

A New Year's spotlight on two years of publication

With this first issue of 2022, *Plant Communications* enters its third year. Over the past 2 years, the activities of plant researchers worldwide have been affected by the COVID-19 pandemic, which has hindered the progress of many ongoing plant science projects. Although the pandemic is not yet over and we currently face many other grand challenges, such as climate change, we have witnessed the global scientific community working boldly together to find solutions for ending the COVID-19 pandemic and tackling other challenges. Climate change threatens global food security and sustainable development. From the 17 Sustainable Development Goals set by the United Nations (<https://www.un.org/sustainabledevelopment>) as well as reports of the United Nations Climate Change Conference (COP26) in Glasgow, UK (<https://unfccc.int/conference/glasgow-climate-change-conference-october-november-2021>), and the 2021 Conference of Parties to the Convention on Biological Diversity (CBD COP15) in Kunming, China (<https://www.cbd.int/conferences/2021-2022/cop-15/documents>), we see an urgent need for promotion of plant sciences and developing diverse approaches exploiting abundant plant genetic resources to provide more food, fiber, and fuel with fewer resource inputs and lower carbon emissions, thereby tackling climate change and achieving sustainability. As mentioned in our inaugural editorial (Cui and Han, 2020), *Plant Communications* aims to provide an open access platform for publishing a wide range of important research advances in all areas of plant sciences, which will surely contribute to the development of sustainable agriculture and the maintenance of diverse ecosystems on our planet. As the new year of 2022 arrives, we would like to take this editorial as an opportunity to summarize a portion of articles we have published to reflect our efforts, aims, and vision.

Unlike mammals, higher plants undergo post-embryonic development to generate lateral organs throughout their morphogenesis and have evolved a so-called double-fertilization mechanism to produce seeds for multiplication and dispersal. The mechanisms underlying plant development, growth, and reproduction are a classic topic in plant sciences, on which we have published many exciting and novel findings. For example, Du et al. (2020) discovered that microRNA168 (miR168)-mediated repression of AGO1 maintains RISC homeostasis, thus fine-tuning the miR165/166-HD-ZIP III module to ensure proper stem cell pools in the *Arabidopsis* shoot apical meristem. Interestingly, Tan et al. (2020) characterized three CNGC family members (CNGC5, 6, and 9) as Ca²⁺-permeable channels that are required for *Arabidopsis* root hair elongation, and Zhang et al. (2021a) identified a Golgi-localized Mn transporter (PML3) that is required for pollen tube tip growth and male fertility in *Arabidopsis*. Light is critical for plant morphogenesis, growth, and flowering. Zhang et al. (2020b) reported that SUMOylation and stability of SEUSS are activated by light and contribute to photomorphogenesis. Li et al. (2020a) revealed that the *Arabidopsis* nucleoporin Nup160 regulates CONSTANS protein abundance by affecting the localization of an E3 ligase, HOS1, at the nuclear pore

complexes, thereby preventing precocious flowering in response to photoperiod. In addition to these findings in *Arabidopsis*, several articles reported developmental findings in other species. These included the identification of two MADS-box genes that regulate vascular cambium proliferation and xylem development in poplar (Zheng et al., 2021) and the discovery of the maternally expressed polycomb group gene *OsEMF2a*, which is essential for endosperm cellularization and imprinting in rice (Cheng et al., 2021b).

Plants produce diverse classes of hormones and specialized metabolites during their life cycles. These small molecules are critical for plant growth, development, and responses to environmental stimuli. We published two themed issues, one on phytohormones and another on plant metabolism and synthetic biology, as well as many exciting research and resource articles to embrace new and emerging trends in these areas. For example, Xin et al. (2020) reported a high-sensitivity method that can quantify more than 40 phytohormones simultaneously from only 100 mg of plant tissue. Strigolactones are crucial for shoot branching. Hu et al. (2020) reported that, downstream of the strigolactone receptor complex D14-MAX2, the core transcription factor of BR signaling BES1 interacts with D53-like SMXLs and binds the *BRC1* promoter to repress its expression and thus promote shoot branching in *Arabidopsis*. Interestingly, unexpected findings were also published regarding the auxin efflux transporter PIN2, which was reported to function as a putative arsenite efflux facilitator that modulates arsenite transport in *Arabidopsis* (Ashraf et al., 2020), and the potassium transporter OsHAK5, which was shown to regulate ATP-dependent auxin transport and plant architecture in rice (Yang et al., 2020b).

Medicinal plants are enriched in specialized metabolites, but elucidating the biosynthetic pathways of these compounds in non-model species is not an easy task. Through whole-genome sequencing and integrated -omics analysis, Jiang et al. (2021) dissected the biosynthetic pathway of ginsenoside and identified key enzymes for its biosynthesis in *Panax notoginseng*. Similarly, Cheng et al. (2021a) used whole-genome sequencing and evolutionary analysis to reveal the origin and evolutionary mechanisms of the diosgenin biosynthetic pathway in yam. They also validated a synthetic biology approach for heterologous synthesis of diosgenin in genetically engineered yeast. Moreover, two exciting studies used advanced structural biology and biochemical approaches to reveal the catalytic mechanisms of plant terpene synthases and diterpene glycotransferase, respectively (Chen et al., 2020; Liu et al., 2020). Another interesting work reported the identification of an R2R3

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MYB transcription factor, SIAN2like, that regulates anthocyanin accumulation in the fruit peel of the *Anthocyanin fruit* tomato line. Alternative splicing in the wild-type alleles of *SIAN2like* causes loss of function, explaining why domesticated tomato does not synthesize anthocyanins in its fruits (Colanero et al., 2020).

As sessile organisms, plants cannot move and have therefore evolved a set of sophisticated mechanisms for adaptation to environmental stress, interaction with surrounding (micro)organisms, and response to pest and pathogen attack throughout their life cycles. We have published two special issues and dozens of interesting studies on plant-biotic or -abiotic interactions. Notably, two studies in 2020 reported on the characterization of *Xa1* allelic genes encoding atypical NLRs with unique central tandem repeats (CTR-NLRs) that confer resistance to *Xanthomonas oryzae* pv. *oryzae* (*Xoo*), the causal pathogen of rice bacterial blight disease. The performance of these *R* genes could be attenuated by interfering TAL effectors from *Xoo* (Zhang et al., 2020a; Ji et al., 2020). Following these reports, another two studies successfully cloned the long-sought *XA7* gene that confers durable broad-spectrum resistance to *Xoo* (Chen et al., 2021b; Luo et al., 2021). Focusing on plant-virus interactions, Sukarta et al. (2020) found that *NbDBCP*, a bromodomain-containing chromatin-associated factor, could interact with *Rx1*, a nuclear-localized NLR protein, and reduce *Rx1*-mediated immune responses to *Potato virus X* by acting synergistically with *Rx1* to reduce the DNA-binding activity of the immune-activating Golden2-like transcription factor *NbG1k1*. Interestingly, a study by Pasin et al. (2020) revealed a defense and counter-defense network between the phytohormone abscisic acid (ABA), which promotes antiviral defense, and a self-controlled RNA virus from the genus *Potyvirus*. In the area of plant-abiotic interactions, Ho et al. (2020) performed integrative multi-omics analyses of two barley accessions with contrasting root growth under salt stress and characterized two distinctive root-zone-localized growth and salinity tolerance mechanisms during the early stage of barley development. Wu et al. (2021b) revealed that hypoxia-triggered elevation of gamma-aminobutyric acid (GABA) restores membrane potential and maintains ion homeostasis in *Arabidopsis*, and Chen et al. (2021a) demonstrated that two *Arabidopsis* NPF transporters, NPF5.9 and NPF5.8, act redundantly to mediate long-distance Fe transport and homeostasis, independent of their nitrate transport function.

The adaptation differences in plants are attributed to the force of natural selection they experienced in various habitats. To illustrate the evolutionary events that shape plant diversity, dispersal, and genetic variation, we published a special issue on plant evolutionary adaptation in 2020. This issue included four excellent reviews discussing the importance of selection at the gametophytic stage for plant adaptive evolution (Beaudry et al., 2020), convergent evolution of plant genomes during adaptation to extreme environments (Xu et al., 2020), adaptive significance of loss-of-function mutations in natural populations (Xu and Guo, 2020), and strategies for landscape genetic studies in plants (Cruzan and Hendrickson, 2020). Among five research articles in this issue, Meeus et al. (2020) reported that whole-genome duplication contributes to hybrid fertility recovery and reproductive isolation from parental species in monkeyflowers. Becher

et al. (2020) revealed the allopolyploid origin of three closely related tetraploid species of eyebrights and suggested that an exchange of adaptive variants has led to their adaptive divergence. Willi et al. (2020) assessed the impact of demographic processes on genomic diversity and positive selection in *Arabidopsis lyrata* by analyzing re-sequencing data from 52 populations collected worldwide. Vaidya and Stinchcombe (2020) used the *Medicago truncatula-Ensifer meliloti* system to demonstrate that genotype-by-environment interactions make a significant contribution to maintaining genetic variation in mutualisms, and Hodgins et al. (2020) found that invasive populations of Canada thistle show rapid adaptation with no trade-off between stress tolerance and performance. Beyond this special issue, Yang et al. (2020a) used sequence data of 1,594 nuclear genes from 151 angiosperm taxa to investigate the angiosperm phylogeny, providing new phylogenomic insights into the origin of major lineages. Li et al. (2020b) revealed the evolutionary timing and events that led to the production of medicinally valuable benzylisoquinoline alkaloids (BIAs), such as noscapine, and inferred that morphine biosynthesis evolved fewer than 18 million years ago in the genus *Papaver*.

Like its sister journal *Molecular Plant*, *Plant Communications* also publishes resource articles reporting technical advances, bioinformatic tools, and -omics datasets and databases. The rapid development of plant biotechnologies such as CRISPR/Cas-mediated genome editing and synthetic biology is profoundly shaping crop breeding and chemical synthesis, and is poised to create revolutions in the agricultural, chemical, and medicinal industries. To showcase our interest in promoting plant biotechnologies, we published a special issue on technology and applications in plants in 2021. In this issue, four review articles discussed cutting-edge technologies and their applications, including proximity labeling for probing molecular interactions *in planta*, organelle genome transformation and editing, transkingdom RNAi and related strategies for crop improvement, and CRISPR ribonucleoprotein-mediated genetic engineering (Li et al., 2021a; Zhang et al., 2021b; Yang et al., 2021; Zhao et al., 2021). Among the five original articles in this issue, two reported on the development of new CRISPR-based genome editing tools (Grutzner et al., 2021; Sretenovic et al., 2021); the other three reported an another culture-based system that enables highly efficient and genotype-independent creation of transgenic and gene-edited plants from commercial barley varieties (Han et al., 2021), a high-throughput micro-computed tomography (micro-CT) imaging system integrated with deep learning for extracting and analyzing rice morphological traits (Wu et al., 2021a), and a nanopore-based single-molecule approach for characterizing plant polysaccharides (Cai et al., 2021), respectively. Apart from those in the special issue, we also published several other methods and tools, including a technique for quantifying the total and individual abundance of root-colonizing microbes (Guo et al., 2020), a 3' ribosome-profiling sequencing (3'Ribo-Seq) method for transcriptome profiling and genome annotation (Zhu et al., 2021), a novel genotyping approach based on high-resolution multiple-single nucleotide polymorphism (SNP) arrays that combines improved genotyping by target sequencing with liquid chip technology (Guo et al., 2021), and a Split-HaloTag imaging assay for studying protein-protein interactions *in planta* (Minner-Meinen et al., 2021).



Figure 1. The cover images of 12 issues published in 2020 and 2021.

In addition to original research articles, we have also published dozens of review articles covering a wide range of topics. These reviews not only provide readers with an up-to-date understanding of multiple aspects of plant sciences but also introduce new ideas and forward-looking perspectives that can guide future plant research. For example, [Zhang and Fernie \(2021\)](#) introduced and detailed a newly emerging concept, the metabolon, which is defined as a transient multi-protein complex of sequential enzymes that mediates substrate channeling to promote efficient catalytic reactions. They discussed approaches for the identification and characterization of putative plant metabolons and outlined their roles in plant metabolism. After reviewing major achievements and unsolved questions in the molecular genetics of plant nitrogen-fixing symbioses, [Huisman and Geurts \(2020\)](#) proposed a strategic roadmap for engineering nitrogen-fixing nodulation in non-legume plants. [Wu et al. \(2021c\)](#) proposed that plant cell cultures can be used as bio-factories for the synthesis of high-value secondary metabolites in a safe, inexpensive, and environmentally friendly manner, and discussed recent advances and current challenges. A review by Dr. Wagner Araújo and colleagues summarized recent progress in the engineering of improved photosynthesis through synthetic biology strategies and discussed potential biotechnological applications ([Batista-Silva et al., 2020](#)).

We believe that the articles highlighted above showcase the breadth and diversity of plant science content we have published over the past 2 years (Figure 1), reflecting—at least in part—the scope and aims of *Plant Communications*. The academic publishing landscape is rapidly evolving, and at *Plant Communications* we advocate the “open access, open science” philosophy. We welcome all of you to submit your important discoveries for consideration and possible publication in a Gold Open Access model. In the coming years, we will strive to provide rigorous and speedy peer-review processes, offer informative decisions with constructive comments, and use multiple channels and social media to share valuable research discoveries as broadly as possible with the global community. We have been committed to hosting and supporting we-

binars and meetings. We would like to dedicate more efforts to holding in-person or remote gatherings on different topics, either independently or collaboratively, to promote scientific education, academic exchange, and collegial collaboration. Finally, we sincerely thank all our authors, reviewers, and members of the production and marketing teams for their joint efforts to make our first 2 years of publication possible. With all of us working together, we are confident that we can build *Plant Communications* into a high-quality journal, contributing to addressing the pressing global issues of our day.

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