis approach that provides fully-automatic extraction of complex root system architectures from a range of plant species in varied imaging setups. Driven by modern deep-learning approaches, RootNav 2.0 replaces previously manual and semi-automatic feature extraction with an extremely deep multi-task Convolutional Neural Network architecture. Rather than simply segmenting the images, the network simultaneously locates seeds, first and second-order root tips to drive a search algorithm seeking optimal paths throughout the image. The result is a tool that is faster than semi-automatic approaches and more accurate than current automatic approaches. The output of RootNav 2.0 is the widely accepted RSML standard, allowing reconstructed root systems to be analysed in a variety of tools within the community. This talk will cover the challenges of root phenotyping in varied images. I will outline the benefits deep learning can provide in this setting, and demonstrate good performance even on smaller datasets. I will show results of training and using this tool on three different datasets, wheat (Triticum aestivum L.), rapeseed (Brassica napus) and Arabidopsis (Arabidopsis Thaliana). Results are compared against manual ground truth labelled by a human expert. This tool can also be transferred over to new image types and species, and I will discuss how RootNav 2.0 can act as a platform, retrained as appropriate on new species.

35236: Is Bigger Always Better to train deep learning models for high throughput phenotyping applications?

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Deep Learning algorithms, in particular Convolutional Neural Networks (CNN), are state-of-the-art techniques for most tasks in computer vision. CNN have been recently applied in high-throughput phenotyping systems to estimate automatically traits like organ or plant density or characteristics, or the cover fraction. These algorithms are well suited to exploit the large amount of high-resolution optical imagery acquired from new vectors such as unmanned aerial or ground vehicles or field imaging devices. However, the reliability of a CNN is largely determined by the amount of observations available for training. Generating such dataset is a tedious and expensive process, as images need to be interactively labelled. Therefore, many studies on the application of deep learning in plant phenotyping are limited to small datasets, questioning the capability of the algorithm to perform robustly in other experimental conditions . Considering the cost of labelling such dataset, is the size of the training dataset or rather the its variability (e.g. illumination, camera set-up, development stages, etc.) that drives the CNN performance? To answer this question, field experiments were conducted to detect sugar beet plants during early growth stages in 2017 and 2018. High-resolution RGB images were acquired from a UAV during 12 measurement sessions over different fields. CNNs were trained using two different schemes: (1) increasing the amount of images for training while keeping the number of sessions constant; and (2) keeping the amount of images constant, but increasing the diversity of the dataset including images from a large number of sessions. Results indicate that CNNs performances largely improve by increasing the variability within the training dataset, rather than increasing its size: generalization was enhanced by selecting images acquired under contrasted conditions that were difficult to mimic using simple data augmentation techniques.

Poster

36562: Multi-scale phenomics: to see a world in a grain of seed, and a life in a minute

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The integration of machine learning, computer vision, big-data analytics and life sciences is opening up new opportunities for plant research. Very complicated rules can be dynamically generated from multi-dimensional biological datasets to characterise phenotypic features, as well as to predict complex trends while plants are interacting with their environment. These methodological advances are enabling biologists to unravel the genetics of dynamic plant phenotypes at the level of the cell, organ, tissue, plant, and population. In this talk, the speaker will start with seed-level phenotyping (SeedGerm) in controlled environment, and will then link to in-field phenotyping (AirSurf) based on seed establishment traits. With a focus on multi-scale phenotyping and phenotypic analysis carried out at both Norwich Research Park (UK) and the Nanjing Agricultural University (China), the speaker will introduce distributed field computing system (CropSight), as well as the approach we have developed to manage in-field data management, monitor seasonal crop growth, and quantify key growth-related traits in a multi-year field experiments for both bread wheat and rice.

34666: Comparing computer vision and deep learning for ear detection in wheat

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Ear count is an important yield component and its formation is influenced by environmental conditions. Thus, it is an important trait for plant breeders and high throughput phenotyping methods of ear count would be an important tool to further investigate wheat ear formation in different genotypes. In this contribution, we compare traditional computer vision implemented to a deep learning approach based on faster RCC network architecture for ear detection and counting in very-high resolution (0.5 mm) iamges. A labelled training dataset of 2250 wheat head images containing a wide variety of genotypes and illumination conditions. This annotated dataset was used to train and evaluate a deep learning object detection model and a baseline computer vision method. Additionally, by decreasing the training dataset image resolution, an estimate of the model performance for a UAV camera was determined. The deep learning method had an 88.7% success rate for head count detection on the validation dataset, whereas the computer vision approach had a success rate of 77%. The deep learning approach was very robust against illumination conditions and had an almost linear decrease of performance by means of mean average precision from 45 to 25 with a decreased resolution of 0.5 – 10 mm. Overall, this contribution shows the feasibility of deep learning for ear detection and counting.

34872: Deep learning for plant phenotype: An overview

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Deep learning for plant phenotype: An overview Plant phenotype refers to the morphological characteristics of plants that can be measured. It is the result of the interaction between plant gene expression and environmental impact, and it determines many important factors such as physiological and biochemical characteristics, yield and stress resistance of plants. However, the traditional means for obtaining plant phenotype information is highly dependent on manual labor, which inevitably accompanied by the waste of time and errors caused by subjectivity , limiting the development of phenomics. With the recent advent of deep learning, plant phenotype information acquisition based on deep learning has made breakthrough progress in methods and performance, which provides a new opportunity for the research of phenomics. In this paper, we introduce the background, research direction and research status of plant phenotype and briefly summary several typical deep learning models, based on which the deep learning methods of plant phenotype information acquisition are summarized and analyzed. Specifically, we conclude the main function and existing problems of deep learning in plant phenotype and propose some schemes that hopefully solve these problems. Finally,we present some prospects for future work. Key words: deep learning ,plant phenotype, Convolutional Neural Network

34920: Toward 3D plant modeling of every leaf and branchlet

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We introduce a work-in-progress report towards detailed modeling of plant leaf and branchlets. Although a state-of-the-art study proposed a multi-view reconstruction of 3D branching patterns, leaf modeling and decreasing number of images required to plant modeling remain challenging problems. To this end, we present the following two trials: 1) a multi-view per-leaf 3D reconstruction utilizing leaf instance segmentation, and 2) a single-image branch modeling by jointly estimating branch paths and keypoints (i.e., joints and endpoints). Based on the leaf instances extracted by instance segmentation, the instance matching among multi-view images ore required for per-leaf 3D reconstruction. We, therefore, develop a novel matching method using epipolar constraint and graph optimization. A set of multi-view correspondences of leaf regions allows the 3D reconstruction of each leaf by traditional 3D reconstruction pipelines. We performed a preliminary experiment using simulated plant models. Assuming a correct instance segmentation is given, we simulated the instance images from 10 views by rendering each leaf in separate colors. The matching accuracies were 94.3 % for plants with 16 leaves, showing that the proposed method successfully found the correct matches. Our single-image branch modeling method inputs an RGBD image, which captures both RGB and depth information. Inspired by human pose estimation approaches, which extract keypoints (i.e., person joints) in the human body, we estimate branch joints and endpoints, as well as branch paths, using a GAN-based image-to-image translation network. The proposed approach then connects appropriate keypoints as branchlets, utilizing the depth and spatial information of the estimated branch paths. From an experiment using the simulated plants, our approach successfully generated a spatial branching pattern, while we found there is a room for further improvement on the depth accuracy.

34989: Comparison of 3D reconstructions from UAV RGB images and terrestrial LiDAR imaging for measuring architectural traits of peach trees

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Automated high throughput architectural trait extraction of fruit trees in the orchard is important for making breeding decisions and identifying best management practices. The objective of this work is to compare the 3D reconstructions derived from UAV based RGB images and terrestrial LiDAR for measuring different architectural traits of peach trees. RGB images of three peach trees were collected before and after pruning operation using a UAV. These images were captured in oblique view by following a circular path around the tree. For each of those peach trees, LiDAR data was also collected before and after pruning operation. LiDAR data of each peach tree consisted of scans from four different views. We compared the quality of 3D point clouds generated from UAV based RGB images with LIDAR scans for automated extraction of traits like tree height, tree volume, crown area, etc. before and after pruning.

35025: A Robust Leaf Surface Reconstruction Method for 3D Plant Phenotyping

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Accurately capturing the morphological trait of plant organs such as leaves, is essential for plant phenotyping studies. Recently, there are several approaches to produce three-dimensional (3D) point clouds of plants. However, due to the complex canopy structure of a plant, occlusion, and sensor noise, the generated point cloud often contains severe noise and missing points, leading to the difficulty of capturing the detailed shape of a plant. For example, when acquiring a leaf shape from the 3D point cloud by existing surface reconstruction methods, taking into account the presence of noise and missing points in the point cloud is needed. However, increasing the resistance to noise and missing points by adjusting the hyper-parameters, it loses the detailed shape of the leaf. On the contrary, if we prioritize the acquisition of detailed shape, the resistance to noise and missing points decrease. That is, there exists a tradeoff between the acquisition of leaf shape and the resistance to noise and missing points of the 3D point cloud. In this work, we propose a method that directly acquires the shape from the 3D point cloud of leaves for mitigating this tradeoff. The proposed method first approximates only the degree of bending of the leaf by curve fitting. Then, the shape is acquired directly from the 3D point cloud by flattening this degree of bending to 2D plane. In this way, we can acquire the globally pointed shape, such as leaf tips, without approximating a curve or surface. The performance of the proposed method was evaluated qualitatively in acquired shape from the 3D point cloud of leaves with various shapes, and quantitatively on leaf surface area calculated when applying our method. The results demonstrated that the proposed method is more resistant to noise and missing points of 3D point cloud compared to the existing surface reconstruction methods. Moreover, the well-reconstructed leaf surface has shown great potential for accurate 3D plant phenotyping.

35049: Using DIRT to characterize conidiophore architecture in the model fungus Neurospora crassa

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Characterizing how fungi grow, develop, and form networks is integral for understanding their role in ecosystems and behavior as pathogens. We use the model filamentous fungus Neurospora crassa to study these concepts. To colonize new environments, N. crassa develops specialized fruiting bodies called conidiophores that give rise to new spores for subsequent release. While genetic, temporal, and environmental regulation of conidiophore development has been well characterized in N. crassa, little is known about the architecture of these structures. Interestingly, the highly branched conidiophores resemble plant root systems, allowing us to employ root phenotyping tools to characterize their architecture. We are using Digital Imaging of Root Traits (DIRT) to quantify over 70 structural traits describing N. crassa conidiophore architecture. To assess natural variation, we examined a population collection of 21 wild, genetically unique isolates collected from Louisiana, USA. Our data show high structural variation of conidiophore architecture, a well-conserved development pathway, presenting a novel application of plant phenotyping tools.

35054: Non-destructive identification of weeds from ryegrass based on hyperspectral imaging

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Weed control in ryegrass paddocks is a major biosecurity, environmental and economic burden in New Zealand. Traditional methods for weed control, including manual and chemical methods, are time consuming and costly and the latter has tremendous negative environmental impact. First step towards modern weed control techniques is weed identification. We used machine learning of hyperspectral imaging data to explore the possibility of weed identification. The hyperspectral imaging spectra data of bristle grass, buttercup thistle and wind grass were acquired and pre-processed by standard normal variate (SNV) to avoid spectra band shift and noise. Three classification models were trained using both full and optimal wavelengths of the average spectra from each weed sample, including partial least squares-discriminant analysis (PLS-DA), support vector machine (SVM) and deep learning. The full band and the optimal selected band of spectra of all pixels were used for deep learning model building. All three classification models showed repeatable identification of ryegrass and weeds using both full and optimal wavelengths spectra with 95% accuracy for both calibration and validation sets with high (> 0.91) sensitivity and specificity. The SVM and PLS-DA Models based on the average spectra could lead to over prediction when predicting all pixels of weed hyperspectral data and result in less accuracy. However, deep learning method produced a reliable and robust identification result using both average and full pixels of imaging spectra. Eight significant wavelengths were found as highly informative for discrimination among the four weed species. Our method may provide a rapid and efficient methodology for weed identification in ryegrass paddocks, which could serve as a powerful tool for future targeted weed control in agriculture.

35070: Identification of favorable ideotypes in crops using deep learning to extract dynamic ear/panicle traits

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The spike (or ear) of wheat is the tissue that most directly determines yield potential. Spike traits could play a decisive role in breeding if favorable variants could be quantified easily, and are related to plant productivity. With these objectives in mind, we have developed a novel approach based on deep learning, and using the morphological diversity released by a multi–parent advanced mapping (MAGIC) population to identify spikes as they emerge, quantitatively measure spike traits, and relate these trait measurements to productivity. After training on a large set of time-stamped images acquired during wheat development, testing, and the result optimization, the precision, recall, F-measure, and IoU can achieve a high level of accuracy, reaching more than 0.8. After spike segmentation from the heading stage to mature stage, a total of 40 spike features and 18 spike growth features were extracted. Performance was evaluated by comparing correlation between manually acquired yield related data and the extracted features. The R2 for top internodes length and spike number were 0.686 and 0.719, respectively. A combination of just 4 key parameters could predict plant productivity with an R2 of 0.776. Spike growth curves fit well to a Sine model, providing additional growth-related features to quantify growth period and potential productivity, and also can be used to determine better ideotypes with higher ear weight and shorter growth period. In addition, we also tested the power of deep learning in identification of rice panicles (in greenhouse and field), rice spikelets and tropical crop fruits. In conclusion, we propose a novel analysis pipeline to dynamically assess wheat spike growth, and dissect the genetic architecture of spike growth, combining novel features with QTL analyses.

35118: PlantCV- Open Source Plant Phenotyping Software

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PlantCV is an open-source image analysis software package targeted for plant phenotyping. Traditional phenotyping is time consuming, costly, and often destructive, therefore streamlined processes will allow research to advance beyond this bottleneck. The PlantCV project was started at the Donald Danforth Plant Science Center in 2014, and is under active development. Core values of the project are open communication and collaboration among stakeholders from diverse backgrounds and areas of expertise. The mission of the PlantCV project is to provide a common interface for a collection of image analysis techniques, and utilize a modular architecture that enables flexibility in the design of analysis workflows and rapid integration of new methods. These tools provide a simplified interface for users to utilize underlying tools and build custom analysis workflows without significant experience with programming. Clear and extensive documentation is vital to this mission and is reflected in the currently available 11 static and the 13 interactive tutorials. Common data that users extract while using PlantCV vary from shape, size, and color characteristics, NIR information, measures of fluorescence, and plant morphology information. White balancing and color correction tools using color cards allow users to standardize their dataset. Height, plant area, and other measures of shape are easily standardized in downstream data analysis with the PlantCV size marker tool. Recent tools added to the software include the ability to analyze thermal data and morphological traits such as internode length, individual leaf length, measures of leaf curvature, and measures of leaf angle. The built in workflow parallelization tool allows users to execute a workflow across an entire dataset of images and gather data collected into a CSV file that can be imported into any preferred data analysis tool.

35177: The Controlled-environment Phenotyping Facility (CEPF) at Purdue Universtiy

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As the access to genotypic data has increasingly become inexpensive, the need for quantitative phenotypic data to complement this information becomes more imminent. The Controlled Environment Phenotyping Facility (CEPF) at Purdue University employs a unique automated system that facilitates plant growth experiments that set to assess complex plant traits. The CEPF is featured with a costumer-designed growth chamber and a fully automated fertigation/irrigation system. These system provide the capability to accommodate growing plants up to three meters tall. When it comes time for measurements, the plants in the chamber are carried by an automated conveyor belt system to an RGB camera system which acquires color images of the plants and extract key parameters such as color, size, morphological traits, and number of leaves, length of each leaf, etc of each plant. The plants can also be transferred to a hyperspectral camera system which provides spectral information in the Visible and Near-infrared (VNIR) 400 – 1000nm waveband. The HSI cameras can be used to detect chemical composition of plants to determine relative water content of leaves, nutrient composition, as well as vegetation indices, herbicide damage, and foliar pathogen progression. Both the RGB and hyperspectral imaging systems are housed in cabinets to create optimal, repeatable lighting conditions for image acquisition. The Zegami Plant Phenomics Suite is leveraged to facilitate visualization of the acquired data set. We are working on adding sensing capabilities in CT root scanning which comes online mid-2019 and expanding the spectral capability of the hyperspectral imaging system into short-wave infrared (1000 – 2500 nm). The CEPF can bridge the gap to help explain gene function, provide insight in nutrient use efficiency, and how water stresses impact plant growth.

35229: Improving Cassava root segmentation using AI

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X-ray computed tomography (CT) is increasingly applied for the non-destructive visualization of belowground structures in pots. With X-ray CT the 3D volume information of objects can be visualized using X-ray projections of the object from different points of view. Due to the non-destructive nature of CT it is possible to track the growth of plant organs such as cassava tubers or root systems. However, to do so automatic segmentation algorithms for virtual root excavation are needed. Very often, changes in soil moisture or soil type demanding a new set of parameters for the complex segmentation algorithms. Due to the structural similarity of roots system architectures, the use of AI-algorithms is the next step. We observed the root growth of seven different Cassava varieties over a period of two months. Within this timeframe we periodically analyzed the root system and applied an automated segmentation algorithm, resulting in a huge set of annotated training samples. We used theses training sets to generate a CNN extracting root structures in soil. Within the presentation, I will show how we used the output of the RootForce algorithm to generate a training set for the CNN. After this I compare the results of the automatic segmentation algorithm RootForce with the ones of the CNN in terms of root volume and calculation speed. Additionally, I will discuss the combination of classical algorithms and CNN based algorithms.

35234: Estimation of Vertical Leaf Area Density of Maize with stratified UAV-LiDAR for different planting densities and growing periods

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Leaf area density (LAD) reflects the vertical distribution of a maize canopy and is an important structural parameter for the growth of maize and for the nutritional diagnosis and breeding of maize. This study acquired high-density datasets in three flights of UAV-LiDAR to evaluate the ability of UAV-LiDAR for measuring LAD of a maize canopy at the plot level. Specifically, we used discrete point-cloud data from a RIEGL VUX-1 mounted on a UAV flying at an altitude of 15 m. We propose a method to estimate the stratified correction factor α(θ) to improve the accuracy of estimates of LAD. On August 28, 2018 (the silking stage), the R2 and root-mean-square error (RMSE) of the upper, middle, and lower layers were 0.79, 0.79, 0.51 and 0.31, 0.32, 0.21, respectively; on September 14, 2018 (the blister stage), the R2 and RMSE of the upper, middle, and lower layers were 0.89, 0.90, 0.64 and 0.25, 0.18, 0.16, respectively. Compared with the study of the correction factor α(θ)=1.1, which has been widely used in previous studies,the estimation accuracy for the middle and lower layer all improved significantly. We analyzed the vertical distribution of the LAD for different planting densities and different growing periods, and the results show that a higher planting density of maize corresponds with greater maize height and ear height. At the same time, the vertical distribution of the LAD and the average leaf area density (ALAD) were consistent for different densities, and with the increase in density, the higher LAD corresponded with the smaller ALAD . By comparing ALAD from different growing periods, we conclude that higher maize density corresponds to slower leaf growth. These results show the usefulness of the proposed method to estimate the vertical distribution of maize LAD by using UAV-LiDAR: it can be used as an indicator for maize health and to assist growers to improve irrigation and fertilization.

35239: Development of a pipeline to determine plant organ specific spectral profiles from single high-resolution multi-spectral photos

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Traditionally, plant breeders have assessed their breeding lines through visual inspection of plant canopies across thousands of trial plots. Such approaches are time consuming, subjective and costly. Recent innovations in using multi-spectral sensors on-board unmanned aerial vehicles (UAVs) and machine learning algorithms have enabled frequent, fast and reliable data collection at fine spatial and narrow spectral band resolutions. However, extracting crop features from single photos for each plot remains a challenge. In this study, we analysed the use of UAV imagery captured by a multi-spectral sensor (Micasense RedEdge) to determine crop traits in a large sorghum breeding trial consisting of 940 plots. Specifically, we investigated the use of high-resolution multi-spectral photos over multiple dates to determine the number of plants and heads per plot and heading date. The utility of spectral band and/or index combinations is explored using various machine-learning approaches. In each of these approaches, we also compared using an ortho-mosaiced reflectance map stitched from thousands of images or using single images per plot. In order to calculate reflectance from a single image we developed a processing pipeline to extract single RedEdge images for each plot. The process involves determining of NADIR images in each plot, automatically detecting the calibrated reflectance panel and calibration information, radiometric calibration, spectral bands alignment and plant index calculation. Preliminary results from this approach showed a significant increase in accuracies of organ detection from single photos compared to the use of stitched ortho-mosaics. It is envisaged that the implementation of this pipeline will allow for more accurate determining of crop characteristics at individual plot level across a large range of genotypes.

35241: Analyzing on the dynamic phenotype changes of soybean plant during the whole growth period based on machine vision technique

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The accurate extraction and analysis of crop phenotype are of vital importance for the design breeding that combines molecular with phenotypes. With the development of digital agriculture, 3D reconstruction and deep learning techniques are widely used in the fields of crop phenotypes. In the study, we try these techniques to acquire automatically phenotypes of soybean plant during the whole growth period. On the one hand, we design a simple 3D reconstruction sampling platform that can take pictures to potted plant all the time, and the plant 3D models are reconstructed based on those pictures and 3D reconstruction techniques. On the other hand, we design a simple flower-pod image sampling platform that can take pictures to the local flower-pod area of soybean. And we calibrate and identify detailed local and quantities of flowers and pods based on deep learning. Then we discover law of soybean growth development and law of flower dropping and pod dropping of soybean based those phenotypes during the whole growth period. Besides some basic biology laws being found, our results adequately show that machine version technique can improve greatly extraction phenotype methods and improve greatly accuracy of genome mapping during molecular breeding. Thus the process of crop breeding will be speed up.

35365: deep learning based approach for weed and maize semantic segmentation

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Weed segmentation under field conditions remains a challenging problem due to variables in the appearance of plants, illumination changes, foliage occlusions, and different growth stages in agricultural environments. Current approaches for weed and crop segmentation and detection rely predominantly on conventional machine-learning techniques that require a large set of hand-crafted features for modelling. These might fail to generalize over different fields and environments. Here, we present a deep learning-based approach that develops a deep convolutional neural network (CNN) with an encoder-decoder configuration for weeds and maize semantic segmentation. there are 5000 field images which were manually labelled in a pixel-wise way. The model was trained with 4700 images and an adaptive learning rate. And the hyperparameters were tuned with 200 images as a validation dataset. Finally, the model was tested in 100 field images, demonstrating a good result in difficult field image segmentation. The mean intersection over unions (IOUs) for soil, weed and crop class are 0.981, 0.694, and 0.833 respectively. We also compared the proposed method with other conventional neural networks used for semantic segmentation such as FCN, UNet. It shows that the proposed model provides the best performance.

35497: Detection of highly occluded immature tomatoes on plant using deep learning

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Automatic detection of intact tomatoes on plant is highly expected for low cost and optimal managements in tomato farming. However, green tomatoes especially when occluded with leaves were seldom successfully detected by traditional image analysis. In this study, we aimed to develop a method to accurately detect intact tomatoes regardless of occlusions and fruit growing stages by using deep learning approaches, thus propose a map to locate tomatoes and show their maturing stages based on the detection. The proposed method worked on tomatoes photos, which were collected in green houses and distributed to train, validation and test dataset in proportion of 7:2:1. Then 28835 tomatoes were manually labeled by a web-based interactive labeling tool, and the photos with annotations were cropped into sub-images. Three tomato detecting models were built on Tensorflow object detection API, using Faster R-CNN with the pre-trained (on the COCO dataset) Resnet-50, Resnet-101, Inception-Resnet-v2, as convolutional neural network model, respectively. With learning rate as 0.00003, random horizontal flip as data augmentation method, models ran in 100 epochs on both training dataset (1779 sub-images) and validation dataset (571 sub-images). Model accuracy evaluation showed the model using Resnet-101 achieved the highest average precision (0.82) with high location accuracy (intersection of union ≥ 0.5), so was selected as the optimal detecting model. By inferring it on test dataset and filter out detections of score < 0.5, correlation analysis of the number of labeled and detections in per sub-image showed high coefficient of determination (R2=0.87). The merged detections constituted a map from which it could easily find ripe or immature tomatoes on cultivation bed. In conclusion, by using deep learning technique, the highly occluded immature tomatoes on plant could be accurately located and counted. It is of great potential for yield mapping, robot harvesting, and optimal farming.

35823: Phenotypic traits of tomato seeds obtained by X-ray microCT imaging predictive of seed germination

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The identification of predictive morphological traits of tomato seed quality and their germination has long been attempted using conventional radiography as a technique to observe internal seed structures and to guide the seed sorting. Many studies observed that the main obtained feature, namely the amount of internal free space, cannot be used alone to predict germination behavior. In addition, the huge variation of the internal structural abnormalities and structural damages affect germination depending on their extent and localization and their detection is not always possible by means of conventional radiography. Although the three-dimensional X-ray imaging has been increasingly common in seed science as allows much more accurate visualization of the internal seed parts, such approach has never been used to analyze tomato seeds. The aim of this work was to test the use of the X-ray microCT imaging for the identification of phenotypic traits of tomato seeds related to the germination capacity. A 100 seeds sample was scanned by a X-ray microtomograph and the internal and external seed traits were quantified using morpho-densitometric parameters. Then a germination test was carried out on the same seeds whose identity remained traced. The internal fragmentation degree and the Sauter mean diameter resulted as the morpho-densitometric parameters better correlated with not germinated individuals. Although such identified predictive traits are not quite rapidly detectable, further studies could allow identification of correlations with some external parameters suitable for a rapid determination in a high-throughput sorting system.

36236: Above-ground biomass estimation and yield prediction in potato by using UAV-based RGB and hyperspectral imaging

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Rapid and accurate biomass estimation and yield prediction enables efficient plant phenotyping and site-specific crop management. RGB and hyperspectral imaging data of potato canopy were acquired with a low altitude unmanned aerial vehicle (UAV) platform at two growth stages for estimating biomass and predicting yield. These field experiments included six cultivars subject to multiple treatments of nitrogen (N), potassium (K) and mixed compound fertilisers. Crop height was estimated by the difference between a digital surface model (DSM) and a digital elevation model (DEM) derived from the RGB imagery, and together with two narrow-band vegetation indices (VIs) selected by the RReliefF feature selection algorithm. Random Forest (RF) regression models achieved high prediction accuracy for both fresh and dry above-ground biomass (AGB), with the coefficient of determination (r2) between the observed and predicted > 0.90. Similarly, crop yield was predicted from six narrow-band Vis (r2 = 0.63) with the imagery data obtained 90 days after planting. A Partial Least Squares (PLS) regression model based on the spectra of full wavelength improved yield prediction (r2 = 0.81). This study demonstrated that UAV-based RGB and hyperspectral imaging can predict potato AGB and yield, which can be used to assist in site-specific crop management.

36315: The shape of plants revealed: A shape theoretic perspective on statistics of trait measurements

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Almost everyone already used the sentence “My plant looks happy”. Most likely one was interpreting the shape of the plant that changed in response to irrigation and fertilization. The response of plant architecture to abiotic stresses is therefore a phenomenon that everyone knows. However, we hardly look below-ground where the root system alters its tip-driven growth. Typically, we observe roots in encapsulated containers and remove all interactions that would normally occur in a field. Alternatively, we try to find a typical root architecture in the field between all root systems of a crop population. We asked the question if we do not miss essential information by simplifying the phenotyping problem to plants in pots or only dominant phenotype observed in the field. We will present a computational method that shows repeatable pattern for drought and well-watered conditions in populations of common bean (DOR 364, L88 57, SEQ 7) and demonstrate how we found initial pattern in existing data. Additionally, the same pattern was observed across years and locations. The observed pattern varies between stress conditions and are hypothesized to optimize above ground biomass. Evidence for this optimization was collected at field sites of the Apache Root Biology Center in Wilcox, Arizona.

36316: Computer Vision in Plant Growing Period Identification, Seed Conting and 3D Leaf Segmentation

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The classification model named GL-CNN (Local-Global Convolutional Neural Network) were designed. The model merges the features together through the network fusion strategy to expand the feature representation based on the whole leaf and leaf patch image sets. Furthermore, we developed a method that would combine density estimation-based methods and Convolution Neural Network (CNN)-based methods to accurately estimate the seed count from an individual soybean pod image with a single perspective. Finally, we proposed an efficient learning and model-free approach for individual vegetable seedling partition using 3D colored point clouds obtained by a low cost RGB-D camera.

36317: Growing Period Classification of Gynura bicolor DC Using Convolutional Neural Network

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There is of great significance to determine the growth period of leafy vegetables for their suitable harvesting. Despite the availability of many intelligent programs designed for the plant classification, identifying the growth stage of a vegetable from its leaf features remains a major challenge. Gynura bicolor DC (G. bicolor) is an important vegetable and its leaf is harvested at a specific growth period. To solve such problems, a classification model named GL-CNN were designed based on convolutional neural networks. The model merges the features together through the network fusion strategy to expand the feature representation based on the whole leaf and leaf patch image sets. Further, the networks were conducted on a new dataset of G. bicolor planted and collected by ourselves. In addition, in order to verify the rationality of the network fusion location, the "early fusion" and "late fusion" networks were designed to compare with GL-CNN. The test accuracy of GL-CNN reached 94.3%, which was best in the classification task

36318: An Efficient Processing Method for Colored Point Cloud-Based High-Throughput Seedling Phenotyping

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Individual vegetable seedling quick segmentation plays an essential role in high-throughput seedling phenotyping in order to monitor the growth status of each single seedling in plug tray. Traditional phenotyping scheme is time-consuming and not suitable for continuously monitoring plant growth. This paper proposes an efficient learning- and model-free approach for individual vegetable seedling partition using 3D colored point clouds obtained by a low cost RGB-D (RGB-Depth) camera. Firstly, noise reduction is conducted on the original point cloud through processing of useable-area filter, depth cut-off filter and neighbor count filter. Secondly, the surface feature histograms-based technique is used to automatically remove complicated natural background. And then the VCCS (Voxel Cloud Connectivity Segmentation) and LCCP (Locally Convex Connected Patches) algorithms are employed for individual vegetable seedling partition. Finally, the height and projected leaf area of each seedling are calculated based on segmented point cloud and validation is carried out. The experimental results show that the proposed method could be used to quickly calculate the morphological parameters of each seedling and it is practical to use this approach for high-throughput seedling phenotyping. Compared with other state-of-art segmentation methods, there is no need for this approach to create new training data and to accompany annotated ground truth images

Session 6: Modelling

Oral Presentations

Crop Nitrogen Phenotyping from Leaves to Grains

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Rapid and accurate monitoring of crop nitrogen (N) status is crucial for timely recommendation of topdressing fertilizers and prediction of grain quality. With ground-based phenotyping platforms, many studies have been dedicated to the estimation of crop N concentration and grain protein content (GPC) from reflectance spectra. However, the physical mechanisms underlying most empirical models remain to be poorly understood, and reliable models across crops and growth stages are highly expected. On the other hand, unmanned aerial vehicle (UAV) has been increasingly popular as a flexible field phenotyping platform but the useful information (e.g., texture and observation angle) in UAV imagery is not yet fully exploited.

In this presentation we will introduce our progress on phenotyping of field crops (wheat and rice) for quantifying the nitrogen status in leaves and plants and predicting the GPC with ground-based hyperspectral data and UAV-based aerial imagery. For these purposes, multi-year small plot trials were conducted in the field with variations in genotype, N rate, and planting density to cover broad ranges in N status and GPC. We used different high-throughput phenotyping devices to quantify the N dynamics in two research lines. One focused on developing advanced spectroscopic methods for accurate estimation of leaf N concentration (LNC) and GPC. To make better use of the N and protein absorption features in the shortwave infrared (SWIR) region, we applied continuous wavelet analysis to leaf and grain power reflectance spectra for constructing sensitive wavelet features. These new spectral parameters exhibited significantly better performance in characterizing the spectral variation in SWIR regions, and yielded higher accuracies for quantifying LNC and GPC than the commonly used spectral indices. The other focused on exploiting the potential of multi-source and multi-angle information from UAV images for improving the leaf and plant N status. We found the textural information derived from multispectral UAV imagery was complementary to spectral information and its integration with spectral information could enhance the estimation of N uptake and N concentration. In combination with commonly used nadir images, oblique images were found to be useful for increasing the estimation accuracy for N concentration but not for N uptake. These findings suggest that the new methods developed in this study have great potential for improving the phenotyping accuracy of crop N status, better understanding the N flow dynamics from leaves to grains, and designing more accurate prescriptions of N topdressing for different crops and growth stages.

34844: Prediction of lettuce fresh weight using optical flow and machine learning in a closed-type plant factory

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Productivity stabilization is an important issue facing closed-type plant factories. As such, researchers have been investigating growth prediction with the overall goal of improving productivity. The projected area of a plant is usually used for growth prediction, by which the growth of a plant is estimated by observing the overall approximate movement of the plant. To overcome this problem, we focused on the time-series movement of plant leaves, using the optical flow (OF) analysis to acquire this information for a lettuce. OF analysis is an image processing method that extracts difference between two consecutive frames caused by the movement of the subject. Experiments were carried out at an actual commercial large-scale plant factory with a daily output of 6,000 lettuces. By using a microcomputer with a camera module placed above the lettuce seedlings, images of 338 seedlings were taken every 20 min over 9 days (from the 6th to the 15th day after sowing). Then, the features of the leaf movement were extracted from the image by calculating the normal-vector in the OF analysis. These features were applied to machine learning to predict the fresh weight of the lettuce at harvest time (38 days after sowing). The growth prediction model using the features extracted from the OF analysis was found to perform well with a correlation ratio of 0.743 which were improvement over the former growth prediction model, thus pointing to the accuracy of our model. Furthermore, our method proved capable of predicting the fresh weight at 22 days in the future with a high level of accuracy, whereas a former study only addressed that at 11 days in the future. This study displayed the capabilities of OF when applied to a plant-growth prediction model. The results obtained from the models show the contribution of the features using OF to the machine learning. Our results were obtained using an MPI system which uses only image data, and thus could easily be industrial implementation.

35217: Deep learning approaches to evaluate morphological and physiological parameters in model plants and wheat

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Deep neural networks (DNNs) are leading enabling unprecedented improvements in data science. We have developed two DNNs for (1) morphological analysis of Arabidopsis thaliana and (2) correlation of wheat ear hyperspectral reflectance with photosynthetic capacity. (1) Mask segmentation using DNNs have dramatically improved accuracy in segmentation of individual objects. In plant phenotyping, this pixel-level allows leaf level segmentation, even when they are overlapping or obscured. We train a Mask R-CNN (regional convolutional neural network) model on annotated Arabidopsis images to study morphological development of different ecotypes. We generated bounding boxes and pixel-level masks on target objects. We tracked Arabidopsis plants over 3 weeks and measured multiple traits, including leaf count, area, length and average leaf colour from time-lapse images. Our results reveal ecotype-specific trends that develop over time. (2) Wheat ear photosynthesis contributes significantly to yield especially under limiting water conditions. Traditional photosynthesis measurement are slow and compounded by organ structure and inability to account for refixation of the respired CO2. Consequently, little work has been done on wheat ears photosynthesis. Hyperspectral reflectance of leaves have been used to generate machine learning models to predict wheat photosynthetic traits in the field. However, these are not suited for wheat ears. Here we describe a method to generate a large training set and predictive algorithms for electron transport rate in wheat ears derived from a combination of pulse amplitude modulated chlorophyll fluorescence images and visible/NIR hyperspectral images. This pixel level mapping method enlarges the effective size of the training data set to produce robust predictions of parameters underpinning genetic variation in photosynthetic performance. This approach may be scalable to field plots and drone-based imaging and thus overcome the screening bottleneck.

35455: High-throughput phenotyping wheat canopy light interception in the field using multi-directional RGB imagery

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Under given environment, crop genotypes owing higher capacity in light interception are always preferable to pursuit more production. However, as the complexity of the canopy structure and its interaction with the illumination that varies over short time under field conditions, quantifying canopy light interception in the field is thus challenging in the context of high-throughput phenotyping. To deal with this problem, here we put our focus on wheat and propose to use the turbid medium assumption to represent canopy structure with two parameters, i.e. green area index (GAI) and average leaf angle (ALA). Through in-silico experiments using the Digital Plant Phenotyping Platform (D3P) and field trials, the turbid medium model demonstrates its capacity to simulate accurately the directional green fraction (GF) over a wide range of wheat structural variability. This permits to derive the canopy structural traits, i.e. GAI and ALA, and integrated light interception trait, i.e. the fraction of intercepted photosynthetic activate radiation (FIPAR), from GFs observed from multi-directions. Further, using D3P, we compare the estimation of FIPAR with GFs observed under several combinations of directions. The combination of GF from 0o and 45o provides the best FIPAR estimation. Accordingly, field experiments were conducted from 2016 to 2018 over six genotypes under two irrigation regimes with three replicates. Phenomobile carrying two RGB cameras with 0o and 45o viewing angles imagined each plot around 10 times over the whole growth season. Using the retrieval method proposed here, we are able to monitor the dynamics of GAI, ALA and FIPAR over the growth cycle. More importantly, our method could generate these light interception traits in the field with heritability higher than 0.85. This would be of high interest to compare genetic variability over genotypes with respect to photosynthetic capacity. The potential of using this HTP method for other crops will be discussed.

Poster

35021: Individual Tree Phenotyping Unlocks Competition, Micro-site and Genetic Effects

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Improving yields, efficiency, and sustainability to meet future demand for forest products will require forest managers to apply precision management practices. This requires the optimal matching of elite tree breeds, having well-defined phenotypic traits, with both forest sites and management practices. High-throughput phenotyping to characterise trees is making this a reality as it allows the effects of genetics and environment to be separated. While this paradigm may be familiar to growers of major crop species such as wheat and rice, it is novel for forest species. Research trials will continue to play an important role in understanding the interactions of tree breeds with their environments, but there is now the potential to also phenotype trees in the operational forest setting using remote sensing. Using remotely sensed airborne laser scanning data, we phenotyped 10,328 trees in a 36 ha operational forest stand and 990 individual trees in a 2 ha single-tree plot breeding trial, both having high tree-to-tree genetic variation. After tree top detection and segmentation of individual tree crowns was completed, several morphological crown size metrics were generated. These data enabled the formulation of individual tree competition and micro-site metrics. Accounting for these environmental effects by incorporating terms for competition and micro-site in the models for two tree size traits allowed the genetic component of observed phenotypic variation to be isolated more accurately. Results showed significant levels of micro-site and competition effects in the phenotypic data, which varied both between and within the two contrasting study sites. This study demonstrates the utility of remote sensed airborne laser scanning as a tool for phenotyping individual forest trees. Furthermore the modelling approach shows strong potential for segregating environmental and genetic effects in phenotypic data for forest trees, with relevance for other crop species.

35098: Sequential forward selection of time series UAV measurements in combination with support vector regression for wheat grain yield prediction

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Plant breeding requires a robust assessment of large numbers of individual plots under different environmental conditions. Breeding based on grain yield is time-consuming and costly, therefore new innovative, rapid and non-contact methods are in high demand in innovative agricultural market. This study investigates the application of multispectral unmanned aerial vehicle (UAV) platform in time series to predict wheat grain yield. The field trial used in this study, contained 396 different wheat cultivars in 600 plots planted in 9th of May, 2018 located at Vollebekk Research Farm (59° 39’N 10°45’E) in Ås, Norway. Five different spectral bands including Red, Green, Blue, RedEdge, and NIR were measured during different growth stages of plants and different vegetation indices maps including NDVI, EVI, and MTCI were generated for each time of measurement. Five spectral bands along with three different indices for each date were used as input data for the support vector regression model and the best value for C parameter in the model was estimated. Sequential forward selections were applied as a feature selection method. Results showed that MTCI was as an important feature for all growing stages. Maturity date was added to the input features to train the model and make a comparison between two models with and without maturity date. Support vector regression demonstrated a strong capability to estimate grain yield based on UAV measurements during the growing season as the correlation coefficient value of 0.92 and mean absolute error of 26.6 was obtained with this model.

35216: Estimation of grain protein content in wheat from reflectance spectra of dried grain powder with continuous wavelet analysis

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The methods for GPC estimation were based on the reflectance spectra in the visible and near infrared (VNIR) region. Since the spectral shape in the VNIR region is dominantly determined by pigments (such as chlorophyll), GPC is estimated based on the empirical correlation of protein and chlorophyll. Considering most protein absorption features are located in the shortwave infrared (SWIR) region, the utilization of the SWIR region could help understand the physical mechanism of GPC estimation. However, the absorption features of protein are masked by other chemicals (such as cellulose and sugar) in the SWIR region. Therefore, it is required to enhance the absorption features of protein and reduce the confounding effects by other chemicals. In this study, the performance of continuous wavelet analysis (CWA) in estimating GPC by enhancing the absorption feature of protein was evaluated by a two-year wheat experiment with varying planting density and nitrogen treatment. After the reflectance spectra of dried grain powder were collected with a ASD FieldSpec Pro spectrometer, the GPC data were measured using semi-micro Kjeldahl method. Our result indicated that the bending and stretching of chemical bond of protein at 1510 nm, which was not observed in the reflectance spectra, was well captured by the wavelet spectra at the scale 4. Based on the absorption feature of protein at 1510 nm, the wavelet feature at scale 4 (WF1510,4) performed well in capturing the link with GPC (2018: R2=0.92, 2019: R2=0.77), with a high validation accuracy for pooled data (R2=0.78, RMSE=0.52%). Our results demonstrated that enhancing the absorption features of protein in the SWIR region could improve the estimation of GPC by applying CWA. The performance of CWA in estimating GPC at the canopy level should be explored in the future. Keywords: Grain protein content, Continuous wavelet analysis, Absorption feature, Shortwave infrared

35646: Outline-based morphometrics and geometric analysis for leaf shapes in a three-dimensional space

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Leaf is one of the most important organs in a plant since it plays crucial roles in light interception, thermoregulation, and hydraulic conductance. Although there are many studies aimed at analyzing leaf shape have been reported, most of them were studied in terms of their outlines in 2D plane and in a destructive way, where 3D spatial information are missed (e.g. curvature, leaf angle). Currently, high-resolution 3D point cloud data can be acquired easily and cost-effectively. For example, a pipeline using Structure from Motion (SfM) and Multi-View Stereo (MVS), which is a promising technique to reconstruct a 3D surface as point cloud data from a series of 2D images taken from different angles, has been implemented in several libraries and software products. In this study, we proposed a morphometric method for quantifying leaf shape from 3D point cloud data. 3D point cloud data of a leaf were generated based on a numerical simulation or SfM and MVS pipeline. A leaf surface was reconstructed from point cloud data by using B-spline surface fitting with any parameterization method (e.g. principle component analysis). A leaf outline was extracted from 2D images by using instance segmentation methods. The 3D outline of a leaf was estimated from the outline in the 2D images based on camera parameters. Finally, we fitted several models to the 3D leaf outline data for characterizing leaf shapes. To examine the accuracy and the precision, we applied the proposed method to virtual measurement data generated by using a theoretical model with several parameters.

Session 7: New sensor technology

Oral Presentations

34965: Virtual phenomics - use of robots and drones in combination with genomics accelerate genetic gains in wheat breeding

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Wheat breeding is a lengthy process that usually takes 10-15 years and depends heavily on the ability to identify superior progeny lines by visual inspection and manual scoring of traits. Two emerging technologies are now offering potential for more precise selection and faster genetic gains: genomic prediction of breeding values based on genome-wide SNP markers and use of high throughput phenotyping technologies. In the innovation project “Reliable and efficient high-throughput phenotyping to accelerate genetic gains in Norwegian plant breeding (virtual phenomics; vPheno), 2017-2022” we are combining multispectral imaging with genomic prediction. This is a collaborative project between the industry partners Graminor AS and Making View AS and world-leading research groups in genetics, robotics and image analysis at the Norwegian University of Life Sciences, Boston University and the International Maize and Wheat Improvement Center (CIMMYT) in Mexico. In order to follow the growth of the plants during the season and calculating vegetation indices that can be used to predict grain yield, the project makes use of drones fitted with multispectral camera that are flown at weekly interval during the field season. In addition, a custom built field robot is being used for gathering close-up images of field plots that will be used for counting the number of heads per square meter and other plant features that cannot be reliably recognized from drone images. One major use of the data is to improve the precision of linking genome and phenome, the other is to enable plant breeders to visit field trials in "virtual reality", by integrating information from the drone and robot images with other available data on the field plots (grain yield, disease resistance, quality traits, marker data etc.). A prototype of the VR tool will be presented along with the progress on improving grain yield prediction by use of the multispectral drone images.

35059: Quantification of temperospatial root water upatke by means of a very precise soil water profiler

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Local root water uptake (RWU) is dependent on shoot transpiration rates as well as several root characteristics and their surrounding soil water content (q). Quantification of local RWU is difficult since it induces very small local changes of q and simultaneously water within the soil is redistributed. Moderate sensitivity and low spatial resolution of currently available soil water sensors pose additional challenges. We present a new, affordable soil water sensor, the Soil Water Profiler (SWaP) with very high sensitivity and adequate spatial resolution. It envelopes, and thereby can be shifted along, a cylindrical plant container. We can scan single cylinders in a few minutes to determine total change of water in the column (mL plant water uptake) as well as the local changes in q with a precision of 3e-5 cm3/cm3 (~ 2mL per slice) at a 1D resolution in the order of 1cm. Due to the sensors' high precision and fast dynamics we can derive local RWU values utilizing light intensity changes. Using 4 sensors, we continuously scanned four plants while they were subjected to different light intensities provided by a home-build, water-cooled, programmable LED panel (up to 1400 mM/(m2.s). In this manner we could calculate local RWU of a variety of plants. We show that not only the amplitude of the RWU profiles changes rapidly, but also the shape of the RWU profiles changes with time and light intensity.

35127: A physically-based model to exploit UAV radiometric observations under heterogeneous illumination conditions

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Multispectral optical devices mounted on Unmanned Air Vehicles (UAVs) have become increasingly popular in field phenotyping thanks to their ability to provide high-throughput observations of relevant plant structural traits. Different studies have successfully applied empirical methods or deep learning algorithms to derive phenotypic traits directly from the raw data provided by cameras mounted on UAVs. Nevertheless, the radiometric information contained in the images is highly valuable to estimate traits using our understanding of radiative transfer in canopies. Accessing that information requires deriving spectral reflectance from the raw images, which is a challenging task. We first review briefly the critical steps needed to retrieve crop reflectance from the raw images. This includes camera characterization (radiometric calibration, vigneting, stray light) as well as systems used to measure the incoming radiation: reference panels or incoming light sensors placed in the field, and DLS (Downwelling Light Sensors) aboard the UAV. Then, we illustrate how both spatial and temporal heterogeneity in incoming radiation due to the intermittent presence of clouds during the flight may severely affect accurate retrievals of canopy reflectance, even when the incoming radiation is measured on the ground or on the UAV. To overcome this frequent issue in the operational use of UAVs on phenotyping, we developed a new physically based approach that permits characterizing jointly the spatial and temporal variability of the incoming radiation, and the canopy bidirectional reflectance distribution function (BRDF), thus providing additional information on canopy structure. To do so, this new method exploits the multiple views of each microplot in the field at different sensor zenith angles along the UAV trajectory. Both in silico and field experiments have been conducted to validate the proposed approach.

36464: Wheat phenotyping using X-ray technology and the effect of X-ray radiation during flowering time

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Sensors such as X-ray systems have in comparison to optical sensors the possibility penetrating through material. Thus, they are not obstructed by opaque structures like leafs or shells. Using X-ray technology in plant phenotyping is becoming more common in the past last years. Normally this kind of technology is only usable inside a labor or a greenhouse environment, due to the shielding requirements and the size of X-ray systems. I will present the possibility to use the advantages of X-ray technology outside on the field. Using a mobile phenotyping platform from PhenoKey we captured 2D X-ray projections of X different plots. This approach allowed us to measure phenotypic data of wheat such as the biomass of seeds and tillers even when the canopy is closed. For each plot, we captured LIDAR and GPS Data to correct the captured data with the movement of the phenotyping platform. For future applications, the effect of X-ray radiation on the individual plants needs to be quantified. Each variety may react differently on X-ray exposures. In a first step I will discuss the effect of X-ray radiation during the flowering time of wheat. For this, we tested 360 plants divided into a control group and five different treatments of radiation during flowering time. After harvesting, we measured different phenotypic traits to compare the groups of X-ray treatments and did a germination test on the harvested seeds.

Poster

32001: An overview of using multispectral imaging and machine learning techniques for seed phenotyping

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Due to their advantage in providing three-dimensional data across a wide range of electromagnetic spectrum, the state-of-the-art multispectral imaging along with various multivariate chemometric analyses has been successfully utilized for various applications in food quality and safety control. This work gives a birds-eye view of the multispectral imaging techniques in regards of fundamental configuration of the system, acquisition approached and image processing scenarios for various applications in seed phenotyping and quality determination. The paper comprehensively highlights research attempts devoted to real implementations of fully-operated multispectral imaging systems and does not consider those ones that just utilized key wavelengths extracted from hyperspectral data analyses without building independent multispectral imaging systems. The paper attempted in briefing multispectral imaging applications for seed phenotyping and quality monitoring and provides examples and research results in characterizing physicochemical quality traits, predicting physiological parameters, detection of defect, pest infestation and seed health.

34936: Technology for high-accuracy analysis of the projected leaf area in a nursery room in a closed-type plant factory

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Predicting individual plant growth is important to improve productivity in plant factories, and the projected leaf area of lettuce is an important indicator in the nursery stage. This study aimed at developing technology for high-accuracy analysis of the projected leaf area in the nursery room in a plant factory. We used lettuce (Lactuca sativa L. cv.) herein, and the study was performed in a commercial large-scale plant factory. We constructed a multiple plant imager (MPI) system, an automatic image acquisition system comprising 12 micro-computers with a camera module; these micro-computers were fixed above the lettuce seedlings. Using MPI, 153 lettuce plants were imaged every 20 min from day 6 to 14 since seeding. On image analysis, the projected leaf area of lettuce was determined by binarizing and separating leaves and the background. Herein, we followed three binarization methods: first, the ExG method, which focuses on the feature that pixels of leaf have a large green value (G) among other color values (R and B) of each pixel; second, the Optimized ExG method (O-ExG method), which automatically determines the ExG threshold; third, the U-Net method, which is a deep-learning method that determines threshold values and automatically sets the threshold values based on learning from the training set. Herein, we used Intersection over Union (IoU) as a metric to determine the overlap of the predicted binary images and annotate the binary images and as the value approached 1, the accuracy was considered to increase. Consequently, although few images displayed more than a 5% difference in the IoU obtained through each method, leaves were not detected in several images in the ExG and U-Net methods. Therefore, our results indicate that the O-ExG method is preferable to determine the projected leaf area in the present case.

35018: SPECALYZER—AN INTERACTIVE ONLINE TOOL TO ANALYZE SPECTRAL REFLECTANCE MEASUREMENTS

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The development of high-throughput plant phenotyping (HTPP) methods aim to resolve the ongoing phenotyping bottleneck by cheap, rapid and accurate assessment of plant traits. The reduction in cost and time associated with phenotyping is important, as it allows for re-allocating resources to larger-scale experiments and field-trials. One of the methods for assessing plant traits is measuring spectral reflectance using proximal sensors which allow for rapid generation of a large amount of data, and often require knowledge of programming to analyze these large data sets. We developed an online tool called Specalyzer for interactive analysis of non-imaging spectral data generated by proximal spectrometers. The aim of Specalyzer is to make the analysis of plant reflectance data accessible to users without significant knowledge in programming. Using Specalyzer, users can pre-process and analyze spectral data directly in the browser. Pre-processing functions include identification and removal of spectral ranges with low signal-to-noise ratio, and sample-level outlier detection. Data analysis functions cover interactive data visualization, the estimation of 140 vegetation indices and their correlation to the plant trait of interest. Specalyzer was evaluated with case study data from a winter wheat fertilization trial with 10 breeding lines and two fertilizer treatments. Specalyzer is available online at www.specalyzer.org.

35198: Estimating full season organ and aboveground biomass in rice with terrestrial laser scanning data

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Non-destructive and accurate estimation of crop biomass is critical for precision crop management and yield estimation. Terrestrial laser scanning (TLS) has been recently used in crop monitoring, especially to complement optical sensing under high biomass conditions. Previous studies focused on the estimation of crop aboveground biomass (AGB) but only for organ biomass, which led to the poor understanding of TLS technology in monitoring biomass partitioning among organs. The objective of this study was to evaluate the performance of LiDAR-derived canopy structural metrics for the estimation of organ and aboveground biomass in rice plants and to examine the feasibility of developing universal models for the entire growing season. The experiments were conducted in 2017 and 2018 in Xinghua, Jiangsu of eastern China and involved different N rates, planting patterns and rice cultivars. Two regression approaches, stepwise multiple linear regression (SMLR) and linear mixed-effects model (LME), were explored to estimate organ and aboveground biomass from TLS data. The results demonstrated that growth stage in LME modeling was selected as the most significant random effects on rice growth among the three candidates, which were rice variety, growth stage and planting technique. The most significant improvement with a LME model grouped by growth stage was obtained for panicle biomass, with an increase of 0.74 in R2 (LME: R2 = 0.90, SMLR: R2 = 0.16) and a decrease of 1.15 t/ha in RMSE (LME: RMSE = 0.79 t/ha, SMLR: RMSE = 2.94 t/ha). SMLR was only suitable for the estimation of AGB over pre-heading stages, but LME performed consistently well across all growth stages. The results suggest the TLS is a promising technology to overcome the saturation of canopy optical signals at post-heading stages and has great potential in yield estimation under all-weather conditions. Keywords: Terrestrial laser scanning; LiDAR; Height metric; Biomass; Mixed-effects; Rice

35313: Green Fraction: a review of this highly desired trait accessible from multiple sensors and methods for estimating several higher order traits

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The green fraction (GF) is the fraction of green pixels in the image. For nadir observation, GF(0°) is very useful to describe the installation of the crop and the competition between plants and weeds. GF(0°) has been used successfully to score disease resistance. GF observed in at least two directions is used to compute the green area index and to characterize leaf inclination and the efficiency of light interception by the canopy. GF was used to document diurnal changes due to leaf rolling and wilting as observed under water stress. GF is mandatory to minimize the impact of soil temperature on canopy temperature. Finally, dynamic structural and functional models describe the seasonal course of GF, allowing assimilating GF observations and retrieving few functional traits that control the impact of environmental factors. GF appears therefore to be a key structural trait to estimate. High-resolution LiDAR systems allow estimating GF using both the distance and intensity. Concurrently, high-resolution RGB or multispectral and even thermal infrared images provide accurate estimates of GF based on the contrast between the optical properties of the background and the green vegetation elements. Alternatively, coarse resolution observations provide also accurate estimates of GF when the interpretation method is adapted to the illumination conditions and optical properties specificities of the crop and background. The several sensors and methods to estimate GF are compared with due attention to their cost, throughput and uncertainties. Their possible complementarity is discussed, either by combining high-resolution local calibration samples with coarser resolution exhaustive coverage of the platform, or fusing optimally GF estimated from several sensors and methods. Finally, this presentation reviews critically the usages of GF for higher order trait estimation, with emphasis on the directionality of the observations and the propagation of the GF uncertainties.

35314: MonitRice: A semi-automatic system to monitor rice structural and biochemical traits under field conditions

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Several key structural traits can be derived from high resolution RGB images and LiDAR point clouds including the green fraction, green area index, fraction of intercepted radiation, leaf orientation, crop height, row compactness, organ density and characteristics. Few biochemical traits can be also accessed from high spatial resolution multispectral camera including leaf chlorophyll content, photochemical reflectance index and disease symptoms. Monitoring the dynamics of these structural and biochemical traits along the growth cycle is required to describe crop functioning and thus access functional traits. However, this requires specific vectors to be able to sample all the microplots of phenotyping platform within a limited time. Although UAVs offer a very high throughput, the spatial resolution that can be accessed may be limiting for few traits over crops such as rice with small leaves, because of the minimum flight altitude necessary. Further, other ground systems may be difficult to move in the muddy environment associated to most rice crops. For this reason, we developed a mobile structure that can carry several instruments including four LiDARs, 4 high resolution RGB cameras as well as two multispectral cameras. The system moves at a speed ranging from 0.3 to 0.5 m/s over tracks thanks to electric wheels. Tracks are 5 m width and 60 m length. Several tracks can be sampled, the system being able to move from track to tracks. The system acquires automatically the measurements according to a predefined scenario. Measurements are triggered thanks to RTK-GPS with centimeter accuracy. The autonomy of the system is larger than 5 hours with a throughput of about 100-200 microplots per hour depending on their dimensions. First results acquired with this cost-effective system over a rice experiment in Danyang (Jiangsu, China) are presented.

35766: MicroScan - For small digital phenotyping tasks requiring high flexibility and fast results.

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Phenospex introduces a new end-to-end, non-invasive phenotyping device. It is a light weight, stand-alone system, that uses a PlantEye F500 sensor to create 3D models and spectral images of plants and extracts +15 morphological- and spectral traits within seconds. The tool has an assembly time of less than 5 minutes and comes in a protective case including all components that weighs just below 28kg. Microphen scans a footprint of (50 x 50 cm) enabling you to phenotype medium sized plants of max. 45 cm height or up to 25 smaller plants at the same time. It is equipped with our automated analytics platform PHENA and our data visualization software HortControl and provides plant traits like height, 3D leaf area, digital biomass, projected leaf area, leaf inclination, leaf area index (LAI), light penetration depth, color information (Hue), NDVI and greenness in any environment. The Microphen is a tool for small-scale applications in phenotyping, germination assays, bioceutical- and chemical screenings, quality control. This saves time and money and provides accurate and objective information flexibly wherever needed and in real time.

35926: High throughput phenotyping in the field under elevated CO2 with the Fieldsnake

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The throughput of field phenotyping is dependent on the target plant trait and associated sensor, the size of the field as well as the maximum speed a position system can move over the field. For high throughput measurements under elevated CO2 a custom made positioning system called "Fieldsnake" was developed. The Fieldsnake enables relatively stable measurements from a horizontal measurement platform moving along a bridge. The bridge itself is moved by 4 track wheels. Sensors on the platform are positioned via a custom made GPS steering system. The Fieldsnake returns to the same spot within 2 cm and performs automatized measurements. The measurement platform is compatible for multiple sensors. In this presentation we show photosynthesis measurements under elevated CO2 in the field. Photosynthesis is determined by via active and passive chlorophyll fluorescence approaches. In the active approach the Light Induced Fluorescence Transient (LIFT) is used and for the passive approach an automated spectroscopy device called the Fluorescence Box (FLOX). CO2 concentration [CO2] was elevated to 600ppm in the field using the BreedFACE during the entire growing season of wheat. Wheat varieties were chosen from an historical collection with 42 varieties spanning a release date from 1950s-2015. Each variety was grown in 1.5 x 3m plot in 3 replications. To scan a plot with the LIFT or measure with the FLOX takes less than a minute such that the full experiment of in total 252 plots in a 2ha field could be measured in about 4hrs. Results for wheat will be presented in comparison to results for soybean in the previous year that showed a decrease in photosynthetic efficiency (Fq/Fm') and increase in Solar Induced Fluorescence under elevated CO2. These experimental results confirm the functionality of the Fieldsnake an unique new tool for field phenotyping.

Session 11: Satellite Event: Root Phenotyping

Oral Presentations

35250: Rhizo-Rice: a novel ideotype for deeper roots and improved drought tolerance

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Drought stress is one of the major constraints limiting rice production in rainfed and poorly irrigated environments. Understanding and defining traits enhancing drought tolerance is therefore of considerable importance. This project has received funding from the Newton Fund Sustainable Rice Research Initiative that integrates leading rice researchers and breeders in Thailand, leading crop physiologists and root biologist at the Pennsylvania State University in the US and at the University of Nottingham in the UK and at the International Rice Research Institute (IRRI) in the Philippines, and leading root modelers in the UK. This 3-Year Newton Fund project aims to improve drought stress tolerance in rice by developing Rhizo-rice, new rice lines that have root traits that permit them to have both improved soil exploration and more efficient water capture under drought conditions. We evaluated the benefits of Rhizo-rice lines in the field and recently developed high-throughput phenotyping platforms and computational simulation modeling to test hypotheses regarding root traits that improve drought tolerance. This project delivers the root ideotype, phenotypic and genotypic selection targets, and trained Thai scientists in methods to incorporate root traits in rice breeding programs. The results showed that rice varieties with small xylems and deeper root systems would have a better capability to adapt to drought conditions. Genes conferring root traits were also identified which would be extremely beneficial for rice germplasm improvement for drought tolerant in the near future. The simulation modeling is being validated for improving its precision. Our results will have direct benefits for food security, as our team includes UK leaders in computational modeling, US leaders in root biology and crop physiology, Thai leaders in rice genomics and breeding, and partnership with IRRI, which deploys new technologies throughout the rice-growing world.

35240: An algorithm to measure root hair response to abiotic stresses in microscopy images

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Improving nutrient and water uptake in crops is one of the major challenges to sustain a fast-growing population that faces increasingly nutrient limited soils. Root hairs, which are specialized epidermal cells, comprise up to 70% of the total root surface area. Therefore, root hairs are important drivers of nutrient and water uptake from the soil. Microscopy provides a mean to record root hairs as digital images. However, due to their geometry and complex spatial arrangements quantifying root hairs in microscopy images manually remains a bottleneck. This process is often based on a limited manual selection of representative root hairs, which can result in inaccurate estimations of root hair traits and misrepresentation of root hair functions. We present a method to automatically quantify phenotypic traits of all individual root hairs in digital microscopy images. Our method uses a machine learning approach that classifies root hair, parent root and the image background. We define metrics to evaluate segments of root hairs that intersect or form blobs of two or more root hairs. Using combinatorial optimization we can reconstruct individual root hairs by resolving these complexities in a globally optimal way. As a result, we measure the root hair traits, length and straightness, as well as the distribution of these traits in each image. We demonstrate our method on examples of rice, maize and common bean under phosphor, nitrogen and potassium stress. Results show that our measurements of root hair traits strongly correlate with manually measured validation data in mean and maximum root hair length (Pearson-correlation: both >0.95) and in root hair number (Pearson-correlation: 0.84). We expect that our method distinguishes subtle differences between genotypes and treatments on the basis of the extracted traits. We believe our study paves a way towards identifying the genetic control of root hair traits and increased agricultural production in future.

35246: Cassava root phenotyping and its application in phytoremediation technology

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Phytoremediation is the use of plants to clean up hazardous contaminants in the environment. Despite its great potential, the use of such technology in actual contaminated environments is often overlooked because it requires a long-term commitment in the application. Another obstacle includes the lack of attraction from local farmers and governments due to low economic values and small biomass yields from many hyperaccumulating plant species. Cassava can be produced efficiently without the need for mechanization or purchased fertilizer inputs. It can also be grown in various climates and soil types making it feasible to be cultivated in contaminated areas. Here we 1) developed a high throughput phenotyping method "Cassava Shovelomics" and implemented Digital Imaging of Root Traits to evaluate cassava root phenotypes and 2) investigated the potential of using commonly grown Thai cassava varieties for remediating arsenic (As) contaminated soils. In the As experiments, the plants were grown in a pot system under various As concentrations. We found that high As concentration reduced photosynthesis rate, stomatal conductance, and transpiration rate by 43%, 69%, and 61%, respectively. Root system width at both moderate and high As concentrations was significantly reduced by 16% and 26.67%, respectively. Additionally, high As concentration significantly reduced basal root number (35%), and total root number (37%). Significant reduction of root dry weight was observed in all genotypes, except for Rayong 9 variety. Maintaining basal root, nodal root, and total root number at high As concentration was likely the key for sustaining growth in this variety. We also found that up to 66 mg kg-1 of As was accumulated in roots. We further investigated the use of the contaminated cassava starch for biofuel production, which may help generate income to farmers as well as enhance the success of the implementation of the phytoremediation technology.

Session 8: Satellite Event: Forest Phenotyping

Oral Presentations

35069: Use of Advanced Remote Sensing Tools for Phenotyping Evaluation

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Ongoing individual tree evaluations is essential for ranking and selecting the best genotypes to ensure target growth, yield attributes and adaptation are maximised. Currently, approaches for assessing which trees exhibit the greatest realised gains are often based on the simple field measures of diameter and height. With advances in remote sensing technology, the potential to derive a suite of more targeted, accurate and broadly applicable structure indices is now possible and has the potential to revolutionize the way progeny testing trials are maintained, measured and analysed. In this presentation we describe how these new technologies can provide spatially detailed and accurate measurements of tree and crown structure which will allow the genetic evaluation of tree breeding progeny testing activities. Specifically we focus on the application of super-dense Light Detection and Ranging (LiDAR) data acquired from unmanned aerial vehicles and aircraft over long-term progeny testing installations on Vancouver Island, Canada. We demonstrate how these data can be used to develop individual tree crown, and stand level metrics to assess key crown structural traits of elite trees within the progeny testing sites and compare these new metrics to existing information on the performance of progeny testing of trees, to demonstrate how LiDAR-derived attributes can yield additional and innovative insights into how these trees will likely perform with respect to productivity in the future. We conclude the use of airborne LiDAR technology to routinely and operationally acquire data over tree breeding sites, and to utilize the derived information to bolster decisions as to which genetic traits and genotypes are most suitable for a sustainable and profitable forest industry globally.

Poster

35052: Forest Phenotyping: Uncontrolled Biological System Under CatBoost

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High-throughput phenotyping (HTP) has unlocked new prospects for field-based phenotyping. The genomics revolution has provided rapid gains in crop productivity by shortening the breeding cycle of many commercial species. Genomic data is most useful when carefully linked to crop phenotypic expression and environmental conditions. Forest tree phenotyping is challenging due to the size, long growth cycle and structural complexity of forests, developing a forest-scale HTP in such variable environments therefore requires outstanding technologies. Advances in remote sensing and permanent monitoring applied in a well-characterised forest have resulted in a deluge of data which provide new insight in the complex interactions in biological systems. Forest phenotypic is highly affected by the interaction of environmental conditions, genetic material and forest management but the understanding of these complex dynamics is incomplete. Using the CatBoost machine learning method, we model forest productivity from an extensive set of 2.7 million observations composed of 62 variables describing environmental surfaces, genetic and management records, and remotely sensed data. The most important drivers of productivity were ranked from genetic, environmental conditions, leaf area index, topology and soil properties, thus describing the complex interactions of the forest. The phenotyping method developed here can be used to identify superior and inferior genotypes and select the best genetic material for breeding and optimise the current and future deployment of genetic material across the forestry landscape. The overall aim of the phenotyping platform is to increase forest productivity and sustainability by matching trees with improved genetics to specific sites for deployment. This precision-based approach is the foundation of future forest planting that will ensure the right tree goes in the right place, with the right purpose and management to realise the best outcomes.

35243: Geographic Image Object Analysis of UAS imagery for plant structure extraction.

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UAV for field-based plant phenotyping in agronomy is limited by payload (weight and size), altitude (regulations) and total flight time (hence, total covered area). Depending on wind conditions, the UAV is also subject to issues with platform stability. Sensors on these platforms are often similar to the sensors deployed for other types of vegetation remote sensing applications such as RGB (reg,green,blue) or multispectral sensors capable of measuring light reflected in the near-infrared. As the prices have decreased for LiDAR scanners and software for SfM data, integration of structural data is increasing as well. There are still several challenges facing the use of remote sensing tools for crop phenotyping including environmental variation in solar illumination, plant movement, data processing, and even sensor selection. Here, we present early work considering the implementation of Geographic Object-Based Image Analysis for extracting plant structure information from UAS derived data.

Session 9: Utilization of genetic resources

Oral Presentations

33184: Phenotyping for stress tolerance in spring wheat

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The climate change is predicted to cause severe changes on the future crop productivity. One of the main challenges for the global food security is maintaining the wheat productivity within the increasing population and subsequent higher food consumption. Thus, new cultivars particularly tolerant for maintaining yield under abiotic stress conditions are needed. The panel used in the experiment for initial screening for heat tolerance was based on 200 Nordic breeding lines and previously selected lines with known QTLs for heat tolerance. The screening was based of maximum quantum efficiency of PSII photochemistry (Fv /Fm) allowing us to select heat tolerant/sensitive lines. Our aim was to analyze the effects of combined heat and drought stresses under two different CO2 concentration, ambient CO2 (400 ppm) and elevated CO2 (800 ppm) using both gas exchange and chlorophyll fluorescence. Four cultivars were selected for in-depth analysis, two as heat sensitive and two as heat tolerant. The results showed that under all stresses, plants grown under elevated CO2 has significantly higher saturated rate of photosynthesis (Amax) compared to plants grown under ambient CO2. Under both CO2 levels, the rate of photosynthetic electron transport (Jmax) was significantly lower under heat and combined stress in all cultivars while the carboxylation rate by Rubisco (Vcmax) was significantly lower under combined stress only in GN5. The cultivars under combined stress had a significantly higher maximum quantum efficiency of PSII photochemistry (Fv /Fm) at elevated CO2 compared to ambient CO2 while in the tolerant cultivars under heat stress, the Fv /Fm was significantly higher at elevated CO2 compared to ambient CO2. These findings are important for understanding the underlying response mechanisms of cultivars to combined abiotic stresses under elevated CO2 that differs from the effect of an individual stress

34843: Phenomics for the improvement and selection of forage genetic resources

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Forage quality and composition are two of the hardest and most costly traits to measure in forage breeding and selection as they require harvest, manual separation and/or wet chemistry analysis. The aim of this study was to evaluate the potential capacity of hyperspectral imaging (HSI) for non-invasive assessment of forage chemical signature. Hyperspectral image data within the visible near-infrared range into the extended near-infrared and short wave infrared covering 900–2500 nm wavelengths were obtained from ryegrass (Lolium perenne) and white clover (Trifolium repens). Medium to high predictive power was observed for the HSI models of total sugars, high molecular weight sugars, %Ash and %Nitrogen. Significant HSI models with low R2 validation of 0.1–0.5 were also obtained for low molecular weight sugars, NDF (%), ADF (%), DOMD (% DM), ME (MJ/kg DM), DM (%), Ca (mg/g) and OM (%). We also observed significant differences in the chemical composition between the pseudo-stems and leaves of the plants for each accession of ryegrass and also between ryegrass and white clover. The power of HSI for prediction of these differences within plants was also demonstrated. Different modelling approaches and machine learning were employed to automatically identify white clover from ryegrass in the field with high accuracy of ~0.9 for clover content. This study paves the way for the HSI technology to be used for rapid forage composition measurement in mixed swards providing a non-destructive and high throughput screening tool to the current visual (inaccurate) or manual (expensive and laborious) methods.

35155: Phenotyping of wheat genebank accessions using RGB and hyperspectral data

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RGB imaging and spectral reflectance analyses represent a promising technology for field and laboratory phenotyping. Although these methods are well established in the remote sensing, the open question is the reliability of the methods for phenotyping of the leaf traits when applied in genebank or breeding accessions of wheat characterized by an enormous phenotypic diversity. To answer this, the hyperspectral field records as well as the subsequent leaf analyses were made in 100 wheat genotypes from the collection of Slovak Genebank. Moreover, the automated phenotyping of 25 wheat genotypes grown in pots were performed at a PlantScreen phenotyping facility of SUA. The traits of the fully developed flag leaves (chlorophyll content, leaf area, leaf thickness, etc.) were correlated with 132 hyperspectral indices developed to estimate different properties of crop aboveground biomass. The genotypes provided high diversity in all observed traits, providing good background for correlation analyses. We identified a group of parameters with a high correlation (MCARI, red edge parameters), which can be useful for the automated field phenotyping of wheat genetic resources. The RGB analyses enabled to collect the phenotyping data related to the plant height, leaf area, but also the color characteristics of plants and leaves. The study represents the initial step of the program aimed at phenotyping of wheat germplasm, towards developing the methodological approaches to assess the genotypes, including traits related to adaptability, plasticity and tolerance to abiotic stress factors. The study was supported by the national grants VEGA 1- 0589-19, APVV-18-465, and APVV-15-0562.

35121: NordPlant - a new climate and plant phenomics university hub for sustainable agriculture and forest production in future Nordic climates

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Climate change is a global challenge, and new plant breeding and protection efforts are urgently needed. Part of the core activities of NordPlant are application and development of novel methods for plant phenotyping and climate facilities. Advanced and precise methods for rapid screening of plant material is central to identify high-performing lines and cultivars suitable for the future climate scenarios. This is also key to make full use of available genetic resources. Therefore, five Nordic universities with versatile and complementing research and infrastructures established NordPlant in 2018 to promote education, research mobility and technological development in order to meet future challenges in Nordic agriculture and forestry. NordPlant has two branches. One stimulates knowledge-exchange by seminars, site-visits and joint education for PhDs, post docs and researchers. The other is to stimulate and support joint research projects between the universities by reduced user fees and mobility grants to build on each other's strengths and knowledge. NordPlant will address a number of focus areas: plant pathogens in new Nordic climate conditions, retained biomass production in climate change, forestry in automated phenotyping, microscopy and plant cell phenomics, modelling including remote sensing and ecosystem modeling and field phenotyping. NordPlant will especially focus on plants important for the Nordic countries both economically and culturally, namely potato, wheat, oat, Nordic berries, apples, sugar beet and birch. NordPlant is one out of a total of six Nordic University Hubs funded by NordForsk, which support research as part the Nordic Council of Ministers. The founding universities are University of Copenhagen, University of Helsinki, Lund University, Swedish University of Agricultural Sciences and University of Tromsø.

Poster

35831: GENETIC DISSECTION OF DURUM WHEAT ROOT SYSTEM AND CANOPY MORPHOLOGICAL TRAITS BY MEAN OF HIGH-THROUGHPUT PHENOTYPING PLATFORM

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In this study we report the characterization of a 183 accessions élite durum wheat association panel for RSA and shoot morphological traits. Plants were grown in controlled conditions up to the 7th leaf (late tillering) using the high-throughput phenotyping platform GROWSCREEN-Rhizo, a rhizo-box-based system integrated with automatic root RGB imaging. The experimental set-up permitted the dynamical assessment of the length of the three main root classes (seminal, later and nodal), the distribution of each root class in the rhizo-box profile, maximum root system depth and width. Leaf area and both leaf and tiller number were measured twice per week. A genome-wide association study (GWAS) revealed 180 QTLs controlling RSA and/or shoot growth traits ($P < 0.0001$). Root and shoot QTLs were mostly independent each other as well as QTLs for different root classes traits. For nodal root traits only most of the QTLs (6/9) overlapped with shoot QTLs. Among others, three chromosomal regions on chromosome 1BS, 6AL and 7AC exhibited a marked influence in root and shoot morpho-architectural traits. Indeed, in a relatively short portion (7.5 cM) of chromosome 1BS we observed significant segregation for 10 root and shoot traits. A QTL cluster on chromosome 6AL confirmed the role of this region in the control of root gravitropism observed in Maccaferri et al., 2016. A QTL cluster on chromosome 7AC was found to be significantly associated with root length and depth and shoot/root dry biomass ratio. Haplotypes segregation at this QTL cluster revealed a contrasting selection pattern between sub-populations of the panel. Indeed, the most root-oriented haplotypes clearly prevail in lines selected in the Mediterranean basin (Italy and ICARDA) while shoot-oriented haplotypes are predominant in lines selected by CIMMYT in well-watered breeding set-up. These results suggest an indirect but major role of RSA and root/shoot equilibrium in durum wheat breeding and environmental adaptation.

31621: GENETIC DIVERISTY ANALYSIS OF COWPEA ACCESSIONS USING DIVERSITY ARRAYS TECHNOLOGY SEQUENCING (DArTseq) TECHNIQUE

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The objective of this study was to assess genetic diversity and population structure of 85 cowpea genotypes using DArTseq genotype by sequencing technique. From a total of 15 284 SNPs tested, only 640 (48.09%) were polymorphic. Chromosome 2 had the highest percentage of polymorphic loci (56.51%) while chromosome 5 had the lowest (39.12%). The highest and the lowest Ho, He and PIC values were recorded from Chromosome 10 and chromosome 2, respectively. The genetic distance value estimated on the basis of SNP markers ranged from 0.14 to 0.44, with a mean value of 0.35.The mean values of total Shonnan information index (I) for genetic diversity was 0.355 while average observed gene diversity (Ho) within genotypes per population was 0.050. Average gene diversity (He) within genotypes per population was 0.232.Average inbreeding coefficient (FIS) was 0.740 and overall mean percentage of polymorphic loci (%P) was 83.68. The Shonnan information index (I) values ranged from 0.325 to 0.381; Ho values varied from 0.047 to 0.050. He values were from 0.216 to 0.247; FIS from 0.717 to 0.770 while %P was from 73.59 to 92.31. Variance among populations was (8 % of the total variation), while the variance among individuals was high (78 % of the total variation). Red cluster only had four accessions (4.76% of the population) blue cluster had 29 accessions (34.5% of the population) while the black cluster had the majority of accessions at 51 (60.71%).GH43, GH45 and GH50 were from IITA while GH 47 was from South Africa.

35798: EXPLORING GENETIC RESOURCES WITH SHOOT AND ROOT HIGH THROUGHPUT PHENOTYPING to increase DURUM WHEAT ADAPTATION TO DROUGHT

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Water availability is a major limiting factor of crop production world-wide, especially in rainfed agricultural systems, such as those of durum wheat. Genetic resources can provide new source of variability that can be exploited to improve crop performance under drought. Among a wide range of traits linked to drought resistance the root system plays an essential role in ensuring plant productivity. In this study we explored the possibility of identifying genotypes more adaptable to the upcoming climate change exploiting high throughput phenotyping (HTP). We first selected a set of genotypes showing high resilience to water stress on the basis of above-ground measurements. Second, we characterized the root system architecture of the selected genotypes. Root phenotyping was carried out using a GrowScreen-PaGe platform, which allows acquisition of time series of the developing root system, and quantification of short-term variations. Fifteen genotypes were selected for drought-stress resistance, based on the above-ground traits, namely responses to different spectral ranges of illumination. Phenotypic RGB analysis accurately measured plant digital biovolume, while fluorescence image (UV) was used to study plant health linked to stress index. Low throughput measurements of chlorophyll density (SPAD), stomatal conductance, RWC, ABA and proline content were also performed. Most root traits showed large variation between the fifteen selected genotypes. In general, root length contributed more than shape and branching to the overall variability of the root system architecture among genotypes. Preliminary data about root density distribution in rhizoboxes under drought conditions were also collected. These data indicate that high-throughput phenotyping is a powerful tool to better and more rapidly select genotypes resistant to drought and more generally to climate change constraints.

Session 10: Yield improvement

Oral Presentations

34868: High-throughput phenotyping of canopy radiation use efficiency and its component traits to improve sorghum productivity

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In the absence of water limitation, radiation use efficiency (RUE), which quantifies how much biomass can be accumulated per unit of light intercepted by a crop canopy, determines its productivity. Once harvest index has been maximised, further increases in potential yield can only come from increased RUE. Plant breeders may have indirectly improved RUE through selection for grain yield. Measuring canopy RUE, let alone gaining a quantitative understanding of the leaf and canopy characteristics that contribute to RUE, has previously not been possible for a large enough number of breeding lines to consider making it a direct selection target. We are using UAV- and tractor-based sensor platforms and targeted data analysis pipelines that combine 2-D spectral information with 3-D point cloud data to estimate leaf and canopy traits associated with canopy RUE in the C4 crop sorghum. Canopy traits include leaf area index, plant height, light interception and light distribution, leaf angle, biomass. Examples of leaf-level traits we are targeting are stomatal conductance (as a surrogate for photosynthetic rate), chlorophyll content and biochemical photosynthetic parameters, such as maximum Rubisco carboxylation (Vcmax) and electron transport rate (Jmax). Using these high-throughput methods to phenotype a large and diverse sorghum association-mapping population gives plant breeders an insight into the natural variation for traits associated with canopy photosynthesis in a C4 crop and will allow them to identify the underlying genetic regions. This then will enable direct selection of traits that improve plant productivity.

34937: How to bring value to agriculture: phenotyping technologies and applications at BASF Agricultural Solutions

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Since over 20 years, CropDesign is home to imaging and automation experts who are developing a variety of phenotyping applications. First there was TraitMill, a unique plant genomics platform for gene and trait discovery to improve yield, drought tolerance or nutrient use efficiency. Since 2016, CropDesign has developed ASAP-platform, one of the largest corporate platforms for automated precision spraying and high-throughput phenotyping. Using different imaging technologies, 10's of agronomical traits (incl. yield components) are captured at high throughput in a standardized way to build functional knowledge of our agricultural products and to make project advancement decisions for BASF Agricultural Solutions. Case studies will summarize and illustrate the value and benefits of different emerging imaging technologies such as Multi- and Hyper-spectral for a broad range of applications within BASF businesses.

36560: From phenomics to yield improvement in a changing climate: a trait-based probabilistic approach

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Seeking alleles for high yield in a variable environment poses a massive problem of time scales. Yield involves feedbacks operating over months, whereas physiological mechanisms of acclimation operate over minutes, following the variability of environmental conditions. Phenomics needs to analyze the genetic variability at these different scales under a range of environmental conditions, with a suite of installations with different temporal definitions and measured traits. Multi-site field experiments show that a given allele, resulting in a given value for trait measurement in a given environment, can result in positive, negative or null effects on yield depending on environmental scenarios. Breeders solved this difficulty by directly selecting for high and stable yield across environments. Retrospective analyses of the genetic progress suggest that, doing so, they selected for constitutive traits. The allelic diversity that governs adaptive traits was probably left largely unexploited because it results in positive or negative effects on yield depending on environmental scenarios. We propose a probabilistic approach that estimates the benefits and risks of vectors of alleles/traits in the most likely environmental scenarios in each region, with current or future climates and different management practices. A combination of phenomics, modeling and genomic prediction allows one to identify which vectors of traits/alleles are most likely to be positive for yield in each region and each field over e.g. 30 years. For that, we use phenotyping platforms in controlled conditions and multi-site field experiments to identify genotype-dependent parameters of models, in particular those driving the responses of grain number to temperature, intercepted light and soil water potential. Those parameters can in turn be predicted based on allelic values for new genotypes. This 'big data' approach potentially allows one to model yield for hundreds of genotypes in hundreds of fields in current and future environmental conditions. It may allow exploiting new sources of allelic diversity for yield in drought-prone regions, by explicitly taking into account the alleles that optimize adaptive responses in expected environmental scenarios for each region.

Poster

33114: Lipidomic study reveals the effect of morphological variation and other metabolite interactions on the lipid composition in various cultivars of Bok choy

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Bok choy is an important Brassica vegetable which is also known for its wide range of cultivars that differ in their appearance, leaf color, size and shape. For the purpose to investigate the effect of these phenotypic differences on their lipid composition, seven morphotypes of NHCC (Suzhouqing, Aijaohuang, Wutacai, Yellowrose, Ziluolan, Xiangqingcai and Zicaitai) were selected for this study. For this reason, extensive metabolic approach was adopted which was mainly focused on lipidomics. The overall metabolic position of lipids was determined and the isolated lipid compounds were characterized on the basis of their lipid classes. Moreover, discriminative analysis was applied to monitor the distribution pattern of lipid in different cultivars. Aijiaohuang was the leading cultivar which contained highest lipid levels, whereas least proportion was found in Zicaitai. We proposed that leaf color might have an effect on the lipid composition such as purple cultivars were dominated in glycerophopholipids, light green in fatty acids and dark green were rich in glycerolipids. The level of metabolites differed greatly among different genotypes. Lipid-metabolite interactions revealed the positive correlation of lipids with flavonoid and hydroxycinnamoyl derivatives, whereas negative correlation was noticed in case of phenylamines. This is the first comprehensive study based on lipidomics in order to evaluate the substantial impact of various phenotypes on the metabolic composition of NHCC.

33377: Above-ground biomass estimation and yield prediction in potato by using UAV-based RGB and hyperspectral imaging

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Rapid and accurate biomass estimation and yield prediction enables efficient plant phenotyping and site-specific crop management. RGB and hyperspectral imaging data of potato canopy were acquired with a low altitude unmanned aerial vehicle (UAV) platform at two growth stages for estimating biomass and predicting yield. These field experiments included six cultivars subject to multiple treatments of nitrogen (N), potassium (K) and mixed compound fertilisers. Crop height was estimated by the difference between a digital surface model (DSM) and a digital elevation model (DEM) derived from the RGB imagery, and together with two narrow-band vegetation indices (VIs) selected by the RReliefF feature selection algorithm. Random Forest (RF) regression models achieved high prediction accuracy for both fresh and dry above-ground biomass (AGB), with the coefficient of determination (r2) between the observed and predicted > 0.90. Similarly, crop yield was predicted from six narrow-band Vis (r2 = 0.63) with the imagery data obtained 90 days after planting. A Partial Least Squares (PLS) regression model based on the spectra of full wavelength improved yield prediction (r2 = 0.81). This study demonstrated that UAV-based RGB and hyperspectral imaging can predict potato AGB and yield, which can be used to assist in site-specific crop management.

34706: Estimation of Potato Chlorophyll Content Based on Continuous Wavelet Transform

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Chlorophyll content is the main biochemical parameter of potato. Monitoring the chlorophyll content is of great significance for the analysis of growth status of potato. The traditional method for measuring chlorophyll content has high accuracy, but it destroys the leaf tissue, and it can’t achieve large-scale real-time monitoring. UAV remote sensing technology has become a hot spot in the agricultural research field with the advantages of low cost, easy operation, and large-scale regional research. In this paper, the continuous wavelet transform is used to estimate the chlorophyll content of potato by using the hyperspectral camera on the UAV. The research contents are as follows: First, the continuous wavelet based on 21, 22, 23,... 26 was used as the basic principle and the UAV canopy hyperspectral reflectance of potato at different growth stages was decomposed. Then, the wavelet energy coefficient was calculated, and the correlation between the wavelet energy coefficients and the chlorophyll content of potato was analyzed. After analyzing the decomposition scale and the number of different bands matched by each correlation value, the optimal wavelet characteristics of the top 10 correlation coefficients in different growth stages under different scales we reobtained. At last, a potato chlorophyll content estimation model by using a stepwise regression analysis method was constructed. The results showed that the modeling R2 and validation R2 in the bud stage were 0.79 and 0.66 respectively, and the modeling R2 and validation R2 in the tuber formation stage were 0.79 and 0.63 respectively, which showed that the model had better adaptability. Due to the chlorophyll content decreases gradually with plant growth, the model began to be insensitive and its accuracy decreased. The modeling R2 and validation R2 in the tuber growth stage were 0.62 and 0.51 respectively, and the modeling R2 and validation R2 in the starch accumulation stage were 0.54 and 0.66 respectively.

34806: Developing high-throughput screening tools for stomatal conductance in sorghum

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Stomata play a crucial role in regulating plant growth and water loss simultaneously affecting rates of diffusion of CO2 and water vapour. This link to carbon assimilation and water use make stomatal conductance (gs) a trait of interest for selection and a number of studies have shown a positive correlation between gs and yield. Sorghum is adapted to a wide range of agro-ecological zones including hot and dry ones. The ability to select for high or low gs lines depending on the target environment, is of particular interest in sorghum. Direct measurement of gs is not practical and rapid screening tools are needed. Due to the cooling effect of water evaporating at the leaf surface, the difference between air temperature and leaf or canopy temperature (Delta T) can potentially be used to measure gs quickly, e.g. using remotely-sensed infrared thermal imagery. We examined the link between gs and Delta T in sorghum in order to a) establish whether genotypic differences in stomatal conductance under fully irrigated conditions were consistent throughout and between measurement days and b) which time of day was best to detect genotypic differences with an infrared thermal camera. Genotypic differences in stomatal conductance were fairly consistent during and between days. The relationship between Delta T and conductance was significantly negative and strongest between 10 am to 2 pm. The relationship between gs and Delta T within genotypes was not always linear. This study is helpful in developing high-throughput field screening methods to measure gs in sorghum.

35142: High throughput phenotyping technologies for smart farming services development: application for potato crop nitrogen management

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High throughput phenotyping technologies integrating sensors and data processing algorithms have been widely developed for breeding purposes for more than 10 years. The aim is to identify differences of behavior within a large range of genotypes in a limited range of environments. Another use of these technologies is the smart farming. to monitor crop growth to optimize the application of inputs to reach the farmer's yield and quality goals. In both cases, regular measurements of the crop state are required. But if high throughput technologies are not directly used to monitor the crops in the farmers' fields, they can contribute to develop or improve crop management tools and services. We present here the development of a decision support service for nitrogen management of potato crops. The advice concerns the decision of a late nitrogen application to complement if necessary an initial dressing. The aim is to identify a sensor based indicator sensitive and selective enough to take the adequate decision. In practice, a drone equipped with a multispectral camera has been used to monitor a network of field trials in France presenting contrasted nitrogen modalities during 3 seasons. In addition, the final yield has been measured. The most sensitive indicator to the nitrogen conditions has been selected. A threshold value has been determined to maximize the right decision rate. Once prototyped, the service has been adapted to large scale fields using satellite images. A first test campaign has been managed in 2019 and evaluation of the service will be done after harvest, in September. There are several ways to use high throughput phenotyping technologies to develop crop management services, from simple indicators to more complex models parametrization. The complementarities between genetic characterization and crop management have been little exploited. It is however a necessity to take the best advantage of the genetic improvement and to optimize the use of resources.

35024: Developing advanced field phenotyping technology for wheat crop improvement

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Pre-breeding and breeding for crop improvement ideally requires trials to be undertaken in the field, with assessment of performance from sowing to final harvest. Large trials sizes and the requirement for high frequency assessments and for complex trait analysis benefits from high throughput and automated technology. A common implementation is that of using drones and the increasing sophistication of hardware and software solutions is providing accurate assessments of germplasm performance in terms of canopy development and maturation assessed by green cover, crop indices and crop height for large scale wheat trials. Examples will be presented on progress on assessing impacts of stress and on the determination of yield components. Limitations still exist due to restrictions in drone and software automation and the achievable resolution. Increasing the latter can be overcome with novel traits now being assessed from drone-based airborne imagery. Complementary to this approach is a field robotic gantry installation (Field Scanalyzer developed by LemnaTec) which allows fully automated high temporal and spatial data collection from a large range of sensors, at a fixed site. Developments in interpretation of sensor image data, fusion of this data, automated extraction of features and application to germplasm population studies and pre-breeding material and nutritional input studies will be presented. The fine temporal resolution allows the detection of previously unknown determinants of final performance. The data to be presented are part of the UK Designing Future Wheat programme which focusses on exploiting novel wheat diversity and dissecting key traits associated with yield, sustainability, abiotic and biotic stresses.

35159: Genotype by environment interaction and grain yield stability analysis of elite bread wheat (Triticum durum L.) genotypes at Agro-climatic zones in India

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Considering the importance of genotype by environment (GxE) interactions in controlling response to selection with efficiency of breeding programs in crop improvement, a study was carried out to estimate the effects of environment and genotypic differences on yield and its related traits for elite cultivars of bread wheat (Triticum durum L.) by the assessment of GxE interaction with yield stability in multi environmental trials across different agro-climatic zones of India. 42 wheat cultivars including checks were assessed for 10 phenotypic traits at six different zones for short seasons during 2016 and 2018, and the trial was laid out in balanced lattice design with 3 replications. In order to evaluate GxE interaction, genotype groupings and stability, analysis of variance (ANOVA) and principal component analysis was applied. The ANOVA using additive main effect and multiplicative interaction (AMMI) model revealed highly significant differences among environments, GxE interaction and Interaction Principal Component Analysis (IPCA-II) while, non-significant variations among genotypes and the remaining IPCAs to yield components, which depicted the response of tested entries were different over environments as the test environments were found highly variable. Instead, the IPCA-I and III were found significant and contributed to 68.54 % of total GxE interaction for yield components. Hence, it was suggested that the genotypes HD-3090 and VL 892 are high yielding than HPW 422 with IPCA score near to zero, while their genotype selection index of six each and AMMI stability value of 0.136 and 0.098, respectively. The genotypes HD-3090, VL 892, and DWR 241 have higher stability for grain yield. As per GGE biplot analysis, genotypes WR 849, UP 2358, DWR 241 and MP 1103 were aside towards corner and suitable to specific environments. An environmental effects plays unique role in improvement of grain yield and should be given importance in wheat breeding programs.

35244: Automated detection of wheat tiller number using terrestrial LiDAR data in field

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Tiller number, as an essential phenotypic trait, could provide important information for yield potential and crop management. In general, determining the number of tillers often involves labor-intensive manual measurement, which clearly fails to meet the needs of high-throughput phenotypes. Using current state-of-the-art terrestrial laser scanning (TLS) systems presents an alternative to measure dense field crops and diverse structural parameters to support various crop improvement and agronomic initiatives. In this study, an automatic counting algorithm was developed to estimate the tiller density under the field conditions from TLS data. Field measurement data collected at the tilling and jointing stages was compared with estimated LiDAR-derived data. The new developed algorithm for counting the tills involves two steps: firstly, the adaptive layering algorithm for cluster segmentation and secondly, the hierarchical clustering algorithm for tiller detection in the clusters. Three field trials were conducted to calibrate and validate the method at two ecological sites (Rugao & Xuzhou) with different wheat cultivars, nitrogen levels, and planting densities during the 2016-2018 wheat seasons in Jiangsu Province, China. Estimated LiDAR-derived tiller number were well correlated with reference manual tiller measurements. These results showed that the proposed algorithm performed reasonable accuracy and scalability. Overall, this study shows that TLS data has the potential to high throughput expedite field-based tiller number counting and provides new perspective into enhancing agricultural production.

35331: Sustainable increase of phosphorus efficiency in winter wheat through effective rot-soil interactions

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Wheat is the crop grown on the largest acreage with a crucial role in food security worldwide. Projected future scenarios of demographic and climatic changes require an increase of wheat yield and its resilience. Phosphorus is an essential main element and a sufficient application is mandatory for a qualitative and quantitative plant production. As the available phosphorus resources are limited and will end in a foreseeable time period it is predicted a shortage in supply higher prices.The goal of the research is the phosphorus efficiency in winter wheat by improving the uptake and usage („P-Harvest-Index“) even under application of hardly soluble recycling phosphates. Wheat lines and cultivars differ genetically at their P - efficiency and its improvement permits that raw phosphates in the soil to be better acquired and lead to a sustainable use of limited resource "phosphorus". We have screened 200 wheat genotypes at their juvenile stage in Rhizotrones filled with standard soil under two phosphorus regimes, control (45kg/ha and stress 5kg/ha). Physiological and morphological parameters like biomass, number of leaves, leaf area and chlorophyll content were collected. Root system development, including length primary roots and lateral roots, were recorded every second day using the RGB camera. Scoring of roots at different stages and different levels of depth revealed high correlation of length of lateral roots with shoot dry weight. Furthermore for a better characterization of genotypes the roots are analysed in field using shovelomics and in addition several agronomic traits were evaluated. The root system morphology and growth dynamics in comparison with plant performance parameters like yield components and quality trait will permit to identify proxies in early plant development stages to select for genotypes with higher P-efficiency.

35941: Assessment of water and nitrogen use efficiency in bread wheat using UAV based non-destructive phenotyping approach

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Unmanned aerial vehicle (UAV) based remote sensing can be a promising approach for the assessment of crop water and nitrogen (N) efficiencies with great applicability in evaluating genotypes and cultivation method. This study was conducted to evaluated UAV based sensor for detecting time-series uptake efficiency of three wheat cultivars under 3 water and N treatments and assessing cultivation strategy. Experiment was conducted at two locations with 4 treatments of water (0mm, 80mm, 120mm and 160mm) and N (0, 8kg/mu, 12kg/mu, 16kg/mu). Aerial and ground truth data was measured at critical growth stages for analysis. The results showed great potential of UAV based remote sensing to predict temporal water and N use efficiency in wheat through reflectance of light spectrums. Regression model was built between vegetation indices (VI) and ground based data such as dry biomass and N contents at critical growth stages. VI had strong correlations ranged from R2=70 to R2=0.85 with dry biomass and plant N contents. Water and N use efficiency calculated form destructive method were also strongly correlated with VI. The VI showed significant variation among the genotypes and indicated that Zhongmai895 was highly efficient in up taking water and N across the treatments. VI composed of near-infrared and red edge bands (NDRE or NGDRI) had a good performance for the practical application. UAV can be used to screen genotypes for water and nutrient uptake under field condition and also to establish efficient cultivation methods for resourceful yield production.

36228: Phenotyping from maize seedling to cobs with newly-developed tools

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Crop functional genomics and breeding programs require collecting high quality plant performance data that are normally time-consuming and with less accuracy. Although traditional image analysis holds the promise to automatically acquire the phenotype data, tools for field-based high-throughput plant phenotyping (HTPP) are still lacking. In this study, we employed developed HTPP tools and artificial intelligence (AI) methodologies to collect maize phenotype data over several maize growth and development stages. In the seedling stage, we have developed the standard application for seedling traits. The unmanned aerial vehicle (UAV)-based RGB camera takes photographs of the plants and the ground-level analytical system extracts phenotype data such as plant-plant distance, seedling stability and seed germination rate which can reflect the planting quality and seedling performance. As for the yield component traits, fully convolutional network (FCN) and random forest methods are used to precisely calculate kernel number, kernel row number, and other maize yield components. We showed, through comparing with manually measured data, that the HTPP tools are highly efficient and with high accuracy. Application of these tools in a maize functional genomics analysis and association mapping population led to the identification of several genes associated with maize stability and yield, and further validation of these genes is on the way. The tools we developed may facilitate the functional study and breeding program of maize.