## **IPPS 2022 Conference Book**

# 7<sup>th</sup> International Plant Phenotyping Symposium

# **'Plant Phenotyping for a Sustainable Future'**

Wageningen, the Netherlands September 26-30, 2022

www.ipps7.org

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The International Plant Phenotyping Symposium is a conference jointly organized by:

The International Plant Phenotyping Network (IPPN) e. V. Wageningen University & Research (WUR)
The Netherlands Plant Eco-phenotyping Centre (NPEC)

# Welcome

#### Welcome

#### Plant phenotyping for a sustainable future

Food security, managing population growth and improving crop yields in the face of climate change are some of the greatest challenges facing our global society. We will need to produce food for 9.7 billion people in a sustainable way by 2050, whilst transitioning from a fossil-based economy towards a bioeconomy to mitigate the effects of global climate change. This will require a fast increase in global crop productivity to produce enough plant biomass to achieve both food and nutrition security, as well as to meet the demands of a future bioeconomy.

Crop production must be increased whilst maintaining crop quality. Society will require crops that combine sustainability, efficient use of scarce resources, e.g., water and mineral fertilizer, and are suitable for cultivation schemes and practices that preserve the Earth's biodiversity. Current intensive cropping systems will need to become more sustainable, and more crop varieties must also meet the needs of the agroecology, organic and urban/vertical farming sectors. "Future-proofed" crops must have good yield stability with a high resilience to adverse climate, volatile weather conditions and biotic stresses.

To meet these aspirations, both current and new crop plants need to be optimized and adapted which will require an ultimate effort both from the plant sciences as from the private sector. And in this process, the availability of versatile, high-throughput plant phenotyping methodology and infrastructure will be an absolute requirement for success.

For this reason, we are very excited that over 400 scientists and members of the private sector have come to Wageningen to the  $7^{th}$  International Plant Phenotyping Symposium, IPPS2022, to present and discuss their latest results and developments in the field of plant phenotyping and to advance the field further towards a sustainable future.

As a community, we are together again for the first time in a couple of years, and we have never been with so many experts at one single location. This offers a great opportunity for all of you to interact, launch ideas, make friends, and explore new collaborations!

We wish you all a very inspiring and fruitful symposium,

The Organizing Committee,

Rick van de Zedde, Philippe von Gillhaussen, Judith van Veen-Borsboom and René Klein Lankhorst

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We would like to thank the sponsors of our conference book (in alphabetical order):

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### Local Organizing Committee



Rick van de Zedde Wageningen University & Research, The Netherlands



René Klein Lankhorst Wageningen University & Research, The Netherlands



Judith van Veen-Borsboom Wageningen University & Research, The Netherlands



Philipp van Gillhaussen IPPN, Germany

#### Local Scientific Committee

All members of the local scientific committee are affiliated to Wageningen University & Research or to Utrecht University.

Fred van Eeuwijk (Mathematical and Statistical Methods)

Leo Marcelis (Horticulture & Product Physiology)

Luisa Trindade (Bioresources Breeding and Genetics)

Christa Testerink (Plant Physiology)

Paul Struik (Modelling)

Eldert van Henten (Farm Technology)

Corné Pieterse (Plant-Microbe Interactions

George Kowalchuk (Ecology and Biodiversity)

Mark Aarts (Genetics)

Jeremy Harbinson (Photosynthesis)

Rick van de Zedde (Phenomics & Automation)

Elias Kaiser (Plant Phenotyping)

Gerrit Kootstra (Deep Learning)

Rumyana Karlova (Root phenotyping)

#### International Scientific Committee

Stefan Gerth, Fraunhofer (IIS), Germany

Robert Koller, Forschungszentrum Juelich (IBG-2), Germany

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Heiner Kuhlmann, University Bonn, Germany

Gregoire Hummel, Phenospex b.v., Netherlands

## HIGH-THROUGHPUT PHENOTYPING OF MAIZE GROWTH DYNAMICS UNDER NITROGEN AND WATER STRESS

DR. SOFIJA BOŽINOVIĆ PHD¹; DR. DEJAN DODIG¹; DR. ANA NIKOLIĆ; DR. MIROSLAV ZORIĆ; DR. JELENA VANČETOVIĆ; DR. DRAGANA IGNJATOVIĆ-MICIĆ; DR. NENAD DELIĆ; KATHLEEN WEIGELT-FISCHER; PROF. DR. THOMAS ALTMANN; DR. ASTRID JUNKER

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Limited water availability and nitrogen deficiency are the most restricting factors for maize growth. Although maize susceptibility to drought is the highest at the reproductive stage, water shortage during vegetative development can significantly reduce grain yield. The aim of this study was to assess the genetic variation of growth dynamics in 20 maize inbred lines (ILs) through automated phenotyping based on visible light (RGB) imaging in a greenhouse under optimal (C), nitrogen (N), water (W), and combined nitrogen and water stress (NW) conditions. Thirteen biomass-related and morpho-physiological image-derived traits acquired at 33 time points were selected, covering developmental stages from five fully developed leaves to 10-13 fully developed leaves, depending on treatment. Estimated biomass volume (EBv), a proxy for biomass in our study, showed to be the most sensitive image-derived morphological trait to water and combined water and nitrogen stress with the maximum reduction of 53 and 54% in W and NW compared to C at the time of maximum water stress. Genotypic variation of EBv within each treatment was consistently high and over 80%, while the analysis across treatments showed that as stress got higher the genetic variation got lower (32-38%) and the interaction term became more prominent. Phenotypic correlations between EBv and other image-derived traits at early stages showed that under no stress or mild stress conditions, morphological traits were more appropriate than color-related traits for the prediction of biomass accumulation, while under more severe stress conditions, color-related traits and chlorophyll fluorescence are more useful to differentiate genotypes for high biomass. To investigate whether ILs can express EBv in similar patterns, temporal profiles were clustered by using the fuzzy c-means clustering algorithm, and two temporal dynamics of EBv patterns among the studied ILs in each treatment were identified.