



# Plant metabolic engineering in the synthetic biology era: plant chassis selection

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In the July 2017 Gordon Research Conference on Plant Metabolic Engineering that was held in Waterville Valley, New Hampshire, an intriguing discussion began. This discussion centered on the question—what is the best model species/tissue/engineering platform for plant metabolic engineering? In synthetic biology parlance, the question can be restated, which plant chassis is best for metabolic engineering? Synthetic biology is a transformative combination of DNA technology, engineering principles, and computational tools that makes it possible to design new life processes and to repurpose natural ones for useful purposes. Synthetic biology applications began in microorganisms and are expanding into more complicated systems, like plants, which bring certain challenges (Liu and Stewart 2015). Nonetheless, plant biology tools and experience are rapidly enabling metabolic engineering applications (Vazquez-Vilar et al. 2018). Therefore, numerous metabolite targets are being pursued for production in plants and attempts are being made to either reconfigure or replace various central pathways. This brings us back to the question: which plant species is the best one? The answer, of course, is complex—hence this special issue of Plant Cell Reports.

Nearly all the senior authors of the eight papers in this special issue attended the Gordon Conference, and thus, the flavor of the conference discussion is captured in their

contributions. Indeed, when we envisaged this special issue, we encouraged the authors to state the case for their favorite plant with the same fervor and passion that they argued for them at the conference. Certainly Holland and Jez (2018) have a significant advantage in arguing for “the original plant chassis organism,” *Arabidopsis thaliana*. It is nearly always the first choice of a plant model in genomics and genetic engineering given the long history and extraordinarily deep resources. It is one of the easiest plants to transform and grow under controlled conditions. The main thing that it lacks is ample biomass, but if a researcher can work out a metabolic pathway in *Arabidopsis*, a clear next step for ‘scale up’ and field application is *Camelina sativa*, another member of the mustard family (Brassicaceae), and the species of choice of Snell et al. (2018). *Camelina* is a hexaploid and produces much more biomass than *Arabidopsis* as well as large, oil-rich seeds, but it is also one of the uncanny plant species amenable to floral-dip-mediated transformation using *Agrobacterium*.

Other relatively simple systems include algae, diatoms, and moss. One heterokont microalgal genus of note, *Nannochloropsis*, has emerged as an attractive chassis to manipulate lipid traits with a robust toolkit of systems biology tools for enabling synthetic biology approaches (Benning et al. 2018). The diatom algae group is globally important in marine ecosystems. Diatoms’ silica-based cell walls add an interesting component that may be exploited in synthetic biology and metabolic engineering (Kroth et al. 2018). Like *Nannochloropsis*, -omics and biotechnology toolboxes for diatoms have undergone rapid expansion in recent years. Genome editing has been proven to be especially efficient in diatoms and can yield genetic knockout strains for basic and applied research. Moving to multicellular, albeit relatively simple plants, the moss *Physcometrella patens* is now established as a model for early evolving plant analogous to *Arabidopsis*’ role among angiosperms (Reski et al. 2018). The authors describe its amenability for genome editing via a very efficient homologous recombination system, which has

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provided a number of metabolic engineering examples that are either approaching commercialization or have already reached the market (Reski et al. 2018). The last relatively “simple” system is plastid engineering of higher plants; plastid molecular genetics is a ‘hybrid’ between prokaryotic and eukaryotic (Schindel et al. 2018). The authors review biotechnology and synthetic biology tools—both current and needed—that could enable flexible metabolic engineering systems in tobacco and other angiosperms.

Finally, two angiosperm platforms for specific and powerful metabolic engineering are featured in the special issue: terpenoid biosynthesis using transient expression in *Nicotiana benthamiana* leaves (Osbourne and Reed 2018) and tomato fruit biofortified with phytonutrients (Martin et al. 2018). Agroinfiltration of “benthi” has long been a favorite tool of plant biotechnologists to rapidly assess the effects of heterologous gene expression directly in living and intact leaf tissue. Osbourne and Reed (2018) review the status of this flexible production system with an emphasis on installing various terpenoid pathways to scale the synthesis of valuable products under controlled conditions. Possibly, the most photogenic example of a chassis is tomato fruit—as the authors state “the world’s favorite fruit” (Martin et al. 2018). As a crop, tomato has a number of things going for it, including excellent germplasm resources and robust nuclear and plastid transformation systems. The fruit provide an attractive edible chassis for functional foods as well as an industrial production system for high-value metabolites. The authors make a compelling case for tomato metabolic engineering (Martin et al. 2018).

In conclusion, talented plant metabolic engineers demonstrate, in this special issue, that we are not limited to a single ideal-plant chassis for synthetic biology. The chassis range from single cell algae to the ‘algae within a crop’ (plastids) and from model species and gene expression systems to commercial crops—a case of the right plant for the right job. Thus, the message from this special issue is that chassis diversity gives plenty of attractive options to enable

the next generation of plant synthetic biology and metabolic engineering.

**Author contribution statement** The authors of this editorial are co-editors of this special issue and as such participated in the writing of this article. Each author approves the content.

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