

BOOK REVIEWS

Water: Abundance, Scarcity, and Security in the Age of Humanity. Jeremy J. Schmidt. SAGE, New Delhi, 2018. 324 pages. Price: Rs 995.

Cape Town, South Africa may be the first waterless city, but that humans are drawing more than their geological share of water should make us shudder as things are becoming worse before getting any better. From surplus to scarcity, human interference with global water systems has turned it into an issue of security, requiring new ways of managing water in the age of the Anthropocene. With the idea of stable water thrown into a tailspin, there is an urgent need to define 'safe operating space' for humans to work within the planetary boundaries for sustaining life and life forms.

By altering the planetary systems humans themselves have attained the status of a geological force, influencing the philosophy of water management that connects culture, geography and economics to lose its relevance. Far from inducing equitable access to water across sectors, the global impact of the American approach to water management has triggered brazen water grab not only within the local hydrological limits, but beyond regional and national boundaries. Unless this predominant approach is questioned, argues the author of this book Jeremy Schmidt, addressing inequalities that exist on a geological scale is not possible.

There is no opportune time to question it than now as humanity's total share of natural material and energetic throughput accelerates at a phenomenal pace. While it is agreed that dividing humans from nature may not help in understanding its impact on natural processes, a failed attempt to reject the society/nature dualism in the past had engineered oppressive logic which enhanced the prospects of meeting certain ends rather than others. The book asks: how do contradictions over water, such as those over the right to water, gain civil status?

The trouble with single planetary story on water, triggered by a techno-centric philosophy of water management, is that while it does not deny that alternatives exist, it simply posits that we should do without them. Instead, Schmidt presents three philosophical concerns to counter it: first, water resources should be managed without privileging any particular cultural understanding; second, acknowl-

edge different social relations that take shape around different water-use practices, and third, appreciate the different symbolic ends that others may hold as intrinsically meaningful.

These three concerns – over subjects, social relations, and symbolic goods – could be critical entry points into initiating a new discourse on water management, as the paradigm of 'making things public' is inadequate since it fails to see that water problems are the outcome of a failed 19th century solution associated with the society/nature dualism. Although this argument may seem troublesome to emerging social entrepreneurship around water, the basic contention here is to ask what questions arise for modernity as the result of water management practices instead of thinking about water through a theory of modernity.

Relying on volumes of historical sources, the book attempts to bridge an understanding on engineering solutions to the social ideas that informed them. As we are now part of an 'unfolding water drama', there is a great deal required to depart from the previous ways into new ways of managing water in the Anthropocene. The challenge, however, for the global water governance is that it does not substantively depart from the philosophy that gave rise to the problems it seeks to solve. Schmidt does not offer a solution, but attempts to implicate ideas widely held in water management that have contributed to unequal water relations.

Making a strong case for reimagining water management, Schmidt refuses to think of water as only a resource because it lends credence to the surplus–scarcity–security trilogy which reinforces structures of thought leading to a single planetary story regarding risks to people, the planet and the economy. And such a story, far from generating empathy, offers further justifications for the existing approach to water management. Such an approach fosters unequal practices (of access, allocation, and pricing) that favour one cultural understanding of water over others.

Schmidt does not offer readymade solution, but questions the philosophy of water that had rejected older ideas as too metaphysical or too far down the evolutionary ladder of social development. However, the new philosophy was not without its own mythical elements. Did it not claim that the idea of liberal forms of

life was uniquely equipped to manage water within a vast array of social and economic demands? The end result of the new philosophy is that water which was once abundant is now scarce. If water continues to be managed the way it is, majority of our rivers will only be carrying treated wastewater, if at all.

The book offers refreshing new historical and philosophical insights to address water, which remains ever restless in this new geological era, and the choice to continue pursuing it as a resource may have limited resolution.

SUDHIRENDAR SHARMA

7 Triveni, A6 Paschim Vihar,
New Delhi 110 063, India
e-mail: sudhirendarsharma@gmail.com

Annual Review of Plant Biology, 2017. Sabeeha S. Merchant, Wilhelm Gruissem and Donald Ort (eds). Annual Reviews, 4139 El Camino Way, P.O. Box 10139, Palo Alto, California 94303-0139, USA. Vol. 68. x + 586 pages. Price: US\$ 114.

As always, it was enriching to read this volume of the *Annual Review of Plant Biology (ARPB)*. It has 586 pages covering 20 chapters, each one is an up-to-date review. Broadly these chapters can be categorized into six themes: signal perception and messengers, organelle biology, abiotic and biotic stress responses, cell biology and regulation, new tools and approaches in plant biology and tree biology, and biodiversity and evolution. I will briefly comment on each chapter by picking one theme at a time rather than their chronological order in the volume.

Under the theme of signal perception and messengers, there are five chapters. The review on ligand perception and membrane receptor kinases by Hohmann *et al.* focuses on the architecture of receptor kinases (RKs) containing lysine motifs and leucine-rich repeat (LRR) ectodomains. Each of these has an extracellular region and a cytoplasmic kinase domain. The extracellular region can bind to different ligands and accordingly transduce messages via cytoplasmic domain. These RKs are involved in hormone or peptide signalling for regulating different developmental and defence responses, specifically where the receptor is activated by binding to carbohydrate

ligands or in response to specific symbiotic interactions. This review covers details of the structure of some of these RKs and shows that even in plants the LRR-type RKs can heterodimerize to transphosphorylate, the cytoplasmic kinase module of the receptor.

In an excellent chapter on phosphoinositide (PI) network, Gerth *et al.* discuss the nature of phenotypes associated with modifications of PI and involvement of related modifying enzymes. Lipid signalling via PIs has been covered in earlier volumes of *ARPB*. Wendy Boss covered PI signalling in 2012 and later, one of her colleagues, Heilmann, discussed in detail about role of PIs in a review in *Development* in 2016. The present chapter deals with the key reactions involved in PI network, their subcellular localization and associated proteins which are targets for mediating specific functions in different physiological states. Especially, the functions of PI in secretory pathway, endocytosis, actin dynamics, vesicular trafficking, and tonoplast and plastid associated functions have been well described and illustrated. As also mentioned by the authors, it is still not clear how PIs mediate their specific effects and perform their role in vacuolar functions.

Strigolactone (SL) was first discovered in the root exudates of parasitic weed, *Striga lutea*, in 1966, yet it is only after intensive work that SL was finally recognized as a carotenoid-derived plant hormone. Its importance in signalling in the regulation of shoot branching, root architecture and in symbiotic interactions, and many other interesting information have been presented in a chapter on SL signalling and evolution by Waters *et al.* Table 1 in this chapter describes the genes related to SL signalling and biosynthesis. The mechanism of their action following binding to receptors like D14, has also been well described and illustrated. SL is present in lower land plants and also in charophyte algae, thus suggesting that these must have originated 725–1200 Mya. Effect of nutrition on SL exudation has also been reported and such studies have presented an interesting concept of using trap crops for weed control.

Inter-organellar signalling and systemic long-distance signalling is discussed in two reviews. The first one by de Souza *et al.* describes the model of cooperativity, and discusses the role of calcium and ROS as the master initiators of inter-organellar communication between the

chloroplast, mitochondrion, peroxisome and nucleus. This is very well depicted in figure 2 of the review. The authors have also listed various metabolites implicated in ‘retrograde-signalling cascade’. Recent studies have shown physical interaction of organelles under certain conditions like stress and the manner in which these signals may be integrated towards balancing energy and regulating growth and development.

Systemic signalling via mobile RNAs in phloem is covered by Ham and Lucas. Lucas’ group has for long been working in the area of cell–cell communication through plasmodesmata and also on long-distance macromolecular signalling. They have published a review on this topic in *ARPB* in 2006. In phloem, companion cell and sieve element form the sieve tube system (STS), which is a conduit for the transport of nutrients and signalling molecules. It has been confirmed now that enucleate STS contains several thousand mRNAs which constitute ‘potential phloem mobile systemic signalling agents’. The chapter discusses in length the role of RNP and its phosphorylation in the movement of RNAs from companion cells into sieve elements and also in the transport through STS. Mobility of si/miRNAs and the mechanism thereof are well illustrated in figure 3. Systemic communication through miRNA under phosphate, sulphate and nitrogen signalling is also reviewed along with their role in epigenetic regulation of gene expression. Recent work on bidirectional RNA movement and also on the movement between parasitic plant and host plants is briefly presented.

Under organelle biology there are three reviews, one each on nucleus, mitochondria and plastoglobuli – the plastid microcompartments. The review on cell biology of the plant nucleus by Meier *et al.* is elaborate and has the maximum number of 250 cited papers. In other chapters, the cited references vary from about 120 to 175. It covers in detail the nature of plant nucleoporins (Nups) and nuclear pore-associated proteins. Nups are required for many signalling pathways. Figure 1 depicts the comparison of plants and metazoan proteins of the cytoplasmic region, Y-complex, transmembrane Nups, Nic96 complex, Phe–Gly Nups and nuclear basket proteins. Details of their localization and organismal role are given in table 1, which runs into four pages. This itself reveals the amount of

work that has been done in the last decade on this organelle, which the authors refer to as a gigantic one. The discovery, role and importance of SUN (Sad1/UNC84homolog) proteins and also of LINC (linker of nucleoskeleton and cytoskeleton) proteins in plants in the determination of nuclear morphology, etc. and binding to the nuclear envelope are described in a historical perspective. The authors discuss that though plant genomes do not seem to code for lamin homologs, EM data reveal an ‘inner nuclear membrane associated network similar to animal lamina’. Dynamics of nucleoli and importance of euchromatin and heterochromatin, and organization of chromosomes during interphase nuclei are also discussed. Like in other species, it has been found that ‘individual chromosomes occupy non-overlapping chromosome territories’ in plants too. However, in plants, an understanding of the role of association of chromatin with the nuclear envelope as a regulatory mechanism is still at its infancy. An interesting paper by Feng *et al.* mentioned in this review shows that CAB locus moves from the interior of the nucleus to the periphery in response to light for its activation. Lastly, the authors have also presented how the functional organization of nucleus alters during mitosis and meiosis.

Gualberto and Newton have reviewed the dynamics and mechanisms of mutation of plant mitochondrial (mt) genomes. Compared to mammals, plant mitochondrial genomes are much larger with abundance of repeated sequences and also carry economically important traits like cytoplasmic male sterility. It is found that nuclear genes control mt DNA mutation and stability. Details of various proteins involved in homologous recombination, replication and repair are given in table 1 of the review and the steps involved in these processes are discussed and well illustrated in figures 1–3. The authors have also described the process of appearance of heteroplasmy, which is ‘the existence of additional mitochondrial genome types (mitotypes) within an individual either inherited or resulting from *de novo* mutation’.

Plastoglobuli (PGs) were first seen by TEM in the 1950s and 60s. These are lipoprotein particles present in different types of plastids, and their dynamic nature is regulated during development and also under various stresses. These and other interesting features of PGs,

including molecular profiling have been discussed by vanWijk and Kessler. Tables 1 and 2 of the review list in detail the metabolite content and proteins that are enriched in PGs. Many of these proteins have been found to have enzymatic functions involved in the production of chlorophyll, carotenoids and isoprenoids. Details of chloroplast PGs as sites of prenylquinone metabolism and storage, and carotenoid metabolism are well illustrated in figures 5 and 6 of the review. The functional connection between PG function and carbon metabolism, though not well understood, has also been touched upon.

There are four reviews that directly deal with abiotic and biotic stresses. The review on salt tolerance by Ismail and Horie presents various ionic mechanisms adopted by plants under salt stress. These basically revolve around regulation and operation of various transporters and ion channels in roots and leaves to avoid cytoplasmic sodium toxicity. A knowledge of these and other components, like non-selective channels and those involved in ROS and calcium signalling as well as search for genetic diversity in salt tolerance, is important for developing breeding strategies. In table 1, examples of salt-tolerant rice varieties that have been developed and released for cultivation in specific regions are given. The review also briefly discusses the molecular breeding programmes that are being undertaken based on QTLs associated with salt tolerance.

There are three reviews related to biotic stress on plant–pathogen interactions and innate immunity in legume–rhizobium symbiosis. Mauch-Mani *et al.* discuss priming as an adaptive strategy to improve the defence capability of plants. They discuss various biochemical and molecular events triggered by biotic stressors and abiotic factors. The sequence of events and the changes that occur during priming phase and post-challenged primed state and the long-term transgenerational primed state are well summarized in table 1. The primed memory can be passed onto the next generation and this happens due to epigenetic changes in the plants. The authors discuss that priming events can also occur through airborne signals. While plants can remember and make use of ‘plant immunological memory’ to overcome the stress that follows the priming events, they can sometimes forget that

they were primed, especially if the earlier response was to false alarm signals.

Novel work and interesting findings on insect herbivory have been reviewed by Zust and Agarwal. This is an area that is of interest to plant biologists, ecologists and evolutionary biologists. The authors discuss the models of relationship between growth, defence and plant fitness. It is mentioned that ‘high levels of defense trait may deter mutualists such as pollinators, and indirectly reduce seed production’, a phenomenon studied by Strauss *et al.* and published in 1999. The molecular components that are involved in defence signalling and which also influence growth through crosstalk are given in a working model in figure 4 of the review.

Another review by Cao *et al.* discusses the work on innate immunity as triggered by microbe-associate molecular patterns (MAMPs) and chitin-triggered immunity. During rhizobium–plant interaction, the former also produces MAMPs which induce the expression of a large number of immunity-related genes in host plants following inoculation. The rhizobium signals and plant proteins involved in immunity and symbiosis are given in table 2. There seems to be an important role for extracellular ATP and ROS signalling in symbiosis. Various pathogenic effectors and effector-induced immunity have also been covered in detail. As mentioned in the summary, nod factors are likely to be involved in symbiosis as also in suppressing plant immune response. Plant immunity also determines rhizobial host range, and is helpful in terminal bacteroid differentiation.

Under cell biology and regulation, the chapter on Rubisco by Bracher *et al.* deals not only with the structure of the protein, but more specifically regarding the role of various factors on protein folding, assembly and metabolic maintenance. The list of these factors along with their functions and the organisms in which these were studied is given in table 1 of the review. The steps on their involvement in the biogenesis and maintenance of green-type Rubisco are well depicted in figure 10. It is not sure if an understanding of the chaperone machineries for biogenesis and maintenance will enable engineering of more efficient Rubisco. This, however, is a challenge for the future and will remain a wishful target for improving crop yields.

Norambeuna and Tejos have reviewed the work done on the chemical screening

strategies to understand the processes in endomembrane trafficking. They have described the cargo proteins of the endomembrane system, and targeting to their destination for molecular functions. Both forward and reverse chemical screen methodologies have been presented, including how these could be used as a starting point for forward genetic screen and omics profiling in response to a chemical treatment. Chemical collections that are available and the bioactive compounds which have been identified by chemical genetic screens have been tabulated with all details on phenotype, molecular target, etc. in tables 1 and 2.

This chapter is also a tribute to the vision and work of Natasha V. Raikhel, who ‘envisioned the need for alternative strategies to overcome the challenges associated with studying the mechanisms that underlie the endomembrane system in plants. She anticipated that chemical biology would bring invaluable tools for plant cell biologists’. Incidentally, in this volume, there is prefatory chapter by Raikhel which I recommend everyone to read. From being one who enjoyed music in Leningrad to her move to USA and then over a period of time becoming the founder director of Plant Cell Biology Program and then the director of the Institute of Integrative Genome Biology at the University of California, Riverside, is a story that speaks volumes on the perseverance, passion and personification of Natasha. She took great initiatives for promoting women in science, music and arts. A glimpse into her personal family life is worth reading. Our tributes to her innovative ideas, exemplary work ethics, tremendous contributions and for always working for the cause of science.

Giovannoni *et al.* have presented discussions on the epigenomic and transcriptional changes during fruit ripening. Most of the work has been done on tomato. Role of ethylene as an inducer of ripening and the involvement of MADS box transcription factors like RIN-MADS, Sepellata, TAG, FUL1, etc. have been reported. Some of these are involved in fruits other than tomato. Details of chromatin remodelling proteins and those involved in DNA-methylation dynamics and other transcription factors are compiled in table 1. Expression data of some of the genes, and the model of genome and epigenome changes regulating fruit ripening in different tissues like

locule and pericarp are given in figures 3 and 4. The ‘mutations in ripening transcription factors suggest that the epigenome’s influence over ripening is modulated by some of the same transcription factors that are regulated by epigenome dynamics. Thus the effects of epigenome on ripening are not linear; rather they are subject to additional feedback mechanisms’. There also seems to be some signalling mechanism from seed to maternal fruit tissues to communicate that embryo development is complete for seed development. This seems to be a survival strategy for protecting unripe fruit against damaging animals and attracting animals only when the fruit is ripened and the seeds are ready for dispersal.

Following seed dispersal, the vegetative body of plants dies. However, even during their life cycle following many stresses, plant parts are induced to senescence and death. This controlled cell death, termed as programmed cell death (PCD), is important for development and responses to cell death. These aspects of PCD are discussed in an informative review on the life and death of a plant cell by Kabbage *et al.* They discuss the role of various components of PCD like proteases, and members of the BAG family of proteins, and how these proteins and the process of PCD are similar to or different from animal cell death. In fact, they propose to use the term apoptotic-like PCD for plant cell death. A special section deals with cell death during plant–microbe interactions, and also on the role of sugar and energy homeostasis in autophagy. Briefly, cell death regulation is discussed in those plants which can sustain their life in extreme conditions. In one of our papers cited in this review (#145), we have also discussed the commonalities and differences in anhydrobiosis and PCD in plants.

Though a lot of work on molecular biology of development and plant responses to environment has been done on model plant *Arabidopsis*, and on some other plants like rice, soybean, tomato, etc. which are annuals by nature, it is only recently that work on perennials and tree species has gained momentum following sequencing of different genomes. Neale *et al.* have discussed new information on tree biology. After the populous genome was sequenced in 2006, over 40 tree genomes have been sequenced and the details of genomic resources available are given in table 1 of their review.

The chapter interestingly takes us through phylogenetic analysis of 35 tree species, gives information on genome size variations, whole genome duplications and information on polyploidy, and on the presence of non-coding RNAs. A section covers the genetic basis of perennial habit and the genes which have been found to be associated with flowering, bud dormancy and woody growth. Recent studies have revealed that *FT* is present in angiospermous trees and is absent in gymnosperms, where *FT/TFL1*-like genes exist. How trees respond to abiotic and biotic stresses is also covered in this chapter. In brief the chapter also reviews the expression of genes which have been reported during fruit development as also the metabolism of sugars that results in fruit sweetening, and the genes involved in fruit flavour and quality.

Vellend *et al.* have put their thoughts around the work that has appeared on changes in plant diversity during the Anthropocene. Temporal biodiversity changes have been seen at the local, regional and global level on speciation and also on extinction. At the local level, it seems that the major drivers of change are habitat fragmentation, climate change and nitrogen deposition. As is mentioned, ‘this review focuses on roughly the past 500 years, but ecological impacts of human land use extend back in time to thousand of years’. Further they conclude that ‘predicting future biodiversity changes presents massive challenges especially for regions undergoing rapid economic development and developing models and confronting them with data in the future will provide an improved basis for predicting the future of plant life on earth’.

There are two chapters on the utilization of new tools and techniques. One of these by Novak *et al.* describes recent advances in mass spectrometric-based quantification for identifying and quantifying plant hormones. They also dwell on the use of biosensors to determine temporal and spatial changes in phytohormone concentrations. These techniques are enabling scientists to do hormone profiling in a tissue- and cell-specific manner, in live cells and also from sub-cellular compartments. Use of different electrochemical sensors, antibody-based sensors, electrode-based biosensors and also aptamers and genetically coded biosensors has been described in detail and given in tables 1 and 2. These technolo-

gies are leading us to a new field of ‘hormonomics’.

Bazakos *et al.* have discussed various strategies and tools that are being used to get to the genotype from phenotyping, which is being done in different plants through non-invasive and non-destructive methods. For example, using an automated system called GROWSCREEN-Rhizo, one can simultaneously measure shoot and root growth under various conditions in small- to medium-sized plants. For such kinds of phenotyping, other platforms like MRI or X-ray micro-computing tomography are being used for 3D plant root imaging. Similarly, GLO-roots use luminescence-based reporters. There are reports where the DEPI platform has been used to measure photosynthesis, and many high-end growth chambers have been commissioned to fill the gap between controlled and field studies. The review also takes us through different tools for generating advanced materials like RILs, near-RILs and chromosome substitution lines for QTL analysis. Genome wide association approaches have been reviewed, which have advantage of high mapping resolution. Similarly, one can use new nested association mapping for its advantages of linkage and association mapping. Outcome of the use of all these tools will eventually depend on the ‘heritability and complexity of the trait and the phenotyping conditions’.

In conclusion, I benefited enormously by going through each and every chapter of this volume. To say the least, *ARPB* should be a companion to every teacher and researcher in the field of plant biology. With enormous literature that is coming out on a daily basis, in each and every area of plant research, it is difficult to keep pace with new data and even less likely to deduce the concepts and impact of that research. In this context, the authors of *ARPB* chapters have done a wonderful job. Great appreciation for the editorial board and the editors of this volume for selecting the topics and the authors.

I thank Drs Sneha Lata Singla-Pareek and Neeti Sannan Mishra for their editorial help.

SUDHIR K. SOPORY

*International Centre for Genetic
Engineering and Biotechnology,
New Delhi 110 067, India
e-mail: sopory@hotmail.com*