

CROPINNO

STEPPING UP SCIENTIFIC EXCELLENCE AND INNOVATION CAPACITY FOR CLIMATE-RESILIENT CROP IMPROVEMENT AND PRODUCTION

Grant Agreement No 101059784

D1.2 – Second report from workshops, Training Schools and STSMs



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Due date	31/08/2025
Completion date	29/08/2025

Dissemination level		
PU	Public, fully open	X
SEN	Sensitive, limited under the conditions of the Grant Agreement	
Classified R-UE/EU-R	EU RESTRICTED under the Commission Decision No2015/444	
Classified C-UE/EU-C	EU CONFIDENTIAL under the Commission Decision No2015/444	
Classified S-UE/EU-S	EU SECRET under the Commission Decision No2015/444	

Document History

Version	Issue date	Changes
1.0	22/08/2025	First draft by Aleksandra Radanović with inputs from Dragana Miladinović and Tanja Vunjak (IFVCNS)
1.1	29/08/2025	Final version approved by Project Management Committee

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EXECUTIVE SUMMARY

Second report from workshops, Training Schools and STSMs is a deliverable of the CROPINNO project, funded as a HORIZON Coordination and Support Action type by the European Commission under its Horizon Europe (HE) Programme. It is produced in the scope of Tasks 1.1. Scientific workshops, 1.2. Training Schools and T1.3. Short-Term Scientific Missions within Work Package 1: Strengthening scientific capacity. This document summarizes the activities completed within those three Tasks till the end of the duration of the project (M16-M36).

The Report describes scientific workshops; training schools and short-term scientific missions organized within the second reporting period and in accordance with D6.1 Mobility Plan. The Report includes the following:

- Reports from workshops,
- Report from Training Schools (TS),
- Report from Short-Term Scientific Missions (STSM)

The First report from workshops, Training Schools and STSMs was drafted by IFVCNS, which is the leader of the respective tasks, with input from all partners.

1. INTRODUCTION

The primary objective of the CROPINNO project is to strengthen and accelerate scientific excellence and innovation capacity at IFVCNS in the domain of climate-smart crop improvement and sustainable production. The project aims to enhance IFVCNS's ability to address pressing agricultural challenges—namely, climate change and the growing demand for food—by fostering innovative, responsive solutions. This will be accomplished through the establishment of a synergistic research environment in collaboration with internationally renowned institutions: Universität Rostock (UROS), Università degli Studi di Padova (UNIPD), Forschungszentrum Jülich GmbH (FZJ), and Agencia Estatal Consejo Superior de Investigaciones Científicas – Instituto de Agricultura Sostenible (CSIC). These partners complement IFVCNS's expertise by addressing key gaps in multi-omics, phenotyping, and data analysis, thereby enabling the Institute to broaden its skillset, enhance innovation capacity, and strengthen its autonomy in engaging with farmers, industry, and stakeholders across the agri-food sector. Ultimately, CROPINNO enabled IFVCNS to establish a Centre of Excellence for climate-resilient crop production and improvement in the Western Balkans. Achievement of CROPINNO objectives was achieved by executing a diverse set of training activities planned within the project framework and will be detailed in the following sections of this report.

2. DESCRIPTION OF MOBILITY PLAN

The workshops, TS and STSMs are conducted through activities within WP1 Strengthening scientific capacity and are expected to contribute to the realization of CROPINNO **OBJECTIVE 1 - Improve scientific excellence capacity at IFVCNS in the use of phenotyping and multi-omics in creation and development of climate-resilient crops** and **OBJECTIVE 2 – Strengthen creativity and innovation capacity by development of new collaborations with R&I Institution**, as well as



achievement of the **Expected Impact 1: Improved excellence capacity of the coordinating institution in the particular field of research.**

2.1 Scientific Workshops

From M16 to M36 two scientific workshops were organized (**Table 1**), with combined participation of IFVCNS researchers and researchers from the host and other institution partners, thus exposing IFVCNS researchers to new ideas and research practices. In total, 21 IFVCNS researchers participated in both workshops.

Table 1 Scientific Workshops executed within the first reporting period of CROPINNO

Title	Duration	Location	Provider	No. particip. from IFVCNS	Date
Non-invasive plant phenotyping approaches and research infrastructure management	2 days	FZJ	FZJ	15	04-05/03/24
OMICS in improvement for drought tolerance	2 days	IFVCNS	UROS	17	04-05/09/24
New approaches in crop improvement for increased climate resilience	3 days	IFVCNS	All	30 on average	25-27/06/2025

2.1.1 Non-invasive plant phenotyping approaches and research infrastructure management

The 2-day workshop had the aim to introduce plant phenotyping approaches, research infrastructure and science management. The program of the workshop is given in **Annex 1**.

The workshop started with a short introduction to the host institute, the institute of plant sciences at Forschungszentrum Jülich. This was followed by seven presentations given by phenotyping experts. The following topics were presented and discussed with the participants: 1) Introduction to plant phenotyping; 2) Overview about existing root methods for field and lab-based phenotyping approaches; 3) Field phenotyping approaches for non-invasive quantification of plant traits; 4) Pitfalls and potential of plant phenotyping platforms, what to consider before purchasing, building or using a phenotyping platform for high throughput phenotyping; 5) Low-cost phenotyping approaches for quantifying plants traits in the field and lab; 6) Computer vision approaches for quantitative analysis of root and shoot traits; 7) Management, storage and access of data by addressing FAIR principles'.

On both days of the workshop, a tour to phenotyping platforms developed at FZJ complemented the talks. The last session of the workshop addressed the topic of science management. The stakeholders from EMPHASIS and IPPN (International Plant Phenotyping Network), who joined the workshop, presented the topic of science management for infrastructure operation, including stakeholder engagement, gave some examples of successful acquisition of project funding for plant phenotyping projects and presented the networking activities within IPPN.

2.1.2 OMICS in improvement for drought tolerance

This workshop consisted of two days of presentations and discussions about omics topics in relation to drought. Phenomics, proteomics, genomics, transcriptomics and epigenomics were covered. The program of the workshop is given in **Annex 2**.

The first day started with a session about phenomics with two talks about root cell wall analysis in sunflower in response to drought and phenomic data from rhizotron experiments with sunflower from CROPINNO project. In the afternoon the session about genomics started with an overview of omics research in sunflower regarding drought tolerance covering not only genomics but also proteomics and transcriptomics. The second talk of this session was about results from genomic analysis regarding drought tolerance in potato from another project.

The first session of the second day was about transcriptomics. It started with a talk about results from transcriptomic analysis of two sunflower lines from *in vitro* drought stress experiments, followed by a webinar from Novogene about epigenomic studies. This session was followed by a general discussion round concerning future procedures and improvements when breeding climate-resilient crops. This discussion was held between researches and breeders alike to have an interdisciplinary exchange. The workshop ended with the session about epigenomics, consisting of two talks. The first one was giving a general overview about epigenomics whereas the second one presented first results of epigenomic analysis of sunflower drought stress experiments.

All talks were interrupted by questions and discussion so to make this an interactive workshop.

2.1.3 New approaches in crop improvement for increased climate resilience

This workshop was organized within the final CROPINNO conference. It gathered researchers, project partners, and stakeholders (with special focus on Western Balkans) to present and evaluate the outcomes of a multi-year initiative aimed at enhancing climate resilience in crops through integrative scientific approaches. A comprehensive overview of activities, covering capacity building, multi-omics integration, innovation acceleration, research management, and dissemination was presented. Highlights included the establishment of training schools, short-term scientific missions (STSMs), and collaborative workshops that strengthened institutional and individual competencies across partner institutions. The Climate Crops Centre and associated roadmaps were introduced as key legacy structures to support ongoing innovation and knowledge exchange. The program of the workshop is given in **Annex 3**.

Scientific sessions across the three-day program showcased cutting-edge research in soil health, breeding strategies, and omics technologies. Presentations addressed SNP-based markers for drought tolerance in sunflower, transcriptomic integration into breeding pipelines, and sensor-based detection of parasitic infections. Discussions emphasized the importance of harmonizing field-based physiological measurements with molecular data, and several talks explored the role of artificial intelligence and statistical modelling in unlocking hidden patterns of resilience. The conference also spotlighted regional and international collaborations, including contributions from USDA/ARS, WACWISA, and multiple European research centres.

The final day focused on STSM outcomes, with detailed presentations on methodology development for sunflower HTPP, *in vitro* screening, drought tolerance genotyping, and



transcriptome analysis. These exchanges underscored the project's success in fostering cross-institutional learning and methodological innovation.

2.2 Training Schools

From M16 to M36 two training schools were organized (**Table 2**), with combined participation from IFVCNS researchers and researchers from the host and other institution partners.

Table 2. Training School executed within the first reporting period of CROPINNO

Title	Duration	Location	Provider	No. particip. from IFVCNS	Date
Phenotyping summer school	3 days	FZJ	FZJ	11	06-08/03/2024
Webinar Series: Why are Omics important for plant breeding	5 days	On-line	UNIPD	16 on averg.	April/May 2025

2.2.1 Phenotyping summer school

The 3-day training school had the aim to teach state-of-the art phenotyping methods. The training school gave the opportunity to get hands-on experience on different root and shoot phenotyping approaches. The presented methods included phenotyping tools using soil-filled rhizotrons and agar-filled plates for non-invasive quantification of root traits. The participants learned how to set-up root phenotyping experiments, including how to prepare soil and growth media, how to fill growth containers in a standardized way and how to image the roots.

Furthermore, destructive sampling of roots was presented, including how to wash roots from soil and measure root traits by scanning roots. For shoot phenotyping various non-invasive devices (such as FluorPen, PolyPen, SPAD etc.) were presented and used by the participants to measure chlorophyll fluorescence, spectral reflectance and chlorophyll content of sunflower plants. The non-invasive methods were complemented with demonstrations of destructive methods (scanning of leaves and biomass measurements). Another part of the training school was the hands-on training for different image analysis tools. The participants could test the imaging tools and learned how to meet the different challenges of root and shoot image analysis. The training school ended with a session about data export and data analysis using R-scripts. The program of the summer school is given in **Annex 4**.

2.2.2 Webinar Series: Why are Omics important for plant breeding

This training school was originally planned to be on site (Bioinformatic analysis of large data sets), however to maximize its impact, it was held online with lectures coming from different institutions and discussing different aspects of use of omics tools and its exploitation in crop breeding. The webinar series featured leading experts from Sequentia Biotech, UNIPD, CNR - Institute of Biosciences and BioResources, CREA - Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria, and the University of Udine, who delivered lectures on cutting-edge omics technologies and their applications in crop improvement. Topics included genome decoding, transcriptomics, virus identification, root-soil interactions, drought stress resilience, epigenomics, and chromatin dynamics. Each session consisted of two 45-minute lectures followed by interactive Q&A discussions, fostering knowledge exchange and



engagement among participants from across Europe. The program of the summer school is given in **Annex 5**.

The training school emphasized the role of multi-omics approaches in accelerating plant breeding, particularly in the context of climate resilience and sustainable agriculture. Presentations highlighted how integrating genomics, transcriptomics, and epigenomics can unravel complex traits, guide precision breeding, and support the development of stress-tolerant cultivars. The series also underscored the importance of data analysis, collaborative research, and stakeholder engagement in translating omics insights into practical innovations for the agri-food sector.

2.3 Short-Term Scientific Missions

From M15 to M36 ten STSMs were executed (**Table 3**). During these STSMs an effective scheme for knowledge transfer via mobility of scientists was implemented.

Table 3. STSMs executed within the first reporting period of CROPINNO

Host	Visitor	Topic	Number of participants	Date
UROS	IFVCNS	Phenotyping for drought tolerance	2 researchers from IFVCNS	05-09/02/2024 09-16/04/2025
FZJ	IFVCNS	Quantification of phenotypic differences in root and shoot traits by use of high-throughput phenotyping platforms	2 researchers from IFVCNS	02-26/04/2024 20/01-20/02/2025
UNIPD	IFVCNS	Knowledge transfer: Epigenomics for improved drought resistance	1 researcher from IFVCNS	03-11/07/2025
IFVCNS	UNIPD	Transcriptome analyses for identification of candidate genes for drought tolerance	3 researchers from UNIPD	09-13/12/2024 24-28/03/2025
IFVCNS	UROS	Troubleshooting and protocol standardisation of -omics tools in improvement for drought tolerance	1 researcher from UROS	09-20/09/2024 17-28/03/2025
IFVCNS	FZJ	Troubleshooting and protocol standardization of phenotyping methods	1 researcher from FZJ	30/06-04/07/2025

2.3.1 Phenotyping for drought tolerance

During the STSM (05-09/02/2024) evaluation of three newly developed genotypes was performed, from which two were selected for continued experimentation. A demonstration of phenotypic assessment methods was conducted on these genotypes, including shoot measurements and root scanning, to establish baseline data for comparative analysis. Moreover, tissue samples were collected for RNA extraction.

RNA was subsequently isolated from root and primary leaf tissues. Quality control procedures were performed using agarose gel electrophoresis and spectrophotometric analysis to confirm RNA integrity and concentration.

A strategic discussion was held regarding RNA sequencing services provided by Novogene. This included detailed guidance on metadata preparation and data submission protocols to ensure optimal sequencing output and downstream bioinformatic analysis. Collaborative alignment was reinforced through a virtual meeting with project partners to address cross-institutional updates and coordination.

Further analytical depth was added through a presentation by Prof. Herburger (University of Rostock) on planned cell wall analyses in root and potentially leaf tissues. Integration of these analyses into the broader experimental framework was explored. The initial phenotypic data were statistically analyzed, and the applied methodologies were reviewed to refine future evaluation protocols.

The second research visit to UROS (09-16/04/2025) was strategically aligned with the outcomes of the Short-Term Scientific Mission (STSM) conducted at IFVCNS in March 2025. During this STSM, RT-qPCR results obtained at IFVCNS were validated using sunflower material from UROS. To ensure consistency, identical primer combinations targeting candidate genes involved in ABA biosynthesis and signalling pathways were applied to *in vitro* samples treated with 15% PEG.

Primer efficiencies were assessed, and qPCR experiments were successfully executed. The resulting expression profiles were compared with those previously obtained in Novi Sad. Additionally, novel primer combinations were tested at UROS, with plans for follow-up validation at IFVCNS.

Parallel to the laboratory work, discussions were conducted regarding a joint manuscript aimed at comparing protocols for drought stress application. Candidate genes previously reported by Shi et al. (2024) were analysed via BLAST to identify duplicated and homologous sequences within the sunflower genome. Supplementary ABA-related genes were retrieved from the KEGG database. All candidate gene sequences were sourced from Heliagene.org, and phylogenetic trees were constructed using MEGA12. These trees were then cross-referenced with significantly differentially expressed genes identified through RNA-sequencing data.

2.3.2 Quantification of phenotypic differences in root and shoot traits by use of high-throughput phenotyping platforms

At the beginning of the STSM (02-26/04/2024), the host organised a tour through the institute facilities, and all necessary safety instructions for work with the phenotyping facility GrowScreen Rhizo-III. During their stays, both researchers gave a presentation about their background and home institute and about the planned and conducted experiment at the seminar of the JPPC (Jülich Plant Phenotyping Center) group. In addition, several meetings took place between the participants and the host institute to plan the experimental setup and refine the data analysis.

The experiment started with substrate preparation. It was required to prepare substrate with two levels of water content to quantify traits of plants grown in conditions with sufficient and reduced water availability. Half of the substrate was placed in a thin layer on the greenhouse floor for air drying. The substrate was regularly manually mixed along with sampling for water



content determination for several days until the desired water content was reached. As a next step, half of the rhizotrons were filled with the pre-dried substrate and the other half with non-dried substrate / control treatment using the semi-automated filling line of the high throughput phenotyping platform GrowScreen-Rhizo III at FZJ. Thereafter germinated seeds of the sunflower genotypes were transferred into the rhizotrons after germination on moistened filter paper. The fully automated imaging of all rhizotrons took place within the GrowScreen-Rhizo III platform on a daily basis until first roots reached the bottom of the rhizotrons. Images of roots and shoots from different view angles were acquired to extract root and shoot traits of all ten sunflower genotypes under the 2 different treatments. To allow for destructive sampling before roots reached the bottom of the rhizotrons (same timing as in the previous year's experiment), as well as for sampling of true leaves, the plants were harvested at two different time points. At harvest, chlorophyll fluorescence (Fluorpen; PSI), leaf-level spectral reflectance (Polypen device, PSI), chlorophyll content (SPAD meter, Konica Minolta), leaf area, and shoot biomass were measured manually. For the first harvest, roots were washed, scanned and root dry weight was determined. The host provided support for the development of respective graphic representation and statistical analyses using the open-source software R. The established scripts to analyze root traits (including root length and root system architectural traits like depth and width profiles) can be transferred to root image analysis at IFVCNS. At the second harvest, one leaf per plant was sampled for RNA analysis by IFVCNS.

In addition, the first visit with this STSM included a second rhizotron experiment with small rhizotrons to establish a rewatering protocol, using the similar rhizotron size as available at IFVCNS and seed material from IFVCNS to test different protocols for rewatering drought stress plants.

During the second visit (20/01-28/02/2025), a germination experiment was performed under control conditions. Seed material of two sunflower genotypes with contrasting drought tolerance was previously sorted by FZJ, to be able to quantify germination rate of small, medium and large sized seeds under sufficient water availability and reduced water availability in the soil.

2.3.3 Knowledge transfer: Epigenomics for improved drought resistance

An interdisciplinary program was introduced with the aim of deepening understanding of the significance of plant studies and their essential role in global sustainability. The program was structured into distinct thematic segments. The initial segment focused on the mechanisms of photosynthesis and the influence of environmental conditions on photosynthetic capacity. Topics addressed included photosynthesis under variable environmental stressors, biomass production from photosynthetic organisms, and the thermodynamic principles underlying these processes.

The second segment took place in the northern region of Veneto, Italy, near the Italian Alps—an area of notable environmental significance. Presentations concentrated on the interactions between forest ecosystems and environmental factors, with emphasis on plant water relations, natural disturbances, and the impact of invasive species.

Following the field visit, the final segment was held in Padova and centered on plant genetics, development, and biotic interactions. Topics included developmental genetics, genomics, stress responses, reproductive biology, and the study of rare or non-model species. Further



sessions explored plant–microorganism and plant–animal interactions, including soil microbiota and insect dynamics. The concluding discussions addressed the role of plants in agriculture, phytoremediation, food security, and sustainability, alongside climate change policies such as the EU Green Deal and future legislative frameworks.

2.3.4 Transcriptome analyses for identification of candidate genes for drought tolerance

This STSM (09-13/12/2024) was designed to enhance the technical expertise of IFVCNS researchers in optimizing RNA extraction protocols from challenging plant tissues for downstream gene expression analysis via RT-qPCR. To support this objective, plant material harvested from both *in vitro* and pot-based drought stress experiments was used for RNA isolation.

Through collaborative efforts between IFVCNS and UNIPD researchers, a robust foundation for protocol refinement was established. Various troubleshooting strategies were explored to improve RNA yield and integrity from difficult tissue types. IFVCNS researchers received hands-on training in RNA extraction techniques, gaining practical experience and methodological insight from UNIPD colleagues.

All relevant materials—including protocols, presentations, and training documentation—have been made available to CROPINNO participants via a shared drive, ensuring broad dissemination and fostering continued knowledge exchange across the consortium.

During the second STSM (24-28/03/2025), a new drought stress experiment was initiated under chamber-controlled conditions, focusing on sunflower genotypes with contrasting drought tolerance (tolerant vs. susceptible). The experimental design was jointly defined, including the stress protocol parameters such as watering regime, developmental stage at stress onset, and standardized leaf sampling techniques. The overarching goal is to generate gene expression data from extracted RNA that is as comparable as possible between the UNIPD (greenhouse-based drought experiment) and IFVCNS.

To support downstream molecular analysis, the optimal cDNA dilution for RT-qPCR was determined through a series of preliminary reactions. These assays helped establish the most suitable dilution factor for consistent amplification. Additionally, initial RT-qPCR experiments targeting ABA-related genes were conducted to assess differential expression patterns between the two genotypes under control and drought conditions. These early results were critically evaluated to refine the experimental workflow and improve reproducibility.

2.3.5 Troubleshooting and protocol standardisation of -omics tools in improvement for drought tolerance

This STSM (09-20/09/2024) focused on isolating RNA from sunflower root and leaf tissues. A tissue-adaptable RNA isolation protocol was employed and further refined to accommodate the specific characteristics of root and leaf samples. Several optimization steps were undertaken, including: a) variation in the quantity and type of starting material; b) adjustment of incubation durations for key protocol steps; c) modification of environmental conditions during extraction procedures.

Successfully isolated RNA was prepared for sequencing and submitted to Novogene for quality assessment. Following this STSM, the samples will undergo whole transcriptome sequencing. The resulting data will be jointly analyzed and discussed among project partners. In future

STSMs, RT-qPCR validation of selected genes of interest—identified through RNA-Seq—will be performed to confirm differential expression patterns.

The second STSM (17-28/03/2025) focused on optimizing qPCR protocols to investigate genes involved in abscisic acid (ABA) synthesis and signalling in sunflower. The work was carried out over two weeks, with contributions from IFVCNS, UROS, and UNIPD.

During the first week, efforts were concentrated on refining the qPCR protocol and testing primers targeting ABA-related genes. These primers had been designed in advance based on genes identified in Shi et al. (2024), which showed significant differential expression in RNA-Seq data from *in vitro* drought experiments conducted at UROS. For these experiments, cDNA samples provided by IFVCNS were used. The initial focus was on standardizing reference genes, including a panel of nine candidates. Target gene primers were evaluated, and multiple qPCRs were performed to determine primer efficiencies. This allowed for the selection of the most reliable reference and target genes for future analyses.

Additionally, RNA-Seq results from previous *in vitro* experiments were reviewed and discussed among the partners. A manuscript draft was initiated between IFVCNS, UROS, and UNIPD, with key topics and structure outlined collaboratively.

2.3.6 Troubleshooting and protocol standardization of phenotyping methods

This STSM goal was to discuss troubleshoot challenges from a previous high-throughput phenotyping (HTP) experiment and to standardize protocols for drought stress assessment. FZI and IFVCNS researchers refined measurement workflows, aligned data acquisition methods, and reanalyzed earlier datasets to improve trait resolution.

The visit also marked the start of a joint publication focused on exploiting HTP technologies for drought tolerance screening in sunflower, aiming to share practical insights and scalable methodologies for crop resilience research.

3. DATA AVAILABILITY

Programs, reports, pictures and training material from workshops, STSMs and training schools have been deposited as datasets and other project output as listed below.

Workshops

1. Varotto, S. (2023). Workshop Introduction to Crop Epigenetics held in February 2023 UNIPD program and report [dataset]. Padua : University of Padua. <https://fiver.ifvcns.rs/handle/123456789/5584> (restricted access)
2. Perrella, G. (2023). Chromatin dynamics and environmental response [training material]. Padua : University of Padua. <https://fiver.ifvcns.rs/handle/123456789/5585> (restricted access)
3. Farinati, S. (2023). Chromatin extraction in plants [training material]. Padua : University of Padua. <https://fiver.ifvcns.rs/handle/123456789/5586> (restricted access)
4. Joseph, J. (2023). Collecting plant material for transcriptome studies [training material]. Padua : University of Padua. <https://fiver.ifvcns.rs/handle/123456789/5587> (restricted access)
5. Comino, C. (2023). Epigenetic marks: DNA methylation [training material]. Torino : University of Torino. <https://fiver.ifvcns.rs/handle/123456789/5588> (restricted access)
6. Varotto, S. (2023). Epigenetics signatures to remember drought stress in maize [training material]. Padua : University of Padua. <https://fiver.ifvcns.rs/handle/123456789/5589> (restricted access)
7. Vendramin, S. (2023). How to sequence RNA [training material]. Padua : BMR Genomics srl. <https://fiver.ifvcns.rs/handle/123456789/5590> (restricted access)



8. Varotto, S. (2023). Introduction to (Crop) Epigenetics [training material]. Padua : University of Padua. <https://fiver.ifvcns.rs/handle/123456789/5591> (restricted access)
9. De Paoli, E. (2023). Noncoding-RNAs and their role in chromatin remodelling and plant function [training material]. Udine : University of Udine. <https://fiver.ifvcns.rs/handle/123456789/5592> (restricted access)
10. Molinero-Ruiz, L. (2023). Workshop Sensors and image analyses as tools for plant phenotyping held in February 2023 CSIC program and pictures [dataset]. Madrid : Spanish National Research Council (CSIC). <https://fiver.ifvcns.rs/handle/123456789/5593> (restricted access)
11. Horn, R. (2024). Workshop Omics in Improvement for Drought Tolerance held in September 2024 UROS program and report [dataset]. Rostock : University of Rostock. <https://fiver.ifvcns.rs/handle/123456789/5594> (restricted access)
12. Horn, R. (2024). Overview Omics research in sunflower regarding drought tolerance [training material]. Rostock : University of Rostock. <https://fiver.ifvcns.rs/handle/123456789/5595> (restricted access)
13. Alf, M. (2024). Transcriptomic comparison between two sunflower lines regarding drought response under PEG treatment [training material]. Rostock : University of Rostock. <https://fiver.ifvcns.rs/handle/123456789/5596> (restricted access)
14. Schilling, F. (2024). Whole-genome Sequencing of Tetraploid Potato Varieties Reveals Different Strategies of Drought Tolerance [training material]. Rostock : University of Rostock. <https://fiver.ifvcns.rs/handle/123456789/5597> (restricted access)
15. Nagel, K. (2024). Workshop Non-invasive plant phenotyping approaches and research infrastructure management held in March 2024 FZJ program, report and pictures [dataset]. Jülich : Plant Sciences (IBG-2), Forschungszentrum Jülich GmbH. <https://fiver.ifvcns.rs/handle/123456789/5598> (restricted access)
16. Eiteneuer, C. (2024). FAIR data in plant sciences - management, storage and access [training material]. Jülich : Plant Sciences (IBG-2), Forschungszentrum Jülich GmbH. <https://fiver.ifvcns.rs/handle/123456789/5599> (restricted access)
17. Müller-Linow, M. (2024). Computer vision approaches for quantitative analysis of root and shoot traits [training material]. Jülich : Plant Sciences (IBG-2), Forschungszentrum Jülich GmbH. <https://fiver.ifvcns.rs/handle/123456789/5600> (restricted access)
18. von Gillhaussen, P. (2024). IPPN – A Global & Independent Network [training material]. Jülich : Plant Sciences (IBG-2), Forschungszentrum Jülich GmbH. <https://fiver.ifvcns.rs/handle/123456789/5601> (restricted access)
19. Fiorani, F. (2024). Low-cost phenotyping approaches [training material]. Jülich : Plant Sciences (IBG-2), Forschungszentrum Jülich GmbH. <https://fiver.ifvcns.rs/handle/123456789/5602> (restricted access)
20. Poorter, H. (2024). What do you need to consider before embarking on high-throughput plant phenotyping? [training material]. Jülich : Plant Sciences (IBG-2), Forschungszentrum Jülich GmbH. <https://fiver.ifvcns.rs/handle/123456789/5603> (restricted access)
21. Nagel, K. (2024). Root phenotyping approaches - exploring the hidden half of plants [training material]. Jülich : Plant Sciences (IBG-2), Forschungszentrum Jülich GmbH. <https://fiver.ifvcns.rs/handle/123456789/5604> (restricted access)
22. Ibrahim, H., Fahrner, S., & von Gillhaussen, P. (2024). On Science Management [training material]. Jülich : Plant Sciences (IBG-2), Forschungszentrum Jülich GmbH. <https://fiver.ifvcns.rs/handle/123456789/5605> (restricted access)

STSMs

23. Nagel, K. (2025). STSM Quantification of phenotypic differences in root and shoot traits by use of high-throughput phenotyping platforms held in April 2024 and February 2025 in FZJ report [dataset]. Jülich : Plant Sciences (IBG-2), Forschungszentrum Jülich GmbH. <https://fiver.ifvcns.rs/handle/123456789/5606> (restricted access)
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Annex 1

CROPINNO Workshop**Non-invasive plant phenotyping approaches and research
infrastructure management
4th and 5th March 2024, Jülich, Germany**



Workshop Non-invasive plant phenotyping approaches and research infrastructure management
Location: Forschungszentrum Jülich, Institute IBG-2: Plant Sciences, building 06.2, room 406

Day 1 (Monday, March 4th 2024)

09:00 – 9:15 Arrival / registration

09:15 – 09:30 Welcome/ Introduction to FZJ / Institute of Plant Sciences (Dr. Kerstin Nagel)

09:30 – 10:30 Introduction to Plant Phenotyping (Dr. Laura Junker-Frohn)

10:30 – 11:00 Coffee break

11:00 – 12:00 Root phenotyping approaches - exploring the hidden half of plants (Dr. Kerstin Nagel)

12:00 – 13:00 Lunch

13:00 – 14:00 Tour through institute of IBG-2: Plant Science (JPPC phenotyping platforms - Dr. Henning Lenz)

14:00 – 15:00 Field phenotyping: quantifying plant traits across scales (Prof. Uwe Rascher / Dr. Onno Muller)

15:00 – 15:30 Coffee Break

15:30 – 17:00 Pitfalls and potential of plant phenotyping platforms (Dr. Hendrik Poorter)

Dinner 18:30 Restaurant 'Einhorn', Poststr. 16, 52428 Jülich

Day 2 (Tuesday, March 5th 2024)

09:00 – 10:00 Low-cost phenotyping methods for shoot traits (Dr. Fabio Fiorani)

10:00 – 10:30 Coffee break

10:30 – 11:30 Computer vision approaches for quantitative analysis of root and shoot traits (Dr. Mark Müller-Linow)

11:30 – 12:30 FAIR data in plant sciences - management, storage and access (Constantin Eiteneuer)

12:30 – 13:30 Lunch

13:30 – 14:00 Tour through institute of IBG-2: Plant Science II (MRI (Magnetic Resonance Imaging) and seed phenotyping, Dr. Robert Koller)

14:00 – 15:00 Science management: infrastructure, projects, initiative and networks (Dr. Roland Pieruschka / Dr. Sven Fahrner / Dr. Philipp von Gillhaussen)

15:00 – 15:30 Coffee Break

15:30 – 16:30 Science management (II): infrastructure, projects, initiative and networks (Dr. Roland Pieruschka / Dr. Sven Fahrner / Dr. Philipp von Gillhaussen)

16:30 – 17:00 Summary and closing remarks.



Annex 2

CROPINNO Workshop

OMICS in improvement for drought tolerance

4th and 5th September 2024, Novi Sad, Serbia

					
Workshop "Omics in Improvement for Drought Tolerance".					
Date: 04.-05.09.2024					
Venue: Hotel Pupin, Narodnih heroja 3, 2100 Novi Sad, Serbia					
Wednesday 04.09.2024			Thursday 05.09.2024		
GA-Meeting			Transcriptomics (Session coordinator: Serena Varotto)		
Time	Speaker	Title	Time	Speaker	Title
9.00-9.15	Dragana Miladinović	Intro and activity schedule	9.00-9.45	Malin Alf	Transcriptomic comparison between two sunflower lines regarding drought response under PEG-treatment
9.15-10.30	WP1-5-leads	Recap and plans: WS, TS, STSM, Milestones, Deliverables (15-min each)	9.45-10.15	Coffee-break	
10.30-11.00	Coffee-Break		10.15-11.00	Adrian Kordes, Armaan-Mehra	Epigenomic Webinar Novogene
Phenomics (Session coordinator: Aleksandra Radanović)			Discussion Round		
11.00-11.45	Klaus Herburger	Responses of root-cell walls to drought stress	11.00-11.20	Future Procedures and Improvements	
11.45-12.30	Laura Junker, Frohn (online)	Phenomic data from CROPINNO drought experiments	11.20-11.45	General Discussion: Breeding climate-resilient crops	
12.30-13.45	Lunch		11.45-13.00	Lunch	
Genomics (Session coordinator: Dragana Miladinović)			Epigenomics (Session coordinator: Renate Horn)		
13.45-14.30	Renate Horn	Overview Omics research in sunflower regarding drought tolerance	13.00-13.45	Serena Varotto	General Overview about Epigenomics
14.30-15.00	Coffee-Break		13.45-14.15	Coffee-break	
15.00-15.45	Florian Schilling	Drought tolerance strategies derived from genomic analyses in potato	14.15-15.00	Alessia Ronchi	First results in epigenomics in sunflower drought experiments
15.45-16.15	General Discussion Genomics		15.00-16.00	General Discussion Epigenomics	
18.30	City-Tour and Social-Dinner	Restaurant Terasa, Petrovaradin Fortress			

Annex 3

CROPINNO Workshop

New approaches in crop improvement for increased climate resilience

From 25th to 27th June 2025, Novi Sad, Serbia






Funded by the European Union

PROGRAM

CROPINNO Final Conference

New approaches in crop improvement for increased climate resilience

25-27. 06. 2025, Novi Sad, Serbia, Hotel Pupin – hybrid

DAY 1	25.06.2025	ZOOM Link
9:00 – 9:30	Conference opening and welcome	<i>Prof. Dr. Dragana Latković, IFVCNS, Director</i> <i>Dr. Dragana Miladinović, IFVCNS, Coordinator</i>
<i>Presentation of the WPs – WP1</i>		
09:30 – 10:30	Strengthening scientific capacity	
	Deliverables and milestones	<i>Dr. Renate Horn, UROS</i>
	Workshops, training schools, short-term visits, joint training course	
	Q&A & discussion	<i>All partners</i>
10:30 – 11:00	Coffee break – Group Photo	
<i>Presentation of the WPs – WP2</i>		
11:00 – 12:00	Multi-omics approaches for increased climate resilience	<i>Dr. Serena Varotto, UNIPD</i>
	Deliverables and milestones	
	Mini project	
	Q&A discussion	<i>All partners</i>
<i>Presentation of the WPs – WP3</i>		
12:00 – 13:00	Stepping up excellence and innovation capacity – Work description	<i>Dr. Kerstin Nagel, FZI</i>
	Deliverables and milestones	<i>On-line</i>
	Guidances, roadmaps, Climate Crops Center	
	Q&A discussion	<i>All partners</i>
13:00 – 14:00	Lunch	
<i>Presentation of the WPs – WP4</i>		
14:00 – 15:00	Strengthening research management and administration capacity	<i>Dr Leire Molinero-Ruiz, CISC</i>
	Deliverables and milestones	
	Workshops, training schools and short-term visits	

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	Q&A & discussion	All partners
15:00 – 15:30	Coffee break	
	Presentation of the WPs – WP5	
	Communication, dissemination and exploitation	
15:30 – 16:30	Deliverables and milestones	Dr. Aleksandra Radanović, IFVCNS
	Dissemination activities	
	Q&A & discussion	All partners
	Project coordination and administration	
16:30– 17:00	Deliverables and milestones	Dr. Dragana Miladinović, IFVCNS
	Q&A & discussion	All partners
DAY 2	26.06.2025	ZOOM Link
	Session 1 – Soil and Climate	Chair: Dr. Jegor Miladinović, IFVCNS, Serbia
09:00 – 09:20	CLEARCLIMATE: Providing Clearer Climate Information Services for Resilient and Sustainable Crop Production	Dr. Richard Agyemang Osei, WACWISA, Ghana
09:20 – 09:25	Discussion	
09:25 – 09:40	Soil and its condition allow crops to flourish in challenging environments	Dr. Alan Franzluebbers, USDA/ARS, Raleigh NC, USA
		On-line
09:40 – 09:45	Discussion	
09:45 – 10:05	Advancing Sustainable Solutions for Contaminants in Soil with Carbon-Based Amendments	Prof. Dr. Snežana Maletić, UNS, FS, Serbia
10:05 – 10:10	Discussion	
10:10 – 10:30	Advanced Analytical and Treatment Strategies for Emerging Water Pollutants: Building Institutional Capacity in the Context of the Triple Planetary Crisis	Prof. Dr. Nataša Mladenović Đurišić, UNS, FT, Serbia
10:30 – 10:35	Discussion	
10:35 – 11:05	Coffee break – Group Photo	
	Session 2 – Breeding for Resilience	Chair: Prof. Dr. Renate Horn, UROS, Germany
11:05 – 11:20	Status of Breeding and Seed Production of Major Field Crops in Serbia: Facing the Effects of Climate Change	Dr. Sandra Cvejić, DSSS, Serbia
11:20 – 11:25	Discussion	
11:25 – 11:40	SNP-based Markers for Drought Tolerance in Sunflower	Dr. Florian Schilling, UROS, Germany
11:40 – 11:45	Discussion	
11:45 – 12:00	Reaction of Sunflower Material from IFVCNS to O. cumana Race F and a Sensor-Based Initial Approach for Early Detection of Infections	Dr. Leire Molinero-Ruiz, CISC, Spain

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12.00 – 12.05	Discussion	
12.05 – 13.00	Lunch	
	Session 3 – Omics Tools	<i>Chair: Prof. Dr. Serena Varotto, UNIPD, Italy</i>
13.00 – 13.20	axiomFP.py: SNP-Based Software for Ploidy Level Detection as a Tool for Modern Breeding Strategies	<i>Prof. Dr. Jasmin Grahić, US, FAFS, Bosnia and Hercegovina</i>
13.20 – 13.25	Discussion	
13.25 – 13.45	Seeing the Unseen: Advanced Imaging Approaches in Plant Stress Research	<i>Prof. Dr. Boris Lazarević, UZ, FA, Croatia</i>
13.45 – 13.50	Discussion	
13.50 – 14.05	PHENO-DROP project – Advancing drought resilience in bread wheat through genomics and phenomics innovations	<i>Dr. Dragana Trkulja, IFVCNS, Serbia</i>
14.05 – 14.10	Discussion	
14.10 – 14.25	Introducing Transcriptomics in IFVCNS Sunflower Breeding Program	<i>Dr. Aleksandra Radanović, IFVCNS, Serbia</i>
14.25 – 14.30	Discussion	
14.30 – 15.00	Coffee break	
	Session 4 – Future Trends	<i>Chair: Dr. Vuk Đorđević, IFVCNS, Serbia</i>
15.00 – 15.20	Local Seeds, Global Tools, and the Fight Against Climate Change	<i>Prof. Dr. Mirela Kaljkut Zeljković, UBL, IGR/FA, Bosnia and Hercegovina</i>
15.20 – 15.25	Discussion	
15.25 – 15.45	Breeding the Unseen & Data-Driven Resilience: Unlocking Nature's Hidden Code with Statistical Precision	<i>Prof. Dr. Mirjana Jankulovska, US, FASF, North Macedonia</i>
15.45 – 15.50	Discussion	
15.50 – 16.10	Some Recent Developments in Artificial Intelligence for Biology	<i>Dr. Branislav Kisačanin, IVI, Serbia</i>
16.10 – 16.15	Discussion	
18.00 – 20.00	Petrovaradin Fortress Tour	
20.30 – 23.00	Social Dinner	
DAY 3	27.06.2025	<u>ZOOM Link</u>
	STSMs Presentations	
09.00 – 09.15	STSMs IFVCNS to FZJ: Development of Methodology for Sunflower HTPP	<i>Dr. Nemanja Ćuk, IFVCNS, Serbia</i>
09.15 – 09.20	Q&A	
09.20 – 09.35	STSMs IFVCNS to UROS: Development of <i>In Vitro</i> Screening Methodology	<i>Dr. Svetlana Glogovac and Dr. Aleksandra Radanović, IFVCNS</i>
09.35 – 09.40	Q&A	



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09.40 – 09.55	STSMs UROS to IFVCNS: Development of Methodology for Sunflower Drought Tolerance Genotyping	<i>Malin Alf, UROS</i>
09.55 – 10.00	Q&A	
10.00 – 10.15	STSMs UNIPD to IFVCNS: Development of Methodology for Sunflower Transcriptome Analysis	<i>Dr. Alessia Ronchi, UNIPD</i>
10.15 – 10.20	Q&A	
10.20 – 10.35	Staff Visits: IFVCNS to UNIPD, CISC, FZI and UROS	<i>Tanja Vunjak and Marjana Vasiljević, IFVCNS</i>
10.35 – 10.40	Q&A	
10.40 – 11.10	Coffee break	
11:10 – 12:00	<i>CROPPINO Wrap-up and Next Steps</i>	
	CROPPINO Overview	
	Final Reporting - Responsibilities, Deliverables & Due Dates	<i>Dr. Dragana Miladinović, IFVCNS</i>
	Plans for future – Possible Collaborations, Project Applications, Trainings	<i>All partners</i>
	Q&A & discussion	
	Meeting Closing	<i>All partners</i>
12:00 – 13:00	Lunch	



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Annex 4

CROPINNO Summer School
Phenotyping summer school
From 6th to 8th March 2024, March




Training School: Phenotyping summer school – Program

Day 1 (Wednesday, March 6th 2024)

09:00-09:15 Introduction to the Training School by Dr. Kerstin Nagel (building 06.2, room 406)

09:30-12:00 Hands-on phenotyping training, part I (meeting point: foyer of 06.2)

Group	Who?	What?
Group 1	Jonas Lentz, Anna Galinski	Root phenotyping using soil-filled rhizotrons - Soil preparation - Filling rhizotrons - Imaging roots - Root washing
Group 2	Dr. Henning Lenz, Shiyan Jia, Bernd Kastenholz	Root and shoot phenotyping using the high-throughput platform GrowScreen-Rhizo III - Demonstrations - Shoot harvest - WinRhizo root scanning
Group 3	Dr. Laura Junker-Frohn, Merle Fritsch	Shoot phenotyping - manual measurements (e.g. length of leaves, plant height) - demonstration of different devices (e.g. SPAD, Porometer, Fluopen)

12:00-13:30 Lunch (canteen 'Seecasino', meeting point: foyer of 06.2)

13:30-16:00 Hands-on phenotyping training, part II (meeting point: foyer of 06.2)

Group	Who?	What?
Group 1	Dr. Henning Lenz, Shiyan Jia, Bernd Kastenholz	Root and shoot phenotyping using the high-throughput platform GrowScreen-Rhizo III - Demonstrations - Shoot harvest - WinRhizo root scanning
Group 2	Dr. Laura Junker-Frohn, Merle Fritsch	Shoot phenotyping - manual measurements (e.g. length of leaves, plant height) - demonstration of different devices (e.g. SPAD, Porometer, Fluopen)
Group 3	Jonas Lentz, Anna Galinski	Root phenotyping using soil-filled rhizotrons - Soil preparation - Filling rhizotrons - Imaging roots - Root washing

16:15-16:30 Summary of the day / Outlook (building 06.2, room 406)

CROPINNO – Training School „Phenotyping“
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Day 2 (Thursday, March 7th 2024)

09:00-11:30 Hands-on phenotyping training, part III (meeting point: foyer of 06.2)

Group	Who?	What?
Group 1	Dr. Laura Junker-Frohn, Merle Fritsch	Shoot phenotyping - manual measurements (e.g. length of leaves, plant height) - demonstration of different devices (e.g. SPAD, Porometers, Fluopen)
Group 2	Jonas Lentz, Anna Galinski	Root phenotyping using soil-filled rhizotrons - Soil preparation - Filling rhizotrons - Imaging roots - Root washing
Group 3	Dr. Henning Lenz, Shiyan Jia, Bernd Kastenholz	Root and shoot phenotyping using the high-throughput platform GrowScreen-Rhizo III - Demonstrations - Shoot harvest - WinRhizo root scanning

11:30-13:00 Lunch (canteen 'Seecasino', meeting point: foyer of 06.2)

13:00-14:00 Hands-on training root image analysis (meeting point: foyer of 06.2)

Group	Who?	What?
Group 1	Anna Galinski	Root image analysis (building 06.1, room 010)
Group 2	Ann-Katrin Kleinert	Root image analysis (building 06.1, room 010)
Group 3	Jonas Lentz	Root image analysis (building 06.2, room 313)

14:00-16:30 Hands-on shoot image analysis (building 06.2, room 406)

Group	Who?	What?
Group 1,2,3	Dr. Mark Müller-Linow, Dr. Fabio Fiorani	Shoot image analysis

16:30-16:45 Summary of the day / Outlook (building 06.2, room 406)

Day 3 (Friday, March 8th 2024)

09:00-09:30 Introduction to agar-based phenotyping, part I (meeting point: foyer of 06.2)

Group	Who?	What?
Group 1 (plus half of group 3)	Bernd Kastenholz	Root phenotyping using agar-filled plates Demonstration of filling agar plates
Group 2 (plus half of group 3)	Dr. Henning Lenz	Root phenotyping using agar-filled plates Imaging agar plates using GrowScreen-Agar II imaging station

09:45-10:15 Introduction to GrowScreen Agar, part II (meeting point: foyer of 06.2)

Group	Who?	What?
Group 1 (plus half of group 3)	Dr. Henning Lenz	Root phenotyping using agar-filled plates Imaging agar plates using GrowScreen-Agar II imaging station
Group 2 (plus half of group 3)	Bernd Kastenholz	Root phenotyping using agar-filled plates Demonstration of filling agar plates

10:30-12:30 Data analysis (building 06.2, room 406)

Group	Who?	What?
Group 1,2,3	Dr. Laura Junker-Frohn, Constantin Eiteneuer, Dr. Henning Lenz	Data export / data analysis

12:30-14:00 Lunch (canteen 'Seecasino', meeting point: foyer of 06.2)

14:00-15:00 Presentation of results, discussion of open questions (building 06.2, room 406)

Annex 5

CROPINNO Webinar Series

Why are Omics Important for Plant Breeding

April-May 2025, online



CROPINNO Webinar Series
"Why are Omics important for plant breeding"

CROPINNO Tuesday Webinar Series - Two 45-min lectures followed by Q&A

April 1st 2025, on-line

	Decoding plant genomes: Technologies, insights, and strategies	Felipe Perez de Los Cobos Arnao, Sequentia Biotech, Spain
10:00 – 12:00	Unveiling plant biology through transcriptomics	Marco di Marsico, Sequentia Biotech, Spain

Zoom: <https://us06web.zoom.us/j/89868942938?pwd=J6Ub4XTQ94ahRb0Tlq3a3wAJ5ZcbKB.1>

April 7th 2025, on-line

	Application of omics for virus identification in crops	Prof. Fabio Marroni, University of Udine, Italy
10:00 – 12:00	Omics for investigating root/soil crosstalk	

Zoom: <https://us06web.zoom.us/j/83074925739?pwd=N2jHPbnlaeQ6uHzD6jwktN7QYdATt8.1>

April 15th 2025, on-line

	Omics for decoding recurrent drought stress responses for resilience	Dr. Giorgia Batelli, CNR, Italy Dr. Salvatore Esposito, CREA, Italy
10:00 – 12:00		

Zoom: <https://us06web.zoom.us/j/81778542662?pwd=hoobRPWAC2oGOxXugPgad5bx8b1kaY.1>

April 29th 2025, on-line

	Resequencing and omics integration	Dr. Eduardo Javier Ordonez Trejo, UNIPD, Italy
10:00 – 12:00	Crop Epigenomics	Pasquale Termolino, CNR, Italy

Zoom: <https://us06web.zoom.us/j/89049274484?pwd=y5AwEXsR6cbKfID00Eb8kNa9PFnLOC.1>

May 8th, on-line

	Chromatin and transcriptomic dynamics in tomato	Dr. Irene Luzzi, UNIPD, Italy
10:00 – 12:00		

Zoom:



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