OFFICIAL PROGRAMME

Norwegian Plant Biology Conference

NPBC 2026 — Bodø, Norway

17–19 June 2026

Workshops · Keynotes · Sessions · Excursion · Dinner

VENUE

Scandic Havet, Bodø

SPPS · NORD University · Photosyntech · kelpinor® · PheNo

About the Conference

Norwegian Plant Biology Conference 2026

NORWEGIAN PLANT BIOLOGY CONFERENCE — HISTORY & MISSION

The Norwegian Plant Biology Conference (NPBC) is a recurring national meeting that unites the Norwegian plant science community with international colleagues. Drawing on Norway's strong traditions in marine biology, ecology, and plant science, the NPBC series has grown to encompass not only vascular plants but also macroalgae, microalgae, and allied organisms — reflecting the breadth of modern plant biology research in Norway and Scandinavia.

Previous editions of the conference have rotated among Norwegian university cities, bringing together researchers from academia, research institutes, and industry in an informal and collegial atmosphere — most recently in March 2024 at the Botanical Garden of the University of Oslo, organised with the Norwegian Plant Network and the Photosyntech research school. In 2026 the conference travels north of the Arctic Circle to Bodø for the first time. The NPBC aims to foster cross-disciplinary collaborations, highlight emerging research directions, and provide early-career researchers with a welcoming platform to present their work and connect with the broader community.

NPBC 2026 is organized under the auspices of the **Scandinavian Plant Physiology Society (SPPS)** and is supported by the Norwegian National Graduate School in Plant and Algae Science (Photosyntech), the Norwegian Plant Phenotyping Infrastructure (PheNo), Kelpinor AS, and Nord University. It is the first time the conference is held in Bodø and the first edition to span themes from vascular plants to marine macroalgae and microalgae at full breadth, reflecting the unique research profile of the host institution.

FACULTY OF BIOSCIENCES AND AQUACULTURE (FBA) — NORD UNIVERSITY

NPBC 2026 is hosted by the Faculty of Biosciences and Aquaculture (FBA) at Nord University in Bodø. FBA is a leading Norwegian centre for aquaculture, marine and agricultural sciences, organised into five research divisions: Aquaculture; Ecology; Animal Science, Production and Welfare; Genomics; and Algae and Microbial Biotechnology. Its researchers work across macro- and microalgal biotechnology, microbial interactions, genomics and epigenetics, marine and terrestrial ecology, and sustainable aquaculture. FBA's unique position — situated just north of the Arctic Circle, with direct access to pristine Arctic and sub-Arctic marine environments — gives its researchers a distinctive perspective that links fundamental plant and algal biology to broader questions of sustainability and resource use.

SCIENTIFIC THEMES

Session 1
Signaling, Perception, and Interactions in Plants, Macroalgae, and Microalgae

Session 2
Plant & Algal Immunity, Stress Responses, and Environmental Adaptation

Session 3
Biotechnological Innovations and Emerging Tools

BODØ — CITY AT THE EDGE OF THE WORLD

Bodø is the capital of Nordland county, situated just north of the Arctic Circle on the northwestern coast of Norway. With a population of around 55,000, it is one of Norway's most dynamic smaller cities — known for its dramatic natural scenery, the world's strongest tidal current at **Saltstraumen**, the Midnight Sun from late May through mid-July, and a vibrant cultural scene that earned it the title of **European Capital of Culture 2024**. The city offers excellent connections from Oslo, Bergen, Trondheim, and Tromsø via Bodø Airport (BOO) with flights taking as little as 1.5 hours from Oslo.

In June, Bodø experiences the Midnight Sun — the sun does not set, bathing the city in a warm golden light throughout the night. The coastline is rich in seaweeds, kelps, and marine life, making it an ideal backdrop for a plant and algal biology conference.

Conference Venue	**Workshop Venue**
Scandic Havet, Tollbugata 5, 8006 Bodø	Nord University Campus, Universitetsalléen 11
Modern waterfront hotel in the heart of the city	10–15 min by bus or taxi from the hotel

More visitor information: **visitbodo.com/en** · Airport: BOO (~5–10 min taxi, ~150 NOK)

Programme at a Glance

17–19 June 2026 · Scandic Havet, Bodø

Wednesday

17 June 2026 — Pre-conference

09:00–14:00	**Workshop 1: Science Communication** Andrea Bozman / NorthSciComm · Nord University campus
09:00–16:00	**Workshop 2: AI-assisted Coding** Physalia Courses (Carlo Pecoraro) · Nord University campus

Thursday

18 June 2026 — Conference Day 1

08:00–08:45	*Registration & Coffee*
08:45–09:00	*Opening Remarks*
09:00–09:45	🔑 **Keynote: Cyril Zipfel**
09:45–10:05	*Morning Break*
10:05–10:50	🔑 **Keynote: Lenka Procházková**
10:50–11:30	**Session 1 — Signaling & Interactions** 4 talks
11:30–12:30	Lunch
12:30–15:00	🌊 Excursion — Coastal Walk & Seaweed Safari
15:00–16:00	📋 *Poster Session 1 (with snack)*
16:00–18:00	**Session 2 — Immunity & Stress** 12 talks
19:00–22:00	🍽 Conference Dinner & Conference Quiz

Friday

19 June 2026 — Conference Day 2

08:00–08:45	*Late registration & Coffee*
08:45–09:30	🔑 **Keynote: Caroline Gutjahr**
09:30–10:15	🔑 **Keynote: Gabriel Markov**
10:15–10:45	📋 *Poster Session 2 (with snack)*
10:45–12:00	**Session 3 — Biotechnological Innovations** 8 talks
12:00–12:10	📖 *Store norske leksikon (SNL) — Kjell-Olav Hovde*
12:10–12:40	🏆 *Best Student Oral & Poster Presentation Awards*
12:40–13:00	*Closing Words & Group Photo*
13:00–14:00	Farewell Lunch
14:00–16:00	*Photosyntech Meeting (invitation only)*

Venue: Scandic Havet, Sjøgata 2, 8006 Bodø · **Full talks:** 10 min (incl. Q&A) · **Short talks:** 7 min · **Posters:** A0 portrait, pins only

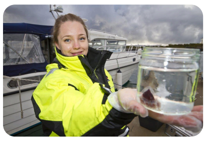
Please note — citrus-aware venue: Out of consideration for an attendee with a citrus allergy that is triggered even by the scent of freshly peeled fruit, we kindly ask **everyone to refrain from bringing, peeling or eating citrus fruit (oranges, mandarins, lemons, etc.) anywhere at the conference venue.** Thank you for helping keep the air citrus-free.

Pre-conference Workshops

Wednesday 17 June 2026 · Nord University Campus, Universitetsalléen 11, Bodø

Separate registration required · contact alexander.jueterbock@nord.no

Workshop 1 — Science Communication Workshop · 09:00–14:00 (includes lunch break)



Andrea Bozman
Workshop Facilitator

Description: A half-day workshop on science communication, led by Andrea Bozman. Participants will develop a science communication project based on their own research, and will work towards preparing text relevant for the Research Council of Norway call *'Communication and Dissemination of Climate, Environment and Ocean Research'*.

Topics covered: (1) What is Science Communication? (2) Knowing Your Audience (3) Crafting Your Message (4) Mediums & Formats (5) Storytelling Techniques for Science (6) Hands-On Practice Sessions

Pre-workshop preparation: Participants are invited to send Andrea a research article related to their own work by **15 May 2026**. Sending an article is not mandatory for participation but helps tailor the workshop. Email to: andrea@northscicomm.com with subject line: *"Science Communication Workshop at NPBC 2026 in Bodø"*.

After the workshop: Participants are invited to email their finished science communication pieces to the workshop facilitator for optional feedback in June or August.

Bring: Laptop with internet access · **Lunch:** Available at university canteen (not included in workshop ticket)

About Andrea Bozman: Award-winning ocean science communicator and creative writer, working across children's literature, narrative essay, eco-poetry, and literary fiction. Funding from Research Council of Norway, Arts and Culture Norway, and European Commission. PhD in Marine Ecology from Nord University. Completing MLitt in Creative Writing at University of Glasgow (July 2026).

Workshop 2 — AI-assisted Coding Workshop · 09:00–16:00 (lunch break 12:00–13:00, self-arranged)

Carlo Pecoraro, PhD
Workshop Lead

Marco Chiarici
Co-instructor (Italy)

Description: A full-day workshop on AI-assisted coding, delivered by **Physalia Courses**, with instructors Carlo Pecoraro, PhD, and Marco Chiarici (Fondazione Bruno Kessler, Trento, Italy). Participants will learn how to effectively leverage AI tools and online solutions to enhance their scientific research and computational workflows — applied to plant biology and bioinformatics.

Venue: Nord University Campus, Bodø (not Scandic Havet!) · **Capacity:** Maximum 30 participants

What you will learn: How to use AI tools (ChatGPT, Claude, Copilot) to assist with coding and data analysis · Practical applications in plant biology, bioinformatics, and scientific computing · Integrating AI assistance into reproducible research workflows · Best practices for prompt engineering and result validation

Technical requirements: Laptop with internet access (mandatory) · RStudio · Selected R packages · AI tools such as ChatGPT or Claude. Detailed software requirements will be sent to registered participants before end of May.

Lunch: Available at university canteen (not included in workshop ticket) · **More info:** physalia-courses.org

About Physalia Courses: Founded in 2016, Physalia-courses has run numerous scientific workshops hosting scientists from institutes worldwide. Attendees are primarily PhD students and postdocs. Named after *Physalia physalis*, a siphonophore that survives through the interaction of specialized zooids — an analogy for how diverse skills combine in science training.

Keynote Speakers NPBC 2026

Cyril Zipfel

Institute of Plant & Microbial Biology, University of Zürich, Switzerland & The Sainsbury Laboratory, University of East Anglia, Norwich, UK

Thursday 18 June · 09:00–09:45 · Storhavet 1

"Roles and recognition of stress-regulated secreted signaling peptides"

Cyril Zipfel studied at diverse French universities before completing his PhD (2001–2005) at the Friedrich-Miescher Institute for Biomedical Research and the University of Basel (CH) under the supervision of Thomas Boller. He then was an EMBO Post-Doctoral Fellow (2005–2007) in the group of Jonathan Jones at The Sainsbury Laboratory, Norwich (UK). From 2007, he has been Group Leader at The Sainsbury Laboratory (which he directed from 2014 to 2018), and since 2018 is Professor of Molecular and Cellular Physiology at the University of Zurich (CH). His laboratory studies the molecular basis of plant innate immunity and receptor kinase-based signaling in plants, as well as how this knowledge can be used to engineer stress-resistant crops. He has published over 200 peer-reviewed papers, holds Starting and Consolidator ERC grants, is a Highly Cited Researcher (since 2014), and received the 2015 Charles Albert Shull Award and the 2018 Tsuneko & Reiji Okazaki Award. Elected to the European Molecular Biology Organization in 2018.

ABSTRACT

Plants must constantly adapt to changing environmental conditions. Cell-surface receptor kinases play an important role in the sensing of stimuli originating from the environment itself or that are produced endogenously often in response to such external cues. I will present our recent work on stress-regulated secreted signaling peptides, their perception mechanisms, and diverse functions in adaptive stress responses.

Lenka Procházková

Charles University, Faculty of Science, Department of Ecology, Prague, Czech Republic

Thursday 18 June · 10:05–10:50 · Storhavet 1

"Snow algae and glacier ice algae biogeography and ecophysiology"

Lenka Procházková is a post-doc at Charles University (Prague, Czech Republic), with research interests in algal ecology, physiological adaptations, strain making, metagenomics, and taxonomy. Her PhD thesis from 2020 was awarded the third prize of the best European PhD thesis in Freshwater Sciences for the period 2019–2020. She has published >45 peer-reviewed papers. Her fieldwork expertise comes from repeated expeditions to Svalbard, the European Alps and High Tatra Mountains. She has described more than three genera and 10 species of algae.

ABSTRACT

Long-lasting, melting snowpacks in sub/polar, alpine and forested regions provide a habitat for specialized microalgae. The main representatives of snow algae belong to the green algal order Chlamydomonadales. The second algal group common in melting snowpacks belongs to the golden-brown algal order Hydrurales. The most prominent glacial ice algae belong to the Zygnematales. Using ice binding assay and genome mining, we demonstrated that filamentous *Ancylonema nordenskioldii* produces ice binding proteins to prevent ice recrystallization. Single-celled *Ancylonema alaskanum* is common in the European Alps while its filamentous sister species dominates the Arctic. Our recent expedition to Colombia also revealed a new *Ancylonema* species. Keywords: snow, glacier, algae, haplotypes, photosynthesis, pigments, fatty acids.

Keynote Speakers NPBC 2026

Caroline Gutjahr

Department of Root Biology and Symbiosis, Max-Planck-Institute of Molecular Plant Physiology, Potsdam, Germany

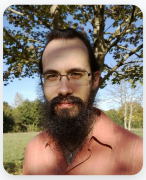
Friday 19 June · 08:45–09:30 · Storhavet 1

"Form and function of a plant-fungal symbiosis"

Caroline Gutjahr is a Director of the Max-Planck-Institute of Molecular Plant Physiology in Potsdam, Germany, where she heads the Department of Root Biology and Symbiosis. Previously she was Professor of Plant Genetics at the Technical University of Munich and before that an independent Emmy Noether group leader at LMU Munich. She gained her PhD at the University of Lausanne in the laboratory of Uta Paszkowski and studied Biology at the University of Freiburg. Her research group aims at understanding the development and function of arbuscular mycorrhiza. The research of her team focuses in particular on the regulation of nutrient exchange, the role of plant hormones and transcriptional networks in physiological, molecular and plant cell developmental changes required to accommodate arbuscular mycorrhiza fungi inside the root and to adjust symbiosis development with environmental conditions.

ABSTRACT

Most land plants form symbioses with Glomeromycotina fungi to acquire mineral nutrients from the soil. This so-called arbuscular mycorrhiza (AM) symbiosis is evolutionarily ancient and found in the oldest fossils of land plants. The fungi form extended hyphal networks in the soil to scavenge mineral nutrients. These are transported into the root and released via beautifully-shaped, highly branched hyphal structures, the arbuscules inside inner root cells. In return they receive up to 20% of photosynthetically fixed carbon from their host in the form of sugars and lipids. Symbiotic infection of single, already differentiated cells within the tissue context requires a poorly understood cellular remodeling program that is intertwined with mechanisms that control plant development and physiology. In my presentation, I will provide examples of how we investigate the molecular mechanisms underlying development and functioning of this fascinating symbiosis.



Gabriel Markov

Laboratory for Integrative Biology of Marine Models, Station Biologique de Roscoff, CNRS / Sorbonne Université, France

Friday 19 June · 09:30–10:15 · Storhavet 1

"Molecular actors in the brown algal oxylipin biosynthesis pathway"

Gabriel Markov is a CNRS researcher at the Laboratory for Integrative Biology of Marine Models in Roscoff, France. He works on the evolution of eukaryotic metabolic pathways, now mainly in brown algae, using genomic and metabolomic data, in order to infer new biochemical reactions and new molecular structures with comparative approaches.

ABSTRACT

Brown algae, key primary producers in coastal marine ecosystems, synthesize a variety of metabolites, such as polyunsaturated fatty acids (PUFAs), their oxidized derivatives (oxylipins), and aldehydes under abiotic and biotic stress. While their biosynthetic pathways and ecological roles (e.g., defense, signaling) remain underexplored, recent evidence suggests that these metabolites may trigger defense reactions against grazers and mediate host-endophyte interactions. To study these pathways, treatments with various elicitors such as aldehydes, OPDA, oligoguluronates and copper have been shown to modulate transcriptomic and metabolomic responses, while CRISPR offers a promising tool to dissect gene-specific contributions. Brown algal pathways share similarities with plant or animal ones, like the involvement of LOX and CYP enzymes, which provide valuable insights for investigations. However, some molecular features are also specific to brown algae, with substantial variation across species and orders. I will illustrate this mainly with examples from Laminariales (kelps) and small filamentous Ectocarpales.

Venue: Scandic Havet, Bodø · **Poster sessions:** Thu 15:00–16:00 & Fri 10:15–10:45 (Storhavet 1)

Wednesday 17 June 2026

Pre-conference Workshops

PRE-CONFERENCE WORKSHOPS · NORD UNIVERSITY CAMPUS, UNIVERSITETSALLÉEN 11, BODØ

Both workshops run in parallel. Separate registration required — contact **alexander.jueterbock@nord.no**

09:00–14:00	Nord Univ.	**WORKSHOP 1** **Science Communication Workshop** **Andrea Bozman** (NorthSciComm) · Half day · includes lunch break Participants develop a science communication project based on their own research. Optional preparation: send a research article related to your work to andrea@northscicomm.com by 15 May (subject: "Science Communication Workshop at NPBC 2026 in Bodø"). Bring a laptop with internet access.
09:00–16:00	Nord Univ.	**WORKSHOP 2** **AI-assisted Coding Workshop** **Carlo Pecoraro, PhD** (Physalia Courses) · Full day · lunch break 12:00–13:00 (self-arranged at university canteen) Learn to leverage AI tools (ChatGPT, Claude) to assist with coding, data analysis, and scientific workflows in plant biology and bioinformatics. Requires: laptop with internet access, RStudio, selected R packages (details sent before end of May).

Workshop participation requires **separate registration**. Lunch is *not* included in workshop tickets (available at university canteen). Main conference registration opens at 08:00 Thursday 18 June.

See full workshop details on the dedicated workshop pages following the Friday schedule. Both workshops run concurrently from 09:00 at Nord University Campus.

Thursday 18 June 2026

Main Conference — Day 1

08:00–08:45	Foyer	*Registration & Coffee*
08:45–09:00	Storhavet 1	*Welcome & Opening Remarks* Alexander Jüterbock, Nord University

Keynote — Signaling & Immunity

09:00–09:45	Storhavet 1	KEYNOTE **Roles and recognition of stress-regulated secreted signaling peptides** *Cyril Zipfel* — University of Zurich
09:45–10:05	Foyer	*Morning Break*
10:05–10:50	Storhavet 1	KEYNOTE **Snow algae and glacier ice algae biogeography and ecophysiology** *Lenka Procházková* — Charles University, Prague

Session 1 — Signaling, Perception, and Interactions in Plants, Macroalgae, and Microalgae

10:50–11:00	Storhavet 1	FULL **Transcriptome analysis of cell wall biomineralization in the large diatom *Coscinodiscus*** Tore Brembu
11:00–11:10	Storhavet 1	FULL **Unravelling the molecular mechanisms of eATP signalling during regulated cell death in *Arabidopsis thaliana*** Leah Gachao ★ STUDENT PRIZE
11:10–11:17	Storhavet 1	SHORT **Role of abscisic acid metabolism in regulation of bilberry fruit ripening** Katja Karppinen
11:17–11:24	Storhavet 1	SHORT **Gene loss and horizontal gene transfer in plants as a consequence of parasitism** Karsten Fischer
11:24–11:30	Storhavet 1	*Buffer / transition*
11:30–12:30	Restaurant	**Lunch**
12:30–15:00	Bodø coastline	**Excursion — Arctic Coastal Walk & Seaweed Safari** Guided coastal walk along the Bodø coastline — included in registration · Depart from Foyer
15:00–16:00	Storhavet 1	POSTER *Poster Session 1 with snack*

Session 2 — Plant & Algal Immunity, Stress Responses, and Environmental Adaptation

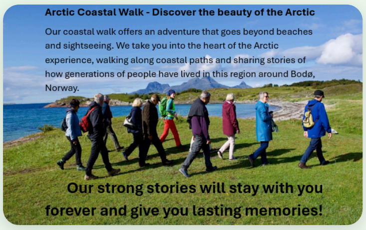
16:00–16:10	Storhavet 1	FULL **Effects of thermal priming on the *Saccharina latissima* transcriptomic response to heat stress** Anne M. L. Nilsen ★ STUDENT PRIZE
16:10–16:20	Storhavet 1	FULL **Environmental Drivers of Phlorotannin Variability in the macroalga *Alaria esculenta*** Ralf Rautenberger
16:20–16:30	Storhavet 1	FULL **The evolutionary origin of the *Arabidopsis* receptor kinase THESEUS1 and its function in plant cell wall integrity maintenance** Steven Zwartkruis ★ STUDENT PRIZE

16:30–16:40	Storhavet 1	FULL **Deciphering the functions of three *Phytophthora cactorum* RXLR effectors involved in strawberry colonization** Anupam Gogoi
16:40–16:50	Storhavet 1	FULL **Extracellular ATP and Metabolomic Fingerprints of Regulated Cell Death in Tomato and *Arabidopsis*** Jo Petter Helstad
16:50–17:00	Storhavet 1	*Short break*
17:00–17:07	Storhavet 1	SHORT **Temperature resilience in different life cycle stages of the kelp *Alaria esculenta*** Pia Anissa Dittmer ★ STUDENT PRIZE
17:07–17:14	Storhavet 1	SHORT **Polyphenolic content and bioactivity in Norwegian brown macroalgae in response to light, temperature, salinity, and UV-radiation stress** Sara Roosvall ★ STUDENT PRIZE
17:14–17:21	Storhavet 1	SHORT **Investigating endocytosis-related candidate genes involved in stress perception** Nelly Braun ★ STUDENT PRIZE
17:21–17:28	Storhavet 1	SHORT **Acquisition and maintenance of environmental stress memory in red algae '*Bangia*' spp.** Puja Kumari
17:28–17:35	Storhavet 1	SHORT **The role of cell wall integrity maintenance mechanisms in hyperosmotic stress and cell wall damage responses** Sara Morghen ★ STUDENT PRIZE
17:35–17:42	Storhavet 1	SHORT **Climate Change Modulates Glyphosate Efficacy and Species-Specific Stress Responses in Key Weed and Crop Species** Zahra Bitarafan
17:42–17:49	Storhavet 1	SHORT **Uncovering the strawberry-crown rot pathosystem and domestication of wild resistance genes** May-Bente Brurberg
17:49–18:00	Storhavet 1	*Discussion / buffer*
19:00–22:00	OHMA Restaurant	**Conference Dinner & Conference Quiz** 3-course dinner with science quiz — included in registration

Excursion

Thursday 18 June 2026 · 12:30–15:00

Arctic Coastal Walk & Seaweed Safari



Arctic Coastal Walk - Discover the beauty of the Arctic

Our coastal walk offers an adventure that goes beyond beaches and sightseeing. We take you into the heart of the Arctic experience, walking along coastal paths and sharing stories of how generations of people have lived in this region around Bodø, Norway.

Arctic Coastal Walk — Discover the beauty of the Arctic

Our coastal walk offers an adventure that goes beyond beaches and sightseeing. We take you into the heart of the Arctic experience, walking along coastal paths and sharing stories of how generations of people have lived in this region.

Join us for an unforgettable walk where natural wonders meet coastal tranquility.

WHAT YOU WILL EXPERIENCE

Norway's Coastal History
Discover the Viking spirit of *Friluftsliv* — the freedom to walk in the open countryside, honouring centuries of tradition in harmony with nature.

The Legacy of the Vikings
Explore the Viking Age and discover our shared history along these shores.

Our Dependence on the Sea
From traditional stockfish trade to modern mariculture — how the sea has shaped Norwegian culture and economy.

Ancient Mountains & Landscapes
Learn how Norway's mountains were formed, where the Norwegian people came from, and why they chose to settle here.

Coastal Seaweed & Kelp
Guided identification of intertidal seaweeds and kelp species by marine biologists from Nord University.

The Arctic Coast
Feel how the weather shapes the coastline; observe the Arctic sky and experience the enduring beauty that has inspired artists for centuries.

Included in registration · **Depart:** 12:30 from Scandic Havet (meet 12:15 in lobby) · **Return:** ≈14:45 · **What to bring:** Comfortable walking shoes, weather-appropriate clothing (layers recommended), rain jacket · **Organised by:** Stella Polaris Bodø (Aleksander Talgø) in partnership with Nord University

"This walk brings history to life in our rugged nature. Our strong stories will stay with you forever and give you lasting memories!"

Friday 19 June 2026

Main Conference — Day 2

Keynote — Symbiosis & Algal Biochemistry

08:00–08:45	Foyer	*Late registration & coffee*
08:45–09:30	Storhavet 1	KEYNOTE **Form and function of a plant-fungal symbiosis** *Caroline Gutjahr* — Max-Planck-Institute of Molecular Plant Physiology, Potsdam
09:30–10:15	Storhavet 1	KEYNOTE **Molecular actors in the brown algal oxylipin biosynthesis pathway** *Gabriel Markov* — Station Biologique de Roscoff, CNRS / Sorbonne Université
10:15–10:45	Storhavet 1	POSTER *Poster Session 2 with snack*

Session 3 — Biotechnological Innovations and Emerging Tools

10:45–10:55	Storhavet 1	FULL **CRISPR/Cas-based genome editing and functional genomics for development of multiple biotic & abiotic stress tolerance in *Solanum lycopersicum*** Banashree Saikia
10:55–11:05	Storhavet 1	FULL **Assisting species differentiation using hyperspectral imaging** Vasili Alexander Balios ★ STUDENT PRIZE
11:05–11:15	Storhavet 1	FULL **Adaptive IoT-enabled automation with multimodal sensing and real-time image analysis for CEA** Arshad Kadevalappil Ajilan
11:15–11:25	Storhavet 1	FULL **Time-series multispectral UAV imaging reveals dynamic N-responses and breeding gains for N-uptake and protein yield in Norwegian spring barley** Morten Lillemo
11:25–11:35	Storhavet 1	FULL **Lithologically diverse Nordic glacial flours as macro- and micronutrient sources for northern plants** Colin Sinclair ★ STUDENT PRIZE
11:35–11:45	Storhavet 1	FULL **Experimental breeding of the diatom *Cylindrotheca* sp. and high-throughput phenotyping of F1 offspring** Chris J. Hulatt — Nord University, Bodø
11:45–11:53	Storhavet 1	FULL **Low-Impact Bioprocessing of *Alaria esculenta* for Next-Generation Agricultural Biostimulants** Paige Heavyside (Kelpinor AS)
11:53–12:00	Storhavet 1	SHORT **The Norwegian Plant Phenotyping Infrastructure (PheNo) – a new era of opportunities for plant research in Norway** Sara Laranjeira
12:00–12:10	Storhavet 1	📖 *Store norske leksikon (SNL)* Kjell-Olav Hovde — Biology Editor, Store norske leksikon (SNL)
12:10–12:40	Storhavet 1	🏆 *Best Student Oral & Poster Presentation Awards* Announcement of the best oral and poster presentations · Cast your votes via the QR codes (see Practical Information — “Vote for the Awards”)
12:40–13:00	Storhavet 1	*Closing Words & Group Photo*
13:00–14:00	Restaurant	**Farewell Lunch** Included in registration

14:00–16:00	Meeting Room	**Photosyntech Leaders Meeting** Invitation only

Poster display: Mount posters **Thursday morning**; remove after Friday poster session. Format: A0 portrait (84.1 × 118.9 cm). **Pins only** — please mount with pins, not tape.

Practical Information NPBC 2026

VENUE

The conference is held at **Scandic Havet**, Sjøgata 2, 8006 Bodø, Norway. Centrally located in Bodø, within walking distance of the railway station and city centre.

HOTEL INTERNET ACCESS

Free WiFi at Scandic Havet · **Network (user):** Scandic · **Password:** ATK83ymw

VOTE FOR THE AWARDS — BEST STUDENT ORAL & POSTER PRESENTATION

Help choose the winners! Every talk and poster marked with a gold ★ **Student prize** badge is presented by a student competing for the **Best Student Oral Award** or the **Best Student Poster Award**. Scan a code (or open the link) to rate the presentations and posters. You can vote any time during the conference — winners are announced **Friday 19 June, 12:10–12:40, Storhavet 1**.

Rate the presentations
forms.gle/vKF9NFL5dkN8JBa68

Rate the posters
forms.gle/myahYXa2y2bgM5Kx7

★ **Student prize** = a student presentation or poster entered in the award competition. Your votes decide the winners — thank you!

ORAL PRESENTATIONS

Full talks: 10 minutes total (incl. questions) · **Short talks:** 7 minutes total (incl. questions)

Accepted formats: PowerPoint (.pptx) or PDF. Upload slides by **15 June** via the Nettskjema link in your confirmation email. Bring a USB backup. Naming: `NPBC2026_[S1/S2/S3/Keynote]_[LastName]_[FirstName].pptx`

POSTER PRESENTATIONS

Format: A0, portrait (84.1 × 118.9 cm) · **Language:** English · **Mounting: pins only.**
Mount Thursday morning; remove after Friday poster session.
Session 1: Thu 18 June, 15:00–16:00 · **Session 2:** Fri 19 June, 10:15–10:45

GETTING TO BODØ

Bodø Airport (BOO) has daily connections from Oslo (Gardermoen), Bergen, Trondheim, and Tromsø via SAS and Norwegian Air. The airport is 2 km from the city centre / Scandic Havet (≈10 min by taxi or bus line 100).

ACCOMMODATION

Discounted rooms available at Scandic Havet — use the booking code provided in your registration confirmation email.

INCLUDED IN REGISTRATION

All registration categories include: **lunches** (Thu & Fri), **coffee breaks**, **conference dinner** (Thu evening), and the **Arctic coastal excursion** (Thu afternoon). Accommodation and workshop fees are not included.

CODE OF CONDUCT

NPBC 2026 is committed to a safe, respectful and inclusive meeting for everyone, regardless of background, career stage, gender or identity. We expect all participants to treat one another with courtesy in talks, discussions and social events; harassment, discrimination or intimidating behaviour of any kind will not be tolerated. Respect every person, every question and every discipline. If you experience or witness unacceptable behaviour, please speak to any organiser (in a white NPBC t-shirt) or email **NPBC2026@nord.no** — all reports are handled confidentially.

CONTACT & WEBSITE

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Organiser: Alexander Jüterbock, Faculty of Biosciences and Aquaculture, Nord University, Bodø

Participants

NPBC 2026 — 57 registered participants

All 57 registered participants listed alphabetically by surname — keynote speakers, oral presenters, poster presenters, and attendees.

NAME	AFFILIATION	ROLE
Ajilan, Arshad Kadevalappil	Grønt fra Nord AS, Fauske, Norway	TALK S3
Alsheikh, Muath	Graminor AS, Norway	PARTICIPANT
Andonova-Lilova, Boyka	AgroBioInstitute, Sofia, Bulgaria	POSTER
Balios, Vasili Alexander	UiT, Tromsø, Norway	TALK S3
Berglund, Liv-Irene	UiT, Arctic and Marine Biology, Tromsø, Norway	POSTER
Bergmann, Pepe	UiT, Arctic and Marine Biology, Tromsø, Norway	POSTER
Bitarafan, Zahra	NIBIO, Ås, Norway	TALK S2
Braun, Nelly	NTNU, Trondheim, Norway	TALK S2
Brembu, Tore	SINTEF Ocean / NTNU, Trondheim, Norway	TALK S1
Brown, Thomas	Graminor AS, Norway	POSTER
Brurberg, May-Bente	NIBIO, Ås, Norway	TALK S2
Cervin, Gunnar	University of Gothenburg, Sweden	POSTER
Debnath, Anirban Jyoti	Institute of Chemistry and Environmental Science, Faculty of Natural Sciences, University of Ss. Cyril and Methodius in Trnava, Slovakia	POSTER
Dills, Michael	Nord University, Bodø, Norway	POSTER
Dittmer, Pia Anissa	Nord University, Bodø, Norway	TALK S2
Fischer, Karsten	UiT, Tromsø, Norway	TALK S1
Fuchs, Maximilian	NTNU, Trondheim, Norway	POSTER
Gachao, Leah	NTNU, Trondheim, Norway	TALK S1
Gannestad, Kristin K.	UiO, Dept of Biosciences, Norway	POSTER
Gogoi, Anupam	NIBIO, Ås, Norway	TALK S2
Grini, Paul E.	UiO, Dept of Biosciences, Norway	PARTICIPANT
Gupta, Anubha	NMBU, Ås, Norway	PARTICIPANT
Gutjahr, Caroline	Max-Planck-Institute of Molecular Plant Physiology, Potsdam, Germany	KEYNOTE
Hamann, Thorsten	NTNU, Dept of Biology, Trondheim, Norway	PARTICIPANT
Heavyside, Paige	Kelpinor AS, Norway	TALK S3
Helstad, Jo Petter	NTNU, Trondheim, Norway	TALK S2
Hornslien, Karina S.	UiO, Dept of Biosciences, Norway	POSTER
Hulatt, Chris J.	Nord University, Bodø, Norway	TALK S3
Iversen, Vegard	UiO, Dept of Biosciences, Norway	POSTER
Karlsen, Stina	Kelpinor AS, Norway	PARTICIPANT

Karppinen, Katja	UiT, Tromsø, Norway	TALK S1
Kinnby, Alexandra	University of Gothenburg, Sweden	POSTER
Klemetsen, Marius Dobbe	UiT, Tromsø, Norway	PARTICIPANT
Krabbe, Jessica	UiT, Tromsø, Norway	PARTICIPANT
Krause, Kirsten	UiT, Tromsø, Norway	PARTICIPANT
Kumari, Puja	SAMS, Oban, UK	TALK S2
Laranjeira, Sara	NMBU, Ås, Norway	TALK S3
Lillemo, Morten	NMBU, Ås, Norway	TALK S3
Markov, Gabriel	Station Biologique de Roscoff, France	KEYNOTE
Minini, Leo	Nord University, Bodø, Norway	POSTER
Morghen, Sara	NMBU, Faculty of Natural Sciences, Ås, Norway	TALK S2
Nilsen, Anne M.L.	Nord University, Bodø, Norway	TALK S2
Patel, Fenilkumar Nirajbhai	Krushak FPO, India	PARTICIPANT
Procházková, Lenka	Charles University, Prague, Czech Republic	KEYNOTE
Quadrio, Francesco Giovanni	Nord University, Bodø, Norway	PARTICIPANT
Rautenberger, Ralf	NIBIO, Ås, Norway	TALK S2
Roosvall, Sara	Nord University, Bodø, Norway	TALK S2
Saffioti, Francesco	NMBU, Faculty of Natural Sciences, Ås, Norway	POSTER
Salvaitis, Dominykas	Nord University, Bodø, Norway	POSTER
Sinclair, Colin	UiT, Dept of Geosciences, Tromsø, Norway	TALK S3
Thode, Sunniva Katharina	UiT, Tromsø, Norway	PARTICIPANT
Windju, Susanne	Graminor AS, Norway	PARTICIPANT
Wiszniewska, Alina	University of Agriculture in Kraków, Poland	POSTER
Zagorchev, Lyuben	Sofia University, Bulgaria	POSTER
Zagorcheva, Tzvetelina	AgroBioInstitute, Sofia, Bulgaria	POSTER
Zipfel, Cyril	University of Zürich / Sainsbury Laboratory, UK	KEYNOTE
Zwartkruis, Steven	NTNU, Trondheim, Norway	TALK S2

Organizing Committee

NPBC 2026 · Nord University, Bodø

The NPBC 2026 is organized by the Faculty of Biosciences and Aquaculture (FBA) at Nord University. Contact the organizing committee at **alexander.jueterbock@nord.no**

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pheno.no

Kelpinor AS

Kelpinor is a Norwegian biotechnology company focused on developing sustainable seaweed solutions for agriculture. Originally based on *Ascophyllum nodosum*, Kelpinor is increasingly focused on cultivated kelp species such as *Alaria esculenta* to produce seaweed-based **plant biostimulants** designed to support crop growth, resilience, and soil health.

The company emphasizes sustainable raw material sourcing and low-impact bioprocessing methods that preserve the natural complexity of bioactive compounds in macroalgae. By combining kelp cultivation with gentle processing approaches, Kelpinor creates consistent, high-quality biostimulant products while reducing pressure on wild kelp ecosystems.

kelpinor.no

Nord University

Nord University is a Norwegian public university with strong research and educational programs in biosciences, aquaculture, biotechnology, and sustainability. With campuses across Nordland and its main campus in Bodø, Nord University plays a central role in developing knowledge for sustainable use of marine and terrestrial resources.

The Faculty of Biosciences and Aquaculture (FBA) hosts internationally recognized research groups working on plant biology, algal biotechnology, microbial interactions, aquaculture innovation, and environmental adaptation. Through close collaboration with industry, public sector actors, and international research partners, Nord University contributes to translating fundamental research into sustainable solutions for society.

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BOOK OF ABSTRACTS

Book of Abstracts

Norwegian Plant Biology Conference 2026
17–19 June · Scandic Havet, Bodø, Norway

24 oral presentations · 18 poster presentations
4 keynote lectures · 3 thematic sessions

Session 1 — Signaling, Perception, and Interactions in Plants, Macroalgae, and Microalgae

Thursday 18 June 2026 · 10:50–11:30 · Storhavet 1

Plants, macroalgae, and microalgae rely on intricate signalling networks to sense their environment, communicate with other organisms, and regulate growth, stress responses, and symbioses. This session spans hormonal and chemical signalling, quorum sensing, and plant–microbe and algae–microbe interactions relevant to nutrient acquisition, stress resistance, and aquaculture productivity.

FULL **S1** 10:50–11:00

Transcriptome analysis of cell wall biomineralization in the large diatom *Coscinodiscus*

Felicity Ashcroft [1]; Per Winge [1]; Fabian Hitz [1]; Pedro Fernandes [2]; Vera Cardoso [3]; Jose Prada-Rodrigo [4]; Johannes W. Goessling [3]; Martin Lopez-Garcia [4]; **Tore Brembu** (presenting author) [1]

[1] Norwegian University of Science and Technology (NTNU) / SINTEF Ocean, Trondheim, Norway
[2]–[4] Affiliation details not provided in abstract submission

A defining feature of diatoms are their silica-based cell wall (frustule), with highly ornate, species-specific structures and pore patterning. While considerable research has focused on the formation of the larger, more elaborate silica structures that make up the valves, the smaller and more uniform girdle bands have received less attention. Recently, the girdle bands of species belonging to the *Coscinodiscus* genus were identified as natural photonic crystals due to their highly ordered arrangement of nanopores. Unravelling the genetic basis of pore pattern formation in these structures could support the development of more sustainable photonic technologies. We wanted to find candidate genes determining photonic crystal properties in *C. granii* and *C. wailesii*, which respectively have square and hexagonal pore lattices. To this end, we combined fluorescence microscopy to monitor girdle band appearance in synchronized cultures with time-resolved RNA-seq transcriptomics. By integrating these experimental approaches, we were able to identify silica-responsive genes specifically upregulated during girdle band formation. We are also in the process of establishing genetic transformation and gene editing in *Coscinodiscus*. We aim to use these results to modify the photonic crystal properties of *Coscinodiscus* girdle bands through genetic manipulation. ---

Diatom · frustule · photonic crystal · transcriptomics ---

Funding: NFR, Enabling natural photonics through genetic manipulation of diatoms/ENIGMA, granted to Tore Brembu

★ STUDENT PRIZE **FULL** **S1** 11:00–11:10

Unravelling the molecular mechanisms of eATP signalling during regulated cell death in *Arabidopsis thaliana*

Leah Gachao (presenting author) [1]; Maximillian Fuchs [1]; Catharina Davies [2]; Astrid Bjørkøy [2]; Daniela Sueldo [1]

1. Norwegian University of Science and Technology, Department of Biology, Trondheim, Norway
2. Norwegian University of Science and Technology, Department of Physics, Trondheim, Norway

As sessile organisms, plants constantly encounter environmental stresses that activate signaling pathways to maintain homeostasis, including regulated cell death (RCD). Under stress conditions, such as heat, RCD eliminates damaged cells to enhance plant survival. Additionally, during stress, plants release various molecules into the apoplast, altering their extracellular environment and generating signals for adaptation. ATP, a universal energy molecule, can be released into the apoplast as extracellular ATP (eATP) and is recognized with high affinity by lectin receptor-like kinases, P2K1 and P2K2. Recent evidence suggests eATP may play a role in cell-cell communication during RCD. However, knowledge regarding eATP as a death signal remains limited, and its spatiotemporal regulation is poorly understood. In my PhD research, I aim to elucidate the molecular mechanisms underlying eATP as a death signal and investigate the spatiotemporal dynamics of eATP release using a genetically encoded fluorescent biosensor. Findings on eATP induced RCD in *Arabidopsis* will be presented. In addition, using the eATP biosensor, findings on the role of eATP in cell-cell communication during RCD will be discussed. ---

Regulated cell death · eATP signalling · biosensor · cell-cell communication · apoplast · *Arabidopsis ---*

Funding: NTNU PhD fund awarded to Leah Gachao

SHORT S1 11:10–11:17

Role of abscisic acid metabolism in regulation of bilberry fruit ripening

Katja Karppinen (presenting author) [1]; Amos Samkumar [1, 2]; Muhammad Furqan Ashraf [1]; Laura Jaakola [1, 3]

[1] UiT The Arctic University of Norway, Department of Arctic and Marine Biology, Tromsø, Norway
[2] The University of British Columbia, Wine Research Centre, Faculty of Land and Food Systems, Vancouver, Canada
[3] Norwegian Institute of Bioeconomy Research (NIBIO), Ås, Norway

Fruit ripening is a complex developmental process involving metabolic and textural changes. Fruit ripening processes are controlled by plant hormones, most importantly ethylene and abscisic acid (ABA), but also affected by environmental factors such as light. Our investigations have focused on hormonal and environmental regulation of fruit ripening and anthocyanin biosynthesis in bilberry (*Vaccinium myrtillus* L.), an economically important wild berry species of the Northern Europe. Bilberries are rich source of health-beneficial anthocyanins which accumulate in berries during ripening. Our studies have shown that ABA level increases at the onset of bilberry fruit ripening preceding anthocyanin accumulation. Although both anthocyanin and carotenoid biosynthesis are upregulated during ripening, only anthocyanin levels increase. This inconsistency is due to simultaneous upregulation of carotenoid cleavage genes, leading to formation of apocarotenoids such as ABA. ABA treatment was shown to induce anthocyanin accumulation and upregulate fruit softening genes, suggesting that ABA plays an important role in the regulation of ripening in bilberry fruit. Light intensity is known to increase anthocyanin accumulation, and we have shown that intense white light given to unripe fruits upregulated the expression of the carotenoid biosynthetic and cleavage genes, indicating that light regulates anthocyanin biosynthesis through ABA metabolism. Also red light increased anthocyanin accumulation and transcriptional studies indicated signaling through ABA metabolism. In addition to anthocyanin biosynthesis, red light elevated expression of fruit softening genes, including pectate lyases (PLs), which have major role in depolymerization of cell wall pectin. Although blue light enhanced anthocyanin accumulation and PL expression, transcriptional studies found this regulation to be less associated with ABA signaling compared to red light, indicating involvement of another signaling route. ---

Vaccinium fruit ripening abscisic acid anthocyanins carotenoids light quality ---

SHORT S1 11:17–11:24

Gene loss and horizontal gene transfer in plants as a consequence of parasitism

Karsten Fischer (presenting author) [1]; Stian Olsen [1]; Rainer Schwanke [2]; Kirsten Krause [1]

[1] UiT The Arctic University of Norway, Department of Arctic and Marine Biology, Tromsø, Norway
[2] Institute for Bio- and Geosciences (IBG-4: Bioinformatics), CEPLAS, Forschungszentrum Jülich, Jülich, Germany

The parasitic flowering plant genus *Cuscuta* (dodder) is a parasitic weed that infects many important crops. Once it winds around the shoots of potential host plants and initiates the development of penetration organs, called haustoria, only a few plant species have been shown to deploy effective defense mechanisms to ward off *Cuscuta* parasitization. In contrast to photosynthetically active non-parasitic plants, *Cuscuta* has only limited need for photosynthesis and an ensuing reduced or absent capacity for autotrophic growth, leading to a different selection pressure on the parasite's genomes. While the chloroplast genome has been intensively studied in the past, the analysis of the other cellular genomes has lagged significantly behind. With the publication of the first parasitic plant genomes in 2018 (*Cuscuta campestris* by Vogel et al. and *C. australis* by Sun et al.), it has finally become possible to investigate what effect the morphological and physiological reductions have had on their overall gene content and coding capacity. An emerging hallmark of *Cuscuta*’s genomes are losses of genes performing redundant or obsolete functions. On the other hand, new genes were gained by trans-species horizontal gene transfer from the genomes of their numerous host plants. Based on an analysis of an extensive dataset including the parasite *Cuscuta campestris* and other parasitic plant species, we identified unique evolutionary histories of some of their genes that will be exemplified here with the gene rpl32 which codes for an essential plastid ribosomal subunit in angiosperm plants. ---

Cuscuta genomics horizontal gene transfer NUP genes parasitic plants ---

Funding: Tromsø Research Foundation, Grant #16-TF-KK to Krause.

Session 2 — Plant & Algal Immunity, Stress Responses, and Environmental Adaptation

Thursday 18 June 2026 · 16:00–18:00 · Storhavet 1

Plants and algae constantly face biotic stressors (pathogens, biofouling organisms, microbes) and abiotic challenges (temperature, UV, salinity, eutrophication). Talks here explore the molecular, physiological, and ecological mechanisms of stress responses — immune signalling, systemic resistance, antifouling strategies, epigenetic priming (stress memory), and climate-driven range shifts.

★ STUDENT PRIZE FULL **S2** 16:00–16:10

Effects of thermal priming on the *Saccharina latissima* transcriptomic response to heat stress

Anne M. L. Nilsen (presenting author) [1]; Niko Steiner [2]; Inka Bartsch [2]; J. Mark Cock [3]; Alexander O. Jueterbock [1]

[1] Faculty of Biosciences and Aquaculture, Nord University, Bodø, Norway
[2] Alfred Wegener Institute, Helmholtz-Centre for Polar and Marine Research, Bremerhaven, Germany
[3] Algal Genetics Group, CNRS, Sorbonne Université, UMR 8227, Station Biologique de Roscoff, Roscoff, France

Saccharina latissima (sugar kelp) is a brown macroalga forming extensive kelp forests along North Atlantic coasts. These habitats are key components of coastal ecosystems, contributing substantially to primary production, nutrient cycling, and biodiversity support. In addition, *S. latissima* is the most common cultivated kelp species in European aquaculture, offering a sustainable source of food, feed, and biomaterials without fertilizer and freshwater demands. However, both natural and cultivated populations are increasingly exposed to elevated sea temperatures and marine heatwaves, posing significant challenges for resilience and sustainable production. Kelp species have a diplohaplontic life cycle, alternating between haploid gametophytes and diploid sporophytes. This alternation enables manipulation of gametophyte stages and testing of transgenerational effects in the resulting sporophytes. Thermal priming, originally described in terrestrial plants, exposes early life stages to moderate heat stress to induce a physiological and molecular memory that enhances stress tolerance at later life stages. We applied this concept to *S. latissima* by exposing gametophytes to moderate heat (20 °C, 3 weeks) before sporophyte induction, while keeping naïve controls at 10°C. Sporophytes grown at 10°C, derived from primed and naïve gametophytes, were subsequently exposed to short-term heat stress (21.5 °C for 48 h) and allowed to recover at 10°C for 72h, during which we assessed transcriptomic responses and photosynthetic performance. Primed sporophytes mounted a stronger transcriptional response to heat stress during the exposure. In contrast, naïve sporophytes displayed delayed and extensive transcriptional downregulation during recovery. These findings indicate that defense mechanisms initiated in the gametophyte stage can be reactivated in the derived sporophyte stage, supporting the view that thermal priming induces a transgenerational stress memory in *S. latissima*. ---

Kelp Stress memory Thermal tolerance Transcriptomics *Saccharina latissima* Thermal priming ---

Funding: Norwegian Research Council, KELPRIME project (project no. 700933)

FULL **S2** 16:10–16:20

Environmental Drivers of Phlorotannin Variability in the macroalga *Alaria esculenta* (Phaeophyceae): Insights from Wild Populations, Aquaculture and Laboratory Studies

Ralf Rautenberger (presenting author) [1]; Michael Streicher [1]; Léo Minini [1]; Sara Roosvall [1]; Sdena Nunes [1]; Oddvar Ottesen [2]

[1] Norwegian Institute of Bioeconomy Research (NIBIO), Division of Food Production and Society, Ås, Norway
[2] AKVATIK AS, Bodø, Norway

Brown macroalgae contain a great variety of unique polyphenolic compounds, the phlorotannins, which are based on phloroglucinol subunits. The polyphenolic compounds possess numerous biological functions, ranging from eco-physiological response to environmental stress and structural cell integrity to novel biotechnological applications. While algae of the taxonomic order Fucales are characterised by high phlorotannin contents, Laminariales are generally known for their low concentrations. However, *Alaria esculenta* from Northern Norway, a member of the Laminariales, seems to be an exemption. It demonstrated a significant variability in its phlorotannin contents and associated antioxidant performance. This presentation compiles results from several integrated projects. First, we examine the spatial and temporal differences in phlorotannin levels and antioxidant capacities across wild-grown populations and seasons in Northern Norway. Second, given the commercial importance of *A. esculenta* to the Norwegian aquaculture industry, we present data from professional cultivation sites near Bodø to understand eco-physiological stress responses and optimize harvest timing. Finally, laboratory stress experiments were conducted to identify the primary environmental drivers—such as irradiance, UV radiation, salinity, and temperature—that trigger phlorotannin accumulation. This research provides a better understanding of the previously unexpected variability of phlorotannins in *A. esculenta*. These insights are not only of ecological interest regarding the alga’s stress management in its natural habitat but also play a critical role in the commercial production of phlorotannins and the blue economic development of Northern Norway. ---

Brown Macroalgae | Marine Polyphenols | Abiotic Stress | Kelp Cultivation | High-Latitude Ecology | Bioactive Compounds ---

Funding: 1. MABIT, Antioxidants of brown and red marine macroalgae as potential new preservatives for freshly caught Atlantic cod (*Gadus morhua*) from Northern Norway (MacroCod), grant BS0083, granted to RR 2. Arktis 2030 - main project (Troms og Finnmark fylkeskommune), Valorisation of marine macroalgae for the industrial development in North Norway (MacVal), grant 384/23, granted to RR and OO

★ **STUDENT PRIZE** **FULL** **S2** 16:20–16:30

The evolutionary origin of the *Arabidopsis* receptor kinase THESEUS1 and its function in plant cell wall integrity maintenance

Steven T. W. Zwartkruis [1]; Nelly K. Braun [1]; Wiebke Häger [1]; Tereza Tichá [1]; Vivien Klein [1]; Christine Ziegler [2]; Gregor Madej [2]; Martijn L. Vandegehuchte [1]; Thorsten Hamann [1]

[1] Norwegian University of Science and Technology (NTNU), Department of Biology, Trondheim, Norway
[2] University of Regensburg, Faculty of Biology and Preclinical Medicine, Regensburg, Germany

Plants actively monitor the state of their cell walls and adapt their structure and composition as needed. This cell wall integrity maintenance is crucial during development and the response to biotic- or abiotic stress, and relies on THESEUS1 (THE1), a receptor kinase. Mutations in THE1 lead to changes in cell wall stiffness, and altered jasmonic acid, abscisic acid and lignin levels in response to stress conditions. However, little is known about the mechanism by which THE1 is activated and very few downstream components have been characterized. To address this knowledge gap, we have generated a set of wild type and the1 loss-of-function plants expressing full length, truncated, and kinase-dead versions THE1-GFP constructs. These lines were tested for tolerance to drought and powdery mildew to find the biological relevance of THE1. We also used these mutant lines to study which domains are essential for the activation of downstream responses, as well as for intracellular localization studies. We performed a GFP-pulldown experiment to identify novel interaction partners of THE1, and discuss the potential proteolytic regulation of THE1. Finally, we find that THE1 is present in all seed plants except for the grasses. This deep conservation in the angiosperm lineage and its role in maintaining CWI during stress makes THE1 an interesting topic of study, providing leads for the knowledge-based development of resilient plant varieties. ---

Plant cell wall | cell wall integrity maintenance | receptor kinase | signaling | plant stress response ---

Funding: Thorsten Hamann and Christine Ziegler acknowledge funding from ERC SYNERGY grant HYDROSENSING (ERC10118769). Thorsten Hamann acknowledges funding from NFR grant WALLINTEGRITY (NFR315325).

FULL **S2** 16:30–16:40

Deciphering the functions of three *Phytophthora cactorum* RXLR effectors involved in strawberry colonization

Anupam Gogoi (presenting) [1]; Bikal Ghimire [2]; Mandeep Poudel [2]; Wyona Hager [1,2]; André van Eerde [1]; May Bente Brurberg [1,2]

1. Department of Molecular Plant Biology, Norwegian Institute of Bioeconomy Research (NIBIO), Ås, Norway
2. Department of Plant Sciences, Norwegian University of Life Sciences (NIBIO), Ås, Norway

Phytophthora cactorum is a destructive pathogen of numerous fruit, ornamental, and landscape plants. Its genome encodes hundreds of RXLR effectors, which are secreted proteins and in general known to manipulate host cell processes and dampen immune responses. However, the functions of most *P. cactorum* RXLR effectors during plant colonization remain poorly understood. We characterized twenty RXLR effectors from *P. cactorum* expressed during infection of strawberry crown tissue. Seven effectors triggered cell death and enhanced callose deposition when transiently expressed in *Nicotiana benthamiana*, indicating activation of the plant immunity. Among the remaining 13 effectors, PcRXLR11 and PcRXLR14 supressed *P. infestans* INF1-induced cell death, whereas PcRXLR17 enhanced INF1-triggered cell death. Infection assays showed that PcRXLR11, which suppressed cell death, enhanced *P. cactorum* virulence. N-terminal YFP tagging of PcRXLR11, PcRXLR14 and PcRXLR17 revealed varied subcellular localisations including chloroplast, cytoplasm and/or plasma membrane. All three effector genes were upregulated during infection of strawberry leaves relative to the mycelial growth. Exogenous application of dsRNA designed to target effector transcripts reduced pathogen colonization in strawberry leaves, indicating that these effectors are required for successful infection. Overall, our results demonstrate that key *P. cactorum* RXLR effectors manipulate host immunity and contribute to pathogen virulence.

Oomycetes | dsRNA | plant immune suppression and defence | strawberry | *N. benthamiana*

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FULL **S2** 16:40–16:50

Extracellular ATP and Metabolomic Fingerprints of Regulated Cell Death in Tomato and *Arabidopsis*

Jo Petter Helstad (presenting author) [1, 2]; Daniela Jorgelina Sueldo [1]; Gaston Courtade [2]; Leah Wanja Gachao [1]; Susanne Hansen Troøyen [2]

[1] Norwegian University of Science and Technology (NTNU), Department of Biology, Trondheim, Norway
[2] Norwegian University of Science and Technology (NTNU), Department of Biotechnology and Food Science, Trondheim, Norway

Regulated cell death (RCD) is critical for plant development, differentiation, and responses to environmental stress. Environmentally induced RCD can be triggered by abiotic and biotic factors to remove damaged cells or limit pathogen infection. Heat stress is an example of an abiotic factor in which increased temperatures trigger RCD. Dying cells release damage associated molecular patterns (DAMPs), including nucleotides like adenosine triphosphate (ATP). Extracellular ATP (eATP) can be recognized by neighboring cells to initiate stress responses or amplify RCD cascades. Ion leakage measurements can estimate RCD, as dying cells lose membrane integrity, leading to the release of cellular electrolytes. Our lab has established a protocol to estimate quantitative RCD after heat shock in *Arabidopsis thaliana* seedlings (Gacho & Sueldo, 2025). Here, we adapt this protocol to assess heat shock-induced RCD in tomato (*Solanum lycopersicum*) leaves using electrolyte leakage, showing that the protocol is easy to adapt to other species. To continue, we infiltrated *A. thaliana* seedlings and tomato leaves with external ATP and observed increased electrolyte leakage. This suggests eATP as a potential signal molecule involved in RCD in plants. Finally, molecules released during RCD can act as a metabolomic fingerprint of stress responses. We are employing nuclear magnetic resonance (NMR) spectroscopy to characterize the metabolomic fingerprint of RCD in *A. thaliana* seedlings and tomato leaves upon heat stress and external ATP infiltration. Our preliminary data suggests that it is possible to characterize heat stressed induced RCD with NMR metabolomic fingerprinting. ---

Cell death | NMR metabolomics | Extracellular ATP | Tomato ---

★ STUDENT PRIZE SHORT **S2** 17:00–17:07

Temperature resilience in different life cycle stages of the kelp *Alaria esculenta*

Pia Anissa Dittmer (presenting author) [1]; Inka Bartsch [2]; Alexander Jüterbock [1]; Niko Steiner [2]

1. Nord University, Faculty of Biosciences and Aquaculture, Bodø, Norway
2. Alfred Wegener Institute, Bremerhaven, Germany

Winged kelp (*Alaria esculenta*), an important ecosystem engineer and farming crop, will face rising sea water temperatures and an increased frequency of marine heatwaves in the rapidly warming Arctic. Until now, its temperature responses throughout the life cycle are largely unknown. As *A. esculenta* has a biphasic lifecycle with a diploid macroscopic stage (sporophyte) and haploid microscopic life stages (spores, gametophytes), it can easily be manipulated in laboratory settings. We tested the effect of temperature on the growth and reproduction of macroscopic sporophytes, as well as the recruitment of microscopic sporophytes, across a temperature gradient ranging from 0 to 15°C and 0 to 21°C, respectively. In addition, we applied a cold and warm temperature pre-treatment to the haploid gametophyte stage, to test how this influences subsequent recruitment responses. Interestingly and hitherto unknown, the temperature optima for macroscopic sporophyte growth differed by several degrees Celsius from the optima for microscopic sporophyte recruitment. In contrast, the fastest reproduction in macroscopic sporophytes (sporogenesis) and microscopic gametophytes (gametogenesis) occurred in a similar temperature range. After 14 days, warm pre-treatment of gametophytes resulted in higher sporophyte recruitment at the tested warm edge (6-12°C) and also induced better survival at lethal temperatures (21°C). These findings can be relevant for application in farming and restoration contexts in a changing climate. ---

kelp | temperature response | temperature priming | climate change | aquaculture resilience | restoration ---

Funding: Norwegian Research Council, KELPRIME, Grant Nr. 334327. The fund has been granted to A. Jüterbock.

★ STUDENT PRIZE SHORT **S2** 17:07–17:14

Polyphenolic content and bioactivity in Norwegian brown macroalgae in response to light intensity, temperature, salinity, and UV-radiation stress

Sara Roosvall (presenting author) [1, 2]; Ralf Rautenberger [2]

[1] Nord University, Faculty of Biosciences and Aquaculture, Bodø, Norway
[2] Norwegian Institute of Bioeconomy Research (NIBIO), Ås, Norway

Phlorotannins are polyphenolic compounds that play a key role in mitigating abiotic stress in brown macroalgae. These bioactive antioxidants are unique to brown algae and vary among species and habitats, reflecting adaptations to environmental conditions such as salinity, temperature, light intensity, and UV radiation. As climate change intensifies these environmental stressors, studying phlorotannins has become increasingly important, both for understanding their ecological role and for exploring their potential applications in nutraceutical, pharmaceutical, food, and cosmetic industries. In this study, three brown macroalgae species (*Saccharina latissima*, *Ascophyllum nodosum*, and *Fucus vesiculosus*) were collected from two environmentally distinct locations: Mørkvedbukta (oceanic) and Evenset (estuarine). Algae were exposed for 24 h to four abiotic stressors: light intensity (22 µmol photons m^{-2} s^{-1}, control; 100 µmol photons m^{-2} s^{-1}, intermediate; 300 µmol photons m^{-2} s^{-1}, high), temperature (10 °C, control; 18 °C, high), salinity (15 psu and 30 psu, depending on site-specific control and stress conditions), and UV radiation (UV-A, 320 nm, stress; PAR, 400 nm, control). Each treatment included three biological replicates per species and location (n = 3). Antioxidant activity was assessed using the DPPH radical scavenging assay, expressed as IC_{50} (mg mL^{-1}), and total polyphenolic content (TPC) was quantified using the Folin–Ciocalteu assay with phloroglucinol as the standard, expressed as mg phloroglucinol equivalents g^{-1} dry weight (mg PGE g^{-1} DW). ---

Brown macroalgae | Bioactive compounds | Polyphenols | Phlorotannins | Antioxidant activity | Abiotic stress ---

Funding: Nord University, Faculty of Biosciences and Aquaculture, Bodø, Norway. Master thesis project (No project nr) Granted to Sara Roosvall

★ STUDENT PRIZE SHORT **S2** 17:14–17:21

Investigating endocytosis-related candidate genes involved in stress perception

Nelly Braun (presenting author) [1]; Wiebke Haeger [1]; Steven Zwartkruis [1]; Francesco Saffioti [1]; Sara Morghen [1]; Thorsten Hamann [1]

[1] Norwegian University of Science and Technology (NTNU), Department of Biology, Trondheim, Norway

Environmental stresses such as drought are becoming increasingly frequent due to climate change, posing a serious threat to plant growth and agricultural productivity. To cope with these conditions, plants must rapidly perceive environmental changes and activate appropriate adaptive responses. The plant cell wall plays a central role in early stress perception, as alterations in cell wall integrity (CWI), mechanical properties, and turgor pressure occur at early stages of water deficit and other abiotic stresses. These changes are monitored by the CWI maintenance mechanism, which integrates mechanical and chemical signals to preserve cellular homeostasis. However, the molecular components and regulatory networks underlying this process remain poorly understood. This project aims to functionally characterize genes involved in CWI-mediated stress perception and signaling using *Arabidopsis thaliana* as a model system. Candidate genes were identified through transcriptomic and phosphoproteomic analyses and screened using hypersensitivity assays under hyperosmotic stress and chemically induced cell wall damage. Promising candidates included a set of genes involved in intracellular trafficking. These trafficking-related genes will be investigated in more detail using expression pattern analysis, stress assays, and possibly complementary molecular and cellular approaches. By exploring the potential link between intracellular trafficking and environmental stress sensing, this project aims to contribute to a deeper understanding of early hydrosensing mechanisms in plants and tries to identify molecular components that may be relevant for improving drought resilience in crops. ---

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SHORT **S2** 17:21–17:28

Acquisition and maintenance of environmental stress memory in red algae ‘*Bangia*’ spp.

Puja Kumari (presenting author) [1, 2]; Koji Mikami [1, 3]

[1] Faculty of Fisheries Sciences, Hokkaido University, Hakodate, Japan
[2] Scottish Association for Marine Science (SAMS), Oban, UK
[3] Department of Integrative Studies of Plant and Animal Production, School of Food Industrial Sciences, Miyagi University, Sendai, Japan

Seaweeds often acquire species-specific and stress stimuli-dependent acclimatory responses to survive in the marine environment. Understanding the acquisition and maintenance of such tolerance mechanism may provide pertinent tool for building environmental resilience. The ability of seaweeds to memorize their past experiences to better acclimate to the changing environment is not much studied. Generally, higher plants acquire a memory after exposure to external stimulus that enable the plants to respond to subsequent stress events with a faster and a stronger defense. This memory persist as a ‘primed state’ even if the stimulus no longer exist. However, the understanding of such stress memory concept is limited in seaweeds. *Bangia* species is a filamentous red seaweed belonging to Bangiophyceae cultivated commercially in South-East Asia. We have showed that *Bangia* sp. acquire thermotolerance based on heat stress memory, but the memory is transient and highly variable among different *Bangia* species. In this study, we investigated the role of stress memory in conferring tolerance to the dilution of seawater that causes hyposalinity, hypoosmatic and low nutrient stress simultaneously. ‘*Bangia*’ sp. ESS1 gametophytes primed with different diluted seawater concentrations for one week showed faster and stronger stress memory responses to recurrent dilution of seawater during triggering stress, which lasted for two weeks. The primed algae showed higher cell viability accompanied with low levels of floridosides and most of the central carbon metabolites during exposure to diluted seawater. This indicated that ‘*Bangia*’ sp. ESS1 may memorize past stress responses to acclimatize to fluctuating seawater conditions in the marine environment. ---

Bangia stress memory priming thermotolerance salinity stress seawater dilution ---

Funding: JSPS KAKENHI (Grant Numbers 25660160 and 18F18388) JSPS postdoctoral fellowship was awarded to Dr. Puja Kumari

★ STUDENT PRIZE SHORT **S2** 17:28–17:35

The role of cell wall integrity maintenance mechanisms in hyperosmotic stress and cell wall damage responses

Sara Morghen (presenting author) [1]; Francesco Saffioti [1]; Luis Alonso Baez [1]; Dhika Amanda [1]; Michaela Tichá [1]; Thorsten Hamann [1]

1. Department of Biology, Faculty of Natural Sciences, Norwegian University of Science and Technology, 7491 Trondheim, Norway

Abiotic stresses have negative effects on agricultural production. Among them, drought is a major cause of agricultural losses, strongly reducing crop yields. The perception of hyperosmotic stress by plants triggers changes in mechanical properties of cell walls and abscisic acid (ABA) production, which is required for plant adaptation to drought stress. Recent results showed that ABA induction requires the presence of intact cell walls and that the receptor kinase THESEUS1 (THE1) is a negative regulator of ABA production induced by hyperosmotic stress and a positive regulator of jasmonic acid (JA) production caused by cell wall damage (CWD). To investigate the role of the receptor kinases THE1 and FERONIA (FER) in hyperosmotic stress and CWD responses, hormone quantification and genetically encoded reporters for ABA and JA dynamics are used. The latest results of this study will be presented and novel insights on the roles of cell wall integrity maintenance mechanisms in the regulation of hyperosmotic stress and CWD response will be presented. ---

cell wall integrity FERONIA THESEUS1 abiotic stress osmotic stress ---

Funding: European Research Council, ERC HYDROSENSING project 101118769 granted to Thorsten Hamann

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SHORT **S2** 17:35–17:42

Climate Change Modulates Glyphosate Efficacy and Species-Specific Stress Responses in Key Weed and Crop Species

Zahra Bitarafan (presenting) [1], Melissa Hamner Mageroy [1], Rafael de Andrade Moral [2], Najmeh Salehan [3], Kristian Schmidt Nielsen [3], Christian Andreasen [1,3]

1. Norwegian Institute of Bioeconomy Research (NIBIO), Division of Biotechnology and Plant Health, Ås, Norway
2. Maynooth University, Department of Mathematics and Statistics, Maynooth, Ireland
3. University of Copenhagen, Department of Plant and Environmental Sciences, Taastrup, Denmark

Increases in atmospheric CO_2 and global temperatures are altering crop–weed dynamics, with implications for herbicide efficacy and future weed management. To simulate anticipated Nordic future climates, we performed controlled herbicide dose–response experiments on one crop species, oilseed rape (*Brassica napus*, C_3), and two weed species, wild oat (*Avena fatua*, C_3) and barnyard grass (*Echinochloa crus-galli*, C_4), under ambient (ca. 400 ppm CO_2, 18/12 °C day/night) and elevated (ca. 800 ppm CO_2, 20.5/14.5 °C day/night) conditions. Glyphosate efficacy was quantified across a range of application rates, and plant responses were evaluated through biomass reduction and transcriptomic profiling. We found that effective dose thresholds (ED_{50} and ED_{90}) for the grass species did not significantly shift under future conditions; however, *B. napus* exhibited enhanced growth reduction at lower glyphosate doses under elevated CO_2 and temperature, indicating species-specific alterations in herbicide sensitivity. Transcriptome analyses revealed species-specific response patterns to glyphosate treatments and environmental conditions, indicating that future climate scenarios may differentially modulate regulatory networks governing growth, stress tolerance, and herbicide responses. These findings highlight the need to consider climate-induced physiological and molecular changes when projecting weed control strategies and herbicide dose recommendations in northern agronomic systems.

Carbon dioxide levels Climate change Elevated CO2 Elevated temperatures Herbicide efficacy Plant stress tolerance

Funding: Part of the project "Weeds vs. Crops: the winner of climate change" financed by NIBIO base funds from the Research Council of Norway (Contract number 342631/L10).

SHORT **S2** 17:42–17:49

Uncovering the strawberry-crown rot pathosystem and domestication of wild resistance genes

May Bente Brurberg (presenting author) [1, 2]; A Gogoi [1]; Nina Elisabeth Nagy [1]; Mandeep Poudel [1, 2]; Jahn Davik [1]

[1] Division of Biotechnology and Plant Health, Norwegian Institute of Bioeconomy Research (NIBIO), Ås, Norway
[2] Department of Plant Sciences, Faculty of Biosciences (BIOVIT), Norwegian University of Life Sciences (NMBU), Ås, Norway

The octoploid strawberry (*Fragaria x ananassa*) with its large red berries is a popular crop that is cultivated all over the world. However, strawberry production suffers major losses due to diseases, among which crown rot caused by *Phytophthora cactorum* is particularly destructive. Infection results in rapid wilting of young leaves, followed by collapse of the entire plant within a few days after the pathogen has attacked the rhizome and roots. With few approved chemical control options and increasing pressure to reduce pesticide use, the development of host resistance represents a sustainable and highly desirable disease management strategy. While modern strawberry cultivars in general are susceptible to crown rot, resistance genes appear plentiful in wild *Fragaria* species. Understanding the molecular basis of plant–pathogen interactions in strawberry is essential for identifying resistance traits that can be deployed in breeding programs. With the help of new high-throughput sequencing and genotyping technologies we are extending plant-pathogen interaction studies from the diploid model plant *F. vesca* to the genetically complex octoploid strawberry crop plant. This transition is facilitated by using two wild octoploid progenitors of cultivated strawberry. Through this approach, we have identified resistance genes present in wild germplasm that were lost during domestication. These genes will be reintroduced into modern cultivars through interspecific hybridization, supported by high-throughput genotyping to accelerate selection. Together, this work aims to restore lost genetic diversity and deliver durable resistance to crown rot in cultivated strawberry. ---

strawberry | *Phytophthora* | disease resistance ---

Funding: This work was funded by the Research Council of Norway and the Norwegian Institute for Bioeconomy through the project FragDef (*Fragaria* defense mechanisms and domestication of wild resistance genes; Project ID 326212; Grant ID 52759) as well as The Norwegian University of Life Sciences (PhD grant MP).

Session 3 — Biotechnological Innovations and Emerging Tools

Friday 19 June 2026 · 10:45–12:00 · Storhavet 1

Advances in biotechnology and computation are transforming plant and algal research. This session covers CRISPR-based gene editing, synthetic biology, metabolic engineering, and strain selection, alongside AI-assisted phenotyping, machine learning, remote sensing, and automated stress detection for sustainable agriculture, aquaculture, and bioproduction.

FULL **S3** 10:45–10:55

CRISPR/Cas-based genome editing and functional genomics for development of multiple biotic & abiotic stress tolerance in *Solanum lycopersicum* L.

Banashree Saikia (presenting author) [1, 2]; Channakeshavaiah Chikkaputtaiah [1, 2]

1. Biological Sciences and Technology Division, CSIR-North East Institute of Science and Technology (CSIR-NEIST), Jorhat-785006, Assam, India
2. Academy of Scientific and Innovative Research (AcSIR), Ghaziabad 201 002, India

CRISPR/Cas is a target-specific, efficient third-generation genome editing technology gaining huge popularity due to its efficiency and robustness. Due to alarming global climate change, the yield and productivity of economically important crops, such as tomato (*Solanum lycopersicum* L.), have been severely affected by various abiotic and biotic stresses. Therefore, there is an urgent need for the development of multiple stress tolerance in crops by utilising the fast-breeding technologies. In this context, a comprehensive study on developing genetic tolerance to biotic and abiotic stress factors in tomato through genome editing and functional genomics are presented. The study has performed systematic CRISPR/Cas9-based precise genome editing of negative regulatory genes of multi-stress tolerance, namely SlHyPRP1 and SlDEA1. Loss-of-function analysis of these genes imparted significant tolerance to drought, salinity, bacterial leaf spot, and bacterial wilt disease in transient and stable lines (GEd2) of tomato. The study showed the key negative regulatory role of SlDEA1, a poorly studied 8CM family gene, functions together as an anchor gene with SlHyPRP1 in imparting multi-stress tolerance in tomato. Given the severe impact of early blight, caused by *Alternaria solani*, and the limited genetic information available, the study further aims to identify disease-susceptibility genes through transcriptome-wide analysis and to generate early-blight-resistant tomato lines using the established state-of-the-art genome editing system. Overall, this study provides a comprehensive framework for developing climate-resilient, multi-stress-tolerant tomato varieties and holds significant promise for field-deployable and sustainable crop improvement. ---

CRISPR/Cas9 · *Solanum lycopersicum* · HyPRP1 · DEA1 · multi-stress tolerance · climate-resilience ---

Funding: The funding was received by Dr Banashree Saikia as Woman in Science and Engineering-Post Doctoral Fellowship (WISE-PDF) from Department of Science and Technology, Anusandhan National Research Foundation (ANRF), Government of India (Sanction No. DST/WISE-PDF/LS-112/2024 (G).

★ STUDENT PRIZE FULL **S3** 10:55–11:05

Assisting species differentiation using hyperspectral imaging

Vasili Alexander Balios (presenting author) [1]; Samuel Ortega [2]; Karsten Heia [2]; Anna Avetisyan [1, 3]; Kirsten Krause [1]

1. Department of Arctic and Marine Biology, UiT The Arctic University of
2. Department of Seafood Industry
3. Department Scientific

Cuscuta species, commonly known as dodder, are parasitic plants infecting a broad range of globally significant crops severely impacting yields. Climate change is expected to further expand *Cuscuta* distribution due to shifts in temperature and precipitation patterns. Effective management of *Cuscuta* infestations is challenging due to limited resistant crop genotypes, drawbacks of mechanical removal, and restrictions on chemical controls. We evaluate hyperspectral imaging (HSI), coupled with machine learning, to differentiate between host plants (*Pelargonium zonale*) and parasitic *Cuscuta* species, including *C. campestris*, *C. monogyna*, *C. reflexa*, and *C. platyloba*. Images were captured using two hyperspectral cameras, covering visible and near-infrared (VNIR, 407–995 nm) and short-wave infrared (SWIR, 950–2518 nm) spectral regions. Multiple segmentation algorithms were evaluated. NDVI-based segmentation emerged as the most efficient and consistent method, significantly improving classification accuracy. Machine learning models, specifically random forest and neural network classifiers, were trained to classify pixels as either host or parasite, as well as distinguishing among the four *Cuscuta* species. High classification accuracy was achieved. Confusion mainly occurred among closely related species pairs (*C. campestris* with *C. platyloba* and *C. reflexa* with *C. monogyna*). Feature importance analysis identified critical spectral bands linked to chlorophyll and carotenoid content, crucial for differentiating host plants from parasites and among parasite species. To optimize data handling, a genetic algorithm and elbow method were employed, significantly reducing the required spectral bands, while maintaining high classification accuracy. These models could be further trained and would be particularly suited for field applications, which could be applied to real-time monitoring and early detection of *Cuscuta* infestations. ---

Cuscuta hyperspectral machine-learning species classification Host/parasite differentiation. ---

Funding: This research was part of a PhD project financed by UiT - The Arctic University of Norway. Work on *Cuscuta* in the group of Kirsten Krause was supported by the Norwegian Research Council FriPro grant 301175. Anna Avetisyan was funded by grant CPEA-LT-2016/10092 from the Norwegian Agency for International Cooperation and Quality Enhancement in Higher Education (DIKU).

FULL **S3** 11:05–11:15

Adaptive IoT-enabled automation with multimodal sensing and real-time image analysis for CEA

Arshad Kadevalappil Ajilan (presenting author) [1]

1. Grønt fra Nord AS, Fauske, Norway

Sustainable controlled environment agriculture (CEA) requires precise environmental regulation, yet manual control of lighting, nutrients and climate remains labor-intensive and difficult to optimize at commercial scale. We are developing an adaptive control framework using ESP32-based sensor nodes and camera modules to monitor physical, chemical and visual plant parameters in real time and support closed-loop environmental regulation. Temperature, humidity, VOCs, CO_2, EC, pH and RGB spectral measurements are collected alongside plant images from an ESP32-CAM. An ESP32 microcontroller functions as the central controller, transmitting data to a cloud computer for multivariate analysis and using image-derived phenotypic indicators to inform actuation of fans, lights, CO_2 injectors and nutrient dosing. To demonstrate feasibility, we developed an MVP prototype that integrates temperature, humidity and image data to regulate LED growth lighting (including brightness and channel combinations) and fan speed. Current image analysis quantifies leaf color metrics and applies a general vision model to derive a proxy health indicator, which is integrated with sensor data for feedback-driven light adjustment. All measurements are transmitted via MQTT and stored in a MySQL database for evaluation and system refinement. Future work will integrate feature extraction, statistical inference and predictive modeling to identify patterns within the commercial growth system at Grønt fra Nord and forecast yield constraints such as etiolation and disease-associated stress signals. Machine and deep learning models trained on accumulated data will capture nonlinear interactions between environmental variables and plant responses, enabling predictive control strategies that reduce the risk of suboptimal growth conditions. Overall, this work outlines a practical pathway toward data-driven, closed-loop environmental control in CEA, with the goal of improving operational sustainability. ---

controlled environment agriculture (CEA) IoT automation multimodal sensing image-based phenotyping machine learning predictive control smart farming ---

Funding: This work was supported by internal research and development funds from Grønt fra Nord AS.

FULL **S3** 11:15–11:25

Time-series multispectral UAV imaging reveals dynamic N-responses and breeding gains for N-uptake and protein yield in Norwegian spring barley

Stefano Zanotto [1]; Constantin Jansen [2]; **Morten Lillemo** (presenting author) [1]

1. Norwegian University of Life Sciences, Department of Plant Sciences, Ås, Norway
2. Graminor AS, Ridabu, Norway

ProteinBar is a collaborative project along the grain value chain in Norway to ensure a better utilization of domestically produced barley for animal feed. Advanced sensor technologies are being used to gain a better understanding of the nitrogen (N) uptake and remobilization in the barley plants and build-up of grain yield and grain protein content. Field trials were carried out over three years with a set of 20 historical barley varieties grown at two different N fertilization levels, 90 kg N/ha and 140 kg N/ha, representing approximately 40 years of barley breeding. The trial was phenotyped weekly with multispectral UAV imaging, and in addition, Yara N sensor measurements from the tillering stage to anthesis. Flag leaf samples were collected at anthesis and analysed for N content. The normalized difference vegetation index (NDVI) was derived from the time-series multispectral data and dynamic phenotypes were calculated as genotype means through Gaussian approximation for each of the two N fertilization treatments. The results revealed a consistent trend with increased N uptake and grain yield in the modern versus older varieties. This trend was apparent for both 2-row and 6-row barley. Conversely, there was a negative trend for protein content, likely due to a dilution effect from the higher yield levels of the modern varieties. Parameters derived from fitted Gaussian curves of the NDVI time-series data could distinguish high-protein content genotypes with a more efficient N-translocation from the canopy to the grains from the high-yielding ones with prolonged grain filling to maximize grain yield at the expense of lower grain protein content. Results from testing this approach in genome-wide association studies to identify genetic loci underlying these different N mobilization strategies in a panel of 250 barley genotypes tested in field trials over two years (2024 and 2025) and two locations (Ås and Bjørke) will be presented at the conference. ---

plant phenotyping | plant breeding | trait improvement | protein content | nitrogen uptake | grain yield ---

Funding: The Research Council of Norway, NFR 336315. Project coordinator: Morten Lillemo

★ STUDENT PRIZE FULL **S3** 11:25–11:35

Lithologically diverse Nordic glacial flours as macro- and micronutrient sources for northern plants

Colin Sinclair (presenting author) [1, 2]; Jemma Wadham [1, 2, 3]; Laura Jaakola [4, 5]; Sabina Strmic-Palinkas [1, 2]

1. The Arctic University of Norway, Department of Geosciences, Tromsø, Norway
2. IC3: Centre for Ice, Cryosphere, Carbon and Climate, Department of Geosciences, UiT The Arctic University of Norway, Tromsø, Norway
3. University of Bristol, School of Geographical Sciences, Bristol, UK
4. The Arctic University of Norway, Department of Arctic and Marine Biology, Tromsø, Norway
5. Norwegian Institute of Bioeconomy Research (NIBIO), Division of Food Production and Society, Ås, Norway

In recent years, rock powders have received renewed interest as slow-release fertilizers that can provide soils and crops with a wide range of macro- and micronutrients. Glacial flour is a naturally occurring, fine-grained rock powder that is found in glaciated regions worldwide. Formed from the erosion of bedrock, the physical and chemical properties of different glacial flours vary widely depending on their sources, influencing their effectiveness as fertilizers. This study aimed to analyze eight lithologically diverse glacial flours collected from glaciers in Iceland, Svalbard, and Norway for their exchangeable and total nutrient concentrations, trace metal concentrations and mineralogy. The flours were then applied to a nutrient-depleted, artificial soil at three different application rates in a controlled greenhouse experiment set up to mimic a short, Arctic/subarctic growing season for the crop, pea (*Pisum sativum* L.). The flours were found to contain low amounts of plant-available N and P. Analyses for potassium, total nitrogen, trace elements, and mineralogy are ongoing. Glacial flour treatments, even at the lowest application rate of 2 tha-1, improved pea biomass and yield over the control, and produced similar results to a low dose of a synthetic PK fertilizer. The magnitude of biomass and yield increases compared to the control varied amongst the glacial flour treatments, but did not always increase with the flour application rate. Trial results indicate that peas benefited from glacial flour amendment of soils over a single growing season under conditions of severe nutrient limitation. Preliminary results indicate that glacial flour has potential utility in organic and regenerative agriculture, but suitable flours must be identified based on total nutrient concentrations, nutrient availability, dissolution rate, and potentially harmful trace metal concentrations. ---

Nutrient Cycling Biogeochemistry Agrogeology Soil Fertility Carbon Sequestration ---

Funding: UiT, Changing Arctic Research School, Glacier GEOHEALTH: A solutions-based approach to the impacts of glacier retreat on ecosystem and human health in a changing Arctic

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FULL **S3** 11:35–11:45

Experimental breeding of the diatom *Cylindrotheca* sp. and high-throughput phenotyping of F1 offspring

Chris J Hulatt (presenting author) [1]; Hirono Suzuki [1]; Alexandre Détain [1]; Noémie Corniaux [1]; Matt C Posewitz [2]

1. Nord Universitet, Norway
2. Colorado School of Mines, USA

Sexual reprduction is widespread in eukaryotes and has profound impacts on the life histories and adaptive diversification of many protist species. In diatoms, mating and recombination is a key activity contributing to their enormous phenotypic and genetic diversity, with perhaps 100,000 or more species inhabiting oceanic, lentic and diverse terrestrial environments. The aim of this project was to investigate the possibilities of a “full cycle” diatom breeding program in the lab, including detecting mating activity between different diatom strains, identifying promising crosses, isolating F1 offspring, and examining their phenotypic traits. We began by isolating strains of *Cylindrotheca* sp. from coastal waters near our lab in Arctic Norway, and introduced them pairwise in crossing experiments. We identified positive mating patterns within three distinct clades, including between parental cells of different genotypes and phenotypes. After selecting the most promising crosses we initiated controlled mating and isolated the F1 offspring. We then examined the F1 phenotypic trait variation, including the cellular morphology, growth rates, and plastid features including chlorophyll content and photophysiology, together with other bioenergetic traits. We detected substantial trait variation amongst F1 strains, including between different parental crosses and between individual offspring within specific crosses. The results shape future experimentation into diatom reproductive biology and advance diatom breeding for studies in ocean microbiology and biotechnology.

diatom breeding phenotyping strain improvement

Funding: Research Council of Norway, ExCell Chris J Hulatt (Nord) Matt C. Posewitz (Colorado School of Mines)

FULL **S3** 11:45–11:53

Low-Impact Bioprocessing of *Alaria esculenta* for Next-Generation Agricultural Biostimulants

Paige Heavyside (presenting) [1], Stina Karlsen [1]

1. Kelpinor AS, Norway

Seaweed-derived biostimulants are increasingly recognized for their potential to enhance crop resilience, nutrient uptake, and stress tolerance in sustainable agricultural systems. However, the bioactivity of seaweed extracts is strongly influenced by both biomass sourcing and processing methods. Conventional extraction approaches often rely on high temperatures or chemical treatments that can degrade sensitive bioactive compounds and alter the natural biochemical complexity of macroalgae. Here we present an industry-focused approach to developing kelp-based biostimulants through low-impact bioprocessing of cultivated *Alaria esculenta*. By prioritizing gentle processing strategies designed to minimize thermal and chemical degradation, this approach aims to preserve the diverse suite of bioactive molecules naturally present in kelp, including amino acids, polysaccharides, phenolic compounds, micronutrients, and hormone-like substances. Maintaining this biochemical complexity may be critical for the synergistic effects associated with seaweed-derived plant biostimulants. In parallel, Kelpinor is leading the transition toward Norwegian cultivated *A. esculenta* to improve raw material consistency while reducing harvesting pressure on wild kelp populations. Together, the integration of sustainable kelp cultivation and low-impact processing represents a promising framework for producing next-generation marine biostimulants with improved reproducibility, environmental sustainability, and agricultural relevance.

Alaria esculenta · seaweed biostimulants · low-impact bioprocessing · macroalgae biotechnology · sustainable aquaculture · sustainable food systems · crop resiliency

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SHORT **S3** 11:53–12:00

The Norwegian Plant Phenotyping Infrastructure (PheNo) – a new era of opportunities for plant research in Norway

Sara Laranjeira (presenting author) [1]; Laura Jaakola [2, 3]; Paul E. Grini [4]; Faouzi Alaya Cheikh [5]; Steinar Trædal-Henden [6]; Hafeez Ur Rehman [7]; Inger Martinussen [3]; Jan Roger Torp Sørby [8]; Odd Arne Rognli [1]; Morten Lillemo [1]

1. Norwegian University of Life Sciences, Department of Plant Sciences, Ås, Norway
2. UiT - The Arctic University of Norway, Department of Arctic and Marine Biology, Tromsø, Norway
3. Norwegian Institute of Bioeconomy Research, Tromsø, Norway
4. University of Oslo, Department of Biosciences, Oslo, Norway
5. Norwegian University for Science and Technology, Department of Computer Science, Gjøvik, Norway
6. UiT -The Arctic University of Norway, Section for Digital Research Services, Tromsø, Norway
7. Norwegian Institute of Bioeconomy Research, Apelsvoll, Norway
8. Norwegian University of Life Sciences, Centre for Plant Research in Controlled Climate (SKP), Ås, Norway

Advanced research facilities are needed to meet the needs for increased food production under the challenging Norwegian climate conditions. The Norwegian Plant Phenotyping Infrastructure (PheNo) addresses these needs by building and operating research facilities using state-of-the-art technology to observe and measure plant traits in detail. By understanding more about how plants react to the environment, we can support the development of stronger, healthier crops that are better suited for future climatic challenges. The infrastructure project is a collaboration between the Norwegian University of Life Sciences (NMBU), the University of Oslo (UiO), the Norwegian University of Science and Technology (NTNU), the Arctic University of Norway (UiT) and the Norwegian Institute of Bioeconomy Research (NIBIO). Investments are being made in new equipment and facilities for phenotyping plants under controlled growth conditions and in the field, as well as automatic phenotyping of seeds, in facilities close to the local research communities across the country. The services tailor both research and teaching needs, covering the entire spectrum from basic plant biology to practical applications in agriculture, horticulture, and plant breeding. The PheNo consortium is part of the International Plant Phenotyping Network (IPPN) and will officially become the Norwegian node in EMPHASIS once it gets its legal ERIC status in 2026/2027. This will provide access to many specialized research facilities across Europe for the entire plant research community in Norway, while European researchers, in turn, will benefit from access to phenotyping services under Norway's unique growing conditions. Overall, PheNo will strengthen the national plant research capacity and position Norway as a leader in plant phenotyping research. ---

plant phenotyping · infrastructure · services · capacity building · research · education ---

Funding: Research Council of Norway, NFR 350254. Project coordinator: Morten Lillemo.

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The urgent need for a transition to sustainable energy systems has renewed interest in molecular hydrogen (H_2) as a clean, carbon-neutral energy carrier. Some cyanobacteria such as *Synechocystis* sp. PCC 6803 can produce H_2 via photosynthetic or fermentative pathways. However, photosynthetic H_2 production is typically short-lived because co-evolved O_2 inhibits hydrogenase (H_2ase). This study focuses on extending the duration and efficiency of H_2 photoproduction in dark-adapted, anaerobic *Synechocystis* cultures through optimization of the pulse-illumination regime. The protocol, originally developed for *Chlamydomonas reinhardtii*, has not previously been applied to cyanobacteria. To evaluate the effect of pulse duration, four light/dark regimes were tested: 200 ms/9.8 s, 500 ms/9.5 s, 1 s/9 s, and 2 s/8 s. Real-time gas exchange was monitored using membrane inlet mass spectrometry (MIMS) and Clark-type microelectrodes. An oxygen scavenging system maintained microoxic conditions to protect hydrogenase from inhibition. In nitrate-containing BG11 medium, longer light pulses triggered rapid but transient H_2 evolution followed by H_2 consumption and enhanced fermentative H_2 release during the dark phase. Shorter pulses induced slower activation but supported more stable H_2 release with reduced subsequent consumption. Replacing nitrate with ammonium in BG11 medium further enhanced and stabilized H_2 production by decreasing electron competition with nitrogen assimilation and redirecting reductants toward H_2ase. Short light pulses shift photosynthetic electron flow from CO_2 fixation and nitrate reduction to H_2 production, resulting in more stable and prolonged photohydrogen generation. These results show that redox balance and nitrogen source are key for sustaining anaerobic photosynthesis and offer a strong basis for improving H_2 production.

hydrogen production · pulse illumination · *Synechocystis* · cyanobacteria · photosynthesis

Funding: Jane and Aatos Erkko Foundation project "PhotoFacts".

Poster Presentations

Session 1: Thursday 18 June 15:00–16:00 · Session 2: Friday 19 June 10:15–10:45 · Storhavet 1

Posters span all four conference themes — Signalling & Interactions; Immunity, Stress & Adaptation; Biotechnological Innovations; and Restoration, Biodiversity & Sustainable Ecosystem Management. Posters marked ★ **Student prize** are entered in the Best Student Poster Award — scan the poster voting code (see Practical Information) to cast your vote.

POSTER P01

A comparison between two flax (*Linum usitatissimum* L.) genotypes, Flanders and Astella, for assaying their salinity adaptation capability

Debnath, Anirban Jyoti [5] *(presenting)*; Harenčár, Ľubomír [3]; Kučka, Matúš [4]; Kovár, Marek [1]; Ivanišová, Eva [2]; Mistríková, Veronika [3]; Gažo, Ján [1]; Ražná, Katarína [1]

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The United Nations-predicted food scarcity creates an urgency in research to assess and improve agriculturally important plants under environmental stress conditions. In this context, lignans are powerful antioxidants that play defensive roles in plants under stress. The roles of lignans in salt stress mitigation are rarely studied or understood, particularly in the multipurpose crop flax (*Linum usitatissimum* L.). Flax is a rich source of lignans. This study assessed the response to salt stress in two flax genotypes, Flanders and Astella. Astella has a higher content of the lignan secoisolariciresinol diglucoside (SDG) than Flanders. The 3-week-old flax plants were stressed with a 100 mM NaCl solution for 1 week. Post-stress treatment, morphological analyses revealed suppressed growth in Flanders, indicating its better stress-adaptive, resource-saving behaviour than in Astella under salinity. The reactive oxygen species (ROS) production and associated cell damage were greater in Astella than in Flanders upon NaCl application. Under salinity stress, higher levels of antioxidants, osmoprotection, and lignan-related microRNAs reflected a superior ROS scavenging and superior cellular protection system of Flanders than Astella. However, multivariate analysis could not provide evidence for the direct involvement of lignans in stress adaptation. Instead, it was hypothesised that microRNAs play a pleiotropic role in the adaptation to salinity. These results depict Flanders' superiority to Astella in salt stress tolerance. The findings could be used to improve the salinity tolerance of flax and other crop plants in future research.

Biochemical analysis · MicroRNA · Morphological analysis · Reactive oxygen species · Secoisolariciresinol diglucoside · Two-tailed quantitative PCR

Funding: This work was supported by the National Scholarship Programme of the Slovak Republic provided by the Ministry of Education, Science, Research and Sport, Government of the Slovak Republic (NSP-SAIA) and COST Action SUSTAIN (CA 22144).

POSTER P02 ★ STUDENT PRIZE

To live and let die - Extracellular ATP signaling in *Arabidopsis* during regulated cell death processes

Maximilian Fuchs [1] *(presenting)*; Leah Wanja Gachao [1]; Daniela Sueldo [1]

1. Norwegian University of Science and Technology, Department of Biology, Trondheim, Norway

As a response to biotic and abiotic stress, a single plant cell can kill itself to increase the chance of survival for the whole organism. During these regulated cell death (RCD) processes, a dying cell communicates with its neighbors, which determines their fate. Being perceived by transmembrane purinoreceptor 2 kinase (P2K) receptors, extracellular ATP (eATP) is a signaling molecule that serves as a damage associated molecular pattern (DAMP). Interestingly, eATP perception can lead to opposite outcomes in the progression of RCD, leading to the survival or death of these neighboring cells, depending on the stress context and the tested plant organism. The objective of this master thesis is to characterize the response of *Arabidopsis* to artificially applied eATP. For this, a double mutant lacking both known P2Ks in *Arabidopsis* (P2K1 and P2K2) was tested in comparison to wild type Col-0. To quantify the occurrence of cell death upon eATP treatment, 14-day old seedlings of both genotypes were vacuum-infiltrated with ATP solution. Subsequently, a time course of electrolyte leakage measurements was conducted and complemented by Trypan Blue cell death staining. To identify novel genes involved in the signaling cascade induced upon eATP treatment, we monitored activity of serine hydrolases (including proteases, lipases and glucanases) using a fluorescent probe that targets enzymes with serine in their active site. Our results show that the wild type, as well as the p2k1/p2k2 double mutant, respond to a concentration of 2 mM artificially applied eATP with a statistically similar increase in electrolyte leakage. Further, preliminary results indicate no change in activity of serine hydrolases up to 60 minutes after eATP treatment. Overall, our data indicates that eATP responses in *Arabidopsis* are not entirely explained by P2K1/P2K2 function and may thereby suggest the presence of additional receptors or other mechanisms involved in eATP signaling.

regulated cell death · stress response · extracellular ATP · electrolyte leakage · purinoreceptor 2 kinase · *Arabidopsis thaliana*

POSTER P03 ★ STUDENT PRIZE

A molecular phylogeny of sea ice microalgae

Dills, Michael [1] *(presenting)*; Campbell, Karley [2]; Præbel, Kim [1]

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2. UiT - The Arctic University of Norway, Faculty of Bioscience, Fisheries and Economics, Institute for Arctic Marine Biology, Tromsø, Norway

Marine Chlamydomonadaleans are a globally distributed clade of green algae populating nearly all photic habitats from sea ice to the tropics. Along with their key role as primary producers in biogeochemical processes, these organisms offer valuable insights into evolutionary processes. Despite being isolated from every major ocean basin, little is known about polar, marine strains – especially those found in the Arctic. This project investigates intraspecific genomic variability and adaptation by applying whole genome sequencing to characterize a selection of Arctic and Southern Ocean *Chlamydomonas* sp. isolates.

ecology · adaptation · comparative genomics · microalgae

POSTER P04 ★ STUDENT PRIZE

Decoding plant drought sensing mechanisms by identifying novel components and characterizing the mechanical properties of cell wall

Saffioti, Francesco [1] *(presenting)*; Morghen, Sara [1]; Alonzo Baez, Luis [1]; Tichá, Michaela [1]; Hamann, Thorsten [1]

1. Department of Biology, Faculty of Natural Sciences, Norwegian University of Science and Technology, 5 Høgskoleringen, Trondheim, 7491, Norway

Climate change poses a major challenge to global agriculture, particularly because of its negative impact on water availability. The development of drought-resistant crops requires the identification and understanding of the key components of drought sensing mechanisms. Currently, the phytohormone abscisic acid (ABA) is recognized as a key element acting as stress signal in response to drought. However, our understanding of how plants detect drought and trigger increases in ABA levels is still limited. Recent findings indicate ABA induction requires interactions between the cell wall and the plasma membrane and is negatively regulated by the receptor kinase THESEUS1 (THE1). THE1 is also required for cell wall integrity maintenance and regulation of cell wall mechanical properties in *Arabidopsis thaliana*. By combining omics experiments and hypersensitivity screens we have identified novel components for sensing drought conditions. At the same time, confocal Brillouin microscopy is used to determine how cell wall mechanical properties participate in drought perception and drought stress responses. This approach will help to uncover how alterations in cell wall mechanics can contribute to improving drought resistance. We will present an up-to-date overview of the components we have found and how they affect responses to drought stress.

THESEUS1 drought cell wall mechanics abiotic stress Brillouin microscopy

Funding: European Research Council, ERC HYDROSENSING project 101118769, granted to Thorsten Hamann

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POSTER P05 ★ STUDENT PRIZE

Immune priming as a novel strategy to enhance disease tolerance in cultivated kelp

Minini, Leo [1] *(presenting)*; Badis, Yacine [2]; Leblanc, Catherine [2]; Engelen H., Aschwin [3]; Weinberger, Florian [4]; Markov, Gabriel [2]; Dittami, Simon [2]; Nolsøe M.J., Jens [1]; Jueterbock O., Alexander [1]

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4. GEOMAR Helmholtz Centre for Ocean Research Kiel, 24148 Kiel, Germany

Diseases pose a major challenge in kelp aquaculture worldwide, reducing biomass yield and quality, which impacts coastal communities that depend on this activity for income. The risk of disease in kelp is increased by human activities and farming intensification, highlighting the need to improve kelp's tolerance to biotic stressors. Selective breeding and species hybridization are currently the main strategies for boosting disease tolerance in farmed kelp in Asia. In Norway, the use of these methods is limited by regulatory and ethical concerns over the risk of genetic pollution in wild kelp populations. Immune priming, which has been successfully used in land crops, could serve as a useful alternative or addition to traditional breeding methods. It is the process where previous exposure to a biotic stressor or an elicitor (such as DAMPs or PAMPs) boosts the speed and effectiveness of the subsequent pattern-triggered immune response against a biotic threat, thereby improving disease tolerance. While oligoguluronates elicit an immune response in kelp, it remains unknown whether they can prime gametophytes and sporophytes to be more resistant to microbial antagonists and biofouling. Additionally, it is unclear how long the priming memory lasts, if it depends on DNA methylation, and whether it can be transmitted from one life stage to the next. We will present ongoing work characterizing the priming effect and its underlying mechanisms in kelp using challenge experiments and multi-omic analyses. If a positive priming effect is observed at the laboratory scale, subsequent field trials in local kelp farms will be conducted to evaluate the potential of immune priming as a novel strategy to enhance kelp resilience and prevent biomass loss due to diseases.

kelp aquaculture disease tolerance immune priming innate immunity oligoguluronates multi-omics

Funding: This work is supported by the Norwegian Ministry of Education and Research through a PhD fellowship awarded to the Leo Minini at the Faculty of Biosciences and Aquaculture, Nord University, under the project "Sugar kelp priming for strengthening host immunity" (st. nr. 30237312)

POSTER P06

Response of *Cuscuta campestris* to gall formation by weevils of the genus *Smicronyx*

Savov, Stefan [1]; Roach, Thomas [2]; Kranner, Ilse [2]; Teofanova, Denitsa [1]; Zagorchev, Lyuben [1] *(presenting)*

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2. Institut für Botanik, Universität Innsbruck, Innsbruck, Austria

Cuscuta campestris is an obligate parasitic plant in the family Convolvulaceae, with North American origin, but is an introduced invasive pest around the globe. Being a parasite, it is also a subject to parasitism by gall-inducing weevils of the genus *Smicronyx* (*Curculionidae*). These galls are characterized by a notable increase in chlorophyll levels of this otherwise non-photosynthetic plant, and are also intriguing experimental object as a potential natural regulator of *C. campestris* fecundity. In the present study, we aimed to elucidate the defense response of the parasitic plant at hormonal and transcription level by HPLC-MS/MS and quantitative PCR analyses. The most notable hormonal changes in the galls were an increase in abscisic acid (ABA), gibberelic acid 4 (GA4) and jasmonic acid (JA), and decrease in salycilic acid (SA) levels. These changes correspond to a typical response expected in insect-induced stress, in combination with growth promotion needed for formation of galls. The increase in α-carotene and lutein, concurrent with β-carotene depletion indicates a stress-induced redirection of carotenoid metabolism toward ABA biosynthesis and photoprotective antenna remodeling, consistent with enhanced ABA and JA signaling and suppressed SA-mediated immunity. Quantitative PCR analysis of defense related genes showed upregulation of osmotin-, thaumatin-, and defensin-like genes together with repression of chitinase, cystatin, and lipoxygenase, which reflects an ABA- and JA-biased stress-adaptation program with suppressed SA-dependent immunity and attenuated jasmonate biosynthesis, consistent with chronic stress or parasitic manipulation. In conclusion, *Smicronyx*-induced galls in *Cuscuta campestris* elicit a coordinated hormonal, metabolic, and transcriptional reprogramming, highlighting gall formation as a finely tuned interaction that facilitates insect development while constraining parasite fitness.

Cuscuta | parasitic plants | pathogenesis-related proteins | plant galls | weevils

Funding: This study is financed by the European Union-NextGenerationEU, through the National Recovery and Resilience Plan of the Republic of Bulgaria, project No BG-RRP-2.004-0008 and grant KP-06-Slovakia/5 of the National Science Fund, Ministry of Education and Science, Bulgaria.

POSTER P07

Genotyping of natural and self-pollinating populations of *Hyssopus officinalis* for utilisation of the biosynthetic capacity

Tzvetelina Zagorcheva *(presenting)*; Zagorchev, Tzvetelina [1,2]; Rusanov, Krasimir [2]; Rusanova, Mila [1,2]; Atanassov, Ivan [2]

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2. AgroBioInstitute, Agricultural Academy, Sofia, Bulgaria, 8 Dragan Tsankov blvd., 1164, Sofia, Bulgaria

The genus *Hyssopus* L. (Lamiaceae) consists of approximately 10–15 species, among which *Hyssopus officinalis* L. is the most commonly cultivated and studied. Hyssop essential oil is widely applied in the cosmetic, perfumery, and beverage industries due to its well-documented antioxidant, anticonvulsant, antifungal, antimicrobial, antihemolytic, antiulcer, and antispasmodic properties. The strong bioactive potential of hyssop essential oil is primarily related to its high concentration of monoterpenoids, particularly pinocamphone, isopinocamphone, and β-pinene. To investigate the genetic determinants of essential oil yield and composition in hyssop, we analysed the genetic structure of two *H. officinalis* natural populations of a total of 59 individual plants employing sequence-related amplified polymorphism (SRAP) molecular markers. Principal Coordinate Analysis and UPGMA clustering of Jaccard indices revealed good genetic differentiation between the two populations, while the delta K approach showed genetic homogeneity within populations. All plants were further characterised by gas chromatography-mass spectrometry (GC-MS) profiling of the essential oil constituents and PCA analysis, showing that essential oil composition varies significantly within populations. Furthermore, genotyping of a self-pollinating, segregating population of an interspecific hybrid *Hyssopus officinalis* ssp. aristatus x *Hyssopus officinalis* ssp. *officinalis* was employed to construct the first genetic map of the species, containing 14 linkage groups and a total of 89 loci. These findings provide a foundation for the sustainable exploitation of hyssop, an essential oil crop that remains relatively underutilised. Furthermore, the identification of elite, high-yielding genotypes with desirable characteristics supports the application of marker-assisted selection and offers a strategy to limit human pressure on natural wild populations.

essential oil | genetic map | hyssopus | SRAP markers

Funding: This study is financed by project No. BG16RFPR002-1.014-0014-C01 “Development Program with a Business Plan for the Laboratory Complex of Sofia Tech Park,” which is implemented under the “Research, Innovation and Digitalization for Smart Transformation” Program, co-financed by the European Union through the European Regional Development Fund.

POSTER P08

Perspective for extremophyte micropropagation in bioreactor system – comparison of physiological responses of halophyte *Lobularia maritima* and metallophyte *Alyssum montanum*

Wiszniewska, Alina [1] *(presenting)*; Makowski, Wojciech [1]; Muszyńska-Sadłowska, Ewa [2]; Kiwer, Agata [1]; Mallepoola, Teja Sree [1]

1. University of Agriculture in Kraków, Department of Botany, Physiology and Plant Protection, Kraków, Poland
2. Warsaw University of Life Sciences (SGGW), Department of Botany and Plant Physiology, Warsaw, Poland

Extremophytes are valuable models for studying plant stress tolerance and have biotechnological and environmental potential but require reliable sources of uniform plant material. Micropropagation enables controlled production of uniform plants, facilitating physiological studies and analysis of intrinsic tolerance mechanisms. Bioreactor-based systems can enhance in vitro culture via improved process control, scalability, and biomass productivity, yet their use in extremophytes is underexplored. We evaluated bioreactor-based micropropagation for two Brassicaceae extremophytes: halophyte *Lobularia maritima* and metallicolous *Alyssum montanum*. Shoot biometry, biomass, biochemical parameters (stress markers, osmolytes, phenolic compounds, antioxidant activity), DNA damage, and methylation were compared between conventional agar solidified medium culture (CC) and temporary immersion bioreactor Plantform (TIB) systems, along with acclimatization fitness of microplants. TIB cultivation enhanced *A. montanum* fresh weight, increased free amino acids, and oxidized glutathione, while reducing stress metabolites (proline, sugars, phenylpropanoids, flavonoids), indicating improved growth and metabolic efficiency with minimal oxidative stress. *L. maritima* also showed increased fresh weight and stress metabolite accumulation, but had elevated MDA, depleted glutathione, reduced phenolics, and activation of an extra SOD isoform, reflecting growth under higher oxidative stress. These contrasting responses highlight species-specific effects of TIB culture: *A. montanum* benefits from stress mitigation and metabolic optimization, whereas *L. maritima* shows a trade-off between growth and stress defence activation. TIB systems support micropropagation in both species, but culture conditions must be optimized to maximize biomass and maintain metabolic stability.

halophyte | metallophyte | in vitro culture | temporary immersion bioreactor | stress response

Funding: Ministry of Science and Higher Education as apart of a research subsidy to the University of Agriculture in Kraków (050012-D011, 050012-D017)

POSTER P09 ★ STUDENT PRIZE

Genomic strategies to accelerate genetic gain in wheat (Wheatboost)

Brown, Thomas Julseth [1,2] *(presenting)*; Lillemo, Morten [1]; Alsheikh, Muath [1,2]; Windju, Susanne [2]; Dieseth, Jon Arne [2]; Mosleth, Ellen [3]; Ruud, Anja Karine [1]; Lin, Min [1]

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2. Graminor AS, Ridabu, Hamar
3. Norwegian Institute of Food, Fisheries and Aquaculture Research (NOFIMA), Ås

Norwegian spring wheat has high potential for good baking quality, yet this potential is frequently compromised by pre-harvest sprouting (PHS) – the premature germination of grain while still in the field during rainy or delayed harvest conditions. PHS reduces baking quality through enzyme activity that degrades starch and gluten, leading to substantial losses across the value chain. Climate variability around harvest and late grain development increases the risk of PHS by reducing dormancy. WheatBoost (indsutrial PhD) integrates quantitative genetics, molecular breeding, and simulation-based optimization to accelerate the development of wheat varieties that combine high baking quality with enhanced resistance to PHS. The project builds on prior identification of quantitative trait loci (QTL) associated with PHS resistance and on advances in phenotyping (including machine learning-enabled single-seed analysis), genomic selection, and speed breeding using single seed descent (SSD). The research expands this foundation through family-based and population-wide genetic analyses, practical marker development for early-generation selection, and simulation-driven optimization of the breeding pipeline. The primary objective is to implement advanced genomics-based speed breeding technologies in the Graminor wheat program to accelerate genetic gain, with a central focus on enhancing resistance to PHS. This will be pursued through specific secondary objectives: Identifying the major genetic factors behind PHS resistance using QTL mapping and genome-wide association studies (GWAS); evaluating and validating KASP-markers for marker-assisted selection (MAS); developing and applying a simulation tool for optimizing breeding under speed breeding; implementing and assessing multi-trait genomic selection (PHS, FHB, and yield).

Wheat breeding | Pre-harvest sprouting (PHS) | Wheat genetics | Speed breeding | Genomic selection

Funding: Funders: Norwegian Research Council of Norway and Graminor AS Project name: Wheatboost Project number: Yet to be determined Authors: Alsheikh, Muath; Lillemo, Morten

POSTER P10

Effects of environmental stress on red seaweeds

Alexandra Kinnby and Gunnar Cervin *(presenting)*; Kinnby, Alexandra [1]; Cervin, Gunnar [1]

1. Department of Marine Sciences, Tjärnö Marine Laboratory, University of Gothenburg, Strömstad, Sweden.

Red macroalgae are key primary producers on rocky substrates as well as high-value aquaculture crops which are increasingly exposed to environmental stresses including potential changes to underwater light regimes or seawater chemistry due to climate change. However, the physiological and biochemical responses of different red seaweed species to these drivers remain poorly understood. We investigate how changes to environmental factors affect growth and biochemical traits in two aquaculture-relevant red macroalgal species. Using *Palmaria palmata* we conducted experiments in which spectral composition of light was manipulated to simulate depth-related changes in underwater light environments. Using *Chondrus crispus* we examined the effects of ocean acidification on physiological performance. Across both experiments, we quantified growth and analyzed biochemical composition, focusing on pigments and fatty acid profiles. This allows us to examine species-specific biochemical changes under changing light and ocean acidification conditions and how they affect seaweed physiology. We consider the responses across different environmental drivers and on different species to develop a more mechanistic understanding of how climate drivers may influence the performance, biochemical quality, and cultivation potential of red macroalgae. Such insights contribute to improving predictions of aquaculture resilience and inform management and cultivation strategies as the marine environment changes.

Seaweed · climate change · ocean acidification · pigments · *Palmaria palmata* · *Chondrus crispus*

Funding: AK was funded by a Young Researcher Mobility Grant from the Research Council FORMAS (grant number 2022/02838) "Effects of ocean acidification on macroalgal forests" and AK and GC are funded by the SBEP project "PalmariaPlus" (grant number 2024/02712). Both grants were awarded to AK.

POSTER P11 ★ STUDENT PRIZE

A group of transcription factors is involved in parasitic *Cuscuta*’s unusual photomorphogenetic behaviour

Berglund, Liv-Irene [1] *(presenting)*; Bawin, Thomas [1]; Olsen, Stian [1]; Krause, Kirsten [1]

1. UiT The Arctic University of Norway, Department of Arctic and Marine Biology, Tromsø, Norway

Species within the *Cuscuta* genus (common name, dodders) have a heterotrophic lifestyle where they attach to other plants vascular tissues in order to get enough water, organic and inorganic nutrients. The study of these interactions between the parasites and their hosts have led to some interesting discoveries. One of them is their reaction to shade: shade avoidance is a common plant response whenever light becomes a limiting factor, while, in contrast, *Cuscuta* species are attracted by shade. This behavior is regulated by far-red light and is dependent on the photoreceptor Phytochrome. Transcriptional studies have revealed that several transcription factor (TF) families are among the genes that are upregulated during far-red-light exposure. Several are described in model plants like *Arabidopsis* and other species with other functions. To explore their potential function in *Cuscuta*, this study focused on selected candidates from one TF family and analyzed their transcriptional patterns as well as their localization in the *Cuscuta* cells upon transient expression of fluorescently labelled transgenes.

Biolistics · *Cuscuta* · parasitic plants · photomorphogenesis

Funding: The Research Council of Norway (RCN), grant 301175 to KK.

POSTER P12 ★ STUDENT PRIZE

Establishing Infrared Thermography for Non-Invasive Monitoring of Transport Dynamics in and Between Vascular Plants

Bergmann, Pepe [1] *(presenting)*; Balios, Vasili [1]; Krause, Kirsten [1]

1. UiT The Arctic University of Tromsø, Institute for Arctic and Marine Biology, Tromsø, Norway

Understanding the dynamic transport processes of vascular plants is important for many biological fields, such as plant physiology, plant parasitology or agricultural science. However, traditional methods for studying these processes are often invasive, damaging or even destroying the plants. This creates a need for repeatable non-invasive tools, capable of monitoring and measuring transport dynamics in real time. Infrared thermography (IRT) offers a promising alternative approach to previously established techniques, by enabling non-contact visualisation of temperature variations within plants, reflecting physiological processes. In this study, a custom-built heating device was used to apply repeated, localized heat pulses to a plant stem, while a thermal camera recorded the propagation of temperature change. Taking this a step further, the same method was applied to observe heat propagation between a host plant and the holoparasitic plant species *Cuscuta reflexa*. The results of this study demonstrate that IRT can capture xylem-transport dominated heat propagation within intact plants at speeds comparable to literature values, while highlighting technical challenges for long-term measurements. In host-parasite systems, testing with *Cuscuta reflexa* showed detectable heat propagation into the parasite, proving the potential, but also the complexity of applying IRT to such studies.

Infrared thermography | Non-invasive imaging | Xylem transport | Plant physiology | Host–parasite interaction

Funding: The project did not receive any funding as it was a bachelor thesis, the lab and resources were provided by Prof. Kirsten Krause (UiT)

POSTER P13 ★ STUDENT PRIZE

New Tools to Investigate Genomic Imprinting using *Arabidopsis arenosa* as a Model System

Gannestad, Kristin K. [1] *(presenting)*; Bjerkan, Katrine N. [1]; Miller, Jason R. [2], Hornslien, Karina S. [1] and Grini, Paul E. [1]

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2. Department of Computer Science and Information Technology, Hood College, Frederick, MD 21701, USA

During double fertilization in flowering plants two fertilization products are generated, the embryo which gives rise to the next generation of plants and the endosperm which supports and nourishes embryo growth. The endosperm is a triploid tissue that requires tight control of the genome dosage (2 maternal:1 paternal) and balance disruptions can infer seed failure due to arrest in embryo development. Genomic imprinting is an epigenetic phenomenon confined to the endosperm, and it has been postulated to regulate gene dosages in a parent-of-origin dependent manner. Deregulation of imprinted genes in the endosperm can be lethal and has been proposed to be a main cause of hybrid seed failure. Imprinting has been widely studied in the inbred model plant *Arabidopsis thaliana*. However, imbalances of maternal to paternal genomes in the endosperm might show stronger phenotypic severities in outbreeding mating systems. The outbreeder *A. arenosa* is a close relative to *A. thaliana*. Here, we developed tools to facilitate the analysis of imprinting in the *A. arenosa* endosperm. We have developed a methodology to generate transgenic *A. arenosa* using *Agrobacterium* transformation. Using this methodology we have generated transgenes expressing nuclear-localised GFP in the endosperm. To isolate pure endosperm tissue for analysis, we have used fluorescence-assisted nuclear sorting (FANS) to isolate endosperm nuclei based on nuclear-localised GFP. Transcript profiles from endosperm nuclei are used to investigate genomic imprinting.

Seed | Endosperm | Genomic imprinting | Fluorescence-assisted nuclear sorting (FANS) | *A. arenosa*

Funding: Funded by a Norwegian Research Council FRIPRO grant EPIHYBRIDS # 276053 to PEG.

POSTER P14 ★ STUDENT PRIZE

Development of an HPLC–DAD Method for Monosaccharide Quantification in Seaweeds Using PMP Pre-Column Derivatization.

Dominykas Šalvaitis [1, 2] *(presenting)*; Hanne K. Mæhre [1]; Alexander Oliver Jüterbock [2]; Jens Mortansson Jelstrup Nolsøe [2]

1. Norwegian Institute of Bioeconomy Research (NIBIO), Division of Food Production and Society, Department of Marine Bioresource Valorization, Bodø, Norway.
2. Nord University, Faculty of Biosciences and Aquaculture, Bodø, Norway

Seaweed polysaccharides comprise a diverse group of carbohydrates with distinct structural and biological functionalities. Structural polysaccharides such as alginate, carrageenan, and agar are widely applied due to their gelling properties, whereas fucoidan, ulvan, porphyran, and laminarin exhibit antioxidant, antimicrobial, and other bioactivities. These functionalities are strongly influenced by monosaccharide composition. However, the commonly used two-step sulfuric acid hydrolysis has not been optimized for macroalgal biomass, and current monosaccharide analysis methods are often time-consuming or insufficiently adapted to complex seaweed matrices. This study aimed to optimize hydrolysis and chromatographic conditions for the quantification of neutral sugars and uronic acids commonly present in macroalgae. Monosaccharides were analyzed using HPLC-DAD following pre-column derivatization with 1-phenyl-3-methyl-5-pyrazolone (PMP). Supplementary methods, including thin-layer chromatography (TLC) and the determination of hydroxymethylfurfural (HMF) and furfural, were developed to evaluate hydrolysis efficiency and sugar degradation. TLC was applied to assess hydrolysis efficiency through changes in degree of polymerization, while HMF and furfural served as indicators of excessive degradation of hexoses and pentoses, respectively. The optimized analytical workflow enables consistent and accurate monosaccharide composition characterisation for seaweed biomass.

Monosaccahrides method development chromatography biotechnology.

Funding: The project is funded by NIBIO.

POSTER P15

In Vitro Comparative Analysis of the Bioactivity of *Rosa* oil Distillation Wastewater Extract and Rose Essential Oil

Assist. Prof. Dr. Boyka Andonova-Lilova *(presenting)*; Andonova-Lilova, Boyka*[1,2]; Rusanova, Mila [1,2]; Rusanov, Krasimir [1]; Zagorcheva, Tzvetelina [1,2]; Atanasov, Ivan [1]

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Rose oils distillation wastewater generated during *Rosa damascena* essential oil production is an waste by-product that may be valorized as a source of natural bioactives. The present in vitro study for the first time compares a polyphenol-rich extract from RODW with rose essential oil (RO) regarding cytocompatibility, antioxidant, antimicrobial, and regenerative activity The experimental design included nine cell lines (including HaCaT, BJ, IPEC-J2, CaCo-2) were exposed to concentrations up to 200 µg/mL for 24–72 h. Viability/proliferation (MTT), mitochondrial oxidative activity (JC-10), and morphopathological analisys (AO/PI) were assessed, DPPH radical scavenging and an H_2O_2-induced oxidative-stress model in IPEC-J2 by AlamarBlue. Antimicrobial effects were evaluated by disc diffusion and MIC with complementary OD600 growth kinetics, regenerative capacity by scratch assay in HaCaT and BJ (48 h). RO showed strong time- and dose-dependent cytotoxicity (72 h IC_{50}: 1.871 µg/mL in IPEC-J2; 9.35 µg/mL in CaCo-2), whereas RODW was substantially less cytotoxic (72 h IC_{50}: 124.307 µg/mL in IPEC-J2; 46.82 µg/mL in CaCo-2; >100 µg/mL in HaCaT). In DPPH, RODW reached 46.09 µg/mL L-ascorbic acid equivalents at 200 µg/mL, while RO achieved 49.34 µg/mL at 100 µg/mL. In the cellular antioxidant model, RO protected against H_2O_2 (AOA-MTT IC_{50} 31.23 µg/mL), whereas RODW was weak/moderate (AOA-MTT IC_{50} >146.6 µg/mL). At 100 mg/mL, RODW produced inhibition zones of 10–16 mm (*E. coli*) and 12–20 mm (*S. aureus*) and reduced peak OD600 by ~40–80% across tested bacteria. RODW promoted HaCaT gap closure at 48 h, with modest effects in BJ. AO/PI double staining indicated that most cells remained viable after RODW exposure. Overall, RODW combines favorable cytocompatibility with measurable antioxidant, notably antibacterial, and keratinocyte-regenerative effects, supporting its development as a sustainable bioactive ingredient, while RO exhibits higher potency but a narrower safety margin.

bioactivity citotoxicity rose oil Rose oils distillation wastewater

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POSTER P16

PheNo at UiO: Advanced High-throughput Phenotyping of Small Seeds and Plants in Controlled Environment

Hornslien, Karina S. [1,2] *(presenting)*; Iversen, Vegard [1,2]; Grini, Paul E. [1,2]

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The national infrastructure for Plant phenotyping in Norway (PheNo) has recently been established. At the PheNo node at the University of Oslo (UiO) we provide state-of-the-art phenotyping of small seeds, seedlings and plants. Using robotics and advanced sensor technologies, we perform precise measurements ranging from seed characters and germination to mature plant growth morphology and plant health. At the UiO node of PheNo we support automated sorting and single-seed measurements, automated sowing of seeds onto agar media according to predetermined matrices, growth and root analysis of seedlings on plates, and phenotyping at later developmental stages in soil-grown plants. Complementary sensors, including RGB imaging, static and kinetic fluorescence, VNIR and 3D scanning facilitate analysis of plant development and architecture, as well as plant health parameters. This includes visual growth analysis (plant morphology and development), detection of biochemical and structural properties in plant material such as abiotic and biotic stresses, pigments, metabolites and fluorescent protein markers. High-throughput, precise measurements integrated with AI technology and machine learning enable automated data analysis and can reveal novel insights into plant growth, physiology and development.

Phenomics · High-throughput phenotyping · Seed morphology · Seed germination · Plant morphology and health · Multi-spectral sensors

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POSTER P17

Precision and consistency for reproducible plant research

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The PlantLab at UiO, Department of Biosciences, can provide an advanced suite of plant growth chambers by the manufacturer Conviron that deliver precision and consistency for reproducible plant research. Features like energy-efficient, high intensity LED lighting, a wide temperature range and extended humidity controls can deliver you parameters tailored to your experimental protocols, and with a multi-tier system that ranges from one to five shelves it offers a flexible and economical solution for your research. This enables studies in plant morphology, photosynthesis and stress physiology. Instrumental ports on the sides of the chambers enables even further flexibility with regards to experimental setups and monitoring. Paired with the advanced control system installed in every chamber it enables you to easily program your experimental setup, at-a-glance monitoring of trend graphs and alarm status, and also to remotely connect and monitor your ongoing projects.

Plants · development · climate control · sensoring

Funding: University of Oslo, CONVIRON

POSTER P18

A Modular AI-Powered Toolbox for Scalable Plant Phenotyping and Data-Driven Analysis

Moosa, Muhammad [1] *(presenting)*

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Plant phenotyping is becoming increasingly data-intensive with the widespread use of UAVs and sensor technologies. However, there is a lack of unified tools that allow both technical and non-technical users to efficiently access and interpret advanced machine learning models for crop analysis. In this work, we present an AI-powered phenotyping toolbox designed as a modular, containerized platform that integrates multiple machine learning and deep learning models into a single, user-friendly interface. The system supports a wide range of tasks including classification, detection, segmentation, and analysis of plant stress and disease using RGB, multispectral, and thermal data. The toolbox is built using a microservice architecture, where each model is deployed as an independent Docker container and accessed through a FastAPI-based backend, while a React-based frontend enables intuitive interaction through model cards, visual outputs, and report generation. This design allows seamless addition of new models and ensures reproducibility and scalability. A key contribution of the toolbox is its ability to bridge the gap between technical and domain experts. Technical users can develop, deploy, and benchmark AI models, while non-technical users such as plant scientists can easily select models, visualize results, and interpret outputs without requiring programming expertise. The platform supports advanced phenotyping applications such as stress detection, disease monitoring, and physiological trait analysis, and is designed to evolve with future integration of multi-modal data and AI-assisted reporting tools, enabling more efficient, accessible, and interpretable phenotyping workflows.

plant phenotyping | deep learning | machine learning | multi-modal learning | disease detection | segmentation | classification