

Fifth webinar of the IRN France-Japan Frontiers in Plant Biology: « Emerging models in plant sciences »

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Abstracts



Dr Sandrine Bonhomme, Institut Jean-Pierre Bourgin ■ ■

URL: <https://ijpb.versailles.inrae.fr/en/research-teams/strigolactones-and-allelochemicals-signaling/presentation>

Strigolactone and KAI2-Ligand signaling in the moss *Physcomitrium patens*

Strigolactones (SLs) are allelochemicals acting in the rhizosphere, as well as plant hormones playing numerous roles in the development of flowering plants. While the SL biosynthesis pathway seems to be conserved across land plants, the signaling pathway that is described in vascular plants could be a much more recent innovation. With my colleagues, we are investigating SL synthesis and signaling in a bryophyte, the moss *Physcomitrium patens* (*P. patens*). We take advantage of the tools available in *P. patens* (e.g. gene targeting through homologous recombination and CRISPR technology), and combine them with biochemistry approaches and use of synthetic analogs to figure out the evolution of SL (and related signaling molecules) function and pathways.



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***Phtheiospermum japonicum*, a new model for root parasitic plants**

The parasitic plants in Orobanchaceae include the devastating parasitic weeds, such as *Striga* spp and *Phelipanche* spp, which parasitize important crops and cause significant yield losses. Parasitic plants form the haustorium, a specialized organ that functions in host invasion and nutrient acquisition. Our research team aims to molecular elucidation of haustorium development and host invasion in Orobanchaceae root parasites. For this purpose, we have established a new model system using the facultative parasitic plant, *Phtheiospermum japonicum*. We have developed the whole genome assembly and hairy root transformation method in *P. japonicum*. Using this system, we have isolated mutants that show defects in parasitism, which allow us to understand the genetic programs underlying host-parasite interaction.



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The role of subcellular topology in shaping microalgal photosynthesis

Eukaryotic phytoplankton have a low biomass but play a major role in primary productivity and climate by carrying out photosynthesis in the ocean. Despite a better understanding of phytoplankton diversity and evolution, we still do not know the cellular basis of their environmental plasticity. In recent years, we have addressed this question through a novel combination of whole-cell approaches, including single-cell spectroscopy and tomography¹⁻². Through these studies, we have shown that bioenergetic constraints modulate environmental acclimation, by controlling the remodeling of subcellular architectures related to respiratory (mitochondria) and photosynthetic (plastids) organelles in response to environmental changes.

Here, I will present examples to support this concept for eight members of dominant phytoplanktonic taxa in the oceans³⁻⁴. Finally, I will recapitulate questions that these data raise in terms of the mechanisms of CO₂ capture in the ocean, an environment that is constantly changing.

[1] J Decelle, et al *Curr Biol.* (2019) 29: 968-978.

[2] Annunziata et al. *Sci Adv.* (2022) 8: eabj9466

[3] C Uwizeye, et al *PNAS* (2021) 118: e2025252118.

[4] C Uwizeye, et al. *Nat Commun.* (2021) 12: 1049.



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Kleptoplasty in dinoflagellates *Nusuttodinium* spp. and insight into evolution of endosymbiosis

Plastid acquisition in algae are originated from endosymbiosis between non-photosynthetic host and algal symbiont. Certain unicellular organisms ingest algae and utilize them as temporal plastids (kleptoplasts) and are interpreted as intermediate phase toward plastid acquisition. The dinoflagellates *Nusuttodinium* spp. ingest unicellular algae cryptomonads retain them in the cell for certain periods. Our studies revealed that *N. poecilochroum* digests cryptomonad nucleus and never enlarges the plastid. By contrast, *N. aeruginosum* enlarges single plastid throughout the cell, retaining a cryptomonad nucleus. To understand how the cryptomonad nucleus contributes to the temporal endosymbiotic relationship, we examined changes in the transcriptome of the ingested nucleus. We show that, after ingestion, genes involved in metabolism and translation are upregulated, especially in photosynthesis-related genes. These results suggest that the cryptomonad cell is enslaved as a “machine” specialized for photosynthetic metabolism and protein synthesis that supports growth of the kleptoplast and dinoflagellate host.



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The embryo of the brown alga *Saccharina* as a model of 4-way cell junction tissue patterning

Saccharina is a brown alga (kelp), which develops a monolayered cell sheet during its embryogenesis. Interestingly, within this sheet, the cells are cuboids arranged in a grid, where each cell vertex is shared by 3 neighbouring cells (in 2D), resulting in the so-called 4-way junctions pattern. This tissue pattern was described as rare and unstable in land plants (D'Arcy Thompson, 1942), whereas it is commonly observed in kelp embryos (Sauvageau, 1918).

I will present how, based on a simple 2D-vertex mechanical model, we simulated the formation of this grid during embryo development and evaluated the impact of fluctuations in cell turgor and cell division dynamics and positions on the final tissue patterning and embryo shape.

In collaboration with Christophe Godin, RDP



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Elucidating molecular mechanisms of sexual reproduction using a trans-activating system of germline cell-like cell induction in the bryophyte *Marchantia polymorpha*

Land plants produce a gametophyte, a multicellular haploid body producing gametes. The bryophyte *Marchantia polymorpha* is a powerful model for elucidating core processes of gametogenesis in land plants mainly due to its low redundancy of regulatory genes and easy access to germline cells. Previously, we showed that BONOBOs (BNBs), members of basic helix-loop-helix (bHLH) transcription factors, regulate differentiation of germline cells in land plants (Yamaoka et al., 2018). However, molecular mechanisms of plant germline development are still largely unknown. Here, we show establishment of a trans-activating system that directly reprograms *M. polymorpha* somatic cells into germline cell-like cells (GCLCs) by expressing MpBNB from its endogenous locus, using an inducible CRISPR activation (CRISPRa) system. A number of GCLCs are ectopically formed in these transgenic plants, of which developmental pattern were similar to that of wild-type germline cells. Time-course RNA-seq analysis revealed that this system recapitulates germ cell differentiation processes in *M. polymorpha* at a transcriptional level. In this talk, we will show transcription factor network modules and metabolic pathways potentially involved in germline cell development.



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Growth, form, and function in *Marchantia*

How does a plant modulate its growth and form according to environmental conditions? We are using *Marchantia spp.* to address this broad question. On the one hand, we are investigating the mechanical control of the germination of vegetative propagules (gemmae) following imbibition. On the other hand, we are exploring how the organs that contain gemmae (gemma cups) adapt their morphology to environmental conditions, possibly to ensure efficient dispersal by rain. In this talk I will briefly introduce our work and illustrate the suitability of *Marchantia* for such research questions.



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Calcium ion-mediated memory and movement system in the Venus flytrap (*Dionaea muscipula*)

Venus flytrap (*Dionaea muscipula*) is a carnivorous plant that catches prey by leaf movement in response to two successive mechanical stimuli. Mechanical stimuli are sensed by sensory hairs on the leaf blade. The first stimulus is memorized and does not trigger the movement, and the second stimulus triggers the leaf closure within 1 second after the stimulus. Previous studies have shown that the mechanical stimulus triggers the propagation of action potentials on the leaf blade. However, it has not been clarified what molecule regulates memory and movement systems. To understand the molecular mechanisms of memory and movement systems, we have established a transformation method of the Venus flytrap and visualized calcium ion dynamics using calcium sensor protein GCaMP6f expressing Venus flytrap. In this webinar, I would like to discuss the mechanisms of memory and movement systems in the Venus flytrap mediated by calcium ions.



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Understanding rose domestication and the mechanisms underlying major floral traits

Roses are among the most prized domesticated ornamental species in human history. They have great cultural and economic importance as garden ornamentals, in cut flowers and for the perfume industry. Their value is mainly determined by their flowers, which have a wide variety of shapes, colors, scents and number of organs, which are highly desirable traits. In recent years, we have invested in the development of a number of resources for *Rosa* sp., including a high-quality assembled and fully annotated genome, a transcriptomic database, and a reproducible genetic transformation protocol for validation of gene function. Using these resources, we investigated the molecular and genetic mechanisms controlling major traits such as double flower, fragrance and color. Our data show that rose can be a new model plant for woody ornamentals and for species of the Rosaceae family that encompasses many tree crops.



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Diversification of circadian properties in duckweed

Many organisms have the circadian clock with a period of about 24 hours and the clock controls various physiological phenomena. The circadian clock system is widely conserved in plants. However, their circadian rhythm properties (period, amplitude, and temperature compensation) display a diversity even within closely related plants. This suggests that variation in circadian rhythms is related to adaptation of the habitat of the plant. In this study, we have compared the circadian properties of closely related duckweed species; seven *Wolffiella* species and eight *Lemna* species. *Lemna* species are widely distributed from low to high latitudes, whereas *Wolffiella* species are mainly found in low-latitude areas. To observe circadian rhythms in duckweed, bioluminescence monitoring systems have been used. Using a particle bombardment method, a circadian bioluminescent reporter was introduced into these species, and their circadian rhythms were measured under different temperatures (20, 25, and 30 °C) and light (constant light or constant dark) conditions. Compared with the genera *Lemna* and *Wolffiella*, *Lemna* species tended to show robust bioluminescence circadian rhythms under these conditions, while *Wolffiella* species showed lower rhythm stability, especially at higher temperatures. These analyses reveal that the circadian properties of species primarily reflect their phylogenetic positions in duckweed. Furthermore, several species inhabiting the tropics showed unstable rhythms. This result suggests that geographic factors also be associated with the variation in circadian properties.

