

the environment or food quality standards are gaining more attention from a growing fraction of the general public. For instance, we hosted the event ‘CRISPR for Us: A Chat with Young Professionals’, which included a variety of young professionals, including a politician, science communicator, entrepreneur, and two academic researchers (Figure 1C)<sup>iii</sup>. Throughout our interactions, we have become more aware of how personal biases affect the assessment of scientific evidence and which societal considerations people with diverse areas of expertise have in common.

### Hosting Positive Activism Events

Activism is about creating social, political, and environmental change and is as a result much aligned with our purpose of actively promoting scientific progress. We want to raise public awareness that we, young plant scientists, are conducting research to build up knowledge and to develop solutions for and with society.

On 5 March 2019, we co-organized a positive activism event, together with Science for Democracy, in front of the European Parliament in Brussels. Together with more than 100 early-career researchers from across the country, we consumed rice pudding prepared with genome-edited rice. We distributed flyers that highlighted our message and informed passersby about the potential of genome-editing applications for agriculture. This event was actively shared on social media with the hashtag #GiveCRISPRaChance and we were able to engage many more fellow researchers to spread the word. In the past summer, students from eight EU member states, who met during their MSc studies at Wageningen University, launched the initiative ‘Grow Scientific Progress’. Together, they submitted a detailed proposal to the European Commission in the format of a European Citizens’ Initiative<sup>iv</sup>. In this proposal, they outlined legal changes to the current regulatory

framework to facilitate responsible innovation for new plant breeding techniques. These initiatives highlight how early-career researchers can become an active part of policy development and public awareness.

### Concluding Remarks

Here, we have illustrated a plethora of possibilities for how young scientists can engage in science communication. Early-career researchers are able to reach out to all stakeholders, including the general public, policy makers, and politicians, to inform and raise awareness for the potential benefits of new technologies in plant science, such as genome editing.

Are you an early-career researcher or student and are you concerned about the future role of technology and innovation in more sustainable food and biomass systems? We encourage you to have a look at the activities of the GeneSprout Initiative on our website and hopefully you will feel inspired to participate in science communication<sup>ii</sup>.

### Resources

<sup>i</sup><https://curia.europa.eu/jcms/upload/docs/application/pdf/2018-07/cp180111en.pdf>

<sup>ii</sup>[www.genesproutinitiative.com/](http://www.genesproutinitiative.com/)

<sup>iii</sup><https://crisprcon.org/crisprcon-2019/>

<sup>iv</sup>[www.growscientificprogress.org/](http://www.growscientificprogress.org/)

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### References

- Shukla, P.R. *et al.*, eds (2019) *Climate Change and Land: An IPCC Special Report on Climate Change, Desertification, Land Degradation, Sustainable Land Management, Food Security, and Greenhouse Gas Fluxes in Terrestrial Ecosystems*, IPCC
- Zhang, Y. *et al.* (2020) A CRISPR way for accelerating improvement of food crops. *Nat. Food* 1, 200–205
- Yang, Y. and Hobbs, J.E. (2020) The power of stories: narratives and information framing effects in science communication. *Am. J. Agr. Econ.* Published online January 3, 2020. <https://doi.org/10.1002/ajae.12078>
- Vergauwen, D. and De Smet, I. (2019) The strawberry tales: size matters. *Trends Plant Sci.* 24, 1–3
- Van Woensel, L. (2020) *A Bias Radar for Responsible Policy-Making: Foresight-Based Scientific Advice*, Palgrave MacMillan
- Lassoued, R. *et al.* (2019) Risk and safety considerations of genome edited crops: expert opinion. *Curr. Res. Biotechnol.* 1, 11–21

### Spotlight

## An Abundance and Interaction Encyclopedia of Plant Protein Function

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Unlike the situation for humans and microbes, the active multiprotein assemblies of plants have not been systematically defined. A recent report by McWhite *et al.* remedies this by analyzing the protein complexes of 13 plant species, thereby defining core assemblies and providing an essential resource for interpreting the genotype–phenotype space of plants.

In the last couple of decades, medical research has made great progress in the functional annotation of proteins and in cataloging multiprotein assemblies, alike [1,2]. By contrast, it has been estimated that only 5% of arabisopsis (*Arabidopsis*

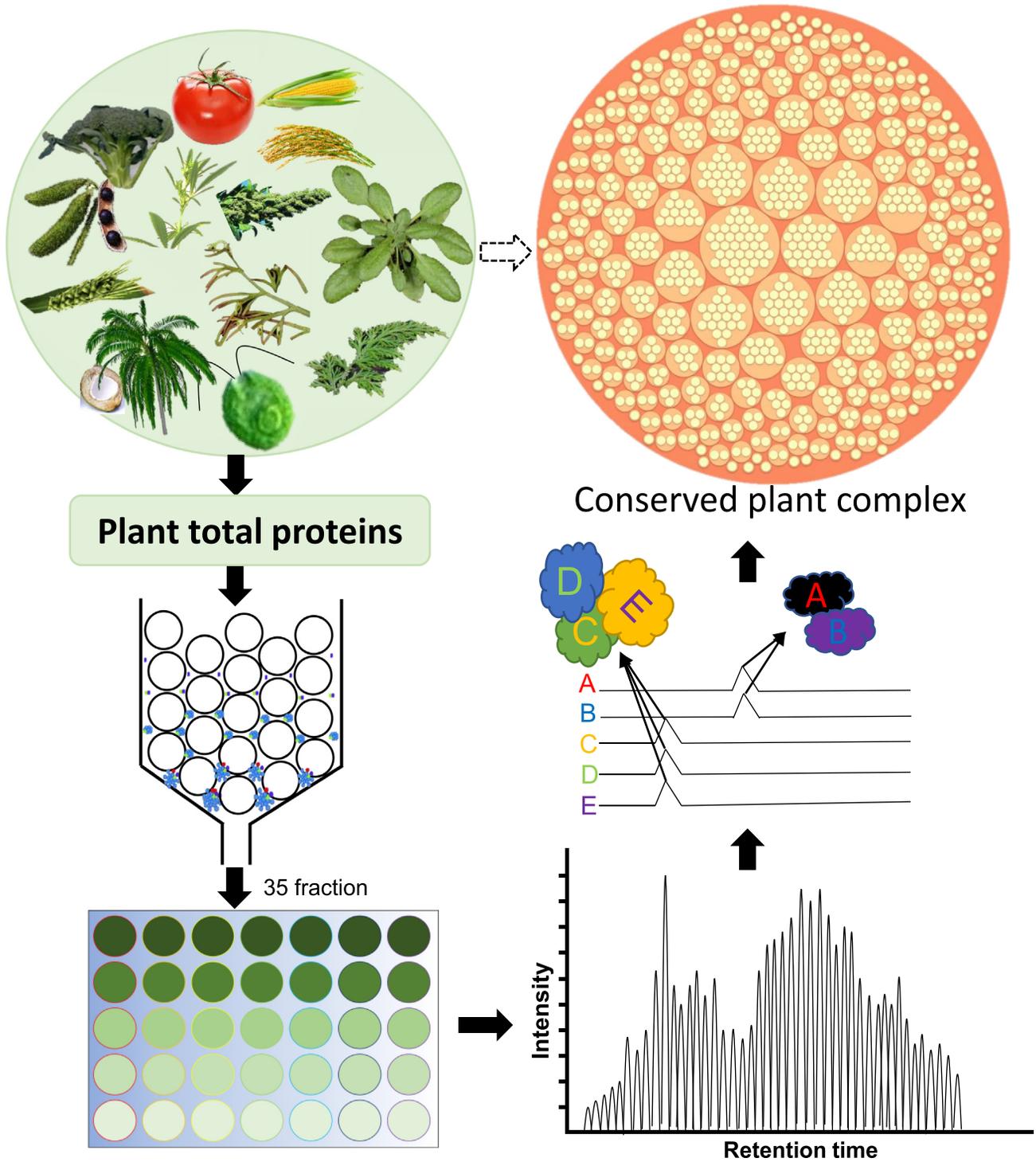


Figure 1. The Identification of Conserved Plant Protein Complexes by Cofractionation Mass Spectrometry. Extracts of 13 species were chromatographically separated and measured by mass spectrometry. Cofractionation indicates that physical association of a conserved protein complex was rebuilt from the results of the cofractionation analysis and can be queried at <http://plants.proteincomplexes.org>.

*thaliana*) proteins and a considerably lower proportion of other plants have been characterized experimentally [3], meaning a massive amount of work lies in front of us if we are going to catch up with human research in this area. Approaches taken to date tend to rely on high-throughput affinity purification (see, e.g., [4,5]), which is limited by its high cost and is only applicable in relatively few species due to issues of transformation efficiency. Whilst the latter issue is likely to become less of a problem in the near future, simpler, readily scalable methods are needed. Cofractionation mass spectrometry fits the bill, being applicable to any organism without the need for antibodies or transgenic epitope tagging of individual proteins. The cofractionation of proteins in a separation serves as evidence of physical interaction and has been used previously in plants (see, e.g., [6]). However, studies in other systems indicate that it needs to be carried out over multiple distinct separations to represent a rigorous means for the detection of interaction proteins [2]. In their recent study, McWhite *et al.* [7] generated a dataset of protein abundances and copurification from 13 plant species [arabidopsis, broccoli (*Brassica oleracea*), soy (*Glycine max*), hemp (*Cannabis sativa*), tomato (*Solanum lycopersicum*), quinoa (*Chenopodium quinoa*), maize (*Zea mays*), rice (*Oryza sativa* ssp. *japonica*), wheat (*Triticum aestivum*), coconut (*Cocos nucifera*), fern (*Ceratopteris richardii*), spikemoss (*Selaginella moellendorffii*), and the green algae *Chlamydomonas reinhardtii*], spanning 1.1 billion years of evolution. This encyclopedic study not only recovered protein complexes previously known in animals but also uncovered novel complexes that can be anticipated as being important in key agricultural traits, including vernalization and pathogen defense. It also maps cross-species conservation of complexes, providing an amazing evolutionary resource as well as a road map for large-scale functional assignment of the many plant genes that

have not yet been experimentally assigned a function (see Figure 1).

To generate this vast compendium, McWhite *et al.* separated each protein extract by either size exclusion- or ion exchange-chromatography or isoelectric focusing, subsequently analyzing the resultant fractions by high resolution liquid chromatography mass spectrometry. In total, over 14.5 million peptide mass spectra were acquired. To circumvent difficulties in orthology mapping between highly diverse species, the authors adopted the approach of interpreting mass spectral observations in terms of protein orthogroups, as opposed to individual proteins. This strategy dramatically increased the recovery of unique spectral counts for highly redundant proteomes such as that of hexaploid wheat without strongly affecting that of diploid organisms. It reduced the nearly 142 000 proteins to approximately 24 000 orthogroups, representing a massive 96.7% of the most conserved Viridiplantae orthogroups. Whilst half of the orthogroups contained one dominantly expressed protein, for the other half expression was similar amongst all members of the orthogroup. Although the coelution of subunits of the 20S proteasome, prefoldin, and the TSET membrane trafficking complex could be eyeballed within the data, a computational classifier and rigorous statistical assessment were required to identify other complexes. These were validated both by scanning literature data and by cross-validation by chemical crosslinking in soy and *Chlamydomonas*.

Having established the reliability of their results, McWhite *et al.* analyzed the conserved protein complexes as to whether they were reported previously, partially reported previously (i.e., some of the subunits being previously reported in complexes), or were novel to the study.

For example, the authors found interactions with RNA polymerase II and oligosaccharyltransferase complexes that had previously only been observed in non-plant systems. Moreover, previously described metabolons such as those of glycolysis and the TCA cycle [5] were noted, as well as novel interactions between consecutive enzymes such as those between OXP1 and GEP enzymes of glutathione degradation. Importantly, all these interactions can be queried at plant.MAP (<http://plants.proteincomplexes.org>). Interestingly, as had already been noted in bacteria and humans [8], homologous gene products are not always assembled in the same manner. In the dataset of McWhite *et al.*, this is perhaps best exemplified by the tRNA multisynthase complex, which in plants is a megadalton complex displaying an architecture and subunit composition distinct from that of animals, fungi, and bacteria. Notably, neither the presence nor absence of orthologs could be used to predict the occurrence or structures of larger complexes. Moreover, plants utilize lineage-specific subunits to co-opt known molecular models; for example, the plant homolog of the RMBX transcription factor, which in mammals regulates liver sterol contents, was found to interact with VERNALIZATION 1 and regulate the FLOWERING LOCUS C (FLC) gene and thereby control rapid and seasonally appropriate flowering [9]. A more complex example is provided by the NDH complex of the chloroplast, which shares architecture and, to some extent, function with the respiratory complex I of mitochondria. These examples demonstrate the way in which this complex dataset can be used to generate testable hypothesis that will undoubtedly allow researchers to go beyond guilt-by-association and lead to functional definitions of constituent proteins. Indeed, McWhite *et al.* provide several other examples of insights from their data that bridge the genotype to phenotype gap, namely: (i) the novel plant–pathogen related

complexes comprised of endochitinase and an osmotin-like protein and that containing proline iminopeptidase and nudix hydrolase; (ii) the interaction between DOMINO and LA1 proteins in embryonic development; and (iii) the interaction between a mitochondrial porin and steroid biosynthesis enzyme. In the third case, the known phenotype of mutants of the first mentioned partner was phenocopied in mutants of the second, highlighting the power of the approach as a means of rapid functional screening.

Following a proverbial, ‘Tell me who your friends are, and I will tell you who you are’ style, identification of protein interactors can be used to unravel the function of uncharacterized plant proteins. By combining multiple separation techniques of protein complexes from 13 plant species with an advanced data analysis pipeline, the work of McWhite *et al.* provides a unique resource that can be readily mined (in a user-friendly manner), for novel, evolutionary conserved protein–protein interactions. We believe that this resource will be a truly fantastic asset in the functional annotation of plant proteins.

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#### References

- Huttlin, E.L. *et al.* (2017) Architecture of the human interactome defines protein communities and disease networks. *Nature* 545, 505–509

- Wan, C. *et al.* (2015) Panorama of ancient metazoan macromolecular complexes. *Nature* 525, 339–344
- Rhee, S.Y. and Mutwil, M. (2014) Towards revealing the functions of all genes in plants. *Trends Plant Sci.* 19, 212–221
- Van Leene, J. *et al.* (2011) A kaleidoscopic view of the *Arabidopsis* core cell cycle interactome. *Trends Plant Sci.* 16, 141–150
- Zhang, Y. *et al.* (2017) Protein-protein interactions and metabolite channelling in the plant tricarboxylic acid cycle. *Nat. Commun.* 8, 15212
- Gilbert, M. and Schulze, W.X. (2019) Global identification of protein complexes within the membrane proteome of *Arabidopsis* roots using a SEC-MS approach. *J. Proteome Res.* 18, 107–119
- McWhite, C.D. *et al.* (2020) A pan-plant protein complex map reveals deep conservation and novel assemblies. *Cell* 181, 460–474 e14
- Marsh, J.A. and Teichmann, S.A. (2015) Structure, dynamics, assembly, and evolution of protein complexes. *Annu. Rev. Biochem.* 84, 551–575
- Levy, Y.Y. *et al.* (2002) Multiple roles of *Arabidopsis* VRN1 in vernalization and flowering time control. *Science* 297, 243–246

## Forum

# Crop Halophytism: An Environmentally Sustainable Solution for Global Food Security

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**This work analyzes the current trends in land salinization and its impact on the global food security. It is argued that reliance on salt-excluding crops is counterproductive and environmentally unsustainable. New breeding paradigms are required to incorporate halophytic traits that were present in wild relatives but lost during domestication.**

The world population currently stands at ~7.77 Billion (Bn) people and is growing rapidly. This increase in the population growth must be accompanied by a massive increase in food production.

However, over the past 50 years, per capita availability of arable land has decreased by about twofold (<https://data.worldbank.org/indicator/AG.LND.ARBL.HA.PC>), as a result of increasing rate of urbanization and land degradation caused by various environmental constraints. One of them is soil salinity. Currently, 4.03 Bn people live in the 13 countries most affected by soil salinity (Figure 1A); this represents 52% of the world’s population. This number may increase to 5.02 Bn by 2050 (Figure 1A). About 1125 million hectares of arable land are currently affected by salinity in those 13 countries [1], and this area is only going to increase, given the climate trends. The progressive increase in mean annual temperatures (Figure 1B) results in a concurrent and rapid increase in the number of drought events (Figure 1C). In the most populated country, China, major drought events are predicted to occur every 5 years, resulting in 25–50% yield losses for major crops [2] and costing the economy up to 12% in gross domestic product (GDP) loss by the end of the 20th century [3]. Thus the food demands in China and other countries affected by salinity can only be met by substantial and increasing reliance on irrigation practices.

The current freshwater withdrawal for irrigation purposes in the salinity-affected countries ranges between 25% and 80% of total freshwater resources (Figure 1D), and both the absolute area of irrigated land (Figure 2A) and its relative share in the agricultural production systems in each country (Figure 2B) have significantly increased over the past 50 years. However, reliance on irrigation for agricultural production comes with an additional very substantial issue of land salinization. The level of dissolved salts in the irrigation water has significantly increased over the past 20 years (Figure 2C). The average electrical conductivity of the irrigation water in the four most populated salinity-