CropXR

2nd Annual Progress Report

July 2024 - June 2025

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Executive summary

CropXR is an international public-private partnership dedicated to making agricultural crops more resilient to climate change and sustainable farming practices.

This second Annual Progress Report highlights the major progress that the partnership made between July 2024 and June 2025 towards its mission: developing smart, AI-powered tools that help the consortium and other breeders create crop varieties capable of thriving under sustainable cultivation in changing climates. These crops are designed to withstand a range of environmental stresses—such as drought, heat, flooding, and poor soil conditions.

People and partnerships

CropXR experienced strong growth during this reporting period. By mid-2025, over 70 researchers and staff were employed, representing more than 45 full-time equivalents (FTEs). This team includes PhD students, postdoctoral researchers, senior scientists, and technical and management personnel.

Through the Holland Innovative Potato consortium, a major potato breeding company joined the already robust public-private partnership. CropXR also strengthened its connections with national and international partners and networks, including SURF, ELIXIR, and AgBioData.

What we did

Over the past year, CropXR and its associated projects—PlantXR, EduXR, DataXR and AgroXR—carried out a wide range of activities:

- They laid the groundwork for the *Resilience Hub*, a digital infrastructure that will enable researchers and breeders to store, access, share, and analyse vast amounts of standardised scientific data.
- Preparations were made for large-scale biological experiments under laboratory and open field conditions to study how plants respond to different types of stress, across various scales and conditions.
- Machine learning techniques were introduced to analyse experimental data and build AI-driven functional plant models. These digital models will predict which combinations of genetic traits help plants cope with multiple stressors—ultimately allowing breeders to develop resilient crops more quickly and more effectively.
- A collaborative community was formed, bringing together academic researchers, applied scientists, leading breeding companies, and policymakers. This ensures that insights from basic research are rapidly translated into real-world crop development and more sustainable agricultural practices.

What we accomplished

Several milestones stand out from this year's progress:

- Phase two of the *Resilience Hub* was completed—a major step towards creating a digital backbone that connects all CropXR activities and will eventually be accessible to external researchers and breeding companies.
- A series of pilot experiments helped establish the best conditions for future large-scale trials. These included setups to test plant responses to drought and nutrient shortages in crops such as potatoes, tomatoes, lettuce, and cauliflower.
- To explore how soil microbes contribute to crop resilience, soil samples from 100 potato fields were collected, stored, and analysed.
- Early AI-based models were developed to simulate plant growth and stress responses, combining biological data with machine learning.
- A new multidisciplinary academic minor on breeding climate-resilient crops—focusing on multi-stakeholder approaches—was designed for Wageningen University.
- Major events like the Annual CropXR Conference and 'Resilient Crops in a Changing World: From Challenges to Solutions' brought experts together to discuss the future of agriculture.
- CropXR researchers and staff actively engaged with the wider community, giving talks, hosting workshops, and contributing to both peer-reviewed journals and trade publications.

Looking ahead

In its third year, CropXR will build on the previous accomplishments and milestones by:

- Launching phase three of the *Resilience Hub* development.
- Initiating pilot and large-scale laboratory and field experiments to study plant responses to various stresses—covering multiple species, multiple stress types, and many measurements related to genetics, growth, and soil health.
- Advancing data management tools, machine learning techniques, and AI-driven plant modelling.
- Continuing to grow a vibrant international collaborative network of researchers, breeders, and policymakers.

Preface

We are proud to present this annual report, documenting the strides we have made during CropXR's second year. From preparations for the large-scale experiments that will give us 'smart data' on how plants respond to multiple stressors, to the first baby steps toward using that data for AI-driven models that can inform future breeding, from the building of a collaborative community to many investments in reaching out to the world, our growing team has turned bold ideas into tangible milestones. The accomplishments listed in this report reflect the growing momentum behind our vision.

CropXR's mission remains clear and unwavering: to develop data-based, AI-driven, reliable tools that empower us and other breeders to digitally model and breed extra-resilient varieties or commercial crops. By providing proof of this revolutionary concept, we aim to accelerate the creation of ever more crop varieties that can withstand multiple environmental stresses while maintaining high yields.

This annual report serves to document and celebrate our collective progress, illuminate key advancements, and chart the path forward. We hope it provides stakeholders—partners in academia, industry, and government—with transparent insights into our activities, outcomes, and strategic priorities in the past and the coming year.

We extend heartfelt thanks to every researcher, data scientist, lab technician, support staff member, advisor, supervisor and others whose dedication has fuelled our work. We're equally grateful for the spirit of collaboration fostered among public and private partners—from university labs to leading breeding companies—which has enriched our research with diverse expertise. Finally, we recognize with deep appreciation the generous support of our funders, without whom these advances would not have been possible.

Looking ahead, we are energized by the promise of further breakthroughs in AI- and modelling-enabled breeding. As we build and refine our tools and expand partnerships, we remain confident that our work will strengthen society's ability to grow more resilient crops—ensuring sustainable food production for a growing global population even in the face of the challenges of climate change.

Utrecht, The Netherlands, October 2025

The CropXR Board of Directors:

Auke Damstra, Technology Director
Hedwich Teunissen, Managing Director
Guido van den Ackerveken, Scientific Director.

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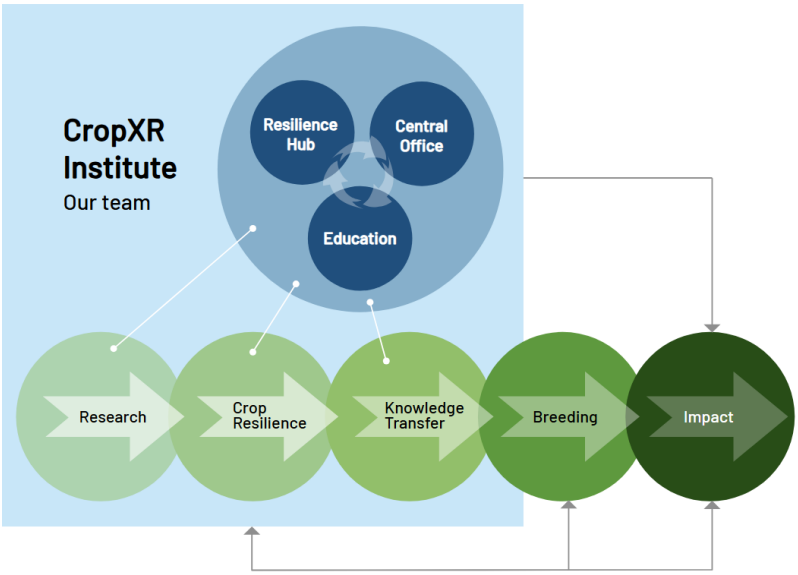
1. Who we are: our context, mission, strategy, and people

IN THE FACE of changing climates, growing populations, and the need for more sustainable agriculture, the world urgently needs more eXtra Resilient ('XR') crops. CropXR, a collaborative public-private partnership in The Netherlands, envisions a world in which breeders can more quickly breed more resilient crop varieties that can withstand multiple stressors like drought, floods, and salinisation while relying less on agricultural practices that harm the environment.

The public-private consortium works towards that vision with a clear mission: to develop revolutionary, data-based tools that will enable them and other breeders to use AI-driven computational models for more efficient breeding. Having those models will enable the world to breed resilient plant varieties far quicker than current breeding methods allow.

The partnership brings together many partners, including multiple universities and leading breeding companies. It will perform large-scale lab and field experiments that produce large amounts of 'smart-data', followed up by phenotype and bioinformatics analysis and state-of-the-art computational modelling. By repeating this cycle iteratively, it will create and gradually improve AI-driven crop models that can predict resilience based on specific combinations of multiple genes and other factors. Those models will enable highly targeted breeding of plant varieties with desired combinations of complex traits, such as resilience.

CropXR uniquely unites contributors from universities and private companies. An Open Science endeavour, it aims to ultimately share its data, knowledge and smart-data breeding tools through a newly built *Resilience Hub*. Its activities range from basic research and the development of computational tools and



methodologies to education, knowledge transfer, and societal outreach.

The CropXR project was launched in 2023 with generous co-funding from the Dutch Research Council (NWO), the National Growth Fund (Nationaal Groeifonds) and the US-based Foundation for Food and Agriculture Research (FFAR). These endowments enable the consortium to carry out its work until at least 2033, after which CropXR plans to continue its efforts with more partners and funders. In the reporting period the Holland Innovative Potato (HIP) consortium—one of CropXR's private sector partners—expanded its membership to include Agrico, among the world's leading potato breeding companies, further strengthening the private sector's involvement in CropXR.

At the end of the reporting period, dozens of people contributed to CropXR's mission.

In all, the collaboration comprised over 50 fulltime equivalents (FTEs) of personnel (see table below), including senior scientists, postdoctoral researchers, PhD students, technicians and central office support staff, involving more than 70 people in all.

Many others took part in a growing community that includes not just scientists and breeders but educators, regulators, and communicators as well.

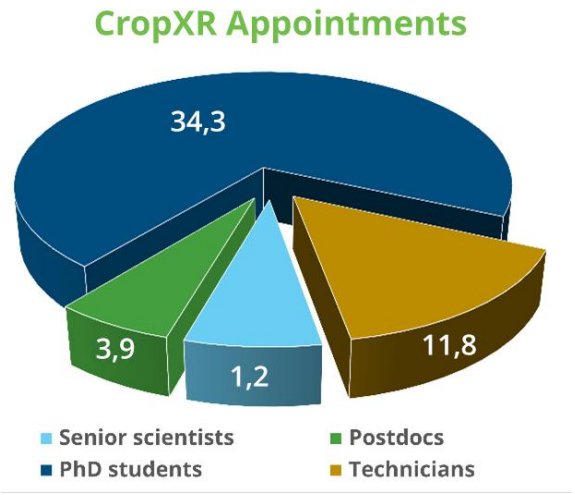
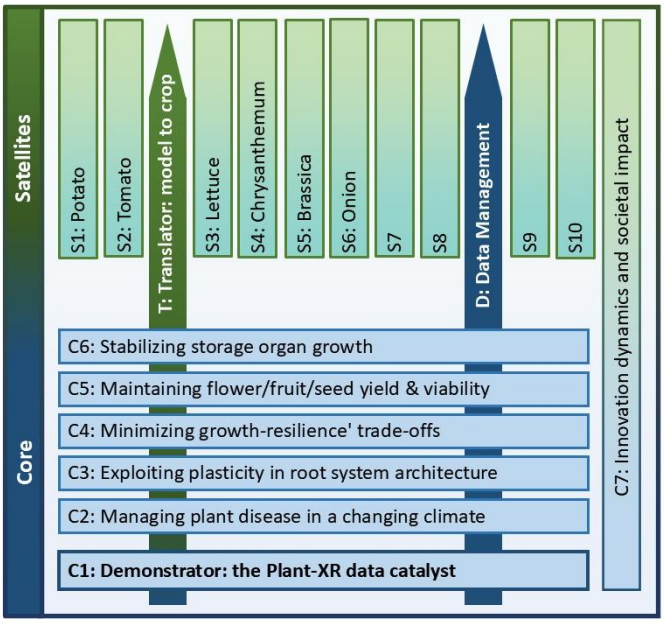


Table 1: CropXR-supported full time equivalent positions at participating universities at the end of the reporting period (30 June 2025).

Work package	Senior scientists	Postdocs	PhD students	Technical staff	Total
AgroXR		0,5	2,6		**3,1**
C1		2,0	5,9	1,5	**9,4**
C2			5,0	0,4	**5,4**
C3			3,0		**3,0**
C4			2,0		**2,0**
C5		1,0	2,9	0,5	**4,4**
C6			2,0		**2,0**
C7			4,0		**4,0**
D/DataXR			1,0	2,5	**3,5**
EduXR	0,7		0,1	1,2	**2,0**
S1		0,4	4,8		**5,2**
T			1,0	2,0	**3,0**
Office	0,5			3,2	**3,7**
Total	**1,2**	**3,9**	**34,3**	**11,8**	**51,2**

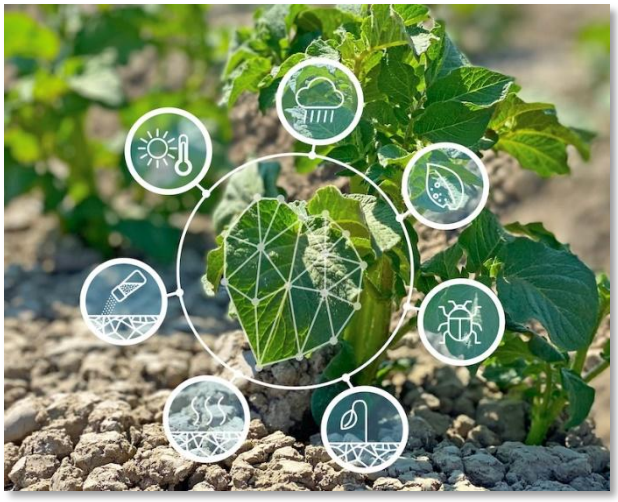
Apart from the **central office** located at the campus of Utrecht University, from where the collaboration is centrally managed, most of CropXR's work is carried out at facilities of its many academic and private partners.

The scientific work, also known as the PlantXR research programme, is structured into **work packages**, seven of which (**C1-C7**) belong to a 'core' that is primarily driven by public and academic partners and Industrial Executing Parties (IEPs)—Genetwister and KeyGene. Others are set up as 'satellites' in which private partners play the most important roles. One satellite work package ('S1'), working on potato, has started. Other satellites will be launched in Phase 2 (2028-2033).



Two work packages intersect with the seven other 'core' packages: **WP-D** (intertwined with DataXR), which covers all data infrastructure, data governance and data sharing in the newly built and developed *Resilience Hub*, and **WP-T** (Translator), which focuses on translating the knowledge that is gained in basic research on the model plant *Arabidopsis thaliana* into various crop species.

Separate projects focus on two specific tasks:
- **AgroXR** studies the breeding of crop varieties suitable for sustainable cultivation systems, and
- **EduXR** focuses on human resource-related challenges and educating a new generation of breeding experts able to bridge the biological and the computational spheres.



This annual report lists accomplishments of all these work packages and projects. For further information, readers are encouraged to visit our website at www.cropxr.org.

2. What we did: collaborate, research, reach out

CROPXR HAS SET THE FIRST STEPS toward what will become tools that can be used to fill a pipeline of more resilient varieties of many crops. Those first steps include preparing large-scale experiments needed for the generation of large amounts of data on how plants respond to environmental stressors such as heat, drought, nitrogen shortages, and so forth.

Other work has focused on the infrastructure to collect, harmonise, store, share and analyse all that data. Computational scientists have begun designing ways to feed all that data to sophisticated models built on machine learning and other forms of artificial intelligence (AI), an explosively growing field.

To enable this technological breakthrough, CropXR has begun building a community in which biologists, data scientists and computational experts from public research institutions, breeding companies, and government bodies meet, interact and collaborate.

CropXR's Central office

In this period, CropXR's central office focused on efforts to ensure communication, interaction, collaboration, cross pollination and synergy between the various projects, work packages and public and private partners. Its outreach was expanded from activities (mostly) limited to the national level to the international level as well.

Much effort was put into CropXR's legal collaboration agreements, necessitated by the fact that the funding arrangements in the National Growth Fund Grant letter did not fully match CropXR as a public-private partnership in the way it was originally intended.
Although CropXR and its components (PlantXR, EduXR, AgroXR, TransferXR) form a coherent whole in terms of content, they are distinct in their funding.
PlantXR, an NWO Long-Term Programme, receives joint public-private funding: 30% from NWO, 30% in cash from private company partners, 10% in-kind contributions from four universities, and 30% from three other sources: the US Foundation for Food & Agricultural Research (FFAR), the National Growth Fund (NGF) and a PPS surcharge from the Dutch Ministry of Economic Affairs. PlantXR is governed by the PlantXR consortium agreement, signed by 19 parties.

The other CropXR components receive public funding exclusively, from NGF. The formal funding order from Rijksdienst voor Ondernemend Nederland (RVO) for CropXR designates four universities (UU, TUD, WUR, UvA) as sole grant recipients. It does not allow private

participation in non-PlantXR components, other than what was originally foreseen. Time and effort therefore had to be invested in modifying the financial and legal arrangements.

A newly drafted and signed CropXR consortium agreement will operate alongside the PlantXR consortium agreement, with governance and data infrastructure provisions applying retroactively to both. Challenges include differing funding structures on intellectual property rights of private partners and interpreting EU's state aid regulations. To maintain commitment and engagement of industrial partners during the long deliberations, the central CropXR managing director role was more clearly defined.

We expect the new CropXR consortium agreement to be signed by all CropXR partners before the end of 2025, as well as a formal request to make some amendments to the RVO funding order. This will lay a robust legal foundation under continued growth of CropXR, which will ultimately facilitate and speed up collaboration.

Since CropXR involves collaboration between many very different parties, cultures, and spheres, internal and external communication is essential. A communications specialist established an infrastructure with several communication channels including a website, a LinkedIn page, a newsletter, and a range of virtual and physical meetings.
The website was expanded to include descriptions of activities of various work packages and profiles of people and work teams, among other things. By the end of the reporting period, it attracted about 1240 unique visitors per month on average. CropXR's LinkedIn page was frequently updated. It has built a worldwide following of about 4,000 people. Five newsletters were produced and distributed to close to 400 e-mail addresses.

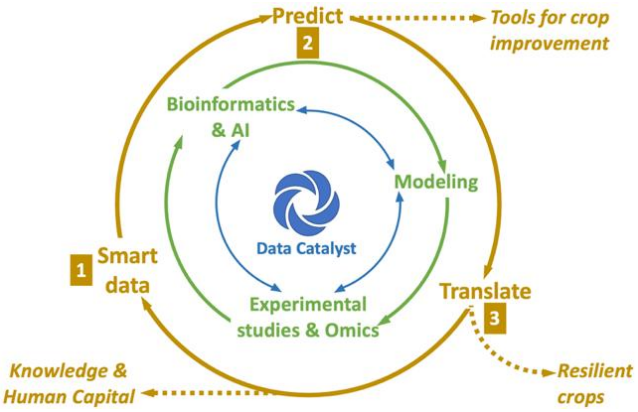
DataXR: Building, managing and sharing the Resilience Hub

Within DataXR (that also encompasses the data management of PlantXR WP-D), develops the *Resilience Hub*, a data and computational infrastructure backbone that supports and interconnects all activities in CropXR through data. The hub integrates data infrastructure, management, and governance to enable secure and seamless data sharing across researchers and work packages.
During the reporting period, existing platforms for data, file, and document storage—such as Slack, Sharepoint, and SURF Research Drive and Research Cloud—were made accessible to CropXR researchers. Two "SAME" (Standard and Metadata Expertise) groups have been established and convene monthly to define best practices, FAIR principles, and select appropriate standards for phenotyping and sequencing. Their work has led to the development of a Metadata Management Procedure, which is now accessible to all CropXR researchers.
To help reduce the administrative workload associated with data management, prototypes of an interactive, AI-powered virtual assistant—*MetaBuddy*—have been developed. A Data Access Committee (DAC) was formed to oversee and implement data access procedures across CropXR.
Additionally, quarterly *user group* meeting were held, engaging 37 participants to define data requirements and produce the first version of the data catalog specifications.
In June 2025, CropXR's technology director Auke Damstra was named co-Head of Node of green life sciences for ELIXIR-Netherlands, which will facilitate interactions between CropXR

and ELIXIR. Furthermore, Auke is member of the AgBioData Phenotyping Data Working Group that is chaired by Jihna Jung from Purdue University, enabling exchange with US initiatives on this topic.

Work Package C1: Demonstrator, the CropXR Data Catalyst

In WP-C1, researchers established experimental conditions for drought and high-temperature stress trials. An RNAseq pilot was used to optimize setup, timing, and sampling protocols, and RNA isolation from small sample sizes was optimized for large-scale implementation. A BoxSeed system was deployed, enabling seed selection based on morphometric features.



On the computational side, a modelling module was developed to describe hypocotyl and root growth responses to temperature, with preliminary insights into drought effects. Initial efforts were undertaken to expand the utilisation of published expression data and to link machine learning approaches to mechanistic models, one of the main challenges of CropXR.

Work Package C2: Managing plant disease in a changing climate

As part of WP-C2, a series of pilot studies were conducted to inform and optimize the design of a forthcoming joint experiment aimed at investigating plant adaptation to abiotic and biotic stressors. Emphasis was placed on elucidating the plant's hormonal crosstalk under combined stress conditions, and its downstream impact on gene expression and metabolite profiles. Insights from these preliminary studies guided the selection of key experimental parameters, including the sequence of combinatorial treatments and the timing of sample collection for RNA isolation and metabolite extraction. A temperature treatment protocol was validated, and specific pattern and hormone treatments were finalized.
To support metabolite profiling, a targeted glucosinolate analysis pipeline was established, encompassing extraction procedures, LC-MS methodology, and data processing workflows. Additionally, preliminary gene regulatory and metabolic models were developed and evaluated using existing datasets, laying the groundwork for integrative analysis in the joint experiment.

Work Package C3: Exploiting plasticity in root system architecture

In WP-C3, pilot experiments were conducted to (1) compare drought responses in soil-based versus plate-based systems, and (2) refine drought simulation protocols in rhizotrons. These efforts led to the planting of the first EcoPanel set in the rhizotron system at the Netherlands Pheno- and Ecotyping Center (NPEC), and preparations for a second experimental run. Following consultations with other work packages, standardized drought-mimicking assays on vertical agar plates were established.

Work Package C4: Minimising growth-resilience trade-offs

In WP-C4, genetic constructs—including the salicylic acid receptor NPR1—and seed materials were produced for proximity labelling proteomics experiments. Assays were standardized for both adult plants in pots and seedlings on vertical plates, combining far-red light treatments with drought stress. Constructs were designed to generate protein-fluorophore fusions for spatial regulation studies.
Preparations were made for a phenomics growth-defence screen involving ~700 Arabidopsis thaliana mutant lines, including detailed protocol optimizations. An RNAseq experiment investigating salicylic acid (SA) regulation of meristem activity was completed. A PhD candidate was recruited under subtask C4.4.

Work Package C5: Maintaining flower/fruit/seed yield and viability

In WP-C5, experiments in NPEC growth chambers were designed to study reproductive effects of heat and drought across *Arabidopsis* developmental stages. In C5.1, a pilot study identified robust methodologies for measuring reproductive output (pollen, seed yield, seed quality).

Initial experiments combining ambient temperature variation with mild drought were launched. In C5.2, an assay was developed to expose Arabidopsis plants to a gradient of drought conditions. Small pilot studies were completed, and a large-scale experiment was initiated. A second PhD candidate joined the team. In C5.3, a newly recruited PhD candidate began compiling all available single-cell RNAseq datasets from Arabidopsis flowers, anthers, and pollen. In C5.4, a theoretical framework was developed to interpret seed-related findings and identify promising directions for future research. In C5.5. the PhD candidate reimplemented components of an existing mechanistic multiscale model to support ongoing analysis.

Work Package C6: Stabilising storage organ growth

In WP-C6, greenhouse experiments related to drought and nitrogen deficiency were conducted with eight potato varieties (Avamond, Desiree, Fontane, Hansa, Lady Rosetta, Russet Burbank, Seresta, Spunta), selected from a larger pool of 20 field-tested cultivars. Drought Treatment: Watering was gradually reduced over four weeks post-tuber initiation, followed by a two-week rewatering phase. Morphological traits (e.g., plant height, stomatal size and density) and physiological traits (e.g., stomatal conductance, photosynthesis, chlorophyll content) were measured. Samples from multiple tissues—leaves, roots, and tubers—were collected for RNA sequencing, metabolite profiling (sugars), and enzyme assays. RNA from four cultivars was sequenced. Tuber and shoot biomass were measured at three harvest points: after 8 and 27 days of drought, and after 15 days of rewatering. Nitrogen Deficiency Treatment: Experimental conditions were initiated at tuber formation and maintained for four weeks, followed by a two-week recovery with normal nitrogen fertilization. Plants were phenotyped for photosynthetic and growth parameters and sampled for transcriptomic and metabolic analyses focused on nitrogen metabolites (nitrate, nitrite, ammonium). Two intermediate harvests were included.
Pilot experiments were also conducted with eight onion cultivars selected by ENZA Seeds and Bejo Seeds. Plants were exposed to early and late drought periods in large crates under

protective cover to simulate drought under near-field conditions. Greenhouse-grown backups were maintained for whole-plant digital imaging.

Work Package C7: Innovation dynamics and societal impact

In WP-C7, three of the four subtasks advanced significantly during the reporting period. Researchers and partners engaged in frequent interactions across CropXR, supported by weekly PhD student meetings and broader team sessions every six weeks. In C7.2, the PhD student developed conceptual and theoretical frameworks for dissertation work, which received approval from two external reviewers. In C7.3, another PhD student began work on two dissertation papers: one on Access and Benefit-Sharing (ABS) mechanisms in global frameworks for genetic resource exchange, and another on emerging ABS regulations related to Digital Sequence Information under the Convention on Biological Diversity. Twelve expert interviews within CropXR were conducted to inform this work. In C7.4, a PhD student completed data collection for a study on plant scientists' perspectives on agricultural resilience. She also began selecting case studies for a comparative analysis of collaboration within CropXR versus other resilience-focused research initiatives.

Work Package T: Translator – from model to crop

In WP-T, experimental work began to establish transcriptomics setups for seedling establishment in four commercial crops—potato, tomato, lettuce, and cauliflower—under heat and drought conditions aligned with WP-C1 protocols. Parameters for climate stress (temperature and watering), phenotyping (e.g., hypocotyl length, shoot and root dry weight), and seedling establishment duration were defined. Genotypes were selected for crop-specific phenotyping and transcriptomics assays. [*Tomato*:] While awaiting Heinz accession seeds (with a fully sequenced genome), pilot experiments were conducted using the Moneymaker cultivar. [*Lettuce*:] Seven lines (Olof, Cobham Green, Salinas, Iceberg, Eldorado, Green Towers, and Salad-bowl) were selected based on high-quality genome assemblies from the Michelmore Lab. [*Cauliflower*:] Pilot experiments with four genotypes helped determine optimal temperature, light, and watering/drought conditions.

In WP-T.2, Genetwister, a private CropXR partner, curated publicly available plant genomes for comparative genomics research. A representative set of 27 species—including key crops, Arabidopsis, and basal species like *Amborella trichopoda*, *Acorus gramineus*, *Aquilegia coerulea*, and *Ginkgo biloba*—was assessed for genome quality. Four genomes were reannotated using public transcriptomes due to low annotation quality or BUSCO completeness. Using OrthoFinder, orthologous gene clusters were identified, including multiple sequence alignments, gene tree construction, and gene-species tree reconciliation for high-resolution ortholog detection. Manual

phylogenetic analyses were performed for key drought and temperature stress signalling genes. Initial analyses of conserved gene expression were conducted to identify regulatory sequence features.
All research data were uploaded to the *Resilience Hub*, CropXR's data-sharing infrastructure. Additionally, leaf and root expression datasets from Arabidopsis, lettuce, and potato were collected.

Work Package S1: Potato

In WP-S1, the satellite work package dedicated to potato, activities included extensive field and greenhouse research alongside mathematical modelling efforts.

Two large-scale field trials were conducted to assess the responses of 20 core potato cultivars to varying nitrogen and water availability—one at SPNA Kollumerwaard and the other at AIKC Rusthoeve (RH). Four irrigation and four nitrogen application treatments were tested, resulting in 16 combinations, of which 12 were successfully completed with two replications each. Intermediate harvests were taken at key developmental stages and under varying water/nitrogen conditions, followed by a larger final harvest. Phenotyping was performed both above and below ground. Drone imagery was captured and processed by Hiphen, contributing to the development of protocols for future aerial trait extraction. Ground-based measurements included leaf area and photosynthetic parameters, while tuber traits were assessed at multiple harvest points.
Insights from these trials—supported by statisticians, agronomists, physiologists, modelers, and breeders from both academic and industry partners—were used to optimize trial designs for the next growing season, balancing workload and data collection.

To investigate the role of soil microbiomes in crop resilience, soil samples were collected from 100 potato fields across the Netherlands for the newly established CropXR Potato Microbiome Soil Library at the NPEC facility, Utrecht University. Samples were sent out for physicochemical analysis, and microbial DNA was extracted for 16S rRNA amplicon sequencing. Farmer experience data was also collected to contextualize microbiome profiles. Preliminary experiments were conducted to refine protocols for a future large-scale study, in which sterile soils will be inoculated with microbiomes from the library and potato growth will be monitored using the advanced imaging technologies available at NPEC. Additional experiments explored how soil microbiota influence potato root development. Microbiome profiles were also gathered from soil surrounding the 20 cultivars used in the field trials.

To advance mathematical modelling of potato growth, a literature review was conducted to evaluate current approaches, including statistical models, process-based models, genomic prediction, and machine learning-based frameworks. Preliminary models were developed to explore nonlinear dynamics and spatial correction effects, laying the groundwork for more sophisticated models.

AgroXR: Studying resilience in crop cultivation systems

AgroXR aims to connect research into more resilient *crops* and research into more resilient *agronomic systems* in which crops are grown. In consultation with CropXR partners and management, AgroXR developed plans for two PhD student research project proposals on the breeding of crop varieties suitable for sustainable cultivation systems. Also, a network of potential collaborators was built, including researchers involved in varietal registration trials (CGO testing) in The Netherlands and abroad (such as INRAE (France) and Agroscope (Switzerland)). Various meetings with CropXR partners were held. Topics include approaches to estimate partial yields or genotype proportions from mixed stands or seed lots and developing methods for leveraging GxE datasets for mixture assembly.

EduXR: building the learning community of CropXR

EduXR worked to build a mature 'learning community' within CropXR. Three times a year, lecturers from universities of applied sciences (HBOs), students, and industry representatives come together to exchange insights on applied research into crop resilience. Key focus crops include potato, onion, cabbage, tomato, lettuce, and chrysanthemum. For each of these crops, dedicated groups have developed long-term visions for applied research, providing a valuable foundation for satellite research plans in the second phase of CropXR.

An academic minor curriculum, tailored to CropXR's mission and the knowledge and insights the collaboration requires, was developed. Efforts were also invested in expanding CropXR opportunities for research at universities of applied science (UAS) and preparations for a new minor curriculum at Wageningen University.

3. What we accomplished

IN CROPXR'S SECOND YEAR, much was accomplished within the various work packages and projects that are part of the collaboration. Almost all began preparing for or carrying out experimental, analytical, and/or modelling studies. Below is a sample of notable examples, which does not claim to be complete.

Hiring and Organisation

Dozens of postdoc researchers, PhD students, technicians, and other support staff were recruited and introduces to their tasks. By the close of the reporting period, nearly all planned CropXR-funded positions had been successfully filled. In total, 45.7 full-time equivalents—spread across 72 individuals—were appointed across the various programmes and work packages.

In addition to the directly funded positions, a substantially larger group of individuals is actively engaged in the research. This includes Principal Investigators (PIs), (co-)supervisors, and representatives from affiliated companies who participate in governance bodies, working groups, and advisory panels. Several hundreds of people contribute to CropXR activities and regularly take part in meetings and events.

At the central office, efforts also focused on the refinement of the legal collaboration agreements that cover intellectual property, governance, access to and use of data in the *Resilience hub*. While the PlantXR collaboration agreement between public and private partners remains in effect, the previously-signed CropXR collaboration agreement needs adapting because of requirements from funders. A new CropXR collaboration agreement will soon be completed, which will ease and speed up collaboration.

In WP-D, through meetings and workshops a robust data management and governance framework took shape. Two Standard and Metadata Expertise (SAME) groups developed a Metadata Management Procedure (MMP), establishing clear guidelines for describing the research data— such as plant phenotyping and sequencing data sets—connecting much of CropXR research and ensuring all data are findable, accessible, interoperable, and reusable (FAIR).

Data infrastructure: the CropXR Resilience Hub

DataXR delivered the second phase of the *Resilience Hub*, CropXR's central data architecture. The Resilience Hub integrates data infrastructure, data management, and data governance to enable secure and seamless data sharing between researchers, work packages and public and private partners. Ultimately, the hub will also be accessible from the world outside.

Initial connections were made with ELIXIR, a European intergovernmental organisation that brings together life science resources from across Europe including databases, software tools, training materials, cloud storage and supercomputers. In effect, it forms a European plant bioinformatics infrastructure.

Criteria and preconditions for pilot testing of CropXR's computing infrastructure were defined.

Early research results

Some work packages defined early results, often preliminary and/or designed mostly to inform bigger experiments that will support firmer conclusions. Below is a sample of them.

In **WP-C1**, early results show that selecting core accessions by ecological data, rather than genetic diversity, yields better performance for environment-driven phenotypic traits than using a larger set. Initial predictive models for *Arabidopsis thaliana* were developed.

In **WP-C2,** preliminary findings demonstrated that a 24-hour exposure to elevated temperatures is enough to elicit measurable changes in gene expression. This provides a validated parameter for temperature-induced stress in subsequent experimental designs.

In **WP-C3,** a robust and reproducible protocol was developed for inducing sublethal drought stress in a soil-based rhizotron system. In parallel, the EcoPanel—a curated set of natural *Arabidopsis thaliana* accessions—was established for genetic diversity studies. Preliminary phenotyping from genome-wide association studies revealed a pronounced effect of soil moisture variation on both shoot growth and root system architecture. Early findings from experiments investigating shoot-to-root signalling under drought stress suggest that applying a sucrose (sorbitol) droplet to the shoot promotes lateral root formation.

In **WP-C4**, preliminary results from the RNAseq experiment investigating salicylic acid (SA) regulation of meristem activity revealed a potential role for SA receptors and suggested significant crosstalk between salicylic acid, jasmonic acid, and ethylene signalling pathways.

In **WP-C5**: pilot studies uncovered notable but contrasting effects of drought conditions on flowering time, indicating genotype-specific responses. Experiments confirmed that mild heat, mild drought, and combinations across the full life cycle negatively impact seed production.

In **WP-C6** the tested potato cultivars exhibited stomatal closure and reduced transpiration under drought conditions, leading to diminished shoot and tuber growth. However, the timing and nature of adaptive responses varied. Some cultivars reinvested in shoot growth, initiated new tubers, or enhanced bulking of existing tubers—suggesting diverse strategies of carbon partitioning during stress and recovery phases. Low-nitrogen conditions reduced overall growth across all cultivars to different extents. Some cultivars prioritized tuber development, with a few initiating tuberization earlier under low-N conditions than under controls. By the end of the low-N period, most cultivars showed reduced leaf area and chlorophyll content, reflecting physiological stress.

In **WP-C7**, a literature review led to the adoption of a philosophical lens to explore the concept of responsiveness within the broader framework of responsible innovation.

In **WP-T**, early results were achieved across four crop species: potato, tomato, lettuce and cauliflower. In potato, using True Potato Seeds from Solynta under long-day conditions, 70% relative humidity, and varying temperatures, lines were identified that showed sustained germination and development. In tomato, germination protocols and drought treatment settings were optimized, and key phenotypic traits were selected for the follow-up studies. In lettuce, the pilot studies revealed different responses to temperature and drought in selected lines. In cauliflower, genotype OB00503 (Enza) was selected for upcoming seedling establishment experiments.
Also, analysis of leaf and root expression data from *Arabidopsis*, lettuce, and potato confirmed prior findings that low-copy orthologs exhibit relatively well-correlated expression—particularly in leaf tissue between *Arabidopsis* and lettuce. The preliminary results suggest a correlation between coding sequence divergence and expression sequence divergence. Early results from our comparative transcriptomics analysis support the hypothesis that gene and genome duplication events contribute to subsequent functional specialization of genes. This finding is particularly significant for the translation of gene modules across species and contexts.

In **WP-S1**, preliminary results indicate that traits such as canopy cover and leaf area index are effective indicators of treatment responses and genotypic variation under different nitrogen levels. Heavy rainfall during the trial limited the ability to assess the effects of different irrigation regimes. Nitrogen application levels had significant but variable impacts on growth, biomass distribution, tuber yield, and quality across genotypes. Early results of experiments on the influence of soil microbiota on potato root development provided valuable insights into the effects of single and combined microbiota. These findings will inform future high-throughput experiments using the CropXR microbiome library. For modelling, use of the Sparse Identification for Nonlinear Dynamics (SINDy) framework to synthetic crop growth data showed promising results, which may offer advantages over traditional process-based models such as WOFOST.

Publications

In the reporting period, five research papers based in part of entirely on CropXR research, were published in peer-reviewed journals. CropXR scientists are marked blue:

- **Monica L García-Gómez, Kirsten H W J Ten Tusscher**: Multi-scale mechanisms driving root regeneration: From regeneration competence to tissue repatterning; *Plant J*. 2024 Aug;119(3):1183-1196. Doi: 10.1111/tpj.16860.
- **Ben Noordijk, Monica L Garcia Gomez, Kirsten H W J Ten Tusscher, Dick de Ridder, Aalt D J van Dijk**, Robert W Smith: The rise of scientific machine learning: a perspective on

combining mechanistic modelling with machine learning for systems biology. *Front Syst Biol*. 2024 Aug 2;4:1407994. doi: 10.3389/fsysb.2024.1407994.

- Vivien I Strotmann, **Monica L García-Gómez** et al.: Root stem cell homeostasis in Arabidopsis involves cell-type specific transcription factor complexes; *EMBO Rep*. 2025 May;26(9):2323-2346. doi: 10.1038/s44319-025-00422-8.
- Scott Hayes, Cheuk Ka Leong, **Francesca Giaume**, Elizabeth van Veen, Wenyan Zhang, Marthe Lamain, Jasper Lamers, Thijs de Zeeuw, Francel Verstappen, Andreas Hiltbrunner, **Christa Testerink:** Warm temperature and mild water stress cooperatively promote root elongation. *Curr Biol*. 2025 Aug 4;35(15):37863795.e5. doi: 10.1016/j.cub.2025.06.062.
- **Ben Noordijk**, **Marcel Reinders**, **Aalt D.J. van Dijk**, **Dick de Ridder**: BADDADAN: Mechanistic Modelling of Time Series Gene Module Expression. *bioRxiv* 2025 Feb 23. (After peer review published in *Quantitative Plant Biology* doi: 10.1017/qpb.2025.10017).

Other publications included contributions to online magazines and trade journals:

- Hedwich Teunissen (interviewed): On the verge of a new era in plant science innovation; *SeedWorld* (seedworld.com), 2024 Sep.
- Guido Van den Ackerveken (interviewed): Met resistentieveredeling is veel winst te behalen in de gewasbescherming; *Bloemisterij (*Dutch flower trade journal), 2024 Nov.
- Rachel Visscher: CropXR werkt aan resistentere gewassen; *Gewasbescherming*, journal of the Royal Dutch Plant diease Association (KNPV), 2024 Dec.
- Rachel Visscher: Transforming Agriculture - The revolutionary smart data breeding technology of CropXR; Community Plant Variety Office (CPVO) website, 2025 Jan.
- Aisha So: *Hero, who cared about the forest and wanted to transform it;* graphic story published in EASST Review, 2024 Dec;43(2) [View online]

Interaction and Collaboration

On 17 and 18 October 2024, CropXR participants gathered in Soesterberg, The Netherlands, for the first scientific CropXR Conference to learn about each other's research. The programme offered talks, (poster) presentations, workshops, and social interaction, including a keynote lecture by Klaas Vandepoele, of Ghent University and the VIB-UGent Center for Plant Systems Biology.

In April 2025, a CropXR Community Event was organised for a broader multi-stakeholder community in Utrecht, The Netherlands including researchers, breeders, growers, and policymakers. Titled *Perspectives. Resilient crops in a changing world: from challenges to solutions*, expert

talks explored topics like impacts of extreme weather on crops, use of fertilisers and pesticides, and alternative cropping systems such as regenerative farming. (Photo: Jelmer de Haas)

The Young CropXR network fosters personal and academic exchange among early-career scientists. Quarterly events feature sessions where PhD students present research and engage in peer discussions. In the reporting period, three *Young CropXR events* were held.

Outreach and Presentations

Dozens of presentations, talks, sessions, and workshops were held and/or produced by CropXR participants. About half of the outreach took place in The Netherlands, about half in other countries. A notable example was a CropXR-hosted workshop on *Scientific Machine Learning for Systems Biology* at the annual Plant & Animal Genomics (PAG) Conference in San Diego, which is visited by around 2,500 scientists from all over the world. The workshop was well received and helped promote CropXR on a global stage.

- July 2024: Presentation by Koen Beumer at the 4S/EASST conference in Amsterdam, The Netherlands
- October 2024: Workshop presented at the Royal General Bulb Growers' Association (KAVB) in Hillegom, The Netherlands.
- October 2024: *CropXR-resilient crops through data-driven design*. Talk by Hedwich Teunissen at Ministry of Agriculture (LVVN), The Hague, The Netherlands.
- October 2024: Talk by Koen Beumers at SISA-4 Workshop in Kassel, Germany.
- October 2024: Talk by Victor Betriu Yáñez at ESDiT Conference 2024, Enschede, The Netherlands.
- October 2024: Talk by Elsenoor Wijlhuizen at the Earth System Governance/TC conference.
- October 2024: *Exploring the breeding implications of diversified cropping systems – GxG or GxM?*; talk by Max Wellens at ARC CoE for Plant Success conference. [Watch on youtube]
- December 2024: Talk by Guido van den Ackerveken, CropXR Scientific Director, for UK researchers, UK research funding organisations and representatives of the Dutch Top Sector Horticulture and Starting materials at the Embassy of the Netherlands in London, United Kingdom.
- January 2025: *Scientific Machine Learning for Systems Biology*, workshop organised and presented by Monica Garcia Gomez and Dick de Ridder at the Plant & Animal Genome Conference (PAG) 2025 in San Diego, USA. [Watch online]
- January 2025: Two talks by Guido van den Ackerveken, CropXR Scientific Director, at Limagrain conference in Barcelona, Spain.

- March 2025: Keynote lecture by Hedwich Teunissen (CropXR managing director) at TU Delft AgTech Congres in Delft, The Netherlands.
- March 2025: Talk by Guido van den Ackerveken, CropXR Scientific Director, at 'Meet the professor' event at Utrecht University, Utrecht, The Netherlands.
- March 2025: *An example of a successful long-term acquisition at national level: CropXR.* Talk by Richard Immink, CropXR Work Package lead, at the kick-off event of the Belgian Plant Science Community (inspired by CropXR) in Meise, Belgium.
- March 2025: *Machine learning in plant science and plant breeding*; talk by Aalt-Jan Van Dijk at Crop Innovation & Business Conference in Cologne, Germany.
- March 2025: *Introduction to machine learning on omics data*, presentation by Aalt-Jan van Dijk at Lorenz Workshop, Leiden, The Netherlands
- April 2025: Talk by Hedwich Teunissen (CropXR managing director) at CPVO's 30th anniversary event in Angers, France.
- May 2025: Integrated Modelling of Plant Life-History Traits, poster presentation by Kyran Wissink at bioSB, Baarlo, The Netherlands.
- May 2025: *Future perspective: AI-driven plant breeding*, presentation by Aalt-Jan van Dijk at SILS 25y anniversary symposium, Amsterdam, The Netherlands.
- May 2025: Future perspective: AI-driven plant breeding; talk by Aalt Jan van Dijk at '25 year Swammerdam institute' symposium, Amsterdam, The Netherlands.
- June 2025: *Reprogramming of defence-related plant hormone networks under temperature stress*; Poster presentation by Julia Ruiz Capella at ICAR2025 Conference in Ghent, Belgium.
- June 2025: Talk by Hedwich Teunissen, CropXR managing director, at the SeedNL Annual Event in Amsterdam, The Netherlands.
- June 2025: Online presentation by Guido van den Ackerveken, CropXR Scientific Director, to the Novo Nordisk Foundation.
- June 2025: Talks by Koen Beumers at IST 25 conference in Lisbon, Portugal.
- June 2025: *Exploring the molecular control of growth-immunity tradeoffs in Arabidopsis thaliana*; poster presentation by Nienke van der Wal at the International Conference on Arabidopsis Research (ICAR) 2025 in Ghent, Belgium.
- Quarterly DataXR Usergroup meetings to connect with CropXR partners on data topics, Utrecht, The Netherlands.

Education

To strengthen participation from universities of applied sciences, project application and funding models were revised to offer more flexible, multi-semester funding opportunities (€15,000–€35,000). Eligibility criteria were expanded to include lecturer-led research projects in addition to student projects. These changes have improved project continuity, enhanced quality, and increased alignment with industry needs.

An interdisciplinary minor study curriculum titled *Climate-Resilient Crops: Interdisciplinary Approaches* was completed. The minor will be launched in September 2025 at Wageningen University.
The new curriculum is aimed at students in the social sciences, life sciences and data sciences who have an interest in the development of climate-resilient crops and the interdisciplinary approaches that are involved. The minor is open to students from both academic universities

and universities of applied sciences. It includes real-world assignments to projects at CropXR partners.

To strengthen the link between fundamental research at academic universities and applied research at universities of applied sciences (UAS), three PhD candidates have been appointed to serve as bridges between these domains.

Two half-day Learning Community events were held, featuring poster presentations, workshops, and strategic discussions. These gatherings fostered meaningful interaction among students, researchers, industry partners, and educators.

4. Looking ahead: plans for the third year

IN THE NEXT reporting period, CropXR will build on the many advances that were achieved during the first two years in its many work packages and projects. The section below highlights a few of them for the various components of the collaboration.

CropXR Central Office

In October 2025, the second Annual CropXR Conference will convene all CropXR participants to share progress, exchange experiences, and strengthen interdisciplinary collaboration across CropXR's work. PhD students and postdoctoral researchers will present their work through dedicated sessions and poster presentations, contributing to the visibility and integration of early-career research. Keynote speakers will include Kathy Roberts Munkvold (Scientific Program Director for Next Generation Crops, FFAR); Elysa Overdijk (Lecturer in Plant Physiology, Wageningen University); Monica Garcia Gomez (Assistant Professor, Utrecht University), Marcel van Verk (Vice-President Crop Data Science, KeyGene); Atoesa Farokhi (Coordinator External Collaboration, Amsterdam Green Campus), and Lidija Berke (Genetwister).
In the new reporting period, the planning of Phase 2 of the CropXR project will seriously kick off. Further opportunities for collaboration and funding will be actively explored. To support these efforts at an operational level, a new position of Research Support Officer will be created. Its responsibilities will also include drafting grant proposals.
CropXR's legal framework will be finalised, providing a robust foundation for effective collaboration between academic institutions and industry partners.

Work packages and projects:

In **Work package D,** the Data Access Committee will review the data access procedures that were established for use across CropXR. Explainer videos will be developed to assist researchers in using the *Resilience Hub* for storage and analysis of data. Collaboration with other NGF and GWI initiatives will be actively explored, as many of these programmes encounter similar challenges in the areas of data and AI. By working together on shared research infrastructure, there is significant potential to achieve greater impact and efficiency within existing budgets—for example, through improved services and security, enhanced computational speed, and expanded access to AI models and capacity.

In **Work package C1,** the modelling module describing hypocotyl and root growth responses to temperature and drought will be expanded to include additional drought-relevant factors and integrate time-of-day dependencies, enhancing its biological realism and predictive

power. To further strengthen harmonization and cross-package synergy, a second full-day coordination meeting with WP-T is scheduled for the fall of 2025. A meeting with WP-C3 principal investigators is planned to strengthen collaboration and reduce potential overlaps in research focus.
In September 2025, we expect to submit a research paper detailing a scalable algorithm for synthesizing barrier functions for biological systems. Software code for generating barrier functions for mass action ordinary differential equations (ODEs) will be finalized.
A large-scale experiment using a matrix of elevated temperature and drought stress will be performed for the transcriptomics analysis of the Arabidopsis thaliana Col-0 reference accession. The data will be used for data-driven models, laying the groundwork for deeper insights into understanding the mechanisms underlying stress responses.

Work package C2 will focus on five activities: 1) Execution of a large-scale joint experiment involving molecular pattern treatments and combinatorial hormone applications under elevated temperature conditions. RNA and metabolite samples will be collected to support the development of Gene Regulatory Network (GRN) and Multi-layer Network Models (MNM). 2) Implementation of a methyl jasmonate (MeJA) treatment experiment at elevated temperature, featuring high-resolution temporal sampling for RNA, metabolite, and protein extraction. These datasets will serve as input for the MNM model. 3) Enhancement and refinement of preliminary GRN and MNM models. 4) Initiation of integrating the two models. 5) Establishing bioassays targeting plant interactions with pathogens and insect herbivores.

Work package C3 will continue experimentation. Subtask C3.1 will complete a second round of EcoPanel genome-wide association studies (GWAS), followed by data processing and early-stage analysis aimed at identifying genes linked to drought-adaptive root system architecture (RSA) traits. In C3.2, a newly recruited PhD student will carry out phenotypic assays to characterize key RSA traits under water deficit conditions and evaluate their correlations with changes in root cell morphology. C3.3 efforts will focus on isolating phloem-mobile mRNAs and validating preliminary findings that suggest shoot-applied sucrose promotes lateral root development. C3.4 and C3.5 will recruit two PhD students and launch its experimental work.

In **Work package C4**, a new model describing salicylic acid (SA) regulation of meristem activity will undergo experimental validation. A large-scale phenomics screen of about 700 *Arabidopsis thaliana* mutant lines is scheduled for September–December 2025 in the NPEC G7 chamber, targeting growth-defence trade-offs. In subtask C4.4, a recently hired PhD student will begin work in September 2025. In C4.5, recruitment of an additional PhD student is planned.

In **Work package C5**, two experiments at NPEC will be completed, with analysis of sampled leaf tissue, meristem-enriched material, and pollen. The NPEC growth chamber will be reconfigured for a second experimental run under revised temperature conditions. In C5.4, experiments at NPEC and Wageningen University will confirm earlier findings on the negative effects of mild heat, mild drought, and their combinations on seed production. These will also assess life-cycle-specific impacts of mild heat. Additional experiments will investigate how parental exposure to mild heat and drought—individually and in combination—affects seed traits such as dormancy and vigor. 'Omics'-based studies will be optimized to assess the effects of both parental and directly experienced stress on germination.

In **Work package C6**, sequenced RNA and other measurements from completed potato experiments (including transcriptomic and metabolomic data) will be analysed. Complementary biochemical assays will help identify physiological and molecular traits linked to drought and nitrogen deficiency adaptation and recovery across cultivars. A new potato trial for the 2025 growing season has been initiated, with cultivars grown under protective covers to simulate drought while maintaining near-field conditions. Onion pilot plants will be phenotyped, with attention to morphological challenges such as hollow, elongated leaves. Onion samples will also undergo RNA and metabolic profiling.

In **Work package C7**, a PhD student will be recruited to resume work on innovation dynamics, following the earlier discontinuation of a contract. In C7.3, the conceptual outline of a paper on Access and Benefit-Sharing (ABS) will be presented at the Earth System Governance Conference in South Africa (TCESG/25) in August 2025. The second half of about twenty interviews with ABS and Digital Sequence Information (DSI) experts—focused on companies and private organisations—will be conducted. Insights from these interviews will inform sessions with private-sector stakeholders on how evolving regulations may influence their strategies and practices.

Work package T will finalise the search for optimal drought levels to support experiments used for studying combined stress responses in potato. In lettuce, results from a pilot study varying temperature and drought will be analysed to identify optimal operating points and select representative lines for the larger follow-up studies. Additional early-diverging plant genomes will be selected and collected to enrich comparative transcriptomics efforts. A large language model-based script for mining journal abstracts will be completed to enhance functional annotation beyond the current capabilities of curated genome databases.

In **Work package S1**, field trials with potato will continue to assess plant and tuber growth under varying drought and nitrogen treatments across twenty cultivars. Remote phenotyping using drone imagery is expected to improve, building on insights from the previous reporting period. Comprehensive physio-chemical and genetic analysis of soil microbiomes in the CropXR Potato Microbiome Soil Library will be completed. New studies will begin on extreme microbiomes from the library, using a broad set of potato genotypes to identify loci of "M genes"—genes associated with maximizing the growth and performance benefits conferred by microbiota.

In the next reporting period, **AgroXR** will begin carrying out stakeholder research; review the connection between digital technologies and cropping systems research; investigate social scientific systems that foster breeding for new cropping systems; and investigate the connections between automation and labour relations in different cropping systems. Research on the effect of mixed cropping systems on crop resilience will be expanded. It is envisioned to also work on cauliflower to link to the Flagship plans.

EduXR will continue strengthening and facilitating CropXR's 'learning community', helping students, lecturers and research teams connected to various work packages and crop species to develop shared visions for basic and applied research.

5. Annex: Founders, partners, funders, governance

Founders

Partners

Vegetable breeding companies

Potato breeding and processing industry

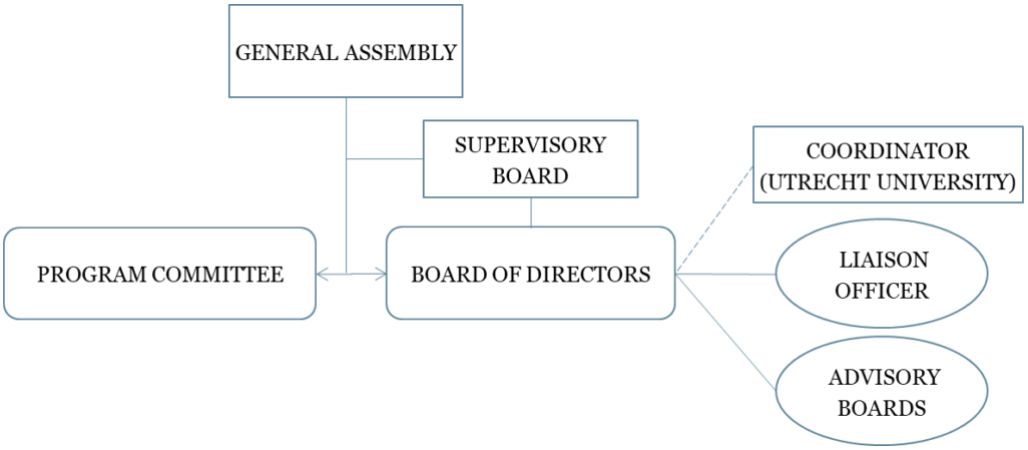
Ornamental breeding companies

Technology companies

Education Partners

Funders

Governance



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