The biologically most fascinating aspect of the work introduced by Mandáková and co-workers [9] is the evolution of a new chromosome (*Heť*) from largely heterochromatic *Het* chromosome, derived from *Boechera* chromosome 1 (BS1). This BS1 chromosome was formed via reciprocal translocation between AK1 and AK2 also constituting a new 'hybrid centromere' being the respective starting point for heterochromatin accumulation (Figure 1 E, F). The *Het* chromosome underwent further mutational steps including a centric fission and pericentric inversion creating another smaller *Heť* version plus a small fragment called *Del* chromosome explaining the cytogenetic situation in apomictic 2n = 15 species. The newly formed chromosomes (*Heť* and *Del*) are persisting in apomictic species and thus can survive in secure "genetic havens". However, because of frequent reticulate evolution and hybridization (Figure 1) this chromosome (*Heť*) can easily move into other genomes and again persists if apomixis is the prevailing mode of reproduction. It will be intriguing to see if there is a potential causal link between occurrence of these aberrant 'apomictic' chromosomes and the apomixis trait. Some first candidate (apo)alleles (APOLLO and UPGRADE), involved in gametophyte and embryo development, have been characterized [11], but direct experimental evidence for their position on *Het* is still lacking. However, their continental-wide occurrence in the various genepools does fit perfectly with the idea of the evolution of apomixis in the genus *Boechera* [9].

The exciting results by Mandáková *et al*. [9] highlight the interplay of cytogenetic analyses, genomics, and evolutionary biology and contribute significantly to our overall understanding of evolution of apomixis in *Boechera*. CCP is a powerful technique to unravel the history of genomes and its chromosomes, and, therefore, will play an increasingly important role in evolutionary biology. It will also substantially contribute, at least within Brassicaceae family, in generating high quality genome assemblies of many species.

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Are karrikins involved in plant abiotic stress responses?

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Recent reports have shown that strigolactones play a positive role in plant responses to drought and salt stress through MAX2 (More Axillary Growth 2). Increasing evidence suggests that MAX2 is also involved in karrikin signaling, raising the question whether karrikins play any role in plant adaptation to abiotic stresses.

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MAX2: a mediator between strigolactone and karrikin signaling

Strigolactones are new plant hormones that are known as root-derived signals for parasitic plant seed germination and arbuscular mycorrhizal fungi hyphal elongation [1]. In addition, strigolactones are involved in regulation of many biological processes in host plants, from growth and development to responses to environmental stresses [1]. In *Arabidopsis* (*Arabidopsis thaliana*), at least four genes have been discovered to be involved in strigolactone biosynthesis, namely *AtD27* (*Arabidopsis thaliana DWARF27*), *MAX3* (*More Axillary Growth 3*), *MAX4* and *MAX1* [1]. AtD27 was demonstrated to catalyze the reversible isomerization

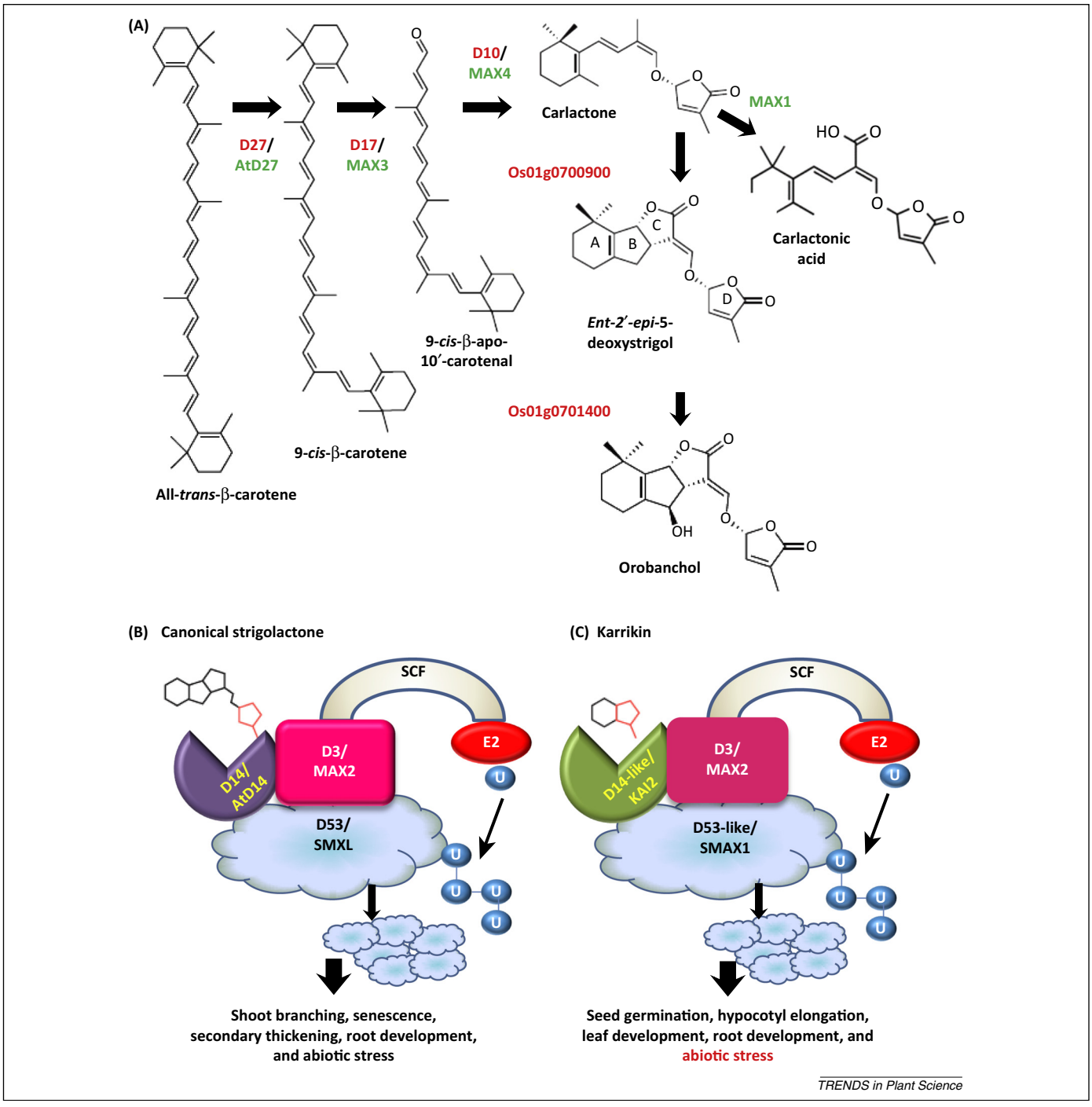

Figure 1. Strigolactone biosynthesis, and strigolactone and karrikin perception modules. **(A)** Proposed model for strigolactone biosynthesis in *Arabidopsis* and rice. Carlactone is synthesized from all-*trans*-β-carotene by three enzymes, D27 (DWARF27)/AtD27, D17/MAX3 (More Axillary Growth 3) and D10/MAX4 in rice and *Arabidopsis*, respectively. Carlactone is converted to strigolactones (orobanchol) by MAX1 homologs (Os01g0700900 and Os01g0701400) in rice. In *Arabidopsis*, MAX1 catalyzes the conversion of carlactone to carlactonoic acid. Red- and green-colored characters indicate proteins of rice and *Arabidopsis*, respectively. **(B)** Strigolactones, after entering a cell, are bound by the α/β-hydrolase fold protein D14/AtD14 (AtD14 is an *Arabidopsis* ortholog of the rice D14), triggering a conformational change in D14/AtD14. Activated D14/AtD14 then interacts with the F-box protein D3/MAX2 (D3 is the rice ortholog of *Arabidopsis* MAX2) in the $SCF^{D3/MAX2}$–E2 complex that tags class I Clp-ATPase D53/SMXL [SMAX1 (Suppressor of MAX2 1)-like protein] (*Arabidopsis* ortholog of rice D53 is unknown, and it might be a SMXL) through polyubiquitination, resulting in degradation of D53. This subsequently leads to induction of strigolactone-responsive genes, resulting in repression of shoot branching, promotion of senescence and secondary thickening, alteration of root growth, and enhancement of stress tolerance. **(C)** In *Arabidopsis*, karrikins, after entering a cell, are bound by the α/β-hydrolase fold protein KAI2 (Karrikin Insensitive 2 or AtD14-like is an *Arabidopsis* ortholog of the rice D14-like), triggering a conformational change in KAI2. Activated KAI2 then interacts with the F-box protein MAX2 in the SCF^{MAX2}–E2 complex that tags class I Clp-ATPase SMAX1 (D53-like rice ortholog of *Arabidopsis* SMAX1 is unknown) through polyubiquitination, resulting in degradation of SMAX1. This subsequently leads to induction of karrikin-responsive genes, resulting in inhibition of hypocotyl elongation, promotion of seed germination, alteration of leaf and root hair growth, and potentially enhancement of stress tolerance. Red color indicates that the karrikin-dependent molecular mechanisms regulating abiotic stress responses are still unknown. Abbreviations: E2, ubiquitin-conjugating enzyme; SCF, Skp–Cullin–F-box protein complex; U, ubiquitin.