Polyamine metabolism and activation of lipid signalling pathways in Arabidopsis thaliana

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Chapter 1

General introduction
Plants in the context of environmental cues

As sessile organisms, plants are continuously challenged by various environmental factors that affect their growth, development and/or productivity. Unlike animals, plants cannot escape from unfavourable conditions yet evolution has resulted in complex, highly coordinated, systems that allow adaptation and acclimation to harsh circumstances. In a plant signal transduction pathway, environmental cues are believed to be perceived by sensor systems that are located at the plasma membrane, which release or activate so-called second messengers, including calcium ($\text{Ca}^{2+}$), reactive oxygen species (ROS), and signalling lipids, that pass on the information by activating downstream effector components, such as protein- and lipid kinases, phosphatases, small G-proteins and ion channels. The signalling cascade often leads to conformational changes of target proteins, causing them to activate, re-localise, or interact with proteins/enzymes, eventually regulating transcription factors, affecting downstream changes in gene transcription, and allowing the plant to adapt and survive. Significant progress has recently been made in elucidating the molecular and genetic pathways involved in these responses (Amtmann, 2009; Hirayama and Shinozaki, 2010; Urano et al., 2010; Nick, 2013; Yuan et al., 2013; Danquah et al., 2014; Gehan et al., 2015). Among these, a well-studied group of compounds that have been seen to play a crucial role in the plant's response to a broad variety of environmental cues, are the polyamines (Takahashi and Kakehi, 2010; Tiburcio et al., 2014; Liu et al., 2015).

What are polyamines?

Polyamines are positively charged small organic compounds, present in most organisms, except for two orders of Archaea, i.e. the Methanobacteriales and Halobacteriales (Hamana & Matsuzaki, 1992). They play versatile roles in regulating fundamental cellular processes and are therefore considered as critical regulators of cell growth and differentiation. If polyamine production is prevented by mutation, or blocked by inhibitors, cells require at least one exogenous polyamine to survive (Wallace, 2009). Spermine (Spm), one of the major polyamines, was first discovered as a crystal in human semen by Van Leeuwenhoek (van Leeuwenhoek, 1678), and was accordingly named at the end of the 19th century (Ladenburg and Abel, 1888). Since then, a long history of research in various fields has accompanied these molecules (Tabor and Tabor, 1964; Bachrach, 2010), which brought, among others, to the discovery in 1971 of the crucial implication of polyamines in cancer (Russell, 1971), placing polyamine research as a major area of interest and driving the quest to understand its cellular function. In this context, an explosive proliferation of scientific literature on polyamines was noticed during the next decades.

The most common polyamines in plants and animals are the diamine putrescine (Put; $1,4$-diaminobutane), the triamine spermidine (Spd; $N$-(3-
aminopropyl)-1,4-diaminobutane) and the tetraamine Spm (N,N’-bis(3-aminopropyl)-1,4-diaminobutane), although other polyamines, such as cadaverine (Cad; 1,5-pentaandiamine), 1,3-diaminopropane (Dap) and thermospermine (Tspm), an isomer of Spm, are also found (Cohen, 1998). Polyamine concentrations and -compositions vary between different organisms. For example, some prokaryotes only contain Put and Spd, whereas in other cases, such as certain thermophilic bacteria, polyamines that are longer than Spm are found (Hamana and Matsuzaki, 1992; Pegg and Michael, 2010). Very long polyamines are also present in diatoms, being mainly used for the biomineralization of the external porous cell wall (Kröger et al., 2000). In plants, the cellular concentrations of polyamines range from $10^{-9}$ to $10^{-5}$ M, which is much higher than the level of the classical phytohormones ($10^{-13}$-$10^{-7}$ M). Nonetheless, like hormones, polyamines are required for various processes like fertilization, embryogenesis, cell division, morphogenesis, autophagy, pathogenesis, senescence, cell death and stress responses (Tabor and Tabor, 1985; Bagni and Pistocchi, 1988; Kaur-sawhney et al., 2003; T Kusano et al., 2008; Shah and Swiatlo, 2008; Alcázar et al., 2010; Lefèvre et al., 2011; Gupta and Sigrist, 2013; Tiburcio et al., 2014; Moschou and Roubelakis-Angelakis, 2014; Miller-Fleming et al., 2015; Aloisi et al., 2016; Li and MacDonald, 2016). Despite all knowledge, scientists also agree that the molecular mechanism by which polyamines generate such different effects in cells, is still one of the biggest mysteries remaining in molecular biology (Miller-Fleming et al., 2015).

Due to the high pK$_a$ of the primary and secondary amino groups at physiological pH, polyamines are mainly protonated. For example, at pH 7.2, 85% of the Spm is in its tetra-cation form (Aikens et al., 1983). Hence, these low-molecular-weight compounds have been suggested to simply function as ‘super-cations’, equivalent to one or two calcium- or magnesium molecules. However, the particular distribution of the charges along the flexible aliphatic chain makes them unique and distinct from the cellular bivalent cations. These features are essential for recognition and to establish specific electrostatic interactions with polyanionic macromolecules within the cell, such as ATP, nucleic acids, phospholipids, and various proteins (Cohen, 1998). Polyamines thus can influence the function of the counter-ion with consequences for fundamental cellular processes, such as ion transport, protein- and lipid-kinase activity, transcription, protein synthesis, post-translational modifications such as S-nitrosylation or hypusination, and stabilization of membrane- and nuclear components (Watanabe et al., 1991; Basu et al., 1993; Miyamoto et al., 1993; Tabor and Tabor, 1999; Igarashi and Kashiwagi, 2010). However, the sheer complexity of their metabolism and regulation argues that polyamines and/or their targets, play other crucial roles, which are not solely based on charge (Wallace, 1998; Wallace et al., 2003).
Polyamine synthesis and catabolism

In plants, polyamine homeostasis is mainly achieved by regulating its biosynthesis and catabolism. Polyamine conjugation also significantly contributes to the regulation of free polyamine levels. This is mainly in the form of hydroxycinnamic acid amides, such as diferuloylspermine, dicoumaroylspermidine, diferuloylspermidine, feruloylputrescine, or coumaroylputrescine (Martin-Tanguy, 1997). The free polyamines levels are tightly controlled and in general only change in response to environmental cues (e.g. salt stress) or during development (e.g. flowering).

The first polyamine synthesized in the biosynthetic pathway is Put (Figure 1). In animals, this polyamine is derived from the decarboxylation of the amino acid ornithine, catalysed by the enzyme ornithine decarboxylase (ODC; Fig. 1). While this enzymatic step is generally believed to be present in all living organisms, there is evidence that the model plant species, Arabidopsis thaliana (thale cress) lacks a functional ODC route. Loss of this pathway might be due to the evolution of an

![Figure 1. Biosynthesis of polyamines in plants. ACL5, ACAULIS5 - thermospermine synthase; ADC, arginine decarboxylase; AIH, agmatine iminohydrolase; CPA, N-carbamoylputrescine amidohydrolase; dcSAM, decarboxylated SAM; ODC, ornithine decarboxylase; SAM, S-adenosylmethionine; SAMDC, S-adenosylmethionine decarboxylase; SPDS, spermidine synthase; SMPS, spermine synthase. In green, genes present in Arabidopsis.]
alternative pathway for Put synthesis in plants and bacteria, i.e. the arginine decarboxylase (ADC) pathway (Alcázar et al., 2010), which uses arginine as substrate (Fig. 1). The conversion of arginine to Put requires three consecutive enzymatic reactions (Fig. 1). Evidence, however, indicates that the rate-limiting step in Put biosynthesis is ADC, hence is typically being targeted by gene modification (Alcázar et al., 2005, 2010). The synthesis of Spd is achieved by adding an aminopropyl moiety to the four-carbon backbone of Put in an enzymatic reaction catalysed by Spd synthase (SPDS). In turn, Spd is converted into Spm or Tspm, by adding an aminopropyl moiety catalysed by Spm synthase (SPMS) or Tspm synthase (ACaulIS5, ACL5), respectively. The donor of the aminopropyl groups is decarboxylated S-adenosyl methionine (dcSAM), which is synthesized by SAM decarboxylase (SAMDC; Fig. 1). The availability of dcSAM limits the biosynthesis of Spd and Spm (Ge et al., 2006), making SAMDC as one of the major regulators of polyamine biosynthesis. Apart from de novo synthesis, polyamines can also be degraded, in particular by oxidative deamination through the action of amine oxidases. Diamine oxidases (DAOs) are copper-containing amine oxidases (CuAO) present at high level in dicots (Cona et al., 2006) that oxidize the diamines, Put and Cad at the primary amino groups, producing 4-aminobutanal, NH₃ and H₂O₂ (Fig. 2). Although they exhibit a higher affinity for Put and Cad than for Spd and Spm, Arabidopsis CuAO enzymes can also utilize Spd as substrate, producing the corresponding aminoaldehyde, NH₃ and H₂O₂ (Moschou et al., 2012; Planas-Portell et al., 2013). Another class of amine oxidases are flavin-containing polyamine oxidases (PAO), which are present at high levels in monocots and have a high affinity for Spd and Spm and their derivatives (Fincato et al., 2012; Kim et al., 2014). They are divided into two groups of which the first catalyses the terminal catabolism of Spd or Spm to produce Dap, H₂O₂, and 4-aminobutanal (Spd catabolism) or N-(3-aminopropyl)-4-aminobutanal (Spm catabolism; Cona et al., 2006; Moschou et al., 2008) (Fig. 2). The second group of PAOs are involved in the back-conversion of Spm to Spd, and Spd to Put with concomitant production of 3-aminopropanal and H₂O₂ (Moschou et al., 2012; Tavladoraki et al., 2016). Whereas only a few PAO genes belonging to the first group have been characterized, several PAO genes belonging to the second group have been identified (Cona et al., 2006; Liu et al., 2014), including, for example, all five PAO genes from Arabidopsis (Liu et al., 2015). As polyamine catabolism leads to the production of H₂O₂, which can function as a signalling molecule at low concentrations or as a toxic compound at higher levels, the proportion of polyamine catabolism vs biosynthesis has been considered as a crucial factor to induce cell death or stress tolerance upon abiotic stress (Moschou et al., 2008; Kusano et al., 2015; Liu et al., 2015). In general, this implies that polyamines can play a key role in ROS homeostasis (Liu et al., 2015).
General introduction

Potential mechanisms of action of polyamines in stress responses

Accumulating evidence suggests that polyamines in plants function in adaptive responses to various environmental stresses. Since the first report published decades ago, describing the accumulation of Put under K⁺ deficiency (Richards & Coleman, 1952), extensive changes in polyamine levels have been found in various plant species subjected to different stresses (Alcázar et al., 2010; Tiburcio et al., 2014; Liu et al., 2015). However, despite the plethora of genetic- and biochemical tools used so far in polyamine research, the cause-effect relationship between polyamine accumulation and the role they exert remains unclear. In that sense, besides its capacity to bind proteins, such as ion channels, kinases and transcription factors, and influence their activity, their role in stress tolerance has also been hypothesized to be associated with its ability to modulate antioxidant systems as described above, e.g. by producing H₂O₂ by amino oxidase-mediated catabolism, and by modifying the expression or activity of various antioxidant enzymes (Moschou et al., 2008; Mitsuya et al., 2009; Yoda et al., 2009; Zhang et al., 2015).

Importantly, there is a crossroad of polyamine metabolism with other stress pathways. An increase of polyamines have been associated with increased levels of nitric oxide (NO) (Tun, 2006; Wimalasekera et al., 2011; Filippou et al., 2013), which seems integral of many defense- and developmental pathways, including stomatal

Figure 2. Polyamine catabolism in Arabidopsis. PAO, polyamine oxidases; CuAO, copper-containing amine oxidases.
movements in response to ABA (García-Mata and Lamattina, 2003; Bright et al., 2006; Neill et al., 2008). In accordance, recent evidence support an NO-dependent functional link under abiotic stress conditions between polyamines and the synthesis of proline, a key compound in abiotic stress tolerance (Filippou et al., 2013; Tanou et al., 2014; Kaur and Asthir, 2015). Moreover, NO is also involved in posttranslational modifications, such as S-nitrosylation, thus could be affecting protein structure and protein-protein interactions (Lounifi et al., 2013). On the other hand, SAM, which is used as precursor to synthesize higher molecular weight polyamines, is also a precursor for the phytohormone ethylene. In this sense, polyamines and ethylene act in an antagonistic manner, competing for the common substrate with subsequent consequences for senescence and plant defense (Suttle, 1981; Apelbaum et al., 1985; Mehta et al., 2002; Nambeesan et al., 2012). Similarly, because of SAM's precursor role in methylation, polyamine metabolism has also been linked to epigenetic changes and to affect gene expression (Fraga et al., 2004; Tiburcio et al., 2014). Increased levels of polyamines have been also associated to alterations in the expression of genes involved in biosynthesis and signalling of other phytohormones, including auxin, ABA, JA and SA (Cuevas et al., 2009; Alcázar et al., 2010; Toumi et al., 2010; Marco et al., 2011; Baima et al., 2014; Tong et al., 2014). In that sense, an interesting concept of a "polyamine modulon" (a group of genes whose expression is enhanced by polyamines at transcriptional level), similar to what is observed in bacteria and mammalian cells (Igarashi and Kashiwagi, 2011; Pegg and Casero, 2011), has been proposed for plants (Tiburcio et al., 2014).

Finally, another interesting view to explain the role of polyamines in stress responses comes from the chemiosmosis theory, in which polyamines are hypothesized to trap protons in acidic compartments to facilitate ATP synthesis (Ioannidis and Kotzabasis, 2014).

**Lipid signalling in plants**

To sense external stimuli, plants have to perceive signals, transduce them across the plasma membrane, and convert them into downstream biological responses that allow the cell/tissue/plant to respond appropriately. The plasma membrane consists of peripheral- and integral (glyco-)proteins, associated with, or embedded in, a bilayer of amphipathic lipids, forming an impermeable barrier to water-soluble and charged molecules, thus limiting the free exchange of molecules and information (Singer and Nicolson, 1972; Goñi, 2014; Lombard et al., 2014; Nicolson, 2014). In this lipid bilayer, hydrophobic fatty acid chains occupy the interior, whereas polar head groups face the cytosolic and extracellular sides, defining an inner- and outer leaflet. Plasma membrane lipids are differentially distributed throughout the bilayer and can be divided into three classes, all with unique biophysical properties, namely (i) glycolipids, which are found mainly in the outer leaflet and can be subdivided into
glycerolipids and sphingolipids, (ii) sterols, which in plants mainly include sitosterol, campesterol and stigmasterol, and (iii) phospholipids, which are typically the most abundant group, forming the body of the plasma membrane (Furt et al., 2011). Phosphatidylcholine (PC) and phosphatidylethanolamine (PE) represent most of the structural phospholipids, 68–80%. The remainder consists of phosphatidylglycerol (PG), phosphatidylinositol (PI), phosphatidylserine (PS), and phosphatidic acid (PA) (Furt et al., 2011). The head groups of PS, PI and PA are negatively charged, and their prevalence in the inner leaflet contributes to the negative charge on the cytosolic face of the plasma membrane, thus leading to potential interactions with positively charged molecules in the aqueous environment.

Membrane proteins constitute around 50% by weight of the plasma membrane, and are responsible for a wide range of membrane functions, including transport and signal transduction. However, the latter is not exclusive executed by proteins: While the majority of membrane lipids has a structural role, a small percentage (~1% of total lipids) function as signalling molecules themselves. Especially, polyphosphoinositides (PPIs) and PA have been shown to play crucial roles in plant development and stress signalling over the last decade (Munnik and Vermeer, 2010; Munnik and Nielsen, 2011; Testerink and Munnik, 2011; Boss and Im, 2012; Wang and Chapman, 2013; Heilmann and Heilmann, 2015; Heilmann, 2016).

**Polyphosphoinositides**

All PPIs are formed from the membrane phospholipid, PI, which via phosphorylation by specific lipid kinases at the D-3, -4 and -5 positions of the inositol ring (Fig. 3) (Munnik and Nielsen, 2011), results in plants in five distinct species, i.e. three PI-monophosphates, PI3P, PI4P and PI5P, and two PI-bisphosphates, PI(3,5)P$_2$ and PI(4,5)P$_2$. Animals cells contain two additional PPIs for which plants lack the enzymes, i.e. PI(3,4)P$_2$ and PI(3,4,5)P$_3$ (Munnik and Vermeer, 2010; Munnik, 2014; Heilmann, 2016). All members of this diverse and dynamic family have been shown to be involved in signalling (regulating structural proteins, enzymes and transporters), membrane trafficking (i.e. endocytosis and exocytosis), and basal metabolism (Xue et al., 2009; Boss and Im, 2012). The specific phosphorylation pattern of PI's head group, act as a distinctive mark that can be recognized by proteins containing PPI specific-binding domains (Lemmon, 2003), which results in the recruitment of target proteins to the membrane. Alternatively, PPIs can regulate the activity of an enzyme or the gating properties of an ion channel (Balla, 2013; Hille et al., 2015).

Besides acting as signalling molecules, PPIs can also serve as second messenger precursors. In this sense, the enzyme phospholipase C (PLC) plays a crucial role (Munnik, 2014; Singh et al., 2015), which in animal systems is known to hydrolyse PI(4,5)P$_2$ to generate the second messengers, diacylglycerol (DAG) and
inositol triphosphate (InsP$_3$). The latter is released into the cytosol where it liberates Ca$^{2+}$ from intracellular stores via a ligand gated-Ca$^{2+}$ channel (InsP$_3$ receptor), while DAG remains in the membrane and activates protein kinase C (PKC) (Irvine, 1992; Carafoli, 2002; Vetter and Leclerc, 2003). However, this model seems inconsistent with higher plant systems, since they lack IP$_3$ receptors and PKC (Zonia and Munnik, 2006; Munnik and Vermeer, 2010; Munnik, 2014). Plants also contain much lower levels of PI(4,5)P$_2$ in their membranes than animals cell, i.e. 20-100 fold less (Munnik and Testerink, 2009). Nonetheless, plant PLCs do hydrolyse PI(4,5)P$_2$ and PI4P, and the resulting products are phosphorylated by inositolpolyphosphate kinases (IPK1 and IPK2) and DAG kinase, (DGK), respectively to produce inositolpolyphosphates (IPPs) and PA, which have been emerging as important second messengers in plants, fungi and animals (Fig. 4) (Arisz et al., 2009; Gillaspy, 2013; Heilmann and Heilmann, 2015; Williams et al., 2015; Heilmann, 2016). PA functions similar to PPIs, i.e. by recruiting target proteins to membranes and by affecting the activity of enzymes and gating properties of channel proteins (Testerink and Munnik, 2011; Liu et al., 2013). The resulting IP$_2$ or IP$_3$ (from PLC hydrolysis of PI4P and PI(4,5)P$_2$,

**Figure 3.** Structure of phosphatidylinositol 3-phosphate, PI3P, as an example of phosphoinositide. The main structure of phosphoinositides consists of two long fatty acid tails esterified to a glycerol backbone, which in turn is esterified to a phosphate group substituted with an inositol, polar head group. In PI3P, the inositol ring is phosphorylated at the D-3 position.
respectively) can be phosphorylated further into InsP$_4$, InsP$_5$, and InsP$_6$, and even up to InsP$_7$ and InsP$_8$, which are pyrophosphorylated molecules of IP$_6$ (Laha et al., 2015; Williams et al., 2015). Several of these IPPs are emerging as signalling molecules. For example, InsP$_6$ releases Ca$^{2+}$ in guard cells upon ABA treatment (Lemtiri-Chlieh et al., 2003), and was found in the crystal structure of the auxin receptor, TIR1 (Tan et al., 2007), which may bear relevance for the auxin perception (Munnik, 2014). Similarly, the JA receptor, COI1 requires InsP$_5$ or its pyrophosphorylated form InsP$_7$ as cofactor for JA signalling and plant defence (Tan et al., 2007; Mosblech et al., 2011; Munnik, 2014; Laha et al., 2016). In yeast and mammalian cells, IPPs have been implicated in regulation of gene expression and in chromatin remodelling. For plants, similar functions are likely (Gillaspy, 2013; Laha et al., 2015, 2016).

PA signalling can also be generated through activation of the phospholipase D (PLD) pathway. PLD hydrolyses structural phospholipids such as PC and PE, to form PA and the corresponding head groups (Fig. 4). Using differential $^{32}$P-labelling techniques (Arisz and Munnik, 2013), combined with transphosphatidylation assays (Munnik and Laxalt, 2013), it is possible to distinguish between DGK- and PLD-generated PA pools.
Enzymes involved in the metabolism of PI4P, PI(4,5)P₂ and PA, and the encoding genes, have been largely characterized and are briefly described below.

Synthesis of PPIs by PI4K and PIP5K
In plants, the main PI-phosphorylated isomer is PI4P, constituting approximately 80% of the plant's PIP pool (Munnik et al., 1994a; 1994b; Meijer et al., 2001; Meijer and Munnik, 2003). The reaction is catalysed by a PI 4-kinase (PI4K), of which Arabidopsis seem to contain three enzymes showing this activity, namely PI4Kα₁, PI4Kβ₁ and PI4Kβ₂ (Okazaki et al., 2015). PI4P can be further phosphorylated into PI(4,5)P₂, which is carried out PI4P 5-kinases (PIP5K), of which Arabidopsis contains eleven isoforms (PIP5K1-11), representing the only known source of PI(4,5)P₂ production in plants (Heilmann, 2016). PIP5K are divided into two groups: group A, consisting of isoforms PIP5K1-9, and group B, containing PIP5K10 and PIP5K11 (Mueller-Roeber and Pical, 2002). Both groups display particular domain structures and features not encountered in PIP5Ks from animal or yeast model systems, suggesting that plant PIP5K enzymes contain additional mechanisms of regulation (Heilmann, 2016). Examples of this are the highly variable linker domains in group B PIP5Ks from animal or yeast model systems, suggesting that plant PIP5K enzymes contain additional mechanisms of regulation (Heilmann, 2016). Examples of this are the highly variable linker domains in group B PIP5Ks from animal or yeast model systems, suggesting that plant PIP5K enzymes contain additional mechanisms of regulation (Heilmann, 2016). Examples of this are the highly variable linker domains in group B PIP5Ks from animal or yeast model systems, suggesting that plant PIP5K enzymes contain additional mechanisms of regulation (Heilmann, 2016). Examples of this are the highly variable linker domains in group B PIP5Ks from animal or yeast model systems, suggesting that plant PIP5K enzymes contain additional mechanisms of regulation (Heilmann, 2016). Examples of this are the highly variable linker domains in group B PIP5Ks from animal or yeast model systems, suggesting that plant PIP5K enzymes contain additional mechanisms of regulation (Heilmann, 2016). Examples of this are the highly variable linker domains in group B PIP5Ks from animal or yeast model systems, suggesting that plant PIP5K enzymes contain additional mechanisms of regulation (Heilmann, 2016). Examples of this are the highly variable linker domains in group B PIP5Ks from animal or yeast model systems, suggesting that plant PIP5K enzymes contain additional mechanisms of regulation (Heilmann, 2016). Examples of this are the highly variable linker domains in group B PIP5Ks from animal or yeast model systems, suggesting that plant PIP5K enzymes contain additional mechanisms of regulation (Heilmann, 2016). Examples of this are the highly variable linker domains in group B PIP5Ks from animal or yeast model systems, suggesting that plant PIP5K enzymes contain additional mechanisms of regulation (Heilmann, 2016). Examples of this are the highly variable linker domains in group B PIP5Ks from animal or yeast model systems, suggesting that plant PIP5K enzymes contain additional mechanisms of regulation (Heilmann, 2016). Examples of this are the highly variable linker domains in group B PIP5Ks from animal or yeast model systems, suggesting that plant PIP5K enzymes contain additional mechanisms of regulation (Heilmann, 2016). Examples of this are the highly variable linker domains in group B PIP5Ks from animal or yeast model systems, suggesting that plant PIP5K enzymes contain additional mechanisms of regulation (Heilmann, 2016). Examples of this are the highly variable linker domains in group B PIP5Ks from animal or yeast model systems, suggesting that plant PIP5K enzymes contain additional mechanisms of regulation (Heilmann, 2016).

Hydrolysis of PPIs by PI-PLC and phosphatases
PI4K and PIP5K are counteracted by several lipid phosphatases (Williams et al., 2005; Zhong et al., 2005; Gunesecka et al., 2007; Thole et al., 2008; Donahue et al., 2013; Gillaspy, 2013; Novakova et al., 2014; Rodriguez-Villalon et al., 2015; Heilmann, 2016), and PI-specific PLCs (PI-PLCs) (Munnik and Testerink, 2009; Munnik, 2014; Heilmann, 2016). All plant PI-PLC enzymes biochemically characterized so far, are activated by Ca²⁺ and display similarity to the human PLCζ subfamily, which represents the most simple group, containing a minimal core structure i.e. a catalytic X- and Y domain, EF-hand domain, and a C2 (calcium- and lipid binding) domain (Tasma et al., 2008; Munnik, 2014; Pokotylo et al., 2014). In the Arabidopsis genome they are encoded by a family of nine isoforms (Mueller-Roeber and Pical, 2002), of which PLC1 to 7 are thought to be responsible for the hydrolysis of PI(4,5)P₂ and PI4P, generating the respective IPP product and DAG (Munnik et al., 1998; Munnik, 2014). PLC8 and PLC9 are thought to be catalytically inactive (Hunt et
How plant PLCs are regulated and activated is still largely unclear (Munnik, 2014).

**DGK and PLD as a source of PA**

In plants, PLC-generated DAG is rapidly phosphorylated to PA by DGK, of which *Arabidopsis* contains seven genes, which are differentially expressed throughout the plant and change in response to many stresses (Arisz *et al*., 2009). PA can also be generated via the PLD pathway. Plant PLDs are classified into 2 subgroups, based on their lipid-binding domains: Those with a combined PX- and PH domain belong to the PLD_ζ_ class, which are homologous to the mammalian- and yeast PLDs. The others, representing the majority of plant PLDs, belong to the C2 class, because of the presence of a Ca^{2+}- and lipid binding C2 domain (Munnik and Testerink, 2009). *Arabidopsis* contains 12 PLDs: 10 C2-PLDs, i.e. PLD_α_1-3, β_1-2, γ_1-3, δ, and ε, and two PX-PH-PLDs, PLD_ζ_1-2 (Bargmann and Munnik, 2006).

**Outline of this thesis**

This thesis focuses on two subjects: *(i)* the role of polyamine metabolism in salt stress and *(ii)* the involvement of polyamines in phospholipid signalling. Polyamine accumulation is usually considered to be a general plant response to abiotic stress. In this sense, genetic manipulation of key genes of its metabolic pathway has been demonstrated to be a useful tool to investigate its mechanism in plant stress responses and adaptation. Whereas most research has focused on the analysis of biosynthetic routes, fewer studies have been reported on the catabolic counterpart. In *Chapter 2*, we investigate the involvement of polyamine back-conversion in *Arabidopsis* salinity tolerance using loss-of-function mutants of AtPAO5 gene, which is the most induced PAO member in salt conditions. We show that the mutants exhibit constitutively higher levels of Tspm, with associated increased salt tolerance. The underlying mechanism is studied and we show a stimulation of ABA, JA and an accumulation of important compatible solutes in the mutant, as well as a Tspm isomer-dependent transcriptional reprogramming.

A different approach to study the mechanism of polyamines is described in the following chapters. A typical early response of polyamines upon environmental cues, such as salt stress, is a polyamine exodus to the apoplast. By applying exogenous polyamines to mimic this effect, we studied its potential early interaction with membrane-associated phospholipid metabolism. For doing so, in *Chapter 3* we describe a ^{32}P_i labelling method that allows to monitor phospholipid synthesis and turnover *in vivo* in *Arabidopsis*. In *Chapter 4* we show that cellular uptake of polyamines trigger within minutes an increase of the lipid-signalling molecule,
PI(4,5)P₂ at the plasma membrane of root cells in Arabidopsis seedlings. Using Spm as a reference polyamine, we identify the lipid kinases PIP5K7 and PIP5K9 as the main enzymes involved in the response. Concurrent with the increase of PI(4,5)P₂, we found a strong Spm-induced K⁺ efflux in which the Spm-sensitive PIP5K enzymes act upstream, indicating its potential role in this Spm-derived effect. In Chapter 5, we show that polyamines trigger in parallel, an independent second lipid-signalling pathway, which generates PA. Using Spm as a reference polyamine, we identified the plasma membrane-associated PLDδ enzyme as the main enzyme responsible for its PA accumulation. We show that the PLDδ-mediated PA response is also upstream of the Spm-induced K⁺ efflux, and we suggest a model in which the combined action of PI(4,5)P₂ and PA involves the lipid kinase PI4Kβ1 and PI4Kβ2. In Chapter 6, all findings are discussed and future perspectives proposed.

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