



# **Molecular Regulation of the Transition from Vegetative Growth to Meiosis in Plants and Model Organisms**

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## **Authors' contributions**

*This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.*

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## **ABSTRACT**

This review examines the molecular mechanisms regulating the transition from vegetative growth to meiosis across plants and other eukaryotic models. It highlights key genetic pathways controlling floral meristem identity, ovule development, and meiotic entry, emphasizing conserved genes and regulatory networks in species like Arabidopsis, rice, yeast, and mice. The roles of hormonal signals, environmental cues, and nutrient sensing in meiosis initiation are discussed, along with mechanisms governing chromosome pairing, recombination, and segregation. Understanding these conserved processes offers insights into reproductive development and provides avenues for crop improvement and fertility management.

**Keywords:** Chromosomes; molecular processes; meiotic regulation; vegetative development.

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## 1. INTRODUCTION

The transition from vegetative to reproductive development is critical for ensuring the species' ability to reproduce and sustain itself. This process, known as flowering, is tightly controlled by a complex interaction of genetic programming and environmental inputs. In many plant species, including the well-studied model organism *Arabidopsis thaliana* and staple crops such as rice, wheat, and barley, the transition to the reproductive phase is managed by integrating stimuli like as light, temperature, and plant hormones (Cheng et al., 2014). The activation of genes involved in defining floral meristem identity, which initiates flowering and gives rise to reproductive organs, is an important step in this transformation (Dreni et al., 2007). These same signals also prompt meiosis, a unique cellular division that reduces the chromosome number and promotes genetic variability in gametes (Kleckner, 1996).

Plants, like other eukaryotes, go through a highly coordinated and complex meiotic process that includes prophase I, metaphase I, anaphase I, and telophase I, followed by a secondary meiotic division (Terasawa et al., 1995). During these stages, homologous chromosomes couple, recombine, and segregate, ending in the formation of haploid gametes. Model systems such as *Arabidopsis*, mice, *Drosophila melanogaster*, *Caenorhabditis elegans*, and *Saccharomyces cerevisiae* have identified a wide range of essential genes that govern meiotic events such as chromosomal alignment, recombination, and division—examples include MSH4 in yeast, Rec8 in mice, and Dmc1 in *Arabidopsis*. Crops such as rice, barley, and wheat also contain unique meiotic genes that are essential for reproductive efficiency (Muralla et al., 2011).

Unravelling the genetic frameworks that control flowering and meiosis is not only important for understanding plant biology, but it also has substantial agronomic implications. By modifying these pathways, we can improve crop output, resistance, and adaptability (Zickler & Kleckner, 1999). This review discusses the molecular pathways that govern the vegetative-to-reproductive transition and meiotic control in plants and other model organisms. It focuses on the conserved genes required for each meiotic phase, stressing their significance in evolutionary continuity and reproductive optimization in species such as *Arabidopsis*, rice, wheat, yeast, and mice.

## 2. GENETIC KEYS THAT DRIVE THE TRANSITION FROM VEGETATIVE GROWTH TO THE FLOWERING PHASE

Flowering plants go through a series of developmental steps as they move from vegetative to reproductive growth. Okada & Shimura, (1994) identify five major steps: establishment of the inflorescence meristem, specification of the floral meristem, determination of floral organ number and placement, identification of organ kinds, and final development of floral organs. Genetic study in *Arabidopsis* mutants has revealed the presence of numerous regulatory genes involved in these stages. Ovule formation is an important element of the reproductive process, with distinct physical distinctions between species. *Arabidopsis* (a dicot) and rice (a monocot) produce anatropous, unitegmic ovules, whereas maize, wheat, barley, and tomato produce bitegmic ovules (Drews & Yadegari, 2004; Wang & Ren 2008; Shi & Yang 2011). The placenta produces ovule primordia, and their development is affected by hormone interactions, particularly auxin and cytokinin, as well as transcription factors such as PIN1, ANT, and the CUC gene family (Balasubramanian & Schneitz, 2000; Elliott et al., 1996; Ceccato et al., 2013). *INO*, *ATS*, and *WUSCHEL* govern the asymmetric development of the outer and inner integuments (Baker et al., 1997; Balasubramanian & Schneitz, 2002; Gross-Hardt et al., 2002). In cereals such as rice, wheat, and barley, orthologs such as *OsMADS13*, *OsINO*, and *OsWOX9 B* play conserved roles that are frequently influenced by auxin gradients. These regulatory components work together to guide precise ovule patterning and megagametophyte growth in both monocot and dicot plants.

## 3. MEIOSIS

In higher plants, meiotic processes are similar to those found in other eukaryotes, with conserved mechanisms for homologous pairing and recombination. However, the molecular signals that begin the shift from the diploid sporophyte to the haploid gametophyte phase are still poorly understood. This generational shift usually happens in the late stages of cell differentiation, but it may also be intentionally induced in undifferentiated tissues, emphasizing the stark distinction between sporophyte and gametophyte development.

Meiosis, a specialized division crucial for all sexually reproducing eukaryotes, consists of a

single DNA replication event followed by two consecutive nuclear divisions. Meiosis I separates homologous chromosomes, whereas meiosis II divides sister chromatids in a manner comparable to mitosis (Gerton & Hawley 2005). The proper production of gametes is dependent on precise regulation during prophase I, which includes homolog recognition, pairing, recombination, and ultimately segregation.

#### 4. ENTRY INTO MEIOSIS I FROM MITOTIC CELL DIVISION IN ANGIOSPERMS

In flowering plants, meiosis begins in ovules and anthers with the transition of subepidermal cells into archesporial cells, which grow directly into megaspore mother cells (MMCs) without going through mitosis (Maheshwari, 1950; Reiser & Fischer, 1993). Normally, a single MMC is present per ovule, although species such as *Paeonia calijolica* can develop 30-40 MMCs (Walters, 1962). Casuarinaceae, Amentiferae, Ranales, and several basic dicots all contain multiple MMCs (Eames, 1961; Maheshwari, 1950).

In Arabidopsis, for sporocyte identity to be established, interactions between the tapetum and meiocytes are essential. Male sterility results from mutations lacking *EMS1/EXS1* or *TPD1*, which overproduce sporocytes and fail to generate tapetal cells (Canales *et al.*, 2002; Zhao *et al.*, 2002). Genes like *AMS*, *MS1*, and *AtMYB103* are activated by the receptor kinase *EMS1/EXS* and are necessary for the differentiation of microspores and tapetums (Yang *et al.*, 2003; Wilson *et al.*, 2001; Sorensen *et al.*, 2003; Higginson *et al.*, 2003). *MSP1* builds the anther wall and limits sporocyte development in rice. Excess sporocytes and deformed anthers are produced by mutants that lack this function (Nonomura *et al.*, 2003). One hypodermal cell in maize serves as the MMC in pseudocrassinucellate ovules, becoming more deeply embedded as the ovule grows (Randolph, 1936; Cooper, 1937).

#### 5. NUTRITIONAL CUES AND REGULATORY PATHWAYS FOR MEIOSIS INITIATION IN YEAST AND OTHER MODEL ORGANISMS

The start of meiosis in *Saccharomyces cerevisiae* is directly related to the availability of nutrients. Carbon and nitrogen deprivation decrease the activity of important metabolic

regulators such as Target of Rapamycin Complex I (TORC1) and protein kinase A (PKA). This activates the transcription factor IME1, which in turn triggers the induction of more than 300 genes required for meiosis (Weidberg *et al.*, 2016; Chu *et al.*, 1998; Primig *et al.*, 2000). By phosphorylating and targeting Sic1, a cyclin-dependent kinase inhibitor, for degradation, another kinase, IME2, promotes entry into meiosis (Dirick *et al.*, 1998; Benjamin *et al.*, 2003). Meiosis is also disrupted by disruptions in tRNA genes like *SUP3*, which affect DNA replication and spore formation by causing incorrect translation termination (Liebman *et al.*, 1976; Rothstein *et al.*, 1977). According to Dirick *et al.*, (1998), Stuart & Wittenberg (1998), and Smith *et al.* (2001), B-type cyclins CLB5 and CLB6 are necessary for premeiotic DNA replication and may also control recombination and the creation of synaptonemal complexes.

Meiosis in *Schizosaccharomyces pombe* is regulated via a unique mechanism. In budding yeast, the transcription factor Ste11 performs a similar role to IME1 (Yamamoto, 1996; Honigberg & Purnapatre, 2003). *Pat1*, a kinase that maintains *Mei2* phosphorylated throughout mitosis, ordinarily represses the RNA-binding protein *Mei2*, which mediates entry into meiosis. *Mei2* can go to the nucleus and start meiosis when *Pat1* is deactivated due to hunger (Yamamoto, 1996; Marston & Amon, 2004). Phosphorylation-based control governs *Mei2*'s interactions with *Mip1p* (Yamashita *et al.*, 1998; Sato *et al.*, 2001; Shinozaki-Yabana *et al.*, 2000; Shimada *et al.*, 2003). Despite continuing mitotic cycles, mutations in *Mei1*, *Mei2*, or *Mei3* stop meiosis at the mononucleate stage (Egel, 1973), while *Mei4* mutants do not advance following DNA replication (Bresch *et al.*, 1968; Egel, 1973; Egel & Egel-Mitani, 1974).

Repetitive routes involving *gld-1* and *gld-2*, which can independently induce meiosis, regulate meiotic entry in *Caenorhabditis* worms (Kadyk & Kimble, 1998). Likewise, in *Drosophila*, meiotic development in both sexes depends on the Cdc25 homolog Twine. Due to reduced meiotic division, sterility resulted from mutations that disrupt twine, such as *mat(2)synHB5* (Courtot *et al.*, 1992; White Cooper *et al.*, 1993). According to Zhang *et al.* (2025), MTR4, a critical cofactor of the nuclear RNA exosome, is essential for sperm production as well as embryonic development. Male infertility results from targeted ablation of *Mtr4* in germ cells, mainly because animals exhibit a marked impairment in the onset of meiosis.

## 6. Sexual Dimorphism in Meiosis Initiation in Mammals: A Complex, Sex-Specific Regulation

Males undergo a cyclical pattern of meiosis after birth, while females undergo it throughout embryogenesis (Juliano & Wessel, 2010; Lehmann, 2012). Gametes are produced by primordial germ cells (PGCs); females generate oocytes before birth, while males produce sperm after puberty. Both sexes undergo meiosis when exposed to retinoic acid (RA) from the mesonephros (Bowles *et al.*, 2006; Koubova *et al.*, 2006). However, Cyp26b1 degrades RA in the embryonic testes, preventing meiosis, whereas in the ovaries, its absence permits meiosis to proceed (Bowles *et al.*, 2010). Meiotic initiation requires the transcription factor Stra8, which is activated by RA. To guarantee exact timing, Cyp26b1 activity regulates Stra8 expression (Koubova *et al.*, 2006). Signalling molecules such as FGF9 and Cyp26b1 inhibit meiosis in the testes to preserve germ cell pluripotency, while RA activates Stra8 in the ovaries and postnatal testes, starting meiotic entry and premeiotic DNA synthesis. For both sexes, MEIOSIN, a partner of Stra8, further guarantees proper meiotic development (Anderson *et al.*, 2008; Ishiguro *et al.*, 2020).

## 7. KEY PLAYERS AND MECHANISMS IN PROPHASE AND ITS SUBPHASES IN MEIOSIS

The extended prophase I stage of meiosis includes leptotene, zygotene, pachytene, and diplotene subphases, and involves numerous gene-mediated steps for chromosomal pairing and synapsis. In maize, the *ameiotic1* (*am1*) gene is indispensable for meiotic initiation; its mutants halt at interphase, similar to defects seen in *Stra8*-mutant mice (Pawlowski *et al.*, 2009). The rice homolog *OsAM1* facilitates the leptotene-to-zygotene transition, and mutants lacking *OsAM1* arrest at leptotene, displaying disrupted recruitment of proteins like *PAIR2*, *ZEP1*, and *OsMER3* (Che *et al.*, 2011).

One important occurrence in early meiosis is telomere migration. Telomere attachment to the nuclear envelope in maize is made possible by proteins such as Ku and Nup145 (Strambio-de-Castillia *et al.*, 1999). Areas of the envelope where the synaptonemal complex anchors are indicated by Lamin C2 (Alsheimer *et al.*, 1999). *Ndj1p* and *Taz1p* are essential for bouquet formation and effective chromosomal pairing in

budding and fission yeasts, and their mutations cause meiosis to be delayed (Conrad *et al.*, 1997; Trelles-Sticken *et al.*, 2000). Through the recruitment of SETDB1 to sex chromosomes and autosomal regions, the germline-specific protein ATF7IP2 (MCAF2) controls heterochromatin organization during male meiosis. Meiotic development is disrupted when it is absent (Alavattam *et al.*, 2024).

## 8. MEIOTIC CHROMOSOMAL PAIRING AND SYNAPSIS: KEY GENES AND THEIR ROLES ACROSS SPECIES

A key component of chromatid cohesion is the cohesin complex. Yeast's *Rec8p* and other meiosis-specific components provide appropriate cohesion (Molnar *et al.*, 1995). When *Smc1 $\beta$*  is mutated in mice, the synaptonemal complex structure is impaired, resulting in meiotic arrest and sterility (Revenkova *et al.*, 2004). Like those without *zip1*, yeast *msh4* mutants show fewer crossovers (Novak *et al.*, 2001).

Multiple conserved genes work together to form the synaptonemal complex (SC), which is necessary for homologous chromosome synapsis and crossover during meiosis. According to Siddiqi *et al.* (2000), mutations in the gene *DYAD* cause univalent formation and interrupted progression, as it is essential for female meiotic synapsis in *Arabidopsis thaliana*. For sister chromatid cohesion and bivalent formation, the yeast *Rec8* homolog *SYN1/DIF1* gene is essential (Bai *et al.*, 1999; Bhatt *et al.*, 1999). Crossover formation is supported during meiosis by RCK, the plant homolog of yeast *MER3* (Chen *et al.*, 2005). The heterodimer of the genes *AtSPO11-1* and *AtSPO11-2* is necessary for recombination and the creation of double-strand breaks (DSBs); as their mutants are unable to establish bivalent bonds or synapses (Grelon *et al.*, 2001; Stacey *et al.*, 2006). Chromosome fragmentation is a symptom of loss-of-function mutants of *MRE11*, *RAD50*, and *COM1*, proteins involved in DSB processing and repair (Puizina *et al.*, 2004; Uanschou *et al.*, 2007).

The HORMA-domain protein *PAIR2* plays a crucial role in the establishment of SC and chromosomal architecture in rice, as evidenced by its association with chromosome axes during early prophase I and persistence at centromeres until diakinesis (Nonomura *et al.*, 2006). *PAIR3* is also essential for homolog synapses, and when it is disrupted, bivalent formation fails, leading to

sterility (Yuan *et al.*, 2009). The deletion of *ZEP1*, which forms the transverse filament of the SC and is comparable to *ZYP1* in Arabidopsis, causes chromosomes to align but not synapses (Wang *et al.*, 2010). Recombination and SC integrity depend on *OsRAD51C*, a homolog of human *RAD51C*; mutations show chromosomal breakage and sterility (Tang *et al.*, 2014). *ZEP1* collaborates with the plant-specific protein *CRC1*, which is similar to *TRIP13* in mice and *Pch2* in yeast, to enhance meiotic growth and construct the SC core (Miao *et al.*, 2013). Homologous pairing and bivalent formation depend on *OsDMC1*, and meiotic abnormalities result from its downregulation (Deng & Wang, 2007). The rice ortholog of *SPO11*, *OsSPO11-1*, controls the development of DSBs and crossovers; its mutants create telomere bouquets but are unable to construct SC and crossover (Yu *et al.*, 2010; Wu *et al.*, 2015). *OsSDS*, *PRD1*, *PRD2*, *AtPRD3/OsPAIR1*, and *DFO* are other DSB-associated genes in rice that show functional conservation with animal meiosis and yeast (Nonomura *et al.*, 2004; De Muyt *et al.*, 2007, 2009; Zhang *et al.*, 2012).

According to Pawlowski *et al.* (2004), *phs1* is essential for homolog detection and recombination in maize. Mutants that lack *RAD51* foci and exhibit nonhomologous pairing demonstrate a breakdown in recombination initiation. *DMC1*'s conserved function in meiotic processes is further supported by the fact that it is essential for appropriate DSB repair and chromosomal segregation in barley (Szurman-Zubrzycka *et al.*, 2019).

In mammals, *SYCP3* is a structural element of the SC that is necessary for cohesion and synapsis; females show decreased fertility and aneuploidy, whereas males that have been knocked out are sterile because of meiotic arrest (Yuan *et al.*, 2000; Kouznetsova *et al.*, 2005). Synapsis and spermatogenesis are disrupted by the *mei1* mutant; male fertility can be partially restored by cisplatin treatment (Libby *et al.*, 2002, 2003). Male infertility results from meiotic disruption caused by loss-of-function in genes such as *Dmc1*, *Msh4/5*, and *Rec8* (Pittman *et al.*, 1998; Yoshida *et al.*, 1998; Edelmann *et al.*, 1999). DSB repair during meiosis is regulated by Cyclin A1, CDK2, and Ku70 (Muller-Tidow *et al.*, 2004; Fuchimoto *et al.*, 2001). Male mice lacking *Miwi* are infertile, whereas female mice are still fertile, and male mice lacking *Mili* are sterile compared to female mice that are fertile (Kuramochi-Miyagawa *et al.*, 2004; Deng & Lin,

2002). DSB induction requires *SPO11*, which is preserved. Males with prophase arrest are infertile, although cisplatin can partially rescue them (Romanienko & Camerini-Otero, 2000). Both Romanienko and Camerini-Otero (2000) and Baudat *et al.* (2000) have reported that female *Spo11*<sup>-/-</sup> mice lose their oocytes after birth.

## 9. HOMOLOGOUS RECOMBINATION: KEY MECHANISMS AND INSIGHTS

The precise segregation of chromosomes and genetic diversity is guaranteed by homologous recombination. In plants such as *Lilium longiflorum*, where *Rad51* and *LIM15* (*DMC1*) localize to recombination sites in early prophase, *Rad51* and *DMC1* play a crucial role in recombination (Roeder, 1995). *LIM15* expression is limited to early meiosis, in contrast to other *LIM* genes with pre-meiotic expression. The existence of similar proteins in yeast (*ISC2/Isc10*) and *Antirrhinum majus* (*fil1*) supports evolutionary conservation (Kobayashi *et al.*, 1994).

According to Meuwissen *et al.* (1992), *SCP1* is necessary for SC formation and pairing in mice. Female oocytes halt postnatally when *Cdk2* is deleted; male meiosis is unaffected (Ortega *et al.*, 2003). *Mei-2* and *asc*(DL243) mutations in *Neurospora* damage pairing, decrease recombination, and result in chromosome missegregation (Smith, 1975; DeLange & Griffiths, 1980).

Recombination and sister chromatid cohesion in Arabidopsis depend on *SWI1* (Mercier *et al.*, 2001, 2003). *OsSUN1* and *OsSUN2* in rice encourage homologous pairing and telomere clustering; double mutants show impaired meiotic chromosomal organization (Zhang *et al.*, 2020). The coordination of recombination and DNA repair is highlighted by mutants such as *Osatm* and *Osdmc1*, where *OsATM* functions downstream of *OsSPO11-1* and interacts with *OsDMC1* to preserve chromosomal integrity (Zhang *et al.*, 2020).

The pachytene-to-diplotene transition in mice requires Cyclin A1, and mutants of *Mlh1* and *Mlh3* halt during meiosis, resulting in delayed meiosis in females and sterility in males because of more stringent checkpoints (Liu *et al.*, 1998; Lipkin *et al.*, 2002; Eaker *et al.*, 2002; Edelmann *et al.*, 1996). While females are unharmed, men with *Fkbp6* deficiency are sterile because of early

prophase I failure (Crackower *et al.*, 2003). Through the activation of mid-meiotic genes, *Ndt80* guides the advancement of *S. cerevisiae* beyond early meiosis; its activation is checkpoint-dependent to guarantee recombination completion (Xu *et al.*, 1995). Meiotic and sporulation abnormalities are revealed at different stages by different *spo* mutants (Esposito and al., 1970; Moens *et al.*, 1974).

## 10. MEIOTIC METAPHASE AND THE ROLE OF KEY GENES IN CHROMOSOME DYNAMICS

Chromosome alignment and segregation preparation occur during the critical meiotic phase known as metaphase I. By facilitating the passage from prophase I to metaphase I, the protein SKP1 is essential to male meiosis. It stops chromosomal pairing structures from disassembling too soon and localizes to the synaptonemal complex (Guan *et al.*, 2020).

Organisms like *Caenorhabditis elegans* and *Arabidopsis* contain several Skp1-related genes, but species like yeast, mice, and humans only have one *Skp1* gene (Nayak *et al.*, 2002; Zhao *et al.*, 2003). By controlling proteins that uphold homologous connections, *ASK1* helps *Arabidopsis* separate homologs before anaphase I (Yang *et al.*, 1999). In *Arabidopsis*, appropriate spindle assembly is controlled by the *ATK1* gene. Spindle structure is disturbed in *atk1-1* mutants, resulting in aberrant multi-axial arrays that cause improper chromosomal segregation during metaphase I (Chen *et al.*, 2002).

In maize, the *afd1* gene interacts genetically with *dv1*, *dys1*, and *as1*, which are likewise important for chromosomal mobility and synapsis, and is necessary for centromere cohesion and spindle orientation (Golubovskaya *et al.*, 1993).

During metaphase I, *OsMTOPIV* in rice transforms multipolar spindles into bipolar ones; if this function is lost, spindle development is flawed (Xue *et al.*, 2019). It is hypothesized that *PRD1* influences sister kinetochores' alignment to promote the development of a bipolar spindle during rice meiosis (Shi *et al.*, 2021). During meiosis I, proteasomal activity is essential in rat oocytes. Protease inhibition slows MPF (maturation-promoting factor) deactivation and prevents polar body extrusion, indicating that the proteasome aids in exiting metaphase I

(Josefsberg *et al.*, 2000). Additionally, rice *OsMRE11* contributes to chromosome integrity; mutants show chromosome breakage and entanglements during metaphase and anaphase I, indicating its significance in structural maintenance and homologous recombination (Ji *et al.*, 2013).

## 11. KEY PLAYERS IN THE TRANSITION FROM METAPHASE I TO ANAPHASE I

In meiosis, precisely regulated regulatory proteins and kinases are involved in the transition from metaphase I to anaphase I. For this transition, the CDC28 kinase's regulatory component CKS2 is necessary. Male mice deficient in CKS2 have anaphase I arrest, which results in sterility (Spruck *et al.*, 2003). Spindle stability and oocyte maturation in mice during this phase are guaranteed by ERK3, another crucial regulator (Li *et al.*, 2010). The anaphase-promoting complex/cyclosome (APC/C) in *C. elegans* is home to the gene EMB-30, which is similar to APC4/Lid1 and regulates the onset of anaphase by ubiquitin-mediated degradation (Furuta *et al.*, 2000).

According to Choi *et al.* (2019), Spindlin1 controls the expression of the spindle checkpoint protein *BUB3*, which is necessary for precise metaphase-anaphase progression in swine during meiosis I. Furthermore, through its interactions with APC/C and increased phosphorylation of APC3, Cyclin B3 (*CycB3*) facilitates the start of anaphase and increases its affiliation with coactivators such as Cdc20 during meiosis and mitosis (Garrido *et al.*, 2020). The expression of *AMA1*, a member of the Cdc20 family, is dependent on the splicing factor MER1 and specifically regulates APC/C activity during meiosis in yeast (Cooper *et al.*, 2000).

## 12. TRANSITION FROM MEIOSIS I TO MEIOSIS II: KEY REGULATORS AND MECHANISMS

Meiosis I to II progression is strictly controlled and varies from organism to organism. The transcription factor SAP is essential for female meiosis in *Arabidopsis*. *Sap* mutants exhibit severe reproductive abnormalities and are unable to initiate meiosis II (Byzova *et al.*, 1999). APC/C targets securin for degradation, which is necessary for this transition, and so activates separase in mouse oocytes. Both *S. cerevisiae* and *C. elegans* share this mechanism (Terret *et*

*al.*, 2003). According to Grandin & Reed (1993), B-type cyclins CLB1 and CLB4 are essential for meiosis II in yeast but not for meiosis I.

In vertebrates like starfish, the proto-oncogene *Mos* controls the progression to meiosis II, preventing oocytes from prematurely reentering the mitotic cycle (Tachibana *et al.*, 2000). To fine-tune APC/C activity and enable oocytes to escape meiosis I and avoid S phase before entering meiosis II, *Emi2* proteins in *Xenopus* induce partial degradation of cyclin B (Tang *et al.*, 2008). *Mes1* controls the interphase between meiotic divisions in fission yeast by modifying APC/C coactivators such as *Fzr1/Mfr1* and *Slp1* (Kimata *et al.*, 2011).

In *Drosophila*, cyclin A levels during the G2 phase are controlled by roughex (*rux*), which controls entry into meiosis II during spermatogenesis. Mutations in *rux* throw off this timing and stop progression (Gonczy *et al.*, 1994). According to Bulankova *et al.* (2010), CDKA;1 activity in plants peaks during metaphase I and II, propelling meiotic progression. According to Marston & Amon (2005), precise exit from meiosis I and entry into meiosis II depend on the proper regulation of cyclin-CDK complexes and APC/C activity during interkinesis.

Although the meiosis regulatory phase is supported by the cyclin-CDK-APC/C network in all species, its molecular actors differ. *Mes1* controls the transition in *S. pombe*, while *OSD1* operates in plants, and *Emi2* does the same in vertebrates (Izawa *et al.*, 2005; Kimata *et al.*, 2008; Madgwick *et al.*, 2006). To guarantee meiotic exit in *Arabidopsis*, genes like *TAM* (a cyclin A), *OSD1* (an APC/C inhibitor), *SMG7* (associated with RNA degradation), and *TDM* work together. *TDM* mutants go through a third aberrant division, whereas *TAM* or *OSD1* mutants stop after meiosis I. Anaphase II advancement depends on *SMG7*, which also shows a link between meiotic regulation and RNA metabolism (Bulankova *et al.*, 2010; Cromer *et al.*, 2012). The RNA-processing domain found in *AtPS1* facilitates this regulatory network as well (d'Erfurth *et al.*, 2008). Lastly, the *STUD* gene is required for *Arabidopsis* cytokinesis during telophase II to promote the generation of viable male gametes (Hülkamp *et al.*, 1997). Spindle reassembly was hampered and abnormal post-meiotic divisions were curbed in *smg7-6* plants due to a CENH3 mutation that

increased meiotic exit by lowering CENH3 levels (Capitao *et al.*, 2021).

### 13. CONCLUSION

Meiosis is controlled by a mix of species-specific regulatory networks and conserved mechanisms that work together to guarantee faithful chromosomal segregation and meiotic cycle completion. The orderly transition from metaphase to anaphase is maintained by essential elements such as *SKP1*, spindle assembly regulators, and the APC/C complex. Tightly regulated cyclin-CDK and APC/C activity support the transition from meiosis I to II, and various species use distinct regulatory proteins such as *Mos*, *TAM*, *OSD1*, and *SMG7* to ensure meiosis integrity.

A delicate balance between shared genetic modules and organism-specific adaptations is highlighted by the evolutionarily conserved core pathways that govern meiotic progression, although regulatory techniques vary among animals. A better comprehension of these mechanisms contributes to our understanding of genetic integrity and reproductive development and offers prospective paths toward increasing fertility and refining crop breeding techniques.

### DISCLAIMER (ARTIFICIAL INTELLIGENCE)

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### COMPETING INTERESTS

Authors have declared that no competing interests exist.

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