

REVIEW

Convergent evolution of gene regulatory networks underlying plant adaptations to dry environments

Mariana A. S. Artur^{1,2}  | Kaisa Kajala² 

¹Laboratory of Plant Physiology, Wageningen University, Wageningen, The Netherlands

²Plant Ecophysiology, Institute of Environmental Biology, Utrecht University, Utrecht, The Netherlands

Correspondence

Mariana A. S. Artur, Laboratory of Plant Physiology, Wageningen University, Droevendaalsesteeg 1, 6708PB Wageningen, The Netherlands.
Email: mariana.silvaartur@wur.nl

Kaisa Kajala, Plant Ecophysiology, Institute of Environmental Biology, Utrecht University, 3584 CH Utrecht, The Netherlands.
Email: k.kajala@uu.nl

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Abstract

Plants transitioned from an aquatic to a terrestrial lifestyle during their evolution. On land, fluctuations on water availability in the environment became one of the major problems they encountered. The appearance of morpho-physiological adaptations to cope with and tolerate water loss from the cells was undeniably useful to survive on dry land. Some of these adaptations, such as carbon concentrating mechanisms (CCMs), desiccation tolerance (DT) and root impermeabilization, appeared in multiple plant lineages. Despite being crucial for evolution on land, it has been unclear how these adaptations convergently evolved in the various plant lineages. Recent advances on whole genome and transcriptome sequencing are revealing that co-option of genes and gene regulatory networks (GRNs) is a common feature underlying the convergent evolution of these adaptations. In this review, we address how the study of CCMs and DT has provided insight into convergent evolution of GRNs underlying plant adaptation to dry environments, and how these insights could be applied to currently emerging understanding of evolution of root impermeabilization through different barrier cell types. We discuss examples of co-option, conservation and innovation of genes and GRNs at the cell, tissue and organ levels revealed by recent phylogenomic (comparative genomic) and comparative transcriptomic studies.

KEYWORDS

apoplastic barriers, comparative genomics, desiccation tolerance, exodermis

1 | INTRODUCTION

The transition of an ancestor aquatic green algae to a terrestrial environment, termed terrestrialization, was a major event in the evolution and diversification of the land plant flora. About 500 Ma after the first ancestor colonized the land, the appearance of a multitude of morpho-physiological adaptations allowed plants to cope with several problems related to terrestrial life, such as water scarcity (Becker & Marin, 2009; Delaux et al., 2012; Kenrick & Crane, 1997; Wodniok et al., 2011). Some of the major adaptations to terrestrial lifestyle include modification of the life cycle, divergence of the plant body

into roots and shoots, the appearance of complex phenolic compounds (e.g., lignin and flavonoids), vascularization and the development of specialized cells (such as stomata) (Delaux et al., 2012). As they colonized land, exposure to high radiations and drought became a recurring problem encountered by multiple plant lineages, and common adaptations at the cell, tissue and organ levels emerged in diverging plant clades. It was until recently unknown how these morpho-physiological adaptations evolved on a genetic level in phylogenetically distant plant species.

Recent advances on whole genome and transcriptome sequencing are now providing evidence that co-option of genes and gene

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regulatory networks (GRNs) underlies the appearance of cell-, organ- and tissue-level adaptations to dry environments. For example, carbon concentrating mechanisms (CCMs) allow photosynthesis under high-light and low-water availability conditions and involve either temporal or spatial separation of the initial carbon fixing from the photosynthetic carbon fixing via anatomical adaptations (Edwards & Ogburn, 2012). Studies have shown that all of the enzymes necessary for the temporally separated Crassulacean acid metabolism (CAM) and the spatially separated C_4 metabolic pathways are present in all plants and function in other processes (Burgess et al., 2016; Christin et al., 2013; Dunning, Moreno-Villena, et al., 2019; Heyduk et al., 2019; Rondeau et al., 2005; Yang et al., 2017). The co-option of these enzymes for CCMs was based on regulatory co-option and neo-functionalization of pre-existing genes, including those involved in C_3 photosynthesis, and rewiring of ancestral GRNs (Figure 1) (Ming et al., 2015; Yang et al., 2017).

Another clear example of plant adaptation to dry environments is desiccation tolerance (DT), the ability to survive extreme drying and remain alive in the dry state (Alpert, 2000; Leprince & Buitink, 2010; Oliver et al., 2000). It has been long hypothesized that DT mechanisms present in the vegetative body of ancestral land plants became confined in small reproductive organs, such as seeds, during the evolution of tracheophytes (Figure 1) (Alpert, 2000; Oliver et al., 2000).

These DT mechanisms of seeds were then co-opted in the vegetative body of angiosperm 'resurrection plants' to be able to survive in extremely dry environments (Artur et al., 2019; Farrant & Moore, 2011). The co-option of DT genes and GRNs has been recently assessed in the genome and transcriptome of resurrection plants (Costa et al., 2017; Giarola et al., 2017; VanBuren et al., 2017; VanBuren et al., 2018; VanBuren et al., 2019). Comparative genomic studies are also revealing that similar gene families and GRNs have expanded and/or being rewired similarly in multiple resurrection plants (Artur et al., 2019; Oliver et al., 2020; VanBuren et al., 2019).

The production of hydrophobic extracellular biopolymers (such as lignin, cutin and suberin) is also an important adaptation to survive on dry land that appeared in specific cells, tissues and organs of diverging plant clades. Comparative genome studies have shown that the ancestral green algae and red algae were already able to produce 'lignin-like' compounds (Delwiche et al., 1989; Labeeuw et al., 2015; Martone et al., 2009), but lycophytes and spermatophytes seem to have independently developed the ability to produce monomers for lignin (Renault et al., 2017; Weng et al., 2010; Weng et al., 2008). Cutin and suberin seem to have also independently evolved in different plant clades, as homologs of genes encoding enzymes necessary for the biosynthesis of their precursors were absent in ancestral non-angiosperm species (Cannell et al., 2020; Philippe et al., 2020; Pollard et al., 2008).

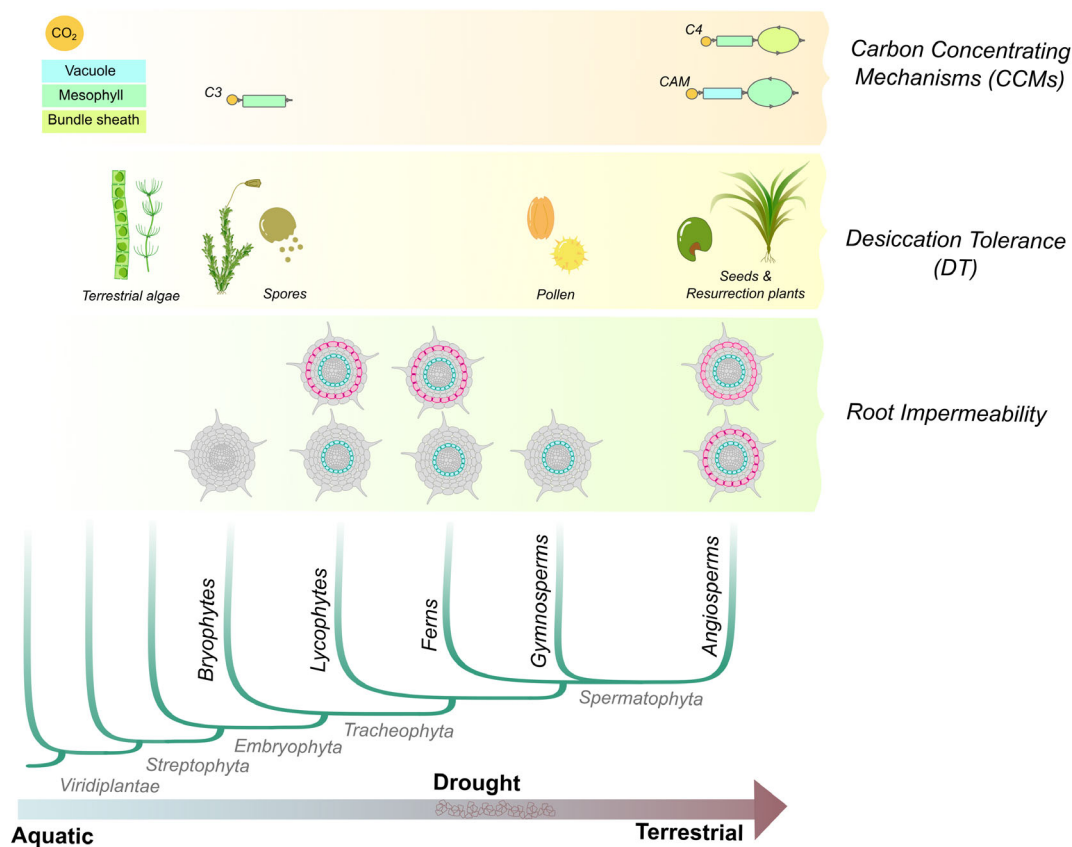


FIGURE 1 Overview of the evolution of plant adaptations to dry environments. The recurring appearance of carbon concentrating mechanisms (CCMs), desiccation tolerance (DT) and root impermeability in Viridiplantae lineages are shown. Root impermeability shows endodermis (yellow), exodermis with suberin only (bright turquoise) and exodermis with suberin and lignin (blue)

The co-option of GRNs for the biosynthesis of these biopolymers in specific root cell types has likely contributed to plant plasticity on dry land. For example, suberin is known to dynamically form barrier for water movement in root endodermis, and it also contributes to plant acclimation to drought when deposited in the exodermis (Ejiri & Shiono, 2019; Enstone et al., 2002; Kreszies et al., 2020; Líška et al., 2016; Reinhardt & Rost, 1995; Taleisnik et al., 1999). The evolution of exodermis remains poorly understood. A suberized exodermis possibly first appeared in early land plants (lycophytes). Its plasticity may have involved the co-option of regulatory genes from the endodermis and may have convergently occurred in some flowering plant lineages (Angiosperms) submitted to constant environmental water fluctuations (Figure 1) (Perumalla et al., 1990). Due to the coexistence of endodermis and exodermis in roots, separation of these cell types for gene expression analyses has been required to understand which genes and GRNs are active in each cell type and to assess co-option and innovation in exodermis GRN evolution (Kajala et al., 2021; Shiono et al., 2014).

In addition to CCMs, DT and root impermeabilization, there are many other adaptations to dry environments that have evolved convergently, such as succulence (Griffiths & Males, 2017), leaf shape (Nicotra et al., 2011; Peguero-Pina et al., 2020) and shallow root system architecture (Griffiths & Males, 2017). However, in this review, we focus on the current knowledge about genes and GRNs recently found to be involved with the convergent evolution of CCMs, DT and root impermeabilization in different plant clades. Using these three examples, we provide insight into the current state of understanding of the following gaps in knowledge:

- How do GRNs convergently evolve to adapt to dry environments?
- Are the same genes and GRNs co-opted or repurposed during independent evolutions?
- What are the shared ancestral GRNs for these traits? What makes ancestral GRNs predisposed for convergent co-option or repurposing?
- What are the different, not shared, pathways taken during independent evolutions?

We will also address how functional genomics can help to generate and to test the novel hypotheses about the evolution and function of these genes.

2 | CONVERGENT GRN EVOLUTION AT THE SPATIAL–TEMPORAL LEVEL: CARBON CONCENTRATING MECHANISMS

Dry habitats are often also sunny, placing further specific restraints on plant physiology and specifically photosynthesis: high-light intensity and high temperature. As plants acclimate to drought by restricting their water loss through closing their stomata, they also restrict CO₂ uptake, reducing the available CO₂ for photosynthesis. High light becomes damaging if the energy obtained from light absorption is not

used by the photosynthetic electron transport chain due to the absence of CO₂. Simultaneously, high temperature reduces the solubility of gases, so that RuBisCO activity shifts away from carboxylation towards more oxygenation, increasing photorespiration and leading to wasted energy (Edwards, 2019). To adapt to these constraints, CCMs have evolved in numerous lineages to enable efficient photosynthesis in dry, hot and high-light environments while improving water-use efficiency.

CCMs work by separating the initial carbon fixing away from the photosynthetic carbon fixing (Calvin cycle) either temporally across the diurnal cycle or spatially across different cell types or compartments. Both the temporal separation, as seen in CAM, and spatial separation, as seen in C₄ photosynthesis, have evolved independently in over 60 lineages (Edwards & Ogburn, 2012). The evolutionary paths to both CAM and C₄ photosynthesis have been recently reviewed and discussed in great detail (Bräutigam et al., 2017; Chen et al., 2020; Edwards, 2019; Heyduk et al., 2019; Niklaus & Kelly, 2019; Schlüter & Weber, 2020; Sedelnikova et al., 2018), and in short, both require two main aspects: (a) an anatomical adaptation and (b) co-option of the carbon concentrating metabolic pathway to the correct spatiotemporal location. The main anatomical adaptation for CAM is enlarged storage vacuole to store the malate synthesized during the night and enable the day–night CCM (Luttge, 1987). In many C₄ plants, the spatial separation is across two cell types, mesophyll and bundle sheath, and to achieve this, C₄ leaves adapt with so-called Kranz anatomy with enlarged bundle sheath cells with increased plastid numbers and increased vein density (Haberlandt, 1904). The regulation of Kranz anatomy is proving to be a complex process (Sedelnikova et al., 2018), and although it has readily evolved convergently in some plant clades, it is starting to appear that not all plant clades are pre-conditioned for the C₄ photosynthesis to evolve (Edwards & Ogburn, 2012). Conversely to complex leaf anatomy and its regulation, all the enzymes required for both the CAM and C₄ metabolic pathways, such as phosphoenolpyruvate carboxylase and malate dehydrogenase, are present in all plants serving other functions. To co-opt these enzymes for CCMs, the expression and regulatory patterns have evolved to be spatially and temporally specific (Brown et al., 2011; Burgess et al., 2016; Christin et al., 2013; Dunning, Moreno-Villena, et al., 2019; Gowik et al., 2004; Heyduk, Ray, et al., 2019; Kajala et al., 2012; Ming et al., 2015; Rondeau et al., 2005; Schulze et al., 2013; Williams et al., 2016; Yang et al., 2017). Whole genome sequencing has enabled a level of understanding of how these CCMs evolved in plants. The first C₄ (*Sorghum bicolor*) (Paterson et al., 2009) and CAM (*Phalaenopsis equestris*) (Cai et al., 2015) genomes provided insights about redirection of genes involved in C₃ photosynthesis and expansion of ancient and recent gene families. Transcriptomic approaches are also offering new evidence about convergent evolution of genes and regulatory pathways underlying these CCMs. For example, the genome and temporal transcriptome sequencing of the CAM species *Kalanchoë fedtschenkoi* revealed that the independent emergences of CAM from C₃ have been based on rewiring of diel gene expression patterns along with protein sequence mutations (Yang et al., 2017). Furthermore, the pineapple genome (*Ananas comosus* [L.] Merr.),

another CAM species, indicated that the transition from C_3 to CAM was based on regulatory neofunctionalization of pre-existing genes and regulation of circadian clock components through evolution of novel *cis*-regulatory elements (Ming et al., 2015).

To resolve how gene expression patterns and GRNs have evolved in convergent C_4 lineages, comparative leaf transcriptomics have been utilized, including comparisons of C_3 , C_4 and intermediate C_3 - C_4 leaves, developmental gradients, specific cell types and environmental cues (Aubry et al., 2014; Bräutigam et al., 2011; Burgess et al., 2016; Dunning et al., 2017; Gowik et al., 2004; Li et al., 2010). From these comparisons, shared routes to C_4 are starting to emerge. Transcriptomic comparison across the monocot-dicot divide revealed deep evolutionary conservation of C_4 leaf development pathways and that certain homologous cell type-specific regulators were co-opted during the independent evolutions of C_4 photosynthesis (Aubry et al., 2014). Not only is it possible to co-opt the same orthologues as another species, but it is also possible to co-opt the very gene from another species. Transcriptomics of closely related *Alloteropsis* grasses revealed that recurrent evolution of C_4 among the group was enabled by co-opting genes across species boundaries, specifically by introgressions of the C_4 components (Dunning et al., 2017). Subsequently, it was discovered that grasses have utilized lateral gene transfer also to speed up C_4 evolution (Dunning, Olofsson, et al., 2019; Phansopa et al., 2020). Furthermore, the understanding of C_4 enzymes' regulatory networks in ancestral C_3 state was elucidated also by a transcriptomics approach: comparison of how light and chloroplasts regulate C_4 enzymes in closely related C_3 and C_4 plants. This linked the C_4 enzymes into a pre-existing C_3 regulatory network, explaining the readiness of C_4 to evolve at the molecular level (Burgess et al., 2016). Regardless of these examples of GRN readiness for C_4 evolution, or 'genetic potentiation', the C_4 lineages are not evenly distributed across the angiosperms (Edwards et al., 2010). This can be due either to the different lineages facing different evolutionary pressures or differences in either genetic or anatomic potentiation (Heyduk, Moreno-Villena, et al., 2019) and remains a question to be addressed in the future.

Counter-intuitively, C_4 and CAM can exist in the same leaf. A recent transcriptomic approach was taken to dissect the behaviour of both C_4 and drought-induced CAM in the same plant, *Portulaca oleracea*, offering insight on how the regulatory networks of shared enzymes might be able to coexist while responding to different environmental and temporal cues (Ferrari et al., 2020). With more C_4 and CAM genomes and transcriptomes becoming recently available (Phytozome v.12.1, Goodstein et al. (2012)), the door is open for better understanding of convergent evolution of CCMs and other parallel drought adaptations in these species.

3 | DESICCATION TOLERANCE GRN IN SEEDS AND RESURRECTION PLANTS

DT, the ability to survive the loss of almost all cellular water without irreversible damage, appeared in the plant lineage during

terrestrialization of their ancestor streptophyte algae (Figure 1) (Alpert, 2000; Leprince & Buitink, 2010; Oliver et al., 2000; Terlova et al., 2021; Wodniok et al., 2011). DT refers to survival after extreme dehydration (below 0.3 g H_2O /g dry weight) where the cellular metabolic activity nearly stops, entering into a state of 'anhydrobiosis' (Hoekstra et al., 2001).

At least six independent major clades of green algae were able to colonize dry environments and to display this remarkable ability to withstand extreme dehydration (Lewis & McCourt, 2004; Terlova et al., 2021). The initial appearance of DT features in the ancestor green algae was a crucial step for plant radiation on land (Oliver et al., 2000; Rensing et al., 2008; Wodniok et al., 2011). Vegetative DT is nowadays documented in about 68 bryophytes, 10 ferns and 10 angiosperms families (Artur, Costa, et al., 2019; Marks et al., 2021; Oliver et al., 2000; Oliver et al., 2020). DT has been retained in reproductive structures (such as spores, pollen and seeds) of most land plant lineages, suggesting that virtually all plants display the genetic potential to become DT but are limited by morpho-physiological constraints (Alpert, 2000; Farrant & Moore, 2011; Marks, Farrant, et al., 2021; Oliver et al., 2000). It has been proposed that vegetative DT in Angiosperm resurrection plants re-evolved by re-directing common regulatory pathways from their reproductive structures (Costa et al., 2017; Farrant & Moore, 2011; Oliver et al., 2000). In fact, common morpho-physiological and biochemical signatures of DT have been found among evolutionarily distant resurrection plants and between desiccation-tolerant vegetative and reproductive structures. One example is the ability that certain groups of resurrection plants have to display leaf curling, rolling or folding, which provide protection against photo-damage during dehydration ('homoichlorophylly'), while other groups undergo chlorophyll breakdown, chloroplast disassembly and synthesis of anthocyanin ('poikilochlorophylly'), a common mechanism involved in seed acquisition of DT (Alpert, 2000; Artur, Zhao, et al., 2019; Charuvi et al., 2019; Dekkers et al., 2015; Rademacher et al., 2019).

Recent developments in sequencing technologies are now also facilitating the assessment of genomic and regulatory adaptations underlying the origin and convergent evolution of DT in plants. In the past 5 years, at least eight whole genomes and several transcriptomes of desiccation-tolerant plant species from distinct phylogenetic groups became available (Artur, Costa, et al., 2019; Oliver et al., 2020). Comparison between desiccation-tolerant and desiccation-sensitive genomes and transcriptomes is revealing loss and repurposing of genes associated with the aquatic lifestyle of the ancestor green algae and the expansion of gene families and refinement of gene expression necessary for survival on dry environments (Khraiweh et al., 2015; Marks et al., 2021; Peredo & Cardon, 2020; Rensing et al., 2008; VanBuren et al., 2019; Xu et al., 2018). The latter is clearly exemplified by expansion of late embryogenesis abundant proteins (LEAs) and early-light induced proteins (ELIPs) families in resurrection plants (Costa et al., 2017; Khraiweh et al., 2015; Rensing et al., 2008; VanBuren et al., 2019; Xu et al., 2018). LEA genes are expressed during orthodox seed maturation, and their corresponding proteins accumulate when the seeds start to dry (Dure et al., 1989; Dure III et al., 1980; Galau et al., 1986; Verdier et al., 2013). These proteins are intrinsically disordered and can undergo disorder to-order transitions, what contribute

to stabilization of membranes, organelles and the cytoplasm (Artur, Rienstra, et al., 2019; Buitink & Leprince, 2004; Crowe et al., 1992; Wise & Tunnacliffe, 2004). A few LEA families were found to be commonly expanded in resurrection plant genomes, what indicates that specific LEAs contributed to the convergent evolution of DT in these species (Artur, Zhao, et al., 2019; Costa et al., 2017; VanBuren et al., 2017). Similarly, ELIPs, known to protect the cells against photo-oxidative damage under high-light intensities (Hutin et al., 2003), have undergone a massive proliferation as tandem duplications in the genome of resurrection plants (VanBuren et al., 2019). Altogether, these studies are shedding light on common patterns of gene family expansion associated with convergent evolution of DT in resurrection plants.

Usually, angiosperm resurrection plants respond to vegetative desiccation by inducing the expression of regulatory pathways typically related to seed DT (Costa et al., 2017; Giarola et al., 2017; Pardo et al., 2020; VanBuren et al., 2017). A recent study has shown, however, that despite conserved seed regulatory networks being activated in vegetative tissues of the poikilochlorophyllous resurrection plant *Xerophyta humilis*, the master transcription factors (TFs) upstream of these pathways in seeds are not activated in vegetative tissues (Lyall et al., 2020). This finding brings novel hypotheses about the evolution of DT. For example, it is likely that the activation of components of seed DT in vegetative tissues involved the appearance of alternative TFs that have evolved in a similar fashion in different resurrection plant genomes. A comparative genome and transcriptome study have recently shown that seed dehydration-related genes shared similar expression patterns among desiccation-tolerant and -sensitive grass species during drought; however, subsets of seed-specific genes were identified as expressing only in desiccation-tolerant grasses (Pardo et al., 2020). With more seed and resurrection plant genomes and transcriptomes becoming available, more information will be provided about the identity of the genes and pathways that underlie the convergent evolution of DT in different plant species and organs.

4 | ROOT CELL TYPE GRN ADAPTATIONS TO DROUGHT: IMPERMEABILIZATION OF ENDODERMIS AND EXODERMIS

The evolution of hydrophobic extracellular biopolymers was a critical innovation for plant terrestrialization, contributing to permeability and water transport control. Some of these compounds include complex phenolic-derived polymers such as lignin, cutin and suberin (Niklas et al., 2017). Lignin generally works in the reinforcement of secondary cell walls; cutin is commonly found as part of the impermeabilizing cuticle of aerial parts and was recently reported as being also part of the root cap cuticle, and suberin is found in many tissues including specialized root cells, tubers, fruit skin and seed coat (Berhin et al., 2019; Niklas et al., 2017; Philippe et al., 2020; Renault et al., 2017). In general, these compounds function in mechanical support, defence against pathogens and herbivores and in the control of

the movement of water, nutrient and gases (Niklas et al., 2017; Philippe et al., 2020; Renault et al., 2017; Pei Wang et al., 2020).

Convergent evolution has also played an important role in the appearance and shaping of the biosynthetic pathways of some of these biopolymers across diverging plant taxa. For example, the ancestral green algae and red algae have the ability to produce 'lignin-like' compounds, leading to the hypothesis that ancient biosynthesis pathways have been rewired in the vascular plant lineage (Delwiche et al., 1989; Labeeuw et al., 2015; Martone et al., 2009). Furthermore, lycophytes and spermatophytes have independently developed the ability to produce monomers necessary for lignin biosynthesis and assembly (Renault et al., 2017; Weng et al., 2008; Weng et al., 2010). It is possible that convergent evolution also played a role on the appearance of cutin and suberin across distantly related plant species. Both cutin and suberin share similar initial biosynthetic steps and lipid precursors; however, different enzymes belonging to the same superfamily and with different mechanisms of action work on their modification and assembly (Philippe et al., 2020; Pollard et al., 2008). A recent large-scale comparative genomic study has revealed that the ability to synthesize precursor molecules of cutin and suberin emerged prior the evolution of land plants; however, the subsequent steps of the biosynthetic pathway may have evolved independently across land plants (Cannell et al., 2020). Still, little is known about how the other parts of the pathway, such as polymerization and distribution in plant cells, evolved in land plants (Niklas et al., 2017; Philippe et al., 2020; Pollard et al., 2008).

The diversification of biosynthetic pathways leading to the production of impermeabilizing hydrophobic compounds has also contributed to the evolution of distinct cell types important for adaptation to terrestrial life and for resilience to drought. For example, the roots of all vascular plants contain an endodermis surrounding the vascular tissues (Doblas et al., 2017; Enstone et al., 2002). The endodermis cell layer forms a diffusion barrier for water, gases and nutrients due to the presence of two cell wall modifications: the Casparian strip and suberin lamella (Barberon et al., 2016; Doblas et al., 2017; Seago Jr. & Fernando, 2013; Vishwanath et al., 2015). Casparian strip is composed of lignin, deposited in the walls of endodermal cells at their junctions, dividing the layer into outward and inward polarities and forming an effective barrier to the apoplastic movement of molecules into the stele and preventing their backflow (Barberon, 2017; Enstone et al., 2002; D. Roppolo et al., 2014; Daniele Roppolo et al., 2011). The suberin lamella is a secondary cell wall modification deposited in the inner surface of the primary cell walls, usually after the Casparian strip is formed in the mature endodermis (Barberon, 2017; Enstone et al., 2002). Different from Casparian strip, the suberin lamella may not form in every root nor in every endodermal cell (the so-called passage cells) (Andersen et al., 2018; Barberon et al., 2016; Enstone et al., 2002; Holbein et al., 2021). Despite debate in the past years, the role of suberin lamella as an apoplastic barrier for water and nutrient uptake from the apoplast to the endodermis cytoplasm has been demonstrated (Barberon et al., 2016; Ranathunge & Schreiber, 2011; Peng Wang et al., 2019).

The roots of several species also develop an exodermis below the epidermis, which is a specialized type of hypodermis with Casparian bands and suberin lamellae depositions (Enstone et al., 2002; Perumalla et al., 1990). The exodermis functions as a dynamic barrier not only against water loss under drought and salinity but also against loss of oxygen under anoxic conditions, against penetration of ions and heavy metals and against pathogen infections (Aloni et al., 1998; Damus et al., 1997; Ejiri & Shiono, 2019; Enstone et al., 2002; Líška et al., 2016; Namyslov et al., 2020; Ranathunge et al., 2011; Tylová et al., 2017). At the same time, the development of exodermis barriers has its downside as it may impair the uptake of nutrients and interaction with beneficial microbes (Kamula et al., 1994). To cope with this problem, many plant species developed the ability to induce an exodermis dynamically in response to abiotic stresses, such as drought (Enstone et al., 2002; Kreszies et al., 2020; Líška et al., 2016; Reinhardt & Rost, 1995; Taleisnik et al., 1999). Interestingly, the development of the exodermis may vary among closely related species displaying distinct stress response phenotypes (Ejiri & Shiono, 2019), indicating that this cell type contributes to plant plasticity and acclimation and may also help plants to adapt and colonize dry environments.

Regardless of its adaptive role, the evolution of exodermis in plants still remains untangled. Perumalla et al. (1990) surveyed 181 species from 53 families of plants from different ecological

groups (hydrophytic, mesophytic and xerophytic) to determine the presence of hypodermis with Casparian bands (exodermis). As the majority (156) of the species assessed presented an exodermis with suberin only (hypodermis) or with both suberin and lignin, the authors hypothesized that the presence of a modified hypodermis is ancestral to flowering plants and has been retained in many species (Perumalla et al., 1990). Furthermore, the authors found that festucoid grasses lack Casparian bands despite presenting cells with similar shape and packing as species with hypodermal Casparian bands, leading to the hypothesis that their recent ancestor may have lost the trait. Interestingly, in seminal roots of modern cultivars of barley (a festucoid species), the exodermis fails to develop even upon severe osmotic stress (Kreszies et al., 2019), while in wild barley, the exodermis is induced in response to osmotic stress (Kreszies et al., 2020). On the other hand, in other crop grasses (non-festucoid), such as rice and maize, an exodermis is present and develops faster in response to stress (Ranathunge et al., 2016; Schreiber et al., 2005).

Understanding how the exodermis evolved in plants can help in the identification of the underlying regulatory networks responsible for its induction in response to drought. To obtain more knowledge about the evolution of exodermis, we compiled the current information about their presence in plant species based on literature search (Figure 2) (Bani et al., 2018; Barrios-Masias et al., 2015; Barykina &

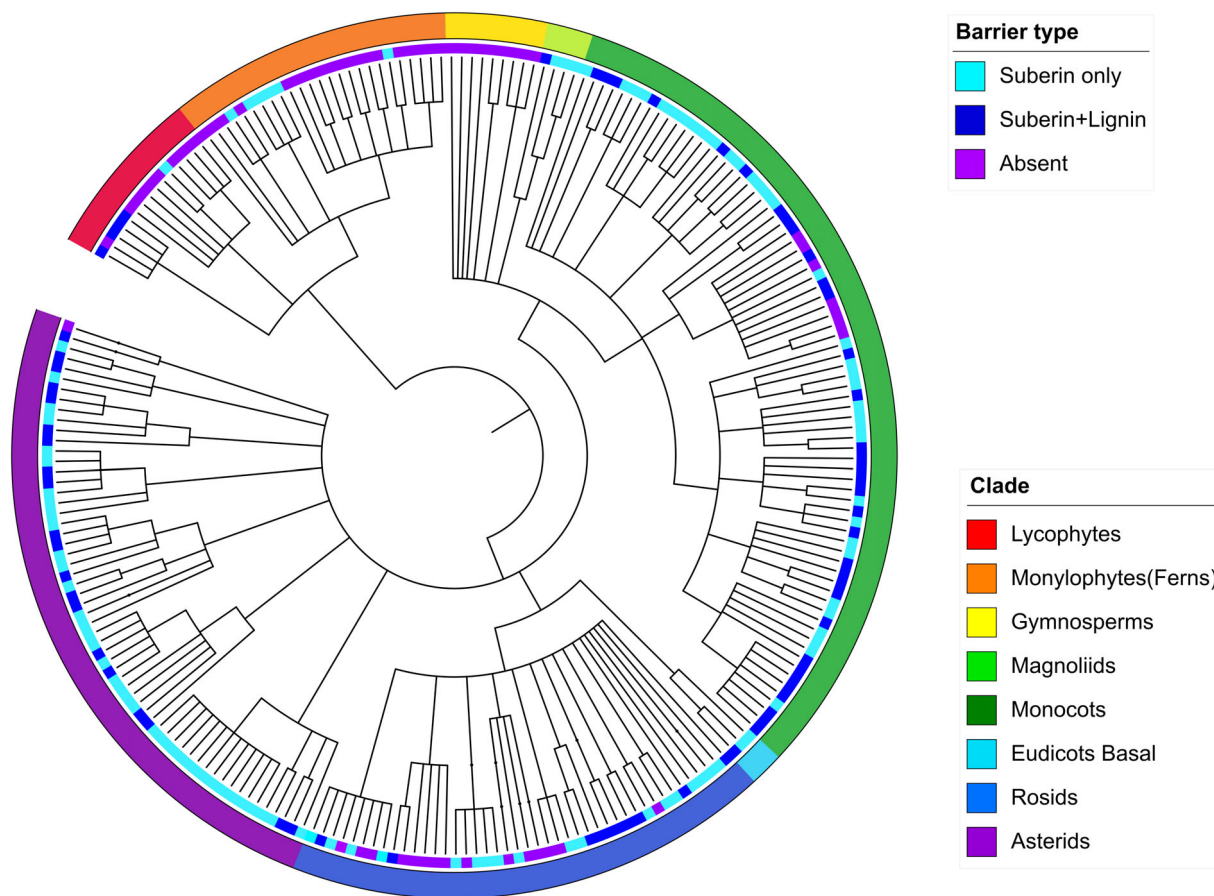


FIGURE 2 Exodermis (hypodermis) evolution across land plants. The inner ring represents the exodermis phenotype and the outer ring, the major clades. The phylogenetic tree was generated using NCBI Common Tree (www.ncbi.nlm.nih.gov/Taxonomy/CommonTree/wwwcmt.cgi) and edited using iTOL (itol.embl.de/)

Kramina, 2006; M. Brundrett et al., 1990; Calvo-Polanco et al., 2014; Damus et al., 1997; Demchenko et al., 2004; Eissenstat & Achor, 1999; Ejiri & Shiono, 2019; Enstone et al., 2002; Ghanati et al., 2005; Kosma et al., 2015; Liu et al., 2019; Perumalla et al., 1990; Ranathunge et al., 2017; Reinhardt & Rost, 1995; Ron et al., 2013; Schreiber et al., 2005; Schreiber et al., 1999; Shiono & Yamada, 2014; Thomas et al., 2007; Zhang et al., 2018). Based on this analysis, the exodermis with suberin first appeared in early land plants (lycophytes), but it is missing from other seedless vascular plants and all but one gymnosperm (Damus et al., 1997). Interestingly, four species in the lycophyte genus *Selaginella* contain exodermis with lignified Casparian strips (Damus et al., 1997). Most flowering plants contain an exodermis with suberization only (hypodermis), while a lignified exodermis appears in about a third of the species. The scattered appearances of the exodermal lignification indicate that it has evolved independently multiple times, suggesting a high evolutionary pressure and pre-conditioning for the characteristic to arise. Species with no exodermis have been identified in seven clades (in purple, Figure 2), and the most parsimonious explanation for presence/absence of exodermis is the loss of the cell type in these lineages. However, the evolutionary hypotheses are restricted by the sparse sampling in families of interest. This is highlighted by the relevant literature containing contradictions (e.g., pea Bani et al. (2018); Perumalla et al. (1990); Talleisnik et al. (1999)), likely due to the dynamic nature of the exodermis.

Evolutionary studies focussed on characterizing the exodermis, for example, by staining suberin and lignin or using barrier property assays (Table S1) will contribute with important information about how this cell type has appeared or disappeared multiple times across the plant lineages. Coupling that with comparative genomics and transcriptomics of phylogenetically close species (e.g., from the same family) but with different phenotypes (e.g., non-exodermal, constitutive and stress-inducible exodermis) will be key to identify the origin of the regulatory networks and how master regulators underlying exodermis development and suberization in response to drought evolved. It is possible that the sporadic appearance of exodermis during plant evolution was possible through rewiring regulatory networks of Casparian strips and suberin lamellae formation in endodermis or similar lignin and suberin biosynthetic pathways from other cell types. The coexistence of endodermis and exodermis in roots has complicated transcriptomic approaches, and to investigate the exodermis gene expression and GRNs in individual species, methods such as laser capture microdissection and translating ribosome affinity purification (TRAP) have been used (Kajala et al., 2021; Shiono et al., 2014). The exodermis-specific gene expression patterns and GRNs are a foundation for understanding the genetic underpinnings of the cell type and enable investigating its evolutionary paths.

Recent studies are showing the importance of distinct clades of the MYB TF family as conserved regulators of suberin deposition in response to osmotic stress in different cell types and in phylogenetically distant plants, linking their evolution with colonization of dry terrestrial environments by early land plants (Capote et al., 2018;

Cohen et al., 2020; Gou et al., 2017; Kajala et al., 2021; Kosma et al., 2014; Lashbrooke et al., 2016; Legay et al., 2016; Shukla et al., 2021; To et al., 2020; Wei et al., 2020). Two of the possible scenarios are: (a) osmotic stress-inducible regulation of suberization diversified from pre-existing developmental pathways and (b) the regulation of suberization in response to drought was re-activated as plants colonized drier environments. Taking that into account, further evolutionary/phylogenetic study of exodermis is needed and selection of a good clade(s) to dissect the gain/loss events is key for understanding exodermis development and how it evolves so readily.

5 | CONCLUSIONS AND PERSPECTIVES

The appearance and diversification of adaptations to dry environments and their underlying GRNs have been tightly shaped at cell, tissue and organismal levels during evolution. These adaptations were crucial for plants to colonize dry lands and survive variations on water availability in the environment. Carbon concentration mechanisms, DT and root impermeabilization are among the main plant adaptations to dry environments and share a similar pattern of convergent evolution in phylogenetically distant organisms. However, we are only starting to understand the evolutionary paths of the GRNs underpinning these adaptations in individual lineages. More comparative research between independent evolutions will inform us of the possible GRN evolutionary paths, including finding out if the same molecular and regulatory changes have occurred in independent lineages.

Detailed physiological and histological studies combined with advanced genome and transcriptome sequencing techniques such as TRAP-seq and single-cell sequencing (Heiman et al., 2014; Reynoso et al., 2015; Thellmann et al., 2020) will allow us to assess how these adaptations evolved through millions of years. This information in combination with novel methods to simulate drought conditions (e.g., Marchin et al. (2019)) and technologies for plant genetic modification (e.g., CRISPR/Cas9) will have the power to help on the improvement of plant performance in dry environments, especially in the current scenario of increasing climate change. These data will also provide knowledge about key TFs working upstream of GRNs controlling DT pathways, which are of potential interest for engineering more drought-tolerant crops.

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CONFLICT OF INTEREST

The authors declare no conflict of interest.

ORCID

Mariana A. S. Artur  <https://orcid.org/0000-0002-6832-2407>

Kaisa Kajala  <https://orcid.org/0000-0001-6483-7473>

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SUPPORTING INFORMATION

Additional supporting information may be found online in the Supporting Information section at the end of this article.

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