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Running title: ABR in the period 2006-2012

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Revisiting ABR editing in the period 2006-2012 and recent developments

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Abstract :

With my colleague Jean-Claude Kader, who unfortunately prematurely passed away in July 2018, we edited eighteen issues of *Advances in Botanical Research*, including ten eclectic and eight thematic volumes. The topics discussed in these articles are briefly described and recent advances in these various fields are reviewed. The main topics concerned developmental biology, cell biology and metabolism, plant-microorganism interactions, environmental and stress biology and, finally, monographs and reviews in genomics.

Introduction

Writing a commemorative review is always challenging, particularly in a scientific journal. However, when Jean-Pierre Jacquot, the present editor, proposed me to review my experience of editing *Advances in Botanical Research*, in order to celebrate the 100th volume of the series, I immediately accepted. This was a unique opportunity to explain how, with Jean-Claude Kader, we managed the series and to evaluate the impact of the topics we selected. After discussions, with Jean-Pierre Jacquot, we decided to split this retrospect in two parts. The first part is presented in chapter 1, which reports the views of the different editors and their experience with ABR. It explains how Jean-Claude Kader and myself met in the late sixties, became friends and collaborators, and finally became editors of this series. It also explains how we worked in selecting articles and inviting co-editors for thematic volumes. The second part (this chapter) summarizes some of the topics on which we focused and examines how these fields have evolved and progressed during the last few years, after we retired from the editorship in 2012.

The period covered by our editorship was marked by the explosion of genomics. The *Arabidopsis thaliana* genome was the first one to be determined (*Arabidopsis* genome initiative, 2000) and that of rice had just been completed (International Rice Genome Sequencing Project, 2005) when we took over after Jim Callow. A major consequence was a tremendous increase in our understanding of developmental processes and cell biology in these two species, and consequently in other plants. Control of pathogens was a major issue for agriculture, but it was also realized that the field should be enlarged to plant-microbe interactions. Another key issue, which was already clearly identified, was the response of plants to various environmental changes. Finally, we anticipated that after *Arabidopsis* and rice, many more genomes will be sequenced and we decided to introduce reviews on specific plants, describing their traits, their systematics and phylogeny, and the

most recent approaches to sequence their genomes. It is certainly not possible to present all the chapters we invited in detail and to update the state of the art for all of them. I have therefore focused on a few aspects we were interested in and simply made a reference for the others.

Reviews in plant developmental biology

Most of the articles on developmental biology addressed to two major topics: root development and flower biology.

Root architecture and development gained much knowledge from studies on *Arabidopsis* (Jovanovic, *et al.*, 2008). This article described the combined effects of plant hormones auxin and cytokinins on root development as well as the roles of ethylene, ABA and brassinosteroids in response to environment and in controlling transcription factors. It also examined the effects of water stress, and of soil concentrations in nitrates and phosphates. A further level of control on root development is at the level of microRNA. Although most of the reported information is derived from *Arabidopsis*, the authors also extend the information to legume roots. An update of root development was also published two years later (Ingram and Malamy, 2010). Another article focused on the role of nitric oxide in controlling lateral root formation (Molina-Favero, *et al.*, 2008) and its crosstalk with plant hormones. The importance of nitric oxide was further recognized by our successors since they invited a thematic volume on this topic (Wendehenne, 2016) in which many updates can be found. Several soil bacteria (PGPR, Plant Growth Promoting Rhizobacteria) promote root growth and they act by producing nitric oxide. Advances in plant interactions with rhizobacteria, including PGPR, were described in another thematic volume (Bais and Sherrier, 2015). Other aspects of root development were also discussed in articles in the series dealing more specifically with interaction with microbes and response to environmental stress. Since the publication of these chapters, numerous reviews have been published (Petricka *et al.*, 2012, Choe and Lee, 2017, Hochholdinger *et al.*, 2018). The hormone interactions have been investigated in much more details (Wei and Li, 2016, Fonouni-Farde *et al.*, 2016, Hu *et al.*, 2017, Du and Scheres, 2018) and a new class of hormones,

strigolactones, has been discovered (Sun *et al.*, 2016). Gravitropism and its relationship with auxin transport and signaling has been elucidated (Su *et al.*, 2017). Reactive oxygen species have been identified as key regulators in the control of root development (Tsukagoshi, 2016). The mode of action of PGPR on root development has been reviewed (Bais and Sherrier, 2015, Verbon and Liberman, 2016).

Flower biology was another key aspect of plant development. The genes controlling flower patterning were already known from pioneer studies in *Arabidopsis* (Drews *et al.*, 1991). They were also discussed in some of the monographs on specific species, such as orchids (Tsay *et al.* 2008) or bamboos (Das *et al.*, 2008). One of the invited chapters reviewed the progress in identifying the gene regulatory network involved specifically in carpel development (Ferrandiz *et al.*, 2010). Flower morphology and symmetry was an important issue. The floral symmetry regulatory gene network, initially identified in *Antirrhinum majus*, was reviewed (Citerne *et al.*, 2010). This domain evolved rapidly, particularly on the evolutionary background, with the development of genomics. An update of the field was recently published (Spencer and Kim, 2018), as well as an update of the development of Inflorescence, flower and meristem determinacy in grasses (Bommert and Whipple, 2018). Flowering time, in most plants depends on photoperiod and circadian clock. The main regulatory factors in this pathway were identified and described (Fekih *et al.*, 2009). Among them were genes involved in histone methylation and demethylation. Since this review, many studies in *Arabidopsis*, in rice and in other plants have focused on control of flowering time by environmental factors, including clock, photoperiod, temperature, drought, salinity, nutrients, hormones and chemicals or pathogens (Fornara, 2014, Cho *et al.*, 2017). A chapter in the thematic volume on rapeseed breeding (Gupta, 2007) deals with self-incompatibility in Brassica (Fujimoto and Nishio, 2007). We also invited a review on pollen germination (Wang *et al.*, 2010) and further one on sex determination (Chuck, 2010). Updates on role of calcium in pollen germination (Zheng *et al.*, 2019), on sex determination (Harkness and Leebens-Mack, 2017, Pannell, 2017) and on the molecular

dialog, involving protein kinases and small peptides, controlling pollen tube guidance (Stegman and Zipfel, 2017) have been recently reported. Similarly, a review of the pollen tube plasma membrane ion transporters was published (Pertl-Obermeyer *et al.*, 2018).

Other aspects of development were the molecular mechanisms underlying vascular development (Jung *et al.*, 2008), the clock control over plant development (Baudry and Kay, 2008) and the impact of phototropism and gravitropism on development (Molas and Kiss, 2009).

Reviews in plant cell biology and metabolism

Several reviews were invited on various aspects of plant cell biology and metabolism. Important classes of proteins were described. They include the expansins (Choi *et al.*, 2008) and the Late Embryogenesis Abundant (LEA) proteins (Shih *et al.*, 2008), as well as plant lectins (Van Damme *et al.*, 2008), aquaporins (Postaire *et al.*, 2008), cytochrome P450 (Schuler and Rupasinghe, 2010) and Arabidopsis histone methyl transferase (Pontvianne *et al.*, 2010). Recent progress in the field of lectins concern the mechanisms of signal recognition at the cell surface, the detection of symbionts and pathogens, the monitoring of cell wall structure and cell growth, and their role in plant immunity (Bellante *et al.*, 2017, Van Holle and Van Damme, 2018). Roles, regulation, and evolution of aquaporins have been further explored (Verdoucq and Maurel, 2018). It has been shown that oscillations in phosphorylation of aquaporins regulate the circadian rhythm of root hydraulics (Prado *et al.*, 2019). Advances in the field of cytochrome P450 are in the understanding of their biological function, as recently illustrated in the case of CYP706A3 from Arabidopsis, which reduces volatile terpene emission in the flowers, thus protecting them from insects and affecting flower-associated bacterial communities. There are also progress in understanding the evolution of these widespread enzymes and their functional role in plant adaptation to their environment (Boachon *et al.*, 2019, Alber *et al.*, 2019). Plant histone methyl transferases are now involved in most epigenetic regulations, such as flowering, control of transposable elements, stress response and plant

immunity (Lee *et al.*, 2016). Structural analysis of certain histone methyl transferases provided insights into the mechanics of DNA methylation (Li *et al.*, 2018). Plant epigenetics has also been recently reviewed in a thematic volume of this series (Mirouze *et al.*, 2018).

Several articles concerned aroma volatiles and metabolism. A first one (Defilippi *et al.*, 2009) addressed the question of fruits aromas and reviewed their metabolism. A second one (Vanavichit and Yoshihashi, 2010) explored the rice fragrance, and finally the more recent (Tamogami *et al.*, 2011) concerned a class of molecules, jasmonates, which were initially discovered as a jasmine perfume, but which are indeed key signaling molecules. Each of these reviews examined biosynthetic pathways and the main genes involved. All these studies require sophisticated analytical chemistry and advanced metabolomics, which have been described later on in these series (Rolin, 2013). A major progress in the field of jasmonate has been the identification of the perception mechanism by the co-receptor COI1-JAZ (Sheard *et al.*, 2010). The role of jasmonate in signaling and manipulation by pathogens and insects has been reviewed (Zhang *et al.*, 2017). The elucidation of the biosynthesis pathway of rose scent was another landmark in the field of volatiles (Magnard *et al.*, 2015).

Several cellular structures or processes were discussed: the plant nucleolus, protein turnover and programmed cell death. The plant nucleolus structure and the process of ribosome synthesis (Saez-Vasquez and Medina, 2008) were described. Since then, nucleolus proteome has been analyzed and comparison of plant genomes with yeast and animal genomes allowed the identification of hundreds of proteins involved in the biosynthesis and assembly of plant ribosome and to analyze their regulation. Several pre-rRNA processing pathways were resolved by analyzing gene expression in mutants (Saez-Vasquez and Delseny, 2019). The role of rDNA and nucleolus in shaping chromosomes organization and 3D structure of the nucleus was recognized (Picart-Piccolo *et al.*, 2019). Programmed cell death (PCD) is an important phenomenon in animal cells but it was in its infancy in plants. The available data were presented (Kacprzyk *et al.*, 2011). Two recent overviews of this

topic analyzed the role of PCD in plant development and control of immunity and the mechanism which are involved in plant cells, compared to animal cells (Kabbage *et al.*, 2017, Locato and De Cara, 2018). The chapter on protein turnover in grass leaves (Irving *et al.*, 2010) addressed the question of the recovery of nitrogen from the most abundant protein in leaves, rubisco, during normal development and senescence in leaves and focused on protein degradation in chloroplasts. Recently, the protein degradation rate was determined for >1200 individual Arabidopsis leaf proteins, showing half-lives ranging from several hours to several months (Li *et al.*, 2017). Factors required for the outer envelope membrane protein degradation were identified in Arabidopsis: they involve the ubiquitin E3 ligase SP1 and allow retro-translocation of ubiquitinated substrates to the cytosol where they are degraded by the 26S proteasome (Ling *et al.*, 2019).

Reviews on plant-microorganism interactions

Interactions of plants with microorganisms constitute an essential domain in botany and plant sciences. It was dominated by interactions with pathogens, which cause considerable losses in agriculture, and by the symbiotic relationship with bacteria or fungi. Some aspects of these interactions have already been mentioned, because they interfere with growth and development (Molina-Favero *et al.*, 2008).

Physiology of legumes nitrogen fixing nodules was analyzed (Qureshi *et al.*, 2010), with emphasis on new developments, such as the role of flotillins in formation of the infection threads, gene regulation and proteomics of the nodule. The response of the nodule to various stresses was also discussed. Two reviews recently addressed the question of immunity of the legumes to rhizobium infection (Cao *et al.*, 2017, Berrabah *et al.*, 2019). Sequencing of at least 10 legume genomes, the last one being pea (Kreplak *et al.*, 2019), as well as several rhizobia strains considerably added to our knowledge of genes controlling this agronomically important symbiosis and on the evolution of nitrogen fixing symbiosis. An update of the proteomic

approach, also including stress conditions, is available (Larrainzar and Wienkoop, 2017). Bacteria are not the only organisms involved in symbiosis and fungi are equally important. The field of arbuscular mycorrhizal fungi was reviewed by Gianinazzi-Pearson *et al.*, 2008. Recent progress in deciphering the mechanisms of establishment of mycorrhiza were described, including the roles of flavonoid, strigolactones and Myc factors. Updates on commonalities in communication in symbioses and plant growth promoting bacteria were presented in a recent thematic volume in the ABR series, specifically addressing the question on how plants communicate with their biotic environment (Bécard, 2017). Another chapter in this volume also examined plant to plant communication through common mycorrhizal networks. Contribution of ectomycorrhiza to tree nutrition was reviewed in a chapter of another ABR issue on molecular physiology and biotechnology of forest trees (Canovas, 2019).

The mechanisms of plant innate immunity were the subject of a thematic volume (Van Loon, 2009) with 15 chapters, covering many aspects of the responses of plant to pathogens. In particular, the concept of PAMP (Pathogen- Associated Molecular Patterns) recognized by receptors, leading to PAMP-triggered Immunity, the concept of Hypersensitive Reaction (HR) and the ways in which pathogens suppress the plant defenses were illustrated. Several examples of plant-pathogen interactions were described in more details. The interplay between the signaling pathways involving salicylic acid, jasmonates and ethylene was discussed as well as the role of iron and volatile organic compounds. A chapter also examined the interaction with Plant Growth- Promoting Bacteria. In addition, we invited a review on the molecular mechanisms of rice resistance to bacterial blight, caused by the bacteria *Xanthomonas oryzae*, pathovar *oryzae* (Lee *et al.*, 2011). This chapter described the disease, the diversity of the bacterial strains, and the disease resistance genes, either dominant or recessive, which have been identified genetically. At the time this article was published, out of 34 known disease resistance genes, only 6 had been cloned! Yet, their mode of action was not always understood. A recent paper reports that 41 genes are identified and that 11 have been cloned (Cao *et al.*, 2018). It discussed the mode of action of dominant versus recessive

genes and pointed to an autophagy-like cell death mechanism for dominant genes and vacuolar-mediated cell death for recessive genes. Numerous papers dealing with plant disease resistance have been published since these early papers and tremendous progress have been achieved in our understanding of the interactions between plants and fungi or bacterial pathogens. A volume in this series documented advances in plant microbe interactions, particularly plant bacteria (Bais and Sherrier, 2015). The signaling cascades initiated by receptor recognition have been reviewed recently (Tang *et al.*, 2017, Kourelis and Van der Hoorn, 2018) and the advances and perspectives in engineering disease resistance have been discussed (Dong and Ronald, 2019).

Interaction between plants and nematodes is also an important issue in agriculture (Abad and Williamson, 2010). Life cycles of root-knot and cyst nematodes were described as well as the various effectors involved in penetration and suppression of plant defenses. The information derived from sequencing the genomes of two root-knot nematodes was discussed and served as a basis for numerous studies which were further analyzed in a specific volume of this series (Escobar and Fenoll, 2015) and in a recent review (Gillet *et al.*, 2017).

The last type of pathogenic interaction we focused on is the plant parasitism (Irving and Cameron, 2009). The anatomical interactions of the host with its parasitic plant were described and different classes of parasites were recognized, some feeding on xylem and others on phloem. The development of the parasite and the host defense mechanisms were described. Finally, the ecological implications of parasite-host physiology were discussed. A major breakthrough occurred with the sequencing of the genome of *Striga*, one of the most devastating parasitic plants (Yoshida *et al.*, 2019). It reveals expansion of the strigolactone receptor gene family as well as evidence for horizontal gene transfers from the host plant. The volume on how plants communicate with their environment (Bécard, 2017) also contains a chapter on communication with parasitic nematodes, an update on the interactions between parasitic and host plants and a review on the roles of allelopathy and allochemicals in plant defence. Finally, a chapter described the defence of marine macroalgae against pathogens (Cosse *et al.*, 2008).

Several topics were missing in this list of organisms interacting with plants, such as pathogenic fungi, insects, viruses. This gap has been at least partially corrected in the most recent issues of ABR (Martin, 2014, Bécard, 2017, Sauvion et al., 2017).

Reviews in plant environmental and stress biology

Adaptation of plants to their environment is a key factor of their evolutionary success and an important issue in the context of climate change, erosion of soils and dramatic changes in agriculture practice in the 20th century. Many sectors are concerned and only a few of them could be approached during the time we were responsible for editing ABR. Two thematic volumes were entirely devoted to stress responses. The first one dealt with oxidative stress and redox regulation (Jacquot, 2009). Oxidative stress begins with the production of Reactive Oxygen Species (ROS). This volume contained 15 chapters including various aspects of oxidative stress, such as the role of ROS in growth and development, the mechanisms of oxidation of proteins, role of the thioredoxin and glutaredoxin pathways, metabolism of glutathione. Several examples of situations in which oxidative stress are important were analyzed such as the exposition of UV-B light and role of antioxidants, the production of ROS in the chloroplast, during establishment of Rhizobium-legume symbiosis, or during lignin degradation by the fungus *Phanerochaete chrysosporium*. Since then, it has become obvious that redox regulation is central in plant development and response to environmental cues (Mittler, 2017). ROS were considered as toxic for living cells but they also appear to be necessary for the progression of several basic biological processes including cell proliferation, cell differentiation, and response to environmental cues. Their production induces many signaling cascades determining the final responses. A recent development in the field is the interaction between redox metabolism and plant epigenetics which turns out to be an essential level of control for plant adaptation to environmental changes (Shen *et al.*, 2016). Other aspects of oxidative stress discussed in different ABR issues are the role of nitric oxide (Molina-Favero *et al.*, 2008), the response and tolerance to heavy metals (Chaffai and Koyama, 2011), the impact and

dynamics of iron (Briat, 2008) and low oxygen tolerance (Licausi and Perata, 2009).

A second major theme in stress physiology is the response to drought and salinity. We have invited several articles in this field, before deciding that a thematic volume should address the question. These early articles reported a description of aquaporins and their role in water transport (Postaire *et al.*, 2008), an analysis of the response of halophytes to salinity (Riadh *et al.*, 2010) and a review on the ecological water-use strategies of succulent plants (Ogburn and Edwards, 2010). Another article examined the situation of culture systems and their optimization to limit stress caused by plant nutrient solutions (Gorbe and Calatayud, 2010). The thematic volume (Turkan, 2011) extended the domain and contained 13 chapters. They described the various strategies of plant adaptation to drought and salinity stresses, the molecular mechanisms of adaptation, including ion transport in halophytes, the role of abscisic acid in triggering plant response to drought or salt, the protective metabolites and the impact of drought and salinity on photosynthetic activity. The molecular genetics of drought stress and approaches to engineer salinity and water stress tolerance were discussed in other chapters. This field also evolved rapidly and numerous articles have been published during the last 10 years. Several reviews can be found in the recent ABR thematic volume on abscisic acid (Seo and Marion-Poll, 2019).

Finally, two other aspects of environmental physiology were discussed: the first one concerns the perception of light and the syndrome of shade avoidance. Several transcription factors which modify the hormone sensitivity and growth response were described (Martinez-Garcia *et al.*, 2010). The second one reviewed cold signaling and cold tolerance (Ruelland *et al.*, 2009). Shade avoidance mechanisms were updated in two recent reviews (Fraser *et al.*, 2016, Yang, 2017). More recently, miRNA (Xie *et al.*, 2017) and histone modification (Peng *et al.*, 2018) were also recognized as part of the regulatory network. Advances and future challenges in signaling and mechanisms underlying cold tolerance have been recently summarized (Ding *et al.*, 2019).

Monographs and Reviews in genomics

Because the series was entitled Advances in Botanical Research, we tried to include some papers on systematics of some emerging species, asking specialists to outline their peculiarities and their interest for various aspects of plant biology. We initiated our role as co-editor of ABR with a thematic volume on rapeseed breeding (Gupta, 2007). This volume had 18 chapters reviewing the evolutionary history of this crop, the breeding methods, oil and meal quality, use of molecular markers for breeding and cultivar identification, self-incompatibility, use of haploid and double haploid technology, breeding for apetalous rapeseed, resistance to herbicides or to black leg, a disease due to the fungus *Leptosphaeria maculans*. Other chapters dealt with development of alloplasmic rape, with the interactions between honeybees and rapeseed, with glucosinolate metabolism, gene flow with wild species, rapeseed biotechnology and oil technology. Although a genetic map of rapeseed already existed at that time, only a few of the important genes for agronomy and breeding of this crop were identified and cloned. Since this volume was published, considerable progress has been made in most of the subjects. A reference genome of rapeseed was published in 2014 (Chaloub *et al.*, 2014) and, more recently, genomes from a world-wide collection of a thousand germplasms have been re-sequenced, shedding light on domestication of this species and its evolution (Wu *et al.*, 2019). Many genes have been identified and introduced in improved varieties including disease resistance genes to black leg disease (Raman *et al.*, 2016), using a variety of techniques. Several genomes of the fungal pathogen *Leptosphaeria* have been sequenced (Dutreux *et al.*, 2018). Glucosinolates pathways have been elucidated (Pietro *et al.*, 2019) as well as fatty acid metabolism (Qu *et al.*, 2017). A volume in this series updates our knowledge on glucosinolates (Kopriva, 2016).

We invited Taiwanese colleagues to write a review on the molecular biology of orchid flowers (Tsay *et al.*, 2008), because this is fascinating model. They had made valuable contributions to the characterization of genes involved in flower morphology and scent metabolism and they had initiated genomic studies

by sequencing ESTs, preparing BAC libraries and molecular tools for functional genomics such as VIGS (Virus Induced Gene Silencing). They have developed their work and reported the first genome sequence of an orchid species, *Phalaenopsis equestris* (Cai *et al.*, 2015), and more recently, the genome of *Apostasia shenzhenica* and transcriptome data for one of each of the 5 orchid subfamilies (Zhang *et al.*, 2017), thus boosting orchid research. Now several genomes of orchid species, including *Dendrobium* and *Vanilla* are available. The role of transposable element in the dark purple spots in some *Phalaenopsis* flowers was elucidated (Hsu *et al.*, 2019).

In the same issue as the one on *Phalaenopsis* we invited a review on citrus fruit quality (Tadeo *et al.*, 2008). It focused essentially on the physiology of fruiting and ripening, composition of the fruit, smell, abscission and conservation. Citrus genomics was just beginning with an EST program. Since then, important advances have been made in the understanding of fruit ripening and of fruit abscission. This progress is due to the development of molecular biology and biochemical approaches to characterize ethylene receptors, although citrus is a non-climacteric fruit (Chen *et al.*, 2018). Important factors in fruit abscission have also been characterized (Merelo *et al.*, 2017). The genomes of lemon, mandarin and orange were determined (Wu *et al.*, 2014) and further sequencing of related species and varieties allowed one to reconstruct the evolutionary history of Citrus domestication. (Wu *et al.*, 2018).

In the same volume, a monography of bamboo was published, (Das *et al.*, 2008). Bamboo is a fascinating genus too, with ~1300 species, either herbaceous or woody, distributed all over the world but mostly in tropical and subtropical era. This is the only grass that can exist as a forest. Some species are characterized by extremely fast growth. Based on flowering time, they can be divided into three categories: some are flowering annually, others flower sporadically and irregularly and the majority flower synchronously at long time intervals ranging from 3 to 120 years. Analysis of DNA content and chromosome numbers indicated different ploidy levels. This article was basically a systematic paper, discussing the

phylogeny and classification of bamboo, using anatomical and biological characters as well as molecular markers such as microsatellites and other PCR derived markers. Here again a tremendous progress has been made by the sequencing of one of the woody species, *Phyllostachys heterocycla*, (Peng *et al.*, 2013). It revealed that bamboo had many more cellulose synthase (*CesA*) genes and cellulose synthase-like (*Csl*) genes than any other grass (19 *CesA* and 38 *Csl*) compared to 11 and 34 in rice and 10 and 29 in Arabidopsis. The gene number in this superfamily is similar to that in poplar, a woody species. More recently 4 genomes were determined (Guo *et al.*, 2019) from different ploidy levels bamboo species and it clarified the phylogeny of the genus: there are one diploid herbaceous lineage and 3 distinct polyploid woody ones which result from allopolyploidy between three extinct diploid parents. Of course, the availability of genomes and transcriptome sequences generated many specific gene studies, including flowering genes, disease resistance genes and many others such as aquaporins.

Along the same lines, we invited review papers on two potential bioenergy crops, *Jatropha curcas* (Carels, 2009) and *Miscanthus* species (Heaton *et al.*, 2010). Both articles reviewed the biology of the two species, their advantages and drawbacks, as well as the perspectives of developing them as a crop. Genomics and sequencing have allowed one to progress. A *Jatropha* genome draft was reported as early as 2011 (Sato *et al.*, 2011) and an improved sequence a few years later (Wu *et al.*, 2015). Similarly, *Miscanthus sinensis* genome sequence was published (Ma *et al.*, 2012). As a result, numerous traits concerning cell wall composition and bioconversion, were identified and now serve as a background in breeding programs (Van der Weijde *et al.*, 2017). A recent article reviews major progress and perspectives in using various crops as a source of bioenergy (Clifton-Brown *et al.*, 2019).

Another aspect of plant genomics was the development of research on three tropical crops: cocoa, coffee, and sugar cane. The review on cocoa (Micheli *et al.*, 2010) was already genomics orientated. One year later, the same group of authors reported a draft genome sequence of *Theobroma cacao*, and, more recently an improved version (Argout *et al.*, 2017). This

work has provided information on genes involved in disease resistance, seed quality, aroma and self-incompatibility, and is now the basis for further breeding. This reference genome has also been very useful to investigate the evolutionary history and domestication of this tree by Amazonian people. Finally, a recent review provides an overview of cocoa production and recent advances in biotechnology for cocoa improvement (Wickramasuriya and Dunwell, 2019). The coffee story (De Kochko *et al.*, 2010) is fairly similar to the cocoa one. The complete genome was reported (Denoëud *et al.*, 2014) and opened the way to further improvement strategies (Tran *et al.*, 2016). Sugarcane is both a food and energy crop (Manners, 2011). Modern sugarcane results from an initial cross between two octoploid species with different haploid chromosome numbers, a male *Saccharum spontaneum* (n=10) and a female *Saccharum officinarum* (n=8). After several generations of breeding, the varieties have chromosome numbers ranging from 100 to 120, 80 % of which have a *S. officinarum* origin, 10-15 % a *S. spontaneum* one and 5-10 % are recombinant chromosomes. Recently the genome of the *S. spontaneum* parent has been reported (Zhang *et al.*, 2018) and the challenges in exploiting sugar cane genomic and transcriptomic data have been discussed (Thirugnanasambandam *et al.*, 2011).

The monography on *Artemisia* addressed another topic (Valles *et al.*, 2011). It reported the description of a genus with more than a 150 species, its phylogeny and the ethnobotanical use of some of the species, including medicinal, food or beverage. The genetic diversity and genome information were fairly limited at the time this paper was published, but the species had great potential in treatment of malaria. A draft genome has recently been published and it shed new insight on the biosynthesis of artemisin, the anti-malarial drug, opening the way to the production of artemisin in transgenic plants (Shen *et al.*, 2018).

Finally, a chapter dealing with genome evolution of plant pathogenic or symbiotic fungi was invited (Aguileta *et al.*, 2009). This chapter examined the evolution of genome organization, chromosomal rearrangements, evolution of gene families, rapid evolving genes, horizontal transfers,

transposable elements, and suppression of recombination around mating type loci. This field also evolved very rapidly, with many more fungi genomes being sequenced. Such studies provided new insights on population biology of fungus invasion (Gladioux *et al.*, 2015) and on the mechanisms which allow a fungus species to adapt specifically to its plant host, as illustrated in a recent example (Badoin *et al.*, 2017). It is worth mentioning that this aspect of plant genomics has been the subject of several thematic volumes in the following years: herbaceous land plants (Paterson, 2014), trees (Plomion and Adam-Blondon, 2015) and fungi (Martin, 2014).

Conclusion

Before concluding, I have to cite four thematic volumes which I have not commented in this review: two volumes reviewed our knowledge on vitamins (Rebeillé and Douce, 2011 A, 2011 B), one volume updated our knowledge on lignin biosynthesis, biodegradation and bioengineering (Jouanin and Lapiere, 2011) and a last volume presented advances and challenges in medicinal plants (Shyur and Lau, 2012). This volume is reviewed in a chapter of this issue, as well as recent advances and trends in the field of medicinal plant research.

I have tried to illustrate a few topics we selected with Jean-Claude Kader a few years ago. These were subjects in which we were interested, although most of the time we were not specialists. We very much enjoyed editing these articles and volumes, exchanging with authors, many of whom became our friends and it has been an exciting experience. I had great pleasure revisiting this period and having a quick look at most recent developments. I feel sad being alone to commemorate this period and I am sure Jean-Claude would have enjoyed, as well, this exercise and would have been impressed, as I have been, by the outstanding advances in such a short time. The most spectacular development is certainly in the field of plant genomics. Many of the current achievements were not even imaginable at the time the articles were written and it is difficult to foresee the future developments. I expect they will occur in the field of the interactions between plants and their microbiote, in the field of ecology and, also, in the applications

of all these findings to a more efficient and sustainable agriculture. I wish a long life to *Advances in Botanical Research* and another bunch of exciting and stimulating articles in the coming years.

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