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Seed Germination Inhibitors: Molecular and Phytochemical Aspects

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Abstract:

Two major stages of seed development are dormancy and germination which finally promotes the growth of a plant. Some internal and external factors such as hormonal, genetic, chromatin development and environmental factors which maintain the seed dormancy with passing time and other suitable factors, these dormancy promoters are gradually decreased causing release of dormancy and promoting germination by the mechanisms of ROS in plant signalling, cell elongation and reverse mobilization. But dormancy has some benefits in protecting the seed from extreme condition even after natural disaster as well as serving as food for predators in order to maintain balance of nature. So, dormancy can be inhibited by some phytochemical components like terpenoids, polyphenoliic compounds, flavonoids, alkaloids and glycosides by the mechanism of inhibiting water uptake system III & II, surface sterilization, reverse mobilization, cell elongation etc.

Abbreviations

ABA- abscisic acid; GA- gibberellic acid; PYL-PYR like; PP2C-Protein phosphatase 2C ; SnRK-SNF1-related protein kinase subfamily 2 ;JA-Ile - Jasmonic acid - isoleucine; QTL- Qualitative trait loci; DOG1- Delay of Germination; AHG- ABA hypertensive germination; AOS- Allene Oxide Synthase; RT-PCR- Reverse Transcription Polymerase chain reaction; HDZip- Homodomain Leucine Zipper; MADS- MDM1 AGAMAMOUS DEFICIENS SRF (all genes so in upper case); CBF- C-repeating binding factor; GPx- Glutathion peroxidase; GST- Glutathion S- Transferase; PAs- Proanthocyanidins; MATE-Multi Antimicrobial Extrusion Proteins ; MRP- Multidrug Resistance Protein; APX- Ascorbate Peroxidase; CAT- Catalase; t-RNA- Transfer Ribonucleic acid; mi-RNA- micro RNA.

1. Introduction

Seeds are one of the most important part of the world's food. Cereal grains only comprise 90% of all cultivated seeds; contribute up to half of the global energy intake per person (Bewley, 1997). Unsurprisingly then, seed biology is one of the most prominently researched areas in plant physiology. With the seed, the development of the next generation of plant begins. The seed, having the embryo as the miniature model of new plant, is structurally and physiologically enabled for its role as a dispersal unit and is pretty much provided with food reserves to sustain the growing seedling until it develop itself as a fully functioning self-sufficient, autotrophic organism. Because the function of a seed is to develop into a new plant, it may seem unusual that dormancy, a phenomenon that blocks germination do exists. But it may not be very meritorious for a seed to germinate freely, even in all favourable conditions. Thus, dormancy is an adaption that optimizes the distribution of germination over time in a population of seeds (Foyer et al., 2016)..

Seed dormancy or rest is the innate inhibition of germination of a viable seed even placed in most favourable environment for germination. Bewley and Black (1994) have divided seed dormancy into two categories, seed coat based and embryo based. Germination inhibitors occur in both.

Despite the fact that many people study dormancy, there is ambiguity in definition of this phenomenon, perhaps because it is manifest and broken in different ways in different species (Bewley & Black, 1994). Simply, seed dormancy is regarded here as the failure of an intact viable seed to complete germination under favourable conditions. The seeds of some species are prevented from completing germination because the

embryo is constrained by its surrounding structures. This phenomenon is known as coat enhanced dormancy; embryos isolated from these seeds are not dormant. In other species, a second category of dormancy is found in which the embryos themselves are dormant (embryo dormancy).

Before considering some of the cellular and metabolic aspects of dormancy, its breaking, and the resultant completion of germination, it is worthwhile pondering why so little progress has been made toward understanding dormancy. Without this information, there are no "baseline" data with which to compare observations made on dormant seeds that exhibit a block to germination. However, studying germination is also difficult because populations of seed do not complete the process synchronously; release from dormancy can be even more erratic because the threshold stimulus required to promote germination varies widely among individual seeds. Recently, a "biotime" concept has been introduced, which incorporates a mathematical model to characterize and predict seed germination behaviour with respect to dormancy and the factors that influence it (Bardford, 1996).

Germination can be defined as emergence and development from seed embryo of those essential structures which for the kind of seed in question indicate its ability to produce normal plant under favourable conditions.

Seed germination, being crucial for next-generation plant growth, is a prerequisite event for crop yield. Typically, seed germination begins with dry mature seed imbibition and ends with radicle protrusion. This process is not an isolated biological process for the dry seed, but a successive process combining seed development/desiccation and seedling establishment. The most important factor for successful germination is selection of the proper environmental condition to initiate this process. Germination depends on regulation of phytohormones, including gibberellic acid (GA), abscisic acid (ABA), ethylene, and auxin. Among them, ABA and GA are proved to be key regulators, which play antagonistic roles in seed germination. Environmental factors, including light, temperature, and soil water content and nutrient, influence seed germination mainly through regulating the metabolism and signaling pathways of GA and ABA.

2. Molecular mechanisms of seed dormancy

2.1 Internal Factors

2.1.1 Hormonal Mechanism

Various genetic studies using ABA (abscisic acid) and GA (gibberellin) biosynthesis and signalling mutants have shown that these two hormones have important and antagonistic roles in dormancy and germination. The equilibrium between the levels of these two hormones and their signalling pathways are much required in regulating both induction and maintenance of dormancy as well as promotion of germination**.** The main importance of ABA biosynthesis and signalling in dormancy in varied species is detailed in the section about conservation of seed dormancy mechanisms.

A recent finding about ABA is the breakthrough identification of PYR/PYL ABA receptors. 14 members of this protein family in Arabidopsis function redundantly in mediating the ABA response by interacting with PP2C, a negative regulators and antagonizing their action. However whether this PYR/PYL receptors have any direct action on the ABA signalling pathway is not known. The PP2Cs like ABI1 and ABI2 were originally identified as ABA insensitive mutants. Consequently, in the presence of ABA, these PP2Cs remain active and repress downstream ABA-activated protein kinases belonging to the SNF1-related protein kinase subfamily 2 (SnRK2). Three Arabidopsis SnRK2s (SnRK2.2, SnRK2.3 and SnRK2.6) have been shown against the transmission of an ABA signal during seed development and dormancy induction (Figure,.1). The triple mutant of those kinases nearly dislodges ABA and exhibits abnormal seed development, produces ABA-insensitive inexperienced seeds kind of like severe alleles of abi3 and germinates precociously below high wetness conditions. Major targets of those kinases are shown to be a gaggle of bZIP-type transcription factors together with ABI5 and AREB3. Amazingly, mutants of those transcription factors usually don't show robust dormancy phenotypes. This will be partially explained by their redundant operation, however there may additionally be necessary targets that act as regulators of ABA responses throughout dormancy induction.

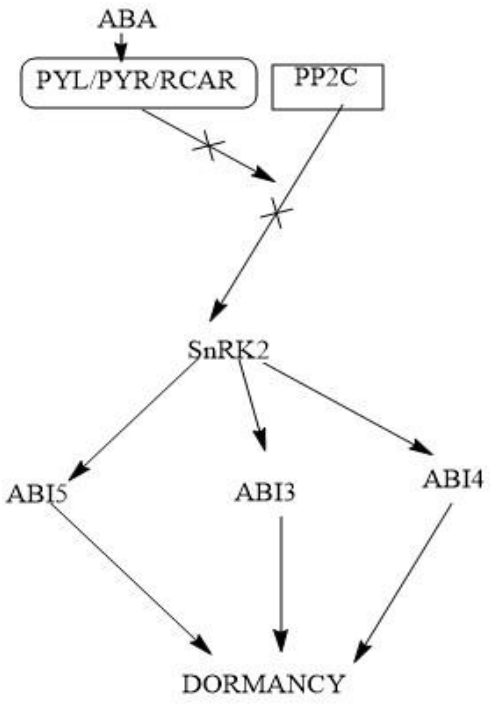

Figure 1: Hormonal control of Dormancy

Antagonistic to ABA action, GA, gas and alternative hormones are shown to push germination. Environmental signals like lightweight and temperature throughout imbibition and germination area unit integrated into GA synthesis and signalling by transcription factors like PHYTOCHROME INTERACTING issue 3-LIKE five (PIL5) and SPATULA (SPT). GAs has been shown to manage reproductive structure cap weakening and rupture in cress, counteracting the action of ABA (Linkies et al., 2009) . Recent reports have incontestable the roles of strigolactones and karrikins (germination-promoting compounds in smoke) in dormancy and germination. Strigolactone signalling is mediate by the F-box supermolecule KARRIKIN INSENSITIVE one (KAI1) that is allelomorphic to a lot of AXILLARY BRANCHES, a pair of (MAX2). The kai1/max2 mutant shows redoubled primary dormancy. It's recently been shown that strigolactones modulate the ABA/GA quantitative relation in secondary dormancy management. These observations reinforce the importance of the coordinated interaction of assorted hormones within the regulation of dormancy and germination. A recent breakthrough proves the effect of jasmonic acid in dormancy. The loss of dormancy caused by maternal herbivory appears to be mediated by jasmonate-dependent changes in the amounts of and/or sensitivity to ABA and GA. When concentrations of JA-Ile in dry seeds are elevated, either as a consequence of parental herbivory or from transgenic overexpression of *AOS* during seed development, dormancy is significantly reduced, and, at least in the case of simulated herbivory, this response is lost in JA signalling mutants. Elevated JA-Ile is associated with elevated gibberellin content and reduced ABA sensitivity in mature seeds (Singh et al., 2017).

2.1.2 Seed dormancy specific genes:

Studies of natural variation have led to the identification of various quantitative trait loci (QTL) controlling seed dormancy (Bentsink et al., 2010). Many of these do not co-locate with reported dormancy regulators and the molecular identification of the first few QTLs indeed revealed novel dormancy genes. The first cloned dormancy genes in Arabidopsis, DELAY OF GERMINATION 1 (DOG1) which encodes a protein of unknown function (Bentsink et al., 2006). The absence of dormancy with non-obvious pleiotropic phenotypes in the *dog1* mutant indicates that it is a key player specific for the induction of seed dormancy. Extensive QTL mapping has also been performed for dormancy/pre-harvest sprouting traits in crop species. Very recently, Seed dormancy 4 (Sdr4) has been identified as one of the main determinants for dormancy in rice. It was noted that Sdr4 is localized in the nucleus and that it affects the expression of several DOG1-LIKE genes. There are Four phosphatases that interact with DOG1 in seeds. Two of them belong to clade A of type 2C protein phosphatases: ABA-HYPERSENSITIVE GERMINATION 1 (AHG1) and AHG3 (Figure: 2). These phosphatases have redundant but essential roles in the release of seed dormancy epistatic to DOG1 (Nww et al., 2017). Yet, its mechanism of action is still not understood properly because Sdr4 encodes a novel protein with unknown function (Kuromori et al., 2010). Characterization of the function of these novel factors and the molecular identification of additional dormancy QTLs will provide us with more clues on the mechanisms that control the induction and maintenance of dormancy (Nelson & Steber, 2017).

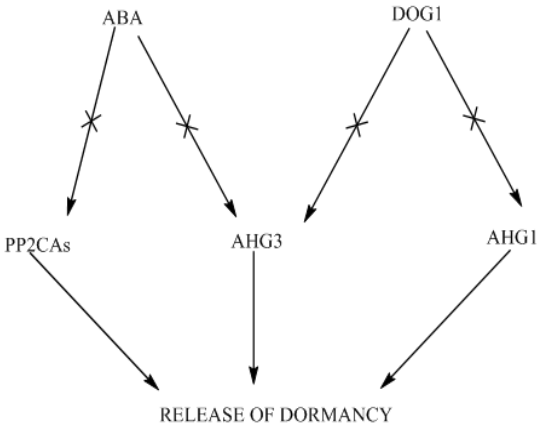

Figure 2: Use of DOG1 gene in Dormancy

Gene approaches by reverse genetics that have become increasingly feasible during the last decade by utilizing large transcriptome and proteome data sets. Recently, two new seed dormancy factors have been identified in Arabidopsis using high-throughput quantitative RT PCR. These are DESPIERTO (DEP), which is a C3HC4 RING finger protein and the HDZip gene ATHB20 (Barrero et al., 2010). A mutation in the DEP gene causes lack of dormancy, whereas the athb20 insertion mutant shows increased dormancy compared with the wild type. Interestingly, both genes modulate ABA sensitivity. It is noteworthy that the dep mutant is completely non-dormant, similar to the dog1 mutant. The biochemical properties of DEP and identification of its downstream targets will be of great interest.

2.1.3 Regulation of Dormancy at Chromatin level:

The organization of chromatin influences gene expression and is therefore important for all developmental processes in the plant, including seed dormancy and bud dormancy (Wolkovich et al., 2012). However, mutations in chromatin factors do not influence all plant processes similarly. The induction of dormancy during seed maturation occurs independent from the simultaneous reduction in nuclear size and compaction of chromatin (Peña-Castro et al., 2011). Genetic and biochemical studies have identified a number of chromatin factors that are required for a proper regulation of seed dormancy and germination. REDUCED DORMANCY 4 (RDO4)/HISTONE

MONOUBIQUITINATION 1 (HUB1) and its homologue HUB2 encode C3HC4 RING finger proteins necessary for histone H2B monoubiquitination. The RDO4/HUB1 gene was originally identified based on its reduced dormancy phenotype (Liu, Koornneef, & Soppe, 2007). The RDO2 gene was found in the same mutagenesis screen for reduced dormancy and encodes transcription elongation factor SII (TFIIS). The HUB and RDO2 proteins are predicted to interact with the RNA polymerase II-associated factor 1 complex (PAF1C) and influence seed dormancy by regulating transcription elongation during seed maturation at a time when transcriptional efficiency is likely to be reduced due to desiccation (Roudier et al., 2011). In accordance, mutants in other components of PAF1C also showed reduced dormancy. Among others, DOG1 and ABA-related genes are differentially regulated in these mutants, which is a potential cause for their reduced dormancy phenotype.

The EARLY FLOWERING IN SHORT DAYS (EFS) gene has been selected as a phase transition regulator during seed germination in a transcriptional network modelling study. EFS codes for a histone H3 methyltransferase involved in histone H3 lysine 4 trimethylation (H3K4me3), which is a transcription activating histone mark. The efs mutant was initially identified by its altered flowering time (Bassel et al., 2011). Interestingly, mutant efs seeds also show a variety of seed phenotypes including precocious germination . Direct targets of EFS associated with dormancy have not been explored yet, but a potential target is FLOWERING LOCUS C (FLC) because its expression was shown to be modulated by EFS in the control of flowering time and it has been implicated to be involved in germination regulation (Chiang, Barua, Kramer, Amasino, & Donohue, 2009). The Arabidopsis protein EARLY BOLTING IN SHORT DAYS (EBS), a plant specific transcriptional regulator, is involved in control of flowering time by repressing the floral integrator FT. The EBS protein binds to the H3K4me3 markand interact with histone deacetylase to modulate gene expression. Transcriptomic analysis in EBS mutant seeds helped to uncover the misregulation for several regulators of seed dormancy including the MADS box gene AGAMOUS-LIKE67 (AGL67). AGL67 interacts genetically with EBS in seed dormancy regulation, indicating that both loci act in the same pathway. Interestingly EBS functions independently of the master regulator gene of dormancy DOG1 and other genes encoding chromatin remodelling factor involved in control of seed dormancy (Narro-Diego, López-González, Jarillo, & Piñeiro, 2017)..

2.2 External Factors:

2.2.1 Environmental Factors affecting seed dormancy:

Seeds act as environmental sensors and adjust their dormancy status as a response to a range of environmental factors (Footitt, Douterelo-Soler, Clay, & Finch-Savage, 2011). Key environmental factors like temperature, nitrate, light, water, oxygen, smoke and allelochemicals influence dormancy levels either during seed development on the mother plant or in the soil seed bank. Thus, a clearly defined dormant state does not exist, and there are only different requirements for germination. Exposure to specific environmental conditions is usually required to bring germination sensitivities back into a range that matches potential environmental exposure (Finch-Savage & Leubner-Metzger, 2006). Thus, drawing a theoretical line, dormancy and germination should be regarded with great care since experimentally derived conclusions might be biased depending on where this artificial line is drawn considering the continuous nature of the transition from dormancy to non-dormancy and germination (Z. Huang, Footitt, Tang, & Finch-Savage, 2017).

Specifically, temperature is a major environmental factor controlling primary dormancy that acts through several identified dormancy regulators controlling ABA and GA contents, as well as DOG1 gene expression (Figure: 3) (Smith & Donoghue, 2008). Kendall et al. (2011) showed that transcription factors of the C-repeat binding factor (CBF) group are necessary for regulation of dormancy caused by low seed-maturation temperatures. CBFs also seem to play a role in the light-mediated induction of bud dormancy. Interestingly, although CBFs are required for dormancy, their transcript abundances are not temperature regulated in seeds. CBF, DOG1 and ABA/GA metabolism have been proposed as central components of a pathway mediating the effect of seed maturation temperature on dormancy (Kendall et al. 2011). In addition, both phytochrome and FLC seem to play important roles in the interaction with seed-maturation temperature. Another gene involved in the low temperature response during seed maturation in wheat is MOTHER OF FT AND TFL1 (MFT). Interestingly, MFT is a candidate for the gene underlying a QTL for pre-harvest sprouting on wheat chromosome 3(Hossain et al., 2011).

Apart from temperature and humidity, allelochemicals represent another environmental factor affecting seed dormancy levels in the soil. Allelopathy is defined as a direct or indirect interaction, whereby allelochemicals released by one organism influence the physiological processes of another neighbouring organism. *Nicotiana attenuata* (wild tobacco) is a post-fire annual plant that germinates from seed banks in response to smoke cues from wildfires. On the other hand, ABA and four terpenes leaching from the litter of the dominant vegetation can induce dormancy of *N. attenuate* seeds (Krock et al. 2002; Preston, Betts & Baldwin 2002; Linkies & Leubner-Metzger 2012).

3. Release of dormancy

Dormancy can either be quickly released in imbibed seeds or relatively slow in dry seeds. The molecular mechanisms controlling dormancy release are less well understood compared to that controlling dormancy induction. The fast release of dormancy requires

imbibition at species specific temperatures and is called stratification. In general, imbibition at low temperatures releases dormancy in seeds of summer annuals, while high temperatures release dormancy in seeds of winter annuals (Probert, 2000). It is largely unclear how stratification drives the release of seed dormancy, and, especially, the temperature sensing mechanism is unknown, but a few genes with role in this process have been identified. The basic helixloop-helix transcription factors SPT and PIL5 have a role in cold stratification (Penfield et al., 2005). SPT is a negative regulator of germination that loses its repressive activity after stratification, whereas PIL5 is not responding to low temperatures, but represses germination in the dark after a cold treatment. Both transcription factors act by inhibiting the GA biosynthesis genes (Penfield, Josse, & Halliday, 2010).

Oxidative processes within the dry seed also influence proteins. Proteomic approaches have been used as a tool to study the dynamics of posttranslational modifications (PTMs) during after-ripening. PTMs have a major role in the regulation of seed development and maturation (Arc et al. 2011). Carbonylation is an irreversible PTM that occurs in response to oxidative stress and that leads to a change in the enzymatic and binding properties of the protein or to its degradation due to a higher sensitivity to proteolytic attack. After-ripening results in an accumulation of reactive oxygen species (ROS), which is associated with the carbonylation of specific proteins in sunflower (Oracz et al. 2007) and in Arabidopsis (Job et al. 2005). It was suggested that the specific carbonylation of seed storage protein helps their mobilization during germination by promoting their proteolytic attack (Job et al. 2005). In mammals, carbonylation is mainly associated with aging and diseases (Stadtman 1992; Agarwal & Sohal 1994), whereas Arabidopsis seeds still germinate and produce healthy plantlets when accumulating carbonylated proteins.

Further support for the important role of ROS in dormancy release comes from wheat, for which it was shown that the antioxidant defence pathway is associated with the maintenance of dormancy. The importance of the ROS-dependent pathway in after-ripening was highlighted by the finding that the signal transduction of hydrogen cyanide (HCN), a compound used to break dormancy artificially, is ROS-dependent and results in an enhanced expression of genes involved in ethylene signalling (Oracz et al., 2007). Moreover, Müller et al. showed that the ROS-producing NADPH oxidase AtrbohB promotes seed after-ripening in Arabidopsis. Interestingly, it has been shown that DELLA repressor proteins, which are negative regulators of GA signalling that are degraded by GA, repress ROS accumulation, leading to an enhanced tolerance to abiotic and biotic stress (Achard et al., 2008).Although this mechanism has not been demonstrated in seeds, it opens the possibility that GA can accelerate after ripening by indirectly increasing ROS. The induction of JA production was dependent on the extent of cold imbibitions and precedes germination. Blocking JA production with acetylsalicylic acid inhibited the cold stimulated germination in a dose dependent manner. There has been exploration of the relationship between JA and ABA in cold regulation of dormancy. An inverse relationship between JA and ABA content in dormant wheat embryos found following stratification. ABA content decreases rapidly in response to stratification (Xu et al., 2016).

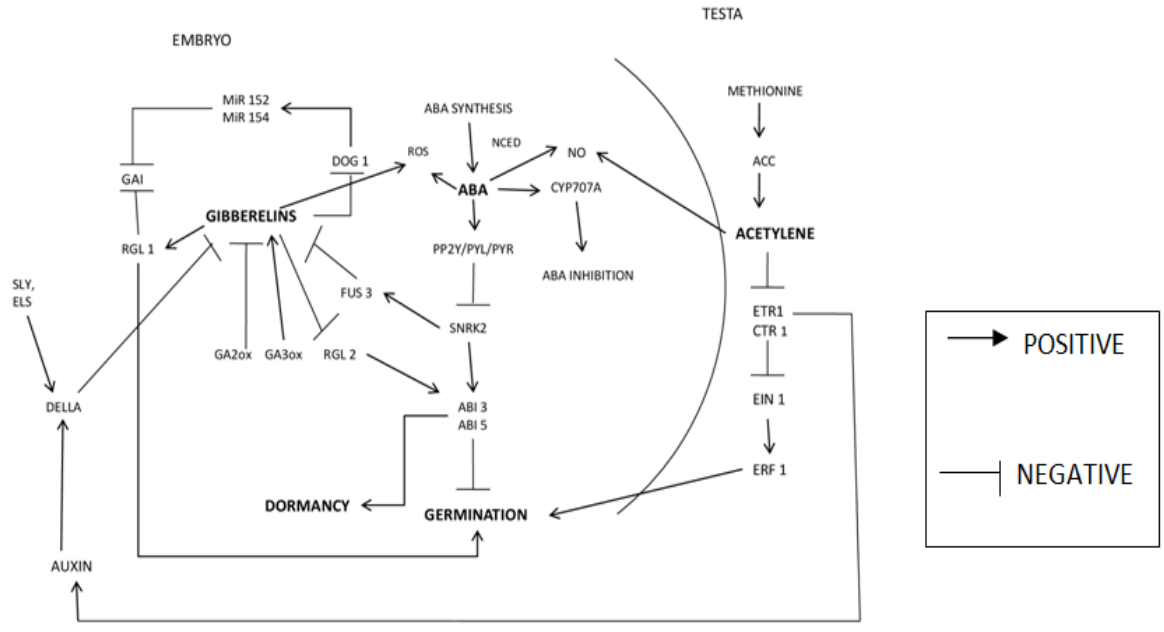

Figure 3: Correlation of Hormones proteins and Genetic factors in Dormancy and Gerrmination

4. Seed germination inhibitors

A large number of substances are capable of inhibiting germination. Compounds which prevent germination without killing the seeds are by far the more valuable in determining the mechanism of dormancy. The simplest type of inhibition is caused by non-toxic chemicals in high concentration. A more complex type of inhibition is that caused by substances which are known to interfere with certain metabolic pathways (Yao et al., 2017). Since germination cannot occur without active metabolism, any substance that would alter normal metabolism, would probably alter the germination pattern of seed. Compounds such as cyanide dinitrophenol, azide, fluoride, hydroxylamine, and others which are respiratory inhibitors, have inhibited germination at concentrations approximating those which inhibit metabolic process (Pošta, Papenfus, Light, Beier, & Van Staden, 2017). Therefore, it seems that inhibition of germination by this class of compounds is a result of their effect on metabolism, but only in the case of cyanide have these chemicals been implicated in natural seed dormancy. Another class of compounds that inhibited germination are auxins. An example of such a case would be the use of low concentrations of 2, 4-dichlorophenoxyacetic acid (2, 4-D) to inhibit germination. On the other hand, growth inhibitors are of general occurrence in dormant seeds, and there is abundant evidence for their involvement in the physiological mechanisms of dormancy (X. Huang, Zhang, Gong, Yang, & Shi, 2017). Evidence for the involvement of growth inhibitors in seed dormancy is the demonstration that they are often present in dormant seeds and that the application of such materials can impose dormancy on seeds in certain cases. Various substances produced by plants prevent the germination of seeds until conditions are favorable for its development. These substances help to insure the survival of different plant species by limiting the density of plant populations and by giving the plants that grow from seeds a better start in life (Nandagopalan, 2017).

4.1 Polyphenolic compounds as seed germination inhibitors

Polyphenolic compounds are an important category of allelochemicals and most of them have inhibitory effects on the seed germination and seedling growth parameters of plants. Low molecular-weight polyphenolic compounds are released by plants and soil microbes, also having major ecological functions. Many polyphenolic compounds containing monomers and polymers are allelopathically important. These have a widespread occurrence and distribution in plants and fruits. Polyphenols are a structural class of mainly natural, but also synthetic or semisynthetic, organic chemicals characterized by the presence of large multiples of phenol structural units (El-Sadek et al., 2017). Aromatic amino acids are the primary components in the synthesis of polyphenols. Polyphenolic compounds are dormancy inducing agents. Numerous benzoic and cinnamic acid derivatives such as high molecular weight tannic acids, protocatechuic, Caffeic and chlorogenic, ferulic, p-coumaric acids have a germination inhibitory activity. Salicylic acid, and in some cases unidentified cinnamic acid derivatives, have strong activity (Mendoza-Sánchez et al., 2016). Most of these inhibitors are washed out or destroyed as the fruit remained on the tree for a prolonged period of time. The major pathway for the formation of these compounds undoubtedly involves phenylalanine via shikimic acid. Other polyphenolic compounds that have shown activity includes (1) Gallic acid (2) Ferulic acid (3) Caffeic acid (4) Vanillic acid (5) Protocatechuic acid (6) Chlorogenic acid (7) p-oxybenzoic acid (8) para coumaric acid (9) Hydroxybenzoic acids (10) Chrysin (11) Luteolin (12) Apigenin (13) Flavonols (14) Galangin (15) Kaempferol (16) Quercetin (17) Flavanones (18) Naringenin (19) Hesperidin (20) Eriodictyol (21) Catechin (22) Epicatechin (23) Epigallocatechin (24) Isoflavones (25) Genistein (26) Daidzein (27) Neobavaisoflavone (Gascó, Cely, Paz-Ferreiro, Plaza, & Méndez, 2016).

4.1.1 Coumarin and coumarin derivatives as seed germination inhibitors

Coumarin and coumarins derivatives are large class of polyphenolic compound widely distributed on the leaf, seed surface, and pollen wall. Coumarin is a strong inhibitor of seed germination. Coumarin is found in several plants, including Tonka beans, lavender, licorice, strawberries, apricots, cherries, cinnamon, and sweet grass (Wu et al., 2016).

Coumarin (2*H*-chromen-2-one) (Figure: 4) the simplest compound of this class, affects root form and function, decreases respiration and photosynthesis, and influences nitrogen uptake and metabolism. Coumarin is a strong inhibitor of seed germination.

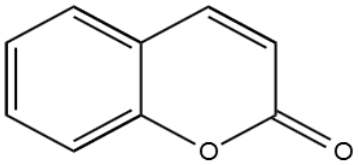

Figure 4: General structure of coumarin

Coumarin is characterized by an aromatic ring and an unsaturated lactone structure. Coumarin reduces water uptake during phase I, but the decrease is recovered during phase II. Coumarin and coumarin derivatives are the seed germination inhibitors, such as 6-Methyl coumarin, 5, 7 dimethoxy coumarin, 7- hydroxyl coumarin, 4- methyl umbelliferone, 4- hydroxy 3-nitro coumarin, Dihydrocoumarin (Chattha, Munawar, Ashraf, Kousar, & Nisa, 2015).

4.1.2 Mechanism of action of coumarin and is derivatives

Water uptake, membrane perturbation, and resumption of respiration may all Water influx into the cells of dry

seeds provokes a transient perturbation to membrane structure. Here, as a consequence of early inhibition of water uptake, coumarin could delay, or even prevent, the recovery of a stable membrane configuration. Interference with membrane functions, and/or delay in taking up an adequate amount of water and inhibition of O2 consumption induced by coumarin during phase I (Chattha et al., 2015; Dastan et al., 2014). Coumarins, being able to perturb the membrane systems that promote the generation of reactive oxygen species (ROS), including superoxide radical anion, hydroxyl radical, and H2O2, during seed germination. During the early stages of germination, seeds are substantially devoid of AsA, APX, and CAT activities, but contain DHAsA and show DHAR activity. Coumarin prevented the activation of the other peroxidase, GPX, well in advance of phase III. Sufficient rehydration in the very early stage of imbibition may prevent or delay the attainment of a stable configuration of membrane systems (Shao, Liu, Zhang, & Zhang, 2016) (Yao et al., 2017). This could lead to a prolonged loss of osmotic ally active substances and substrates, and delay resumption of respiration. This may eventually cause oxidative stress, which explains the enhanced transcription, already occurring during phase II, of genes involved in redox homoeostasis, such as TRX. ETR1 and CTR1 are two types of genes also situated in the testa. During the dormancy stage ETRI and CTR1 genes are also inhibited EIN1 gene and also promoted the auxin transport system (Saleh & Madany, 2015) (Scheel, 2016). As a result DELLA repressor protein and Gibberellin biosynthesis is also inhibited by coumarin and seed dormancy is controlled.

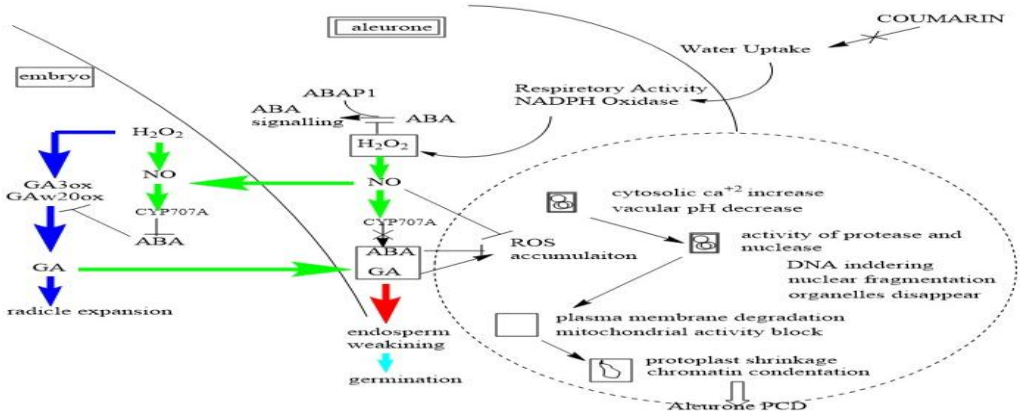

Figure 5: Mechanism of action of Coumarin and its derivatives as seed germination inhibitors

Table 1: Phytochemicals and its mechanism as seed germination inhibitors

Name	Examples	Mechanism of action
Polyphenolic compounds	Ferulic acid, Chlorogenic acid, Ellagic acid (Gawlik-Dziki, Dziki, Świeca, & Nowak, 2017) Caffeic acid (Ho, Kase, Wangensteen, & Barsett, 2017), Gallic acid	Inhibit water uptake system 1,Inhibit electron transport system
Flavonoids	Kaempferol,Quercetin,Isorhamntin, Proanthocyanidin (Mohammed, 2016)	Inhibits water uptake system 3 in seed
Quinazolidine alkaloids	Oflupanine,13- hydroxylupanine(Kouris-Blazos & Belski, 2016)	Inhibition of translation or transcription of seed
Other alkaloids	Emetine, Berberine (Rozmer & Perjési, 2016)	Phenylalanine- tRNA is inhibited in seeds
Glycoside	Rutin (Park, Beaulieu, & Bousquet, 2016)	Inhibition of embryogenesis
Essential oil	Limonene. Camphene, citral, citronelol, α-terpinolene (Grichi, Nasr, & Khouja, 2016) capraldehyde, borneol, 2-hexen-1-ol, α-thujene, β-pinene (Mahajan, Batish, Singh, & Kohli, 2016) ,	Inhibits water uptake system, Inhibition of embryogenesis and inhibition of CYP707A

4.2 Flavonoids as seed germination inhibitor

Flavonoids are secondary metabolites that accumulate in most plant seeds and are involved in physiological functions such as dormancy or viability. Over 6000 different flavonoids have been reported and subdivided into different classes that include flavonols, flavones, nature of the substitutions (hydroxyl, methyl, galloyl, glycosyl) (Marles, Ray, & Gruber, 2003). Flavonoids are found in most seeds and grains. The major types of flavonoids in seeds are flavonols, anthocyanin's, phlobaphenes, isoflavones, and Proanthocyanidin (PAs, also called condensed tannins) (Harborne & Williams, 2000; Holdsworth, Bentsink, & Soppe, 2008).

4.2.1 Mechanism of action of proanthocyanidins as seed germination inhibitor

Proanthocyanidins inhibit seed germination by maintaining a high level of abscisic acid. PAs can cross-link cell wall components (Manz, Müller, Kucera, Volke, & Leubner-Metzger, 2005). GST may participate in the cytoplasmic transport of PAs before they are transported into the vacuole via a tonoplast protein that GST activity has been linked only with transport by MRPs (Dixon, Xie, & Sharma, 2005). Vesicular transport, GST, MATE, and MRP trans-porters and H+-ATPase may all be involved in flavonoid transport and increase testa thickness, which increases physical resistance and suppresses seed germination (Graeber et al., 2010; Marles et al., 2003). C1/Pl1 (R2R3-type MYB pro-teins) and R/B/Lc/Sn-family (bHLH) is also involved in biosynthesis of flavonoid in embryo. Flavonoid also bind to the members of the ATNCED genes family encode cis-epoxy carotenoid dioxygenases enzyme which is the key regulatory step in biosynthesis of ABA (Radchuk et al., 2010). It is also called de novo biogenesis of ABA. ABA concentration is also increased in an embryo. Abscisic acid (ABA) inhibits phase III water uptake (Ali-Rachedi et al., 2004). Then it inhibits CYP707a1 and CYP707a2 genes which are involved in ABA degradation (Linkies & Leubner-Metzger, 2012). Then ABA also stimulates DOG1 (Delay of germination -1) (Weitbrecht, Müller, & Leubner-Metzger, 2011). In the endosperm B-1, 3 Glucanases (glycosyl phosphatidyl inositol a membrane protein) is expressed in the mycopylar endosperm. ABA inhibits the induction of βGlu I in the micropylar endosperm just before its ruptures ((Bentsink, Jowett, Hanhart, & Koornneef, 2006). ABA also inhibits endosperm rupture. As a result the radicle protrusion is also blocked by the help of inhibiting AB15 gene (Wojtyla et al., 2006).

4.3 Alkaloids as seed germination inhibitor

Quinolizidine alkaloids are seed germination inhibitor synthesized in the chloroplast. These alkaloids are consist mainly oflupanine and 13- hydroxylupanine.

In the developing seedling, the 13hydroxylupanine is esterified to 13-tigloyloxylupanine through the action of tigloyl-CoA: 13-hy- droxylupanine 0-tigloyltransferase. The binding of amino- acyl-tRNA to ribosomes and polypeptide synthesis is interfered. Quinolizidine alkaloids are interfered with these processes thus the binding of phenylalanine- tRNA is inhibited and polyphenylalanine synthesis with the tRNA molecule is also interfered. Interactions with RNA and DNA have been reported from other alkaloids, such as emetine (Gilead and Becker 1971) and Berberine (Krey and Hahn 1969). The inhibition of seed germination by lupin alkaloids reflects an inhibition of translation or transcription.

4.4 Essential oil as seed germination inhibitor

Esssential oil like limonene, camphene, citral, pinene have shown promises to be good seed germination inhibitor. Mutation that affects ABA biosynthesis or seed coat structure in arabidopsis , tomato were able to rescue seed germination defect of GA biosynthesis mutants suggesting GA has important effects in seed germination. GA overcomes the inhibitory effect of the seed coat and ABA related dormancy (Zapata et al., 2016). In situ hybridization showed presence of AtKO1, AtGA3ox1, AtGA3ox2 mRNAs in the cortex and endodermis of embryo of germinating Arabidopsis seed indicating synthesis of bioactive GAs from ent- kaurene in these cells. Cortical cells in the embryo axis begin to expand before radical protrusion (Li et al., 2016). Therefore, the site of bioactive GA synthesis seems to occur in rapidly expanding cells, which are likely to be GA responding cells. Although AtGA3ox1, AtGA3ox2 were expressed in same cellular locations in the germinating embryo, only AtGA3ox1 expression was under feedback control by GA response pathway. It was hypothesized that AtGA3ox1 may be required for embryo to produce the higher level of bioactive GA needed to ensure efficient germination. Another surprising finding reported by Yamaguchi et al (2001) is that the location of AtKO1, AtGA3ox1 and AtGA3ox2 expression appeared to be different from that of the early GA biosynthetic gene AtCPS Promoter Glucoronidase (GUS) gene fusion in transgenic Arabidopsis (Yamaguchi, 2008), GUS activity was detected in the shoot apex and provascular in both cotyledons and embryo axes, whereas AtKO1, AtGA3ox1 and AtGA3ox2 were expressed in the cortex and endodermis in embryo axes. Therefore, there is a physical separation steps in the GA biosynthetic pathway in germinating Arabidopsis embryo, implying that the synthesis of active Gas in the germinating embryo requires intercellular transport (if only short range) of a pathway intermediate (CDP or ent-kaurene). Because earlier biochemical studies provided evidence that CPS and KS may form complex in catalyzing the two cyclization reactions, it was suggested that ent kaurene probably is the transported compound. Future analysis of AtKS mRNA localization in germinating seed will be crucial to determine the nature of transported intermediated.

5. Conclusion

Hence from aforementioned text evidences of internal and external factor affecting dormancy can be found. Also it can be seen that specific phytochemical compounds broadly under categories Polyphenolic compounds which inhibit water uptake system, Flavonoid, alkaloids inhibiting translation and transcription in seed, glycosides, essential oils effects very widely on inhibiting germination. On inhibition of germination using these phytochemical products we can assume that cell cycle is arrested in seeds preventing it from germinate. So if these phytochemicals can be specifically identified and works the same way in human preventing cell cycle then it will serve as important breakthrough in the field of medical science as natural anti proliferative agents. Another aspect of these seed germination inhibitors are that seeds survive in adverse conditions, seeds used in research such as gene pool, seed can be stored till next season and can be transported without losing its viability. Some seed kept in cold condition to get better price for it when there is off season which germinates itself later on suitable condition, is also important aspect of seed dormancy aided by germination inhibitors.

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Conflict of interest

None declared

6. References

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