A Molecular Portrait of Arabidopsis Meiosis

Hong Ma

Department of Biology, the Huck Institutes of the Life Sciences, and the Institute of Molecular Evolutionary Genetics, The Pennsylvania State University, University Park, PA 16802; e-mail: hxm16@psu.edu

Key words: pairing, recombination, synopsis, crossover formation, interference, spindle assembly

Abbreviations: DAPI, 4',6-diamidino-2-phenylindole; DSB, double strand break; DSBR, double strand break repair; SC, synaptonemal complex; TEM, transmission electron microscopy

Abstract

Meiosis is essential for eukaryotic sexual reproduction and important for genetic diversity among individuals. Efforts during the last decade in Arabidopsis have greatly expanded our understanding of the molecular basis of plant meiosis, which has traditionally provided much information about the cytological description of meiosis. Through both forward genetic analysis of mutants with reduced fertility and reverse genetic studies of homologs of known meiotic genes, we now have a basic knowledge about genes important for meiotic recombination and its relationship to pairing and synopsis, critical processes that ensure proper homolog segregation. In addition, several genes affecting meiotic progression, spindle assembly, chromosome separation, and meiotic cytokinesis have also been uncovered and characterized. It is worth noting that Arabidopsis molecular genetic studies are also revealing secrets of meiosis that have not yet been recognized elsewhere among eukaryotes, including gene functions that might be unique to plants and those that are potentially shared with animals and fungi. As we enter the post-genomics era of plant biology, there is no doubt that the next ten years will see an even greater number of discoveries in this important area of plant development and cell biology.

Introduction

Meiosis is a specialized cell division characteristic of eukaryotes and is essential for sexual reproduction. The function of meiosis is to generate cells that contain exactly half of the genetic materials of the parental cells and that develop into germ cells. Consequently, the fusion of germ cells can then restore to the offspring the ploidy and level of genetic complexity of the parent(s). In mitosis, DNA replication is followed by one round of nuclear division, which separate sister chromatids. In contrast, in meiosis, a single round of DNA replication is followed by two rounds of nuclear division, meiosis I and meiosis II. Meiosis I is unique and involves the segregation of homologous chromosomes (homologs); this division reduces ploidy by half, thus is also called reductional division. Meiosis II is very similar to mitosis in that it results in the segregation of sister chromatids; therefore, it is also called equational division. Both meiosis I and II are further divided into four phases: prophase, metaphase, anaphase, and telophase, roughly similar to those in mitosis.

Meiotic prophase I is a long and complex process and is further divided into five substages according to cytological features of the chromosomes: leptotene, zygotene, pachytene, diplotene, and diakinesis (Dawe, 1998; Zickler and Kleckner, 1999; Stack and Anderson, 2001; Armstrong and Jones, 2003). Very early in prophase I, chromosomes begin to condense, forming thin thread-like structures called the axial element; this substage is called leptotene. Because the purpose of meiosis I is to properly separate homologs, it is essential for the homologs to recognize each other during early prophase I. The recognition between homologs is achieved through homolog pairing. The term "pairing" has been used to describe various interactions or associations between homologs (Zickler and Kleckner, 1999). In this chapter, it is used with a narrow definition for the transient interaction at localized regions of homologs that occurs prior to synopsis (Zickler and Kleckner, 1999). In most organisms, pairing depends on DNA homology to verify that the interacting chromosomes are indeed homologous. Pairing then progresses to homolog juxtaposition, which is also homology-dependent and refers to the coming togeth-
Synapsis is an extensive and stable interaction between chromosomes that involves the formation of a complex proteinaceous structure called the synaptonemal complex (SC) (Roeder, 1990). When homologs are partially synapsed, parts of homologs can be visibly detected as "fused" together, at a substage called zygotene. Using electron microscopy, the SC can be seen as a tripartite proteinaceous structure (Zickler and Kleckner, 1999; Schwarzacher, 2003; Higgins et al., 2005). The central element consists of the heads of the proteins that form the transverse elements and is connected to the lateral elements by the transverse elements (Zickler and Kleckner, 1999; Higgins et al., 2005). When the homologs are fully synapsed with the completion of the SC, the stage is called the pachytene substage, with each pair of synapsed homologs appearing under a light microscope as a thick thread-like structure, although the SC proper requires electron microscopy to observe. During normal meiosis, SC is formed between homologs and is closely coupled with homolog pairing and juxtaposition; however, in some yeast and maize mutants, SC can also form between non-homologous chromosomes (Leu et al., 1998; Pawlowski et al., 2004) suggesting that synapsis per se does not require homology and can be uncoupled from pairing. After pachytene, the SC is disassembled and homologs partially separate, except at the chiasmata, which are cytological features corresponding to crossing over points between non-sister chromatids; this substage is recognized as diplotene. Subsequent further chromosome condensation results in highly compacted bivalents (attached pairs of homologs), reaching the diakinesis substage, the end of prophase I.

In addition to pairing, juxtaposition, and synapsis, homologs also undergo recombination during prophase I, resulting in crossovers (exchange of chromosomal regions) and gene conversion (copying of sequence from one homolog to the other). Under an electron microscope, electron dense bodies called meiotic nodules can be detected along the chromosome; they are also called recombination nodules because their number and distribution are correlated with those of recombination (Carpenter, 1975, 1987; Sherman et al., 1992; Sherman and Stack, 1995; Anderson et al., 2001). Recombinational crossover, along with sister chromatid cohesion, ensures the formation of chiasmata, which are the physical links between homologs in a bivalent at late prophase I through the metaphase I/anaphase I transition. In the absence of crossovers, homologs would separate following the disassembly of the SC, resulting in detached chromosomes called univalents, which cannot align properly at the metaphase plate and segregate correctly at anaphase I. Therefore, at the level of an individual organism, recombination is critical for the reproductive success, because it maintains homolog association until the metaphase I/anaphase I transition and allows correct segregation of homologs at anaphase I. At the population and species levels, meiotic recombination, along with independent assortment of chromosomes, facilitates the redistribution of genetic material between generations, and increases genetic diversity among individuals in a population. This obviously has great ecological and evolutionary implications, making meiosis and particularly meiotic recombination important genetic mechanisms that have likely contributed to the enormous success of eukaryotes.

In flowering plants, meiosis occurs in both the male organ anther, and the female structure called the ovule, which is housed within the ovary. Both male and female meiocytes produce haploid spores, which then develop further through mitoses and cell differentiation into gametophytes. Because of the ease with which one can obtain male meiocytes and observe chromosome behaviors in a number of flowering plants, male meiosis in these plants has been studied extensively using cytogenetics and genetics (Golubovskaya, 1979; Kaul and Murphy, 1985; Dawe et al., 1994; Neuffer et al., 1997; Dawe, 1998; Zickler and Kleckner, 1998, 1999; Hamant et al., 2006). Chromosomal behavior, including condensation, pairing, and synapsis have been described for a number of plants using light and electron microscopy. Traditionally, plants with many meiocytes and very large chromosomes, such as lily, tomato, and maize, have been favored (Moens, 1969; Stack, 1973; Anderson et al., 1985; Anderson et al., 1988; Sherman and Stack, 1995; Anderson et al., 1997; Peterson et al., 1999; Stack and Anderson, 2001). In particular, maize has been a favorite organism for decades and is an excellent system for genetic and cytological analyses (Golubovskaya, 1979; Anderson et al., 1988; Golubovskaya, 1989; Staiger and Cande, 1991, 1992; Golubovskaya et al., 1993; Dawe et al., 1994; Dawe and Cande, 1996; Golubovskaya et al., 1997; Yu et al., 1997; Franklin et al., 1999; Golubovskaya et al., 2002; Anderson et al., 2003; Pawlowski et al., 2003; Anderson et al., 2004; Pawlowski et al., 2004).

In recent years, cytological procedures have been developed for Arabidopsis thaliana (Pfeirson et al., 1996; Ross et al., 1996; Kimmyuk and Jones, 1997; Ross et al., 1997; Yang et al., 1999; Caryl et al., 2000; Armstrong and Jones, 2001; Grelon et al., 2001; Azumi et al., 2002; Chen et al., 2002; Caryl et al., 2003), even though it is well-known for its small chromosomes. These technical advances in combination with the molecular genetic properties of Arabidopsis (Meyerowitz, 1987, 1989) and the availability of the complete genomic sequence and publicly available collections of insertional lines (Parinov et al., 1999; AGI,
2000; Alonso et al., 2003) have greatly facilitated the identification and characterization of meiotic genes using both forward and reverse genetics. This chapter will first briefly describe normal meiosis in Arabidopsis, and then present a series of discussions of genes that are important for meiosis (Table 1), roughly according to the progression of the meiotic process. For studies in others plants, the reader is referred to a number of excellent reviews (Dawe, 1998; Zickler and Kleckner, 1999; Schwarzacher, 2003; Harper et al., 2004; Pawlowski and Cande, 2005; Hamant et al., 2006). Much information about meiotic genes has been obtained from studies in the budding yeast Saccharomyces cerevisiae; unless otherwise indicated, in this chapter yeast refers to S. cerevisiae. Because meiosis is a conserved process common to eukaryotes, other reviews on meiosis in yeast and other non-plant systems also offer valuable references (Zickler and Kleckner, 1999; Haber, 2000; Page and Hawley, 2003; Bishop and Zickler, 2004; Page and Hawley, 2004).

**Normal Arabidopsis Meiosis**

In Arabidopsis, male meiosis occurs in the anther at anther stage 6 as define by Sanders et al. (1999), when the meiocytes are surrounded by four layers of somatic cells, including the tapetum (Ma, 2005). This is within stage 9 of flower development (Smyth et al., 1990). Each Arabidopsis flower has six anthers, each of which contains four lobes; within each lobe, there are approximately 30 meiocytes, giving rise to about 700 meiocytes per flower. To visualize meiotic chromosomes, a procedure called chromosome spreading is used to partially separate the chromosomes after limited digestion of the meiocytes to loosen the cell walls; this procedure has been widely used to study Arabidopsis meiotic mutants (Peirson et al., 1996; Ross et al., 1996; Klimyk and Jones, 1997; Ross et al., 1997; Yang et al., 1999; Caryl et al., 2000; Siddiqi et al., 2000; Armstrong and Jones, 2001; Grelon et al., 2001; Sanchez Moran et al., 2001; Azumi et al., 2002; Chen et al., 2002; Caryl et al., 2003; Grelon et al., 2003; Yang et al., 2003a; Yang et al., 2003b; Bleuyard and White, 2004; Higgins et al., 2004; Li et al., 2004; Li et al., 2005).

Following spreading, the chromosome preparations are stained with DAPI (4’,6-diamidino-2-phenylindole) before viewing under a fluorescence light microscope (Figure 1). At leptotene, partially condensed meiotic chromosomes are seen as thin lines (Figure 1A). From late leptotene to early zygotene (Figure 1B), homologs pair and become juxtaposed and then synapsed from zygotene through pachytene (Figure 1C). At diplotene (Figure 1D), the SCS are disassembled and the homologs separate in regions other than the chiasma(ta). At diakinesis (Figure 1E), further condensation results in very short chromosomal pairs, seen as five bivalents. The bivalents move to the center of the cell and are aligned at the equatorial plane at metaphase I (Figure 1F), due to the forces of the spindle microtubules. At the metaphase I/anaphase I transition, the removal of cohesins along chromosomal arms allows the separation of homologs, which are then pulled to the opposite poles of the spindle (not seen here) at anaphase I (Figure 1G). At telophase I (Figure 1H), five chromosomes decondense and form a cluster at each pole. The chromosomes re-condense during prophase II (Figure 1I), and the two groups are separated from each other by an organelle band. The two groups of chromosomes are aligned separately at two division planes at metaphase II (Figure 1J). Subsequently at anaphase II, separation and segregation of sister chromatids form four clusters of new chromosomes (Figure 1K). At telophase II, chromosome decondensation results in four haploid nuclei (Figure 1L), which are then packaged into four microspores by cytokinesis.

Unlike male meiosis, Arabidopsis female meiosis occurs in only about 50 cells per flower, one in each ovule. The relatively small number of female meiocytes and the fact that each female meiocyte is surrounded by somatic cells of the ovule make the analysis of female meiosis much harder than that of male meiosis. This is generally true for meiotic studies in other plants, such as maize. Much greater amounts of efforts are needed to obtain female meiotic images at various stages (Figure 2), which are generally very similar to the male counterparts. One important distinction is that female meiosis is asymmetric, resulting in one functional megaspore, which develops into the female gametophyte, and three others that degenerate. Unless specifically indicated, meiosis refers to male meiosis in this chapter.

In addition to DAPI-stained chromosome spreads, fluorescence in situ hybridization (FISH) methods have been applied to plant meiotic chromosomes, and are important for studying homolog pairing and juxtaposition (Zhong et al., 1996; Bass et al., 1997; Yu et al., 1997; Fransz et al., 1998; Peterson et al., 1999; Fransz et al., 2000; Armstrong et al., 2001). Furthermore, SCS and recombination nodules have been observed using transmission electron microscopy (TEM) (Armstrong et al., 2002; Schwarzacher, 2003; Higgins et al., 2004; Li et al., 2004; Li et al., 2005) (Figure 3). Using TEM, it seems that full-length axial elements are formed prior to homolog synapsis (Figure 3), unlike some organisms, in which SC formation is initiated before the axial element is completely formed (Zickler and Kleckner, 1999). The axial elements become the lateral elements of the SC following synapsis (Figure 3). The central element is formed from the heads of the transverse elements, which are connected to the lateral elements (Zickler and Kleckner, 1999; Schwarzacher, 2003). The light and electron microscopic methods provide the means to obtain a morphological basis for genetic and molecular analyses of Arabidopsis meiosis.
<table>
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<th>Gene symbol</th>
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aThe "At" in gene names for Arabidopsis thaliana is not shown here.

bFor additional references, please see text.

### Chromosome Condensation and Sister Chromatid Cohesion

In both mitosis and meiosis, chromosome condensation from long interphase fibers to highly compacted units is essential for successful segregation. In meiosis, chromosomes condense twice, one for each of the meiotic divisions. Analyses in animals and yeast have identified a group of highly conserved proteins, called Structural Maintenance of Chromosomes (SMCs) (Hirano, 2000; Hirano, 2002). In eukaryotes, there are six distinct types of SMC proteins, SMC1-6; among these, SMC2 and SMC4 form a heterodimer that is specifically required for condensation, whereas others have different functions (Hirano, 2002). Because condensation is a common feature of both mitosis and meiosis, genes required for condensation are likely important for mitotic development, such as gametophyte development and embryogenesis. At the same time, due to the highly duplicated Arabidopsis genome, often a specific function is fulfilled by two or more highly related genes. Indeed, a recent report showed that Arabidopsis possesses two highly similar SMC2 genes, called AtCAP-E1 and AtCAP-E2 (Siddiqui et al., 2003). AtCAP-E1 is expressed at a level approximately six times that of AtCAP-E2. In addition, T-DNA insertional mutants in either gene are viable and fertile, although the atcap-E1 mutant (called titan3 for enlarged embryos) exhibits mild embryo development defects (Liu and Meinke, 1998). In contrast, the atcap-E1 atcap-E2 double homozygous plants are embryonically lethal; even the presence of one copy of AtCAP-E2 is not sufficient for embryo viability. Therefore, possible meiotic chromosome condensation defects of the double homozygous plants could not be assessed. Nevertheless, the authors reported that one copy of the AtCAP-E1 gene was sufficient for viability and the male meiocytes in the mutant plants exhibited abnormal chromosomal morphology at metaphase I and anaphase I, consistent with a defect in chromosome condensation. It is not known whether chromosome condensation during early prophase I is abnormal in these mutant meiocytes.
Following DNA replication, the sister chromatids are closely associated with each other via sister chromatid cohesion (Michaelis et al., 1997; Nasmyth, 1999). In mitosis, sister chromatid cohesion is the primary means of chromosomal association until the metaphase/anaphase transition, when sister chromatid cohesion is removed to allow sister separation. As mentioned in the introduction, in meiosis I, sister chromatid cohesion, along with a crossover, is important for maintaining the chiasmata, which hold homologs together prior to the metaphase I/anaphase I transition. Removal of meiotic cohesion along the arm then allows the homologs to separate (Klein et al., 1999; Orr-Weaver, 1999; Watanabe and Nurse, 1999; van Heemst and Heyting, 2000). Therefore, sister chromatid cohesion and its regulated removal is critical for meiosis. Cohesion depends on a multiprotein complex called cohesin, which has at least four proteins; two of the four proteins, SMC1 and SMC3 are related to the SMC2 and SMC4 condensins, whereas the other two, SCC1, and SCC3 are specific subunits of cohesins (Losada et al., 1998; Nasmyth, 1999; Orr-Weaver, 1999). In addition, there is a meiosis-specific SCC1-like protein REC8; both SCC3 and REC8 in yeast are required for meiotic sister chromatid cohesion (Klein et al., 1999; Orr-Weaver, 1999; Parisi et al., 1999; Watanabe and Nurse, 1999; van Heemst and Heyting, 2000).

Figure 1, Arabidopsis male meiosis. A, leptotene. B, zygotene; arrows indicate regions of pairing between homologs. C, pachytene. Fully synapsed chromosomes appear as thick threads in light micrographs. D, diplotene, E, diakinesis; arrows point to the position of chiasmata and arrowheads indicate the centromeric regions. F, metaphase I. G, anaphase I. H, telophase I. I, prophase II; the arrow points to the organelle band between the two groups of chromosomes. J, metaphase II. K, anaphase II. L, telophase II. M, Four newly formed nuclei. The images were obtained from DAPI-stained chromosome spreads following the fixation of floral buds. These images were provided by W. Li and were previously published in Ma (2005).
In Arabidopsis, a gene named SYN1 or DIF1 has been found to be a homolog of REC8 and mutant analysis indicates it is essential for normal meiosis (Peirson et al., 1996; Peirson et al., 1997; Bai et al., 1999; Bhatt et al., 1999). In syn1/dif1 mutant meiocytes, sister chromatid cohesion is abnormal; in addition, chromosome condensation is also affected and mutant meiocytes produce chromosomal fragments. Recent immunolocalization experiments (Cai et al., 2003) using antibodies against the SYN1 protein indicate that the SYN1 protein is localized to the meiotic chromosomes from interphase to pachytene. At diplotene and diakinesis, the amount of SYN1 signal on the chromosomes reduces dramatically and the signal seems to localize to discrete regions of the chromosomes. Concurrent with the reduction of the chromosomal SYN1 signals, there is an increase in nucleoplasm SYN1 staining, suggesting that SYN1 is released from the chromosome to the nucleoplasm. This is consistent with the idea that initially cohesins are cleaved rather than completely degraded. At metaphase I, the SYN1 signal is further reduced and limited to the chromosomes, only detectable at a few loci on the highly condensed chromosomes; at anaphase I, SYN1 signals on chromosomes disappear. These results indicate that SYN1 is localized to the arms, as is the case for Rec8 protein. Although SYN1 signal is not detected at the centromere during prophase I or metaphase I, it should still be present at very low levels before anaphase I, as supported by the loss of centromere cohesion at anaphase I in syn1 meiocytes (Cai et al., 2003).

From anaphase I to metaphase II, the sister chromatids remain associated at the centromeres. Therefore, other cohesins are likely responsible for sister chromatic cohesion at the centromere responsible for sister association until anaphase II. Arabidopsis has at least two other REC8 homologs, SYN2 and SYN3 (Dong et al., 2001). SYN2 and SYN3 are distantly related to each other (18% amino acid sequence identity) and to SYN1 (16% and 19% aa sequence identity, respectively), with greater similarity near the N- and C-terminal regions than the central region. SYN2 and SYN3 are widely expressed, with elevated levels in tissues with dividing cells, such as root and shoot meristems, suggesting a role in mitosis. It is possible that SYN2/3 may also be involved in sister cohesion during meioses I and II. Arabidopsis also has homologs for both SMC1 and SMC3, AtSMC1 and AtSMC3, respectively, which are expressed widely, consistent with a role in both mitosis and meiosis (Lam et al., 2005b). Both AtSMC1 and

![Image](https://bioone.org/journals/The-Arabidopsis-Book on 13 Dec 2019 Terms of Use: https://bioone.org/terms-of-use)
AtSMC3 are expressed more highly in floral buds than other tissues, with AtSMC1 at a higher level, and more non-specifically, than AtSMC3. Both AtSMC1 and AtSMC3 are about 140 kD in size and have predicted domains similar to other SMC1 and SMC3 proteins: an N-terminal ATP-binding domain, two long coiled-coil regions flanking a flexible hinge region, and a C-terminal DA domain (Hirano, 2002). Protein localization studies using cell fractionation and antibodies indicate that AtSMC3 is found in both the cytoplasm and the nucleus (Lam et al., 2005b). In particular, from prophase and anaphase, AtSMC3 is associated with chromosomes in both mitotic and meiotic cells, supporting the idea that AtSMC3 is involved in sister chromatid cohesion, as its homologs do in other organisms. This hypothesis is further supported by the observation that syn1 mutant meiocytes exhibit abnormal AtSMC3 localization, indicating that SYN1 is required for normal chromosomal localization of AtSMC3 in meiocytes. Surprisingly, AtSMC3 is also associated with the spindle from metaphase to telophase in a SYN1-independent manner, suggesting a function previously unknown from studies in other systems (Lam et al., 2005b). Mutations in the AtSMC1 and AtSMC3 genes were previously isolated as titan8 and titan7 mutants, respectively; these mutants have enlarged embryos and arrested embryo and endosperm development (Liu et al., 2002a), indicating that these genes are critical for mitotic development.

Recently, the Arabidopsis homolog of SCC3, AtSCC3, has been characterized (Chelysheva et al., 2005). The AtSCC3 protein was detected in mitotic and meiotic cells; during meiosis, AtSCC3 was localized to the chromosome from leptotene to anaphase I. In addition, atsc3-2, a null mutation, causes embryonic lethality and a weak allele, atsc3-1, also results in defects in mitotic development, indicating that AtSCC3 is important for the mitotic cell cycle. Furthermore, AtSCC3 is required for maintenance of sister chromatid cohesion at centromeres at anaphase I, similar to SYN1 (Cai et al., 2003; Chelysheva et al., 2005). In normal meiosis, the kinetochores of the sister chromatids are oriented in the same direction to allow attachment to microtubules from the same pole of the spindle during the reductional meiosis I. Analysis of the atsc3 mutant meiocytes indicates that this monopolar orientation of the meiosis I kinetochores requires AtSCC3 function.

In addition to cohesin subunits, the Arabidopsis SWI1/DYAD gene is also required for normal sister chromatid cohesion during male and female meiosis (Mercier et al., 2001; Agashe et al., 2002). In mutant male meiocytes, sister chromatid cohesion is lost, resulting in 20 separated chromatids at late prophase I to metaphase I, in contrast to the five bivalents at wild-type diakinesis. Detailed examination of the male meiotic chromosomes in the swi1-2 mutant indicates that formation of the axial element is affected, suggesting that SWI1 is also important for condensation (Mercier et al., 2003). Furthermore, the swi1-2 mutation can suppress the chromosome fragmentation phenotype of dif1-1 (allelic to syn1), suggesting that SWI1 controls an early step in meiosis, as supported by the detection of the SWI1 protein in meiotic G1 and S phases. In the swi1 mutant, the absence of sister chromatid cohesion does not result in chromosome breakage, unlike the syn1 mutant chromosomes. In female meiosis of the swi1 mutant, a mitosis-like division takes place, suggesting that the centromeres behave like mitotic centromeres, although it is not clear how this might have occurred.

The predicted SWI1 protein is a novel protein with 639 amino acids; Arabidopsis has another gene (At5G23610) with a predicted protein of 360 amino acids that shares 38% identity and 52% similarity with SWI1 over the N-terminal 205 aa regions of both proteins. In addition, there is a rice gene (accession number: AK064367) encoding a protein with 33% identity and 48% similarity to SWI1 over nearly the entire protein. Therefore, SWI1 might represent a conserved plant gene family. Although the SWI1 protein lacks clear homologs among proteins with known func-

![Figure 4. Immunolocalization of ZYP1 protein (bright light blue) in wild-type male meiocytes. A, leptotene, showing a small number of foci. B, early zygotene, with some expansion to larger chromosome regions. C, mid-zygotene, showing further expansion of ZYP1 regions. D, pachytene, with ZYP1 distribution to all chromosomes. DNA was stained with DAPI (blue). Bar = 10 µm. This figure was modified from Figure 2 of Higgins et al. (2005), with permission from Genes and Development.](https://bioone.org/journals/The-Arabidopsis-Book)
Homolog Pairing/Juxtaposition and the Synaptonemal Complex

As mentioned earlier, homolog pairing/juxtaposition, synopsis, and recombination promote correct recognition and association of homologs, such that they can properly segregate subsequently. It is thought that telomeres play an important role in chromosome pairing (Dawe, 1998; Scherthan, 2001). In early prophase I of several organisms, including plants (such as maize) and yeasts, dispersed telomeres move and attach to the nuclear envelope, forming a configuration called bouquet with telomeres clustered on one face of the nucleus. Bouquet formation may be important for initiating homolog pairing (Dawe et al., 1994; Scherthan et al., 1996; Bass et al., 1997). In Arabidopsis, the telomeres seem to cluster during interphase to the nucleolus rather than on the nuclear envelope, then pair before synopsis (Armstrong et al., 2001). The paired telomeres then dissociate from the nucleolus and are dispersed during leptotene, suggesting that telomere clustering might also facilitate homolog pairing in Arabidopsis (Armstrong et al., 2001).

Following pairing and juxtaposition, homologs form the synaptonemal complex (SC) between the two aligned chromosomes. In light microscopy, juxtaposed chromosomes can be visualized as thick lines (Figure 1C), which represent synapsed homologs in normal Arabidopsis meiotic cells. The SC consists of three parallel filamentous elements (Figure 3); the two lateral elements and a central element. The lateral elements correspond to the two aligned homologs, with regions of the chromatin in complex with SC proteins and large loops of chromatin emanating away from the SC. The central element is seen in TEM as a thin filament in between the lateral elements; it is known to be composed of the overlapping heads of the transverse elements, which are very fine filaments that are perpendicular to and connecting the lateral elements.

Because pairing, juxtaposition and synopsis are highly coordinated processes, mutants defective in one often are also abnormal in another, and have generally been called synaptic mutants. These can be classified as either asynaptic mutants, which fail to establish synopsis, or desynaptic mutants, which cannot maintain homolog association after forming SC. At diakinesis, both asynaptic and desynaptic mutants have univalents rather than bivalents (Ross et al., 1997; Caryl et al., 2000; Cai and Makaroff, 2001; Armstrong et al., 2002; Bass et al., 2003; Schommer et al., 2003; Nonomura et al., 2004). In Arabidopsis, the Asy1 mutant is asynaptic, unable to form SC in both male and female meiocytes (Ross et al., 1997; Caryl et al., 2000). The ASY1 protein is localized to the axial/lateral elements, suggesting that it plays critical role in SC formation (Armstrong et al., 2002). The ASY1 protein share sequence similarity in its N-terminal domain with the yeast HOP1 protein (Hollingsworth et al., 1990; Caryl et al., 2000), which is known to be important in SC assembly and is localized on axial elements (Hollingsworth et al., 1990). In rice there is an ASY1 homolog called PAIR2, a mutation in PAIR2 causes defects in homolog alignment at pachytene and the formation of univalents instead of bivalents at diakinesis (Nonomura et al., 2004). Therefore, ASY1, PAIR2, and HOP1 are functionally conserved genes in plants and yeast. Another Arabidopsis mutant, aph2, is defective in pairing and bivalent formation (Schommer et al., 2003). The AHP2 protein is similar to the S. cerevisiae HOP2, S. pombe Meu13p, and human TBPIP (Tat-binding protein 1-interacting protein) proteins. Both HOP2 and Meu13p are important for homolog pairing during meiosis.

Figure 5. Models for homologous recombination. The double stranded break repair model (left) and the synthesis-dependent strand annealing model (right). Both start with a DSB, 5’ to 3’ resection to 3’ single strands, the invasion of one end into the intact recombination partner to form a D-loop, and some DNA synthesis. In the traditional DSBR model, the second end invades, leading to the formation of the double Holliday junction, which expand and then can be resolved to either crossover or noncrossover. Recently studies in yeast indicate that double Holliday junctions usually resolve into crossovers. In addition, a number of results support the synthesis-dependent strand annealing model, which branch off following D-loop formation. This alternative model can generate noncrossovers, but not crossovers. This figure was adopted from Figure 1 of Maloisel et al. (2004).
In addition, TBPIP is expressed in the testis. Therefore, AHP2 is a likely functional homolog of HOP2/Meu13p in Arabidopsis.

Although SC is structurally similar among eukaryotes under TEM, SC proteins from yeast and animals do not share any obvious sequence similarity. Nevertheless, analogous protein components do show similarity in secondary structures. For example, in yeast, the ZIP1 protein is a subunit of the transverse element; its counterparts in animals are SCP1 from mammals, SYP1 from C. elegans, and C(3)G from Drosophila (Zickler and Kleckner, 1999; Page and Hawley, 2004). They lack amino acid sequence similarities, but share secondary structural properties, each with globular heads and a long coiled-coil central region. The lack of strong sequence similarity has made it difficult to identify Arabidopsis genes encoding SC proteins. However, recently, Higgens et al. (Higgins et al., 2005) have used a combination of various bioinformatics tools to identify an adjacent pair of divergently transcribed genes, ZYP1a and ZYP1b. They encode highly similar (90% similarity) proteins with structural features of ZIP1 and other related proteins.

Immunolocalization experiments indicate that the ZYP1 proteins are located at 20-25 foci on leptotene chromosomes, and expand during zygotene to cover the entire length of the pachytene chromosomes, consistent with the hypothesis that ZYP1 is a SC component (Higgins et al., 2005) (Figure 4). The appearance of ZYP1 foci is later than the appearance of the ASY1 foci, which are found on the axial element at leptotene. At pachytene, ASY1 signals flank both sides of the ZYP1 signal, both along the synapsed homologs, suggesting that ZYP1 forms part of the central region of the SC. Single mutants in either ZYP1a or ZYP1b genes have reduced fertility, slight reduction in the number of chiasmata and a delay in prophase I. Because these two genes are adjacent, it was not possible to generate the double mutant. Localization analysis in the single mutants indicates that the distributions of the ZYP1a and ZYP1b proteins are indistinguishable from each other and from that in the wild-type. Several RNAi lines in single mutant backgrounds were obtained that had no detectable ZYP1 proteins; these lines produced meioocytes that usually did not have aligned chromosomes but occasionally did have fully aligned chromosomes, although these aligned chromosomes are not synapsed fully. The great increase of the number of cells with unaligned chromosomes suggested a severe delay of meiotic progression. This is further supported by an increase in the period between DNA replication and the completion of meiosis I from ~30 hours in normal meioocytes to ~50 hours in cells of the ZYP1 RNAi lines.

The ZYP1 RNAi lines also display evidence of abnormality in recombination (Higgins et al., 2005). The affected meioocytes have a slightly reduced number of MLH1 foci (7.3), which likely mark crossover sites, in comparison with 10 found in the wild-type cells. In addition, the average number of chiasmata was estimated to between 7 and 8, rather than the normal ~10. These results suggest that recombination is slightly affected. Nevertheless, the fact that MLH1 foci and chiasmata are present in substantial numbers indicates that recombination was able to progress to a relatively late stage. Strikingly, fluorescence in situ hybridization experiments indicate that nonhomologous chromosomes are closely associated, suggesting that pairing might have been affected in the ZYP1 RNAi lines. The results from the analysis of ZYP1 RNAi lines support the idea that pairing, synapsis and recombination are tightly coupled. Clearly, a severe reduction of the ZYP1 protein has a significant effect on pairing and recombination. It is possible that the RNAi lines still have some residual ZYP1 function, which may allow recombination at a level greater than possible if the ZYP1 function were completely absent.

**Meiotic Recombination: Initial Events**

In addition to pairing/juxtaposition and synapsis, homologous recombination occurs during prophase I between homologs. It is initiated around late leptotene to early zygotene and is completed at late pachytene. Using TEM, electron dense bodies called meiotic nodules can be found associated with the chromosome; they are also called recombination nodules because they are thought to be related to recombination (Carpenter, 1975, 1987; Sherman et al., 1992; Sherman and Stack, 1995; Anderson et al., 2001). Late recombination nodules are very well correlated with recombination crossovers (Anderson et al., 2004), which are observed cytologically as the chiasmata. The maintenance of chiasmata also requires sister chromatid cohesion.

A well-known model for recombination called the double-strand break repair (DSBR) model was proposed primarily on the basis of biochemical studies in yeast and animal cells (Szostak et al., 1983). According to this model (Figure 5, left), recombination is initiated by a double-strand break (DSB) in one of two participating chromosomes, usually a non-sister chromatid during meiosis; 5' resection of the DSB produces 3' single-stranded DNAs, one of which then forms a D loop with the intact partner chromatid. DNA synthesis ensues primed from the invading strand using the intact molecular as the template. The invasion of the second broken end and further DNA synthesis yield the double-Holliday junction, which can be
resolved following cutting at alternative strands, effecting either crossovers or non-crossovers.

Recent studies have yielded evidence supporting the idea that the decision for crossover/non-crossover is made very early during recombination, prior to the formation of the double-Holliday junction, prompting a revision of the DSBR model (Bishop and Zickler, 2004; Borner et al., 2004; Haber et al., 2004). This revised model (Figure 5, right) posits that the recombination pathway branches following the formation of the D loop. One branch leads to the formation of the double-Holliday junction, which then progresses to form a crossover, but usually not a non-crossover. In the second branch of the pathway, the invading single strand, with its newly synthesized DNA, dissociates from the homolog and re-anneals with the other broken end; DNA synthesis and ligation then restore the chromosome, resulting in a non-crossover.

Many genes important for meiotic recombination have been identified by studies in the budding yeast *Saccharomyces cerevisiae*, as well as in the fission yeast *Schizosaccharomyces pombe*, *C. elegans*, *Drosophila*, and others (Zickler and Kleckner, 1999). The relatively ease with which to perform reverse genetics and the available sequence information have allowed the testing of the function of Arabidopsis homologs of these known meiotic genes. Because of the intimate relationship between recombination, pairing and synapsis, studies of genes important for meiotic recombination have also yielded insights into their roles in pairing and synapsis. In budding yeast, DSBs are generated by SPO11 (Keeney, 2001; Lichten, 2001), which was discovered a number of year ago as a mutant defective in sporulation (Esposito and Esposito, 1969), the formation of haploid spores from a diploid cell through meiosis. SPO11 encodes a member of a novel family of type II topoisomerase and has a transes-

**Figure 6.** Male meiosis in the atspo11-1 mutant. A, leptotene. B, early diakinesis, showing many univalents. C, prometaphase I, with 10 univalents. D, metaphase I, with one bivalent (arrow) and 8 univalents. E, metaphase II to anaphase II, showing abnormal distribution. F, anaphase II. This figure was modified from Figure 8 of Li et al. (2005).

terase activity that creates DSBs along with several other proteins (Bergerat et al., 1997; Keeney, 2001). SPO11 homologs have been identified in many organisms including *S. pombe*, *Drosophila*, *C. elegans*, mammals, the mushroom *Coprinus cinereus*, and Arabidopsis (Dernburg et al., 1998; McKim et al., 1998; Keeney et al., 1999; Romanienko and Camerini-Otero, 1999; Celerin et al., 2000; Grellon et al., 2001), suggesting a highly conserved function in eukaryotes.

Genetic studies using mutations in the *SPO11* gene in various organisms have revealed differences in the relationship between recombination initiation in the form of DSBs and synopsis. In both budding and fission yeasts, as well as mouse, *spo11* mutants are defective in SC formation, indicating a requirement of DSBs for homolog synapsis (Cervantes et al., 2000; Romanienko and Camerini-Otero, 2000; Zenvirth and Simchen, 2000). In contrast, SPO11-dependent DSBs are not required for homolog synapsis in *C. elegans* and *Drosophila* (Dernburg et al., 1998; McKim et al., 1998). In Arabidopsis, there are three SPO11 homologs (Hartung and Puchta, 2000, 2001). A mutant in one of these SPO11 homologs, AtSPO11-1, was shown to be defective in bivalent formation in prophase I (Figure 6) and has a sharply reduced recombination rate between homologous chromosomes, indicating that AtSPO11-1 is important for recombination (Grellon et al., 2001). The atspo11-1 mutant phenotypes also suggest that AtSPO11-1 is required for homolog pairing, juxtaposition, and/or synopsis. Therefore, meiotic recombination and its relationship to pairing and synopsis may be more similar between yeast, mammals and plants, then between these organisms and *C. elegans* or *Drosophila* (see below for more discussion). The other two SPO11 homologs, AtSPO11-2 and AtSPO11-3, are not known to be involved in meiosis.

After the formation of SPO11-dependent DSBs in yeast, then a complex of RAD50, MRE11, and NBS1 (XR52) proteins carries out the resection step to generate single-stranded ends (Connelly and Leach, 2002). RAD50 and MRE11 are similar in sequence to the bacterial sbcC and sbcD subunits of a nuclease complex; in particular, the MRE11 and sbcD proteins contain conserved phosphoesterase motifs (Sharples and Leach, 1995). The Arabidopsis homologs of *RAD50* and *MRE11* are known, but a NBS1 homolog has not yet been identified in Arabidopsis (Hartung and Puchta, 1999; Gallego et al., 2001). An atrad50 mutant is completely sterile and is hypersensitive to DNA-damaging radiation and chemicals (Gallego et al., 2001). Further studies indicate atrad50 meiotic cells have numerous chromosome fragments in prophase I, suggesting that the repair of DSBs is defective (Bleuayrd et al., 2004b). This is consistent with a role for AtrAD50 just downstream of AtSPO11-1. The predicted Arabidopsis MRE11 protein has 720 amino acids and
shares strong sequence similarity with yeast and human MRE11 proteins in the N-terminal two thirds, which contains four phosphoesterase motifs (Hartung and Puchta, 1999; Bundock and Hooykaas, 2002). A T-DNA insertional mre11 mutant was found to have small and abnormally shaped leaves and enlarged shoot apical meristem (Puizina et al., 2004). In addition, the Arabidopsis mre11 mutant is sterile, has meiotic chromosome fragmentation, is defective in homolog pairing and bivalent formation, and exhibits abnormal chromosome segregation (Puizina et al., 2004). The chromosome fragmentation phenotype is due to a failure to process SPO11-induced DBSs because spo11-1 mre11 double mutant meiocytes do not show chromosome fragmentation. Therefore, similar to RAD50 and MRE11 in yeast, the Arabidopsis AtRAD50 and MRE11 genes are required for normal meiotic recombination. In addition to its meiotic function, AtRAD50 and MRE11 are also needed for normal mitotic growth. In yeast, RAD50 and MRE11 are also important for repair of DSBs by non-homologous end joining (Haber, 1998); therefore, at least some of the somatic phenotypes in the Arabidopsis atrad50 and mre11 mutants could be due defects in this pathway, rather than that in the homologous recombination pathway.

**Meiotic Recombination: The RAD51 Gene Family and DSB Repair**

Another yeast gene important for meiotic recombination is RAD51, which encodes a eukaryotic homolog of the E. coli RecA recombinase critical for DSB repair in homologous recombination (Smith et al., 1987; Smith and Wang, 1989; Cox, 1999). RecA is a 38-KDa protein that has activities in single-stranded DNA (ssDNA) binding, ATP binding, and ATP hydrolysis (McEntee et al., 1980; Weinstock et al., 1981). The yeast RAD51 and E. coli RecA proteins are 30% identical (54% conserved) over a ~210-amino acid region. In addition, the meiosis-specific yeast protein DMC1 is another RecA homolog and is highly similar to RAD51 (Bishop et al., 1992). The RAD51 gene is required for both meiotic and mitotic recombination, whereas DMC1 is specifically required for meiotic progression, synaptonemal-
mal complex formation, and homologous recombination (Bishop et al., 1992; Shinohara et al., 1992). In C. elegans and Drosophila, the RAD51 homologs are required for normal meiosis (Rinaldo et al., 1998; Staeva-Vieira et al., 2003). It is worth noting that Drosophila and C. elegans do not seem to possess a DMC1 gene. In mouse, RAD51 has been shown to interact with DMC1 (Masson et al., 1999; Tarsounas et al., 1999), but its function in meiosis has not been shown genetically because the rad51 mutant is embryonic lethal. The mouse dmc1 mutant is defective in meiosis (Habu et al., 1996; Pittman et al., 1998; Yoshida et al., 1998).

Homologs of RAD51/DMC1 have been identified in several plants, including Arabidopsis and maize (Sato et al., 1995; Anderson et al., 1997; Klimyk and Jones, 1997; Doutriaux et al., 1998; Franklin et al., 1999; Ding et al., 2001; Shimazu et al., 2001). Protein localization studies in maize and Arabidopsis using antibodies indicate that the RAD51 protein is located on the chromosome at a large number of foci at the zygotene stage (Franklin et al., 1999; Franklin et al., 2003; Pawlowski et al., 2003). These results led to the proposal that RAD51 is important for homology search during pairing (Franklin et al., 1999; Franklin et al., 2003; Pawlowski et al., 2003).

The hypothesis that RAD51 is important for pairing/juxtaposition is supported by analysis of a T-DNA insertional mutant in the Arabidopsis RAD51 ortholog (AtRAD51) (Li et al., 2004). The atrad51 mutant is male and female sterile; using both light microscopy of DAPI-stain chromosome spreads and TEM, it was found that mutant meiocytes are defective in homolog juxtaposition, lacking the typical "thin threads" seen at pachytene (Figures 7). Analysis using TEM revealed that mutant meiocytes were able to form axial elements, but they did not progress to form SC (Figure 8). Moreover, consistent with a predicted role in D-loop formation according to the DSBR model of recombination, atrad51 mutant meiotic cells have multiple chromosomal fragments detectable beginning at diakinesis and continuing through anaphase II, suggesting a severe defect in repair of SPO11-induced DBSs. Indeed, meiocytes of the atspo11-1 atrad51 double mutant lack chromosome fragments, indicating the fragmentation in the atrad51 mutant requires the SPO11-1 function (Li et al., 2004).

Figure 6. Transmission electron micrographs of male meiocyte nuclei in wild type and atrad51. A and B, wild type nuclei with SC (arrows) at zygotene (A) and pachytene (B). C and D, atrad51-1 nuclei, with axial elements (arrowheads), which are unpaired in nuclei at zygote (C) and pachytene (D) stages. E, an occasional fragmentary SC in the atrad51-1 mutant. Nu: nucleolus. Bar = 1 µm. This figure is Figure 5 of Li et al. (2004).

Figure 7. A Neighbor-Joining phylogenetic tree of the RecA/RAD51 gene family. Species designation: Arth: Arabidopsis thaliana; Dare: Danio rerio; Esco: Escherichia coli; Hosa: Homo sapiens; Sace: Saccharomyces cerevisiae; Scpo: Schizosaccharomyces pombe. Eukaryotic recARAD51 gene family members form 7 clades; Arabidopsis genes are present in 6 of these clades, indicating an orthologous relationship between each Arabidopsis gene and animal genes. Bootstrap values are indicated near the stem of each clade. The tree in this figure was generated by Z. Lin.
2004). Therefore, AtRAD51 participates in the SPO11-1 dependent meiotic recombination, and the RAD51 meiotic function is similar between yeast and plants.

Protein localization studies also indicate that at the pachytene stage, the number of RAD51 foci is greatly reduced (Franklin et al., 1999; Mercier et al., 2003), consistent with the number of crossovers per cell (Copenhaver et al., 1997). This suggests that RAD51 is also needed for the branch of the recombination pathway that led to crossover formation. In addition, studies of a T-DNA knockout mutant of AtDMC1 indicate that the mutant meiocytes have largely univalents instead of bivalents at late prophase I (Couteau et al., 1999). Because crossovers are needed for maintaining bivalents at diakinesis, the atdmc1 phenotypes indicate that AtDMC1 is crucial for Arabidopsis meiotic crossover formation. Indeed, the recombination frequency is greatly reduced in the atdmc1 mutant (Couteau et al., 1999). Although both AtRAD51 and AtDMC1 are RecA homologs and are required for normal meiosis, particularly meiotic recombination, the meiotic phenotypes of the corresponding mutants are very different. Specifically, atdmc1 mutant meiocytes do not have detectable chromosome fragmentation. It is possible that atdmc1 is primarily functioning to promote crossover formation, and is not required for the non-crossover branch of homologous recombination.

DSBs in chromosomes can occur due to radiation and chemical mutagens, even during DNA replication in a normal cell cycle. These DSBs must be repaired to maintain chromosome stability and cell viability because a single chromosomal break can cause cell death. One of the major pathways of DSB repair is homologous recombination (Masson and West, 2001). As mentioned above, the yeast RAD51 is important for the repair of DSBs caused by DNA-damaging agents, but is not required for mitotic cell viability (Shinnohara et al., 1992; Game, 1993). Similarly, in C. elegans and Drosophila, the RAD51 gene is not essential for mitotic cell viability, unless the animals are exposed to DNA-damaging agents (Rinaldo et al., 2002; Staeva-Vieira et al., 2003). On the other hand, the mouse RAD51 gene is essential during embryogenesis (Lim and Hasty, 1996; Tsuzuki et al., 1996). Consistent with this, RAD51 is important for DNA repair and chromosome stability during the mitotic cell cycle in mammalian and chicken cell cultures (Li and Maizels, 1997; Sonoda et al., 1998; Kim et al., 2001; Lambert and Lopez, 2002; Lundin et al., 2003). Reduction or loss of RAD51 function in these cells cause hypersensitivity to ionizing radiation and methyl methanesulfonate (MMS) and a deficiency in DSB repair and cell death (Taki et al., 1996; Sonoda et al., 1998; Collis et al., 2001). In Arabidopsis, the atrad51 mutant plants appear healthy, identical to the wild type, when grown under normal conditions (Li et al., 2004). The size and number of atrad51 leaves and floral organs all seem normal. In addition, mitosis in the atrad51 mutant appears to proceed normally, unlike the mammalian rad51 knockout, which is embryo lethal. Therefore, the Arabidopsis AtRAD51 gene is not critical for DNA repair during vegetative and floral development.

In addition to RAD51 and DMC1, yeast also has two other distant homologs of recA: RAD55 and RAD57, which were identified as mutants hypersensitive to radiation (Kans and Mortimer, 1991; Lovett, 1994). Several lines of evidence support the hypothesis that RAD57 interacts with RAD51 to promote recombination. It was found that rad57 mutants (Kans and Mortimer, 1991; Game, 1993) can be partially rescued by the overexpression of RAD51 (Hays et al., 1995). In addition, RAD57 promotes RAD51-mediated homologous pairing and strand exchange in vitro (Sung, 1997). Amino acid substitutions in RAD51 that increase its DNA-binding affinity can suppress rad57 mutations (Fortin and Symington, 2002). These observations are consistent with the idea that RAD57 facilitates the binding RAD51 to DNA. In S. pombe, hypersensitivity to DNA damaging agent MMS and gamma-rays were used to identify mutations in the RHP57 gene, which is the putative ortholog of the budding yeast RAD51 (Tsutsui et al., 2000).

Vertebrate animals also possess five other RAD51 paralogs: RAD51B, RAD51C, RAD51D, XRCC2, and XRCC3 (Albala et al., 1997; Cartwright et al., 1998; Dosanjh et al., 1998; Liu et al., 1998b; Pittman et al., 1998; Braybrooke et al., 2000; Havre et al., 2000) (Figure 9). RAD51B, RAD51C, and RAD51D were isolated as cDNAs with similarity to RAD51, and XRCC2 and XRCC3 genes were identified by their ability to counter the sensitivity of hamster mutant cell lines, irs1 and irs1SF, to DNA-damaging radiation and chemicals (Liu et al., 1998b). Phylogenetic analysis suggests that XRCC3 is a putative ortholog of the budding yeast RAD57 and fission yeast RHP57 (Tsutsui et al., 2000). Similar to RAD57, the XRCC3 protein can also associate with RAD51 in a yeast two-hybrid assay (Schild et al., 2000). The human XRCC3 is required for the assembly of RAD51 complexes in vitro (Bishop et al., 1998) and for homology-directed repair of DNA DSBs in cell lines (Pierce et al., 1999; Brennan et al., 2000). In addition, biochemical studies have detected two protein complexes involving these proteins: one containing RAD51B, RAD51C, RAD51D, and XRCC2 and called the BCDX2 complex; the other containing XRCC3 and RAD51C (Masson et al., 2001; Liu et al., 2002b). The BCDX2 complex binds to nicks in duplex DNA, and may play a role in the recognition of nicks during repair of DSBs (Masson et al., 2001). In the XRCC3-RAD51C complex, RAD51C facilitates homolog pairing, and XRCC3 contributes to preferential binding to ssDNAs (Kurumizaka et al., 2001).

Disruption of one of mouse RAD51, RAD51B, RAD51D, or XRCC2 genes causes early embryo lethality (Lim and Hasty, 1996; Tsuzuki et al., 1996; Shu et al., 1999; Deans
et al., 2000; Pittman and Schimenti, 2000), indicating non-redundant essential roles in embryogenesis, consistent with their having important functions in DSB repair in the mitotic cell cycle. Furthermore, the early lethality of rad51 and rad51b mutant embryos can be delayed due to partial suppression by a mutation in p53, a checkpoint control gene, suggesting that the loss of the p53 function can allow cell cycle progression even with a defect in DNA repair. However, the rad51 p53 double mutant embryos eventually also die (Lim and Hasty, 1996; Shu et al., 1999). Therefore, the RAD51-dependent function is linked to mitotic DNA damage checkpoint control. Indeed, RAD51 has been found to interact genetically and physically with tumor suppressor genes p53, ATM, BRCA1, BRCA2, and others (Scully et al., 1997; Sharan et al., 1997; Wong et al., 1997; Marmorstein et al., 1998; Chen et al., 1999), suggesting that it is involved in the normal cellular process that maintains chromosome integrity and stability.

In Arabidopsis, molecular cloning and genomic sequence analysis indicate that there are at least six Arabidopsis RAD51 homologs. In addition to AtRAD51 and AtDMC1, Arabidopsis also has putative orthologs of...
RAD51B, RAD51C, XRCC2, and XRCC3: AtRAD51B, AtRAD51C, AtXRCC2, and AtXRCC3, respectively (Doutriaux et al., 1998; Couteau et al., 1999; Osakabe et al., 2002; Bleuyard and White, 2004; Li et al., 2004; Bleuyard et al., 2005; Li et al., 2005), as supported by phylogenetic analysis (Figure 9). AtRAD51C is expressed at low levels in somatic cells (Li et al., 2005). RAD51C is also expressed in meiocytes, but at a lower level than that of RAD51 (Li et al., 2004; Li et al., 2005). Similar to the atrad51 mutant, an atrad51c T-DNA insertional mutant is also completely sterile and defective in meiosis, with fragmented chromosomes (Abe et al., 2005; Bleuyard et al., 2005; Li et al., 2005) (Figure 10). Moreover, the rad51c male and female meioocytes display pairing/juxtaposition defects, as indicated by fluorescence in situ hybridization experiments (Li et al., 2005). Furthermore, TEM experiments indicate that atrad51c meioocytes have abnormal partial SCs, sometimes with more than two chromosomes, suggesting that non-homologous chromosomes might have partially synapsed (Figure 11). At late pachytene, no SC was detected; therefore, the partial SCs at earlier stages could not progress to complete SCs. Therefore, RAD51C also is required for normal homolog juxtaposition, synopsis, and recombination, following the formation of DSBs during prophase I. Similar to the atrad51 atspo11-1 double mutant, the atrad51c atspo11-1 double mutant also lacks chromosome fragments, indicating that AtRAD51C also acts downstream of AtSPO11-1 to repair DSBs. In addition to the meiotic defectives, the atrad51c mutant is hypersensitive to gamma radiation and a DNA crosslinking agent and is reduced in somatic recombination frequency (Abe et al., 2005; Bleuyard et al., 2005).

The function of the Arabidopsis XRCC3 homolog, AtXRCC3, was revealed by the analysis of a T-DNA insertional mutant, which showed sterility and fragmented meiotic chromosomes (Bleuyard and White, 2004), similar to the phenotypes of the atrad51 mutant. In addition, the appearance of chromosome fragments depends on the function of AtSPO11-1, indicating that the fragmentation is due to failure to repair SP011-induced DSBs (Bleuyard et al., 2004a; Bleuyard and White, 2004). When grown under normal conditions, the atxrcc3 mutant can develop normally; in contrast, mutant cells in culture are sensitive to DNA cross-linking agents but not to DSB-inducing chemicals. Therefore, AtXRCC3 is not required for normal mitotic development, unlike the mammalian XRCC3 gene. The role of AtXRCC3 in DNA repair also seems to be different from that of the XRCC3 gene, which is involved in DSB repair. Insertions in the AtRAD51B and AtXRCC2 genes have no visible developmental defects, but cause DNA repair defects in somatic cells (Abe et al., 2005; Bleuyard et al., 2005; Osakabe et al., 2005). Therefore, AtRAD51, AtRAD51C, and AtXRCC3 are required for normal processing of DSBs induced by AtSPO11-1 during meiosis; in addition, AtRAD51B, AtRAD51C, AtXRCC2 and AtXRCC3 are involved in repair of damaged DNA during the mitotic cell cycle.

Mutant phenotypes from DAPI analysis suggest that atrad51c and atxrcc3 meioocytes might have fewer chromosome fragments than that in the atrad51 mutant, although the number of fragments is difficult to quantify and the possible meiotic phenotypic difference between these three mutants needs to be further investigated. If atrad51c and atxrcc3 meioocytes do have weaker phenotypes than does atrad51, there might be a functional difference between these genes. EM results also support the idea that these genes are not functionally identical, atrad51 cells had almost no SC (Figure 8), except very occasional abnormal ones (Li et al., 2004), additional to axial elements, whereas atrad51c meioocytes had occasional polycomplexes (Figure 11), and xrcc3 cells had abnormal SC, at a frequency greater than those in the atrad51 cells (L. Timofejeva, W. Li, and H. Ma, unpublished data). The fact that each of the three single mutants has such severe meiotic defects indicates that these genes are not genetically redundant. In addition, the fact that separate RAD51, RAD51C, and XRCC3 evolutionary lineages have been maintained and conserved in both animals and plants supports the hypothesis that RAD51, RAD51C, and XRCC3 have distinct essential functions (Figure 9).

Immunolocalization studies indicate that there are numerous (more than 200) AtRAD51 foci in early Arabidopsis prophase I cells (leptotene to zygotene) and this number is reduced to fewer than 20 at pachytene (Mercier et al., 2003). From DAPI-stained images, the numbers of chromosome fragments in the atrad51, atrad51c, and atxrcc3 seem to be far fewer than the number of early AtRAD51 foci (Bleuyard and White, 2004; Li et al., 2004; Abe et al., 2005; Bleuyard et al., 2005; Li et al., 2005). It is possible that each of these proteins is present at a subset of the DSBs. This is consistent with the observation that RAD51 labeled 44% of early meiotic nodules and 79% of late nodules in lily (Anderson et al., 1997). It is possible that AtRAD51, AtRAD51C, and AtXRCC3 are localized to non-identical but possibly overlapping subsets of DSBs, so that some AtRAD51 foci also have AtRAD51C and/or AtXRCC3 proteins. It is also possible that AtRAD51C and AtXRCC3 are localized to fewer foci than AtRAD51.

RAD51 and XRCC are essential for mitotic growth in mammals and birds, but their putative orthologs are not required for cellular viability in yeast, Drosophila, or Arabidopsis. Clearly, AtRAD51, AtRAD51C, and AtXRCC3 are each required for meiosis and fertility, indicating that they cannot replace each other during meiosis. As mentioned above, AtRAD51C and AtXRCC3 are also important for DNA repair when the plant is exposed to DNA-damaging chemicals, as are AtRAD51B and AtXRCC2. Therefore, even though these genes are members of the same fami-
ly, they are not redundant genetically. It is possible that these genes are needed when the numbers of DSBs are large, as in meiosis or when caused by mutagens. The fact these genes are highly conserved suggests that they are also important for meiosis in animals, even though the embryo lethality has thus far prevented a direct test of this hypothesis. The fact that atrad51, atrad51c, and atxrcc3 mutants all appear normal during mitotic development under standard growth conditions suggests two different possibilities. First, DSB repair is not important for normal mitotic cell cycle, although this is not likely because Arabidopsis rad50 and mre11 mutants have vegetative phenotypes. Second, DSBs might be repaired by other pathways, such as those involving other RAD51 paralogs, or the non-homologous end joining pathways.

In vitro studies of mammalian RAD51 indicate that it binds to ssDNA and catalyzes the formation of a D loop by promoting the invasion of the ssDNA into a double stranded DNA (Petukhova et al., 2000). In addition, mammalian XRCC3 and RAD51C form a complex that promotes the loading of RAD51 onto DNA (Masson et al., 2001; Sigurdsson et al., 2001; Wiese et al., 2002; Lio et al., 2003). Also, xrcc3 and rad51c mutant animal cell lines have reduced number of RAD51 foci; furthermore, RAD51C, but not RAD51, is needed for the formation of XRCC3 foci on chromosome (Yoshioka et al., 2003; Lio et al., 2004). Because the Arabidopsis AtRAD51, AtRAD51C, and AtXRCC3 proteins are orthologous to their mammalian counterparts, the Arabidopsis proteins might have similar biochemical properties, suggesting the following model for how these genes function in meiosis. During meiosis, AtRAD51C and AtXRCC3 form a complex that promotes the formation of AtRAD51 foci. It is possible that formation of AtRAD51 foci does not absolutely require AtRAD51C or AtXRCC3; when AtRAD51C or AtXRCC3 are eliminated by mutations, the number of AtRAD51 foci is reduced. This model can explain the residual homolog interaction in the atrad51c-1 mutant. In addition, the observation of a smaller number of chromosome fragments in atrad51c-1 meiocytes than in atrad51-1 meiocytes supports the idea that some DSBs are repaired in atrad51c-1 cells.

Besides the RAD51 homologs, the BRCA1, BRCA2 and ATM tumor suppressor proteins have been linked with DSB repair in animals and interact with each other (Khanna and Jackson, 2001; Thompson and Schild, 2002; Henning and Sturzbecher, 2003). ATM is the gene that is defective in the human disease called ataxia telangiectasia (AT) and encodes a very large protein of over 3000 amino acids with a C-terminal domain, similar to other ATM homologs. MEI1 gene was discovered originally for its mutant meiotic defects and has been recently shown to encode a protein with five BRCT motifs (He and Mascarenhas, 1998; Yang and McCormick, 2002; Grelon et al., 2003). The MEI1 protein is localized to meiotic chromosomes, suggesting that it plays a role in meiosis (Chen et al., 1998), although this has not been demonstrated genetically in part because of the embryo lethality of the mouse mutant.

The Arabidopsis ATM homolog, AtATM, is widely expressed and encodes a protein of 3856 amino acids (Garcia et al., 2000). The predicted AtATM protein has a 350-aa C-terminal phosphatidyl inositol-3 kinase like domain (58% identity and 67% similarity to the same domain in ATM), as well as a RAD3 domain just upstream of the C-terminal domain, similar to other ATM homologs. Two T-DNA insertional mutations in AtATM have been identified and found to cause reduced fertility (Garcia et al., 2003). Meiosis is abnormal in atatm mutants, with chromosome fragmentation and chromosome bridges, although pairing and synapsis seem to be normal. In addition, atatm mutants are partially fertile, but gametophytes often arrest in development. Therefore, AtATM promotes normal meiosis, possibly facilitate DNA repair, but it is not essential for meiosis, as supported by the normal meiotic recombination frequency in the mutant (Garcia et al., 2003). The atatm mutants are hypersensitive to gamma radiation and unable to induce elevated expression of DNA repair genes, such as AtRAD51, in response to DNA damage (Garcia et al., 2003), indicating it plays an important role in regulating DNA damage response.

A true BRCA1 homolog has not yet been found in Arabidopsis; nevertheless, the Arabidopsis MEI1 protein bears some resemblance to BRCA1. The Arabidopsis MEI1 gene was discovered originally for its mutant meiotic defects and has been recently shown to encode a protein with five BRCT motifs (He and Mascarenhas, 1998; Yang and McCormick, 2002; Grelon et al., 2003). BRCT motifs are found in BRCA1 and other proteins involved in DNA repair (Koonin et al., 1996; Grelon et al., 2003). The presence of BRCT motifs in MEI1 suggests that it may have related protein activities. Detailed analysis of mei1 mutants revealed that mutant meioocytes exhibit chromosome breakage during meiosis I (Grelon et al., 2003). Unlike the atrad51, atrad51c, and atxrcc3 cells, mei1 mutant meioocytes exhibit variable phenotypes in terms of
detectable. In about 5% of the cells, the chromosomal
1995; Nakagawa and Ogawa, 1999; Novak et al., 2001;
guisionable from wild-type cells in terms of sensitivity to
ble mutant cells had a phenotype similar to spo11-1 single
mousomes. The me1 somatic cells were indistin-
 be mutant phenotype and the DNA breaks in the me1 mutant
ocyte similar to the severe class of me1 single mutant
cells, indicating that spo11-1 could not rescue the me1
small number of the dou-
bletions at anaphase I, similar to those of the
formation univalents instead of bivalents and mis-segrega-
and UV-C radiations (Grelon et al., 2003).
interactions with the DNA repair
protein involved in DNA repair and are important for the
formation of double-Holliday junctions; they form a het-
erodimer in vitro that recognizes Holliday junctions (Bocker
and DNA breaks in the me1 mutant
not SPO11-1 dependent. A small number of the dou-
with DNA repair process was further supported by the observation that the
et al., 1999; Snowden et al., 2004). MER3 was first discov-
erodimer in vitro that recognizes Holliday junctions (Bocker
Ae, several genes are required for normal crossing over,
including MSH4, MSH5, and MER3 (Hollingsworth et al.,
Nakagawa and Kolodner, 2002a). MSH4 and MSH5 are
two of several eukaryotic homologs of the bacterial MutS
protein involved in DNA repair and are important for the
formation of double-Holliday junctions; they form a het-
erodimer in vitro that recognizes Holliday junctions (Bocker
et al., 1999; Snowden et al., 2004). MER3 was first discov-
ered as a mutant defective in meiosis and sequence com-
parison suggests that the MER3 protein is a DNA helicase
containing a DEXDc-box. The DNA helicase activity was
demonstrated by biochemical studies showing that MER3
can unwind double stranded DNA molecules, including
Holliday junctions (Nakagawa and Kolodner, 2002b;
Mazina et al., 2004).

The msh4, msh5, and mer3 mutant meiocytes produce
a small number of crossovers, about 10-15% of the normal
levels. The remaining crossovers are randomly distributed;
therefore, they are not sensitive to interference. In addition,
mutations in the MUS81 and MMS4/EME1 genes that
encode subunits of a heterodimeric endonuclease affect a
small portion of the crossovers that are not sensitive to
interference (Hollingsworth and Brill, 2004). Thus, there are
two genetically separable pathways in yeast for crossover
formation: one is responsible for the majority of
crossovers, is sensitive to interference, and is dependent
on the function of the MSH4, MSH5, and MER3 genes; the
other is less prominent, insensitive to interference, and
requires the function of the MUS81 and MMS4/EME1
genes (Nakagawa and Ogawa, 1999; de los Santos et al.,
2003; Bishop and Zickler, 2004; Hollingsworth and Brill,
2004; Stahl et al., 2004). In humans, statistical modeling
also supports the existence of two pathways for crossing
over, with only one of these being sensitive to interference
(Housworth and Stahl, 2003). It has been observed that the
numbers of crossovers dependent on the two different
pathways vary in different organisms (Hollingsworth and
Brill, 2004). In contrast to the budding yeast, in which the
MSH4-MSH5 dependent pathway accounts for the major-
ity of crossovers, fission yeast employs the MUS81-
MMS4/EME1 pathway to generate most of the crossovers
(de los Santos et al., 2003; Bishop and Zickler, 2004;
Hollingsworth and Brill, 2004). MSH4 and MSH5 homologs
are also important for meiosis in mammals (de Vries et al.,
1999; Kneitz et al., 2000).

Several recent studies indicate that Arabidopsis, like
yeast, also has two distinct pathways for crossover forma-
tion. Using genetic mapping studies with a quartet
mutant that produces attached pollen grains that are the 4 pro-
ducts of each meiosis, it was shown that the distribution of
crossovers in Arabidopsis is also consistent two different
kinds of crossovers: interference-sensitive and insensitive
ones (Copenhaver et al., 2002; Lam et al., 2005a). In addi-
tion, Higgins et al. (2004) reported that the MSH4 homol-

**Meiotic Recombination: Crossover Formation**

As mentioned before, crossing over is required to maintain
homolog association after disassembly of the SC and the
recombinational exchange of sequences flanking a
crossover is a major mechanism of re-distribution of
genetic information among meiotic products. Crossing
over in many organisms exhibits interference, which refers
to the phenomenon that the presence of a crossover alters
the probability of a nearby second crossover as expected
from random distribution. In the budding yeast _S. cerevisi-
ae_, several genes are required for normal crossing over,
including MSH4, MSH5, and MER3 (Hollingsworth et al.,
1995; Nakagawa and Ogawa, 1999; Novak et al., 2001;
protein has 792 amino acids and is 35% identical and 57% similar to the human MSH4 in amino acid sequence. AtMSH4 expression is highest in floral buds containing meiotic cells, reduced in mature flowers, and not detectable in vegetative organs. The AtMSH4 protein was found at numerous (~100) foci at mid-leptotene, gradually decreasing through zygotene, to only several sites at early pachytene, and completely disappearing by late pachytene, except at the ends of chromosomes (Higgins et al., 2004). This pattern of protein localization is consistent with the idea that AtMSH4 functions in recombination. This hypothesis is further supported by the observation that AtMSH4 and AtRAD51 have similar spatial and temporal patterns of distribution, although AtRAD51 might be loaded onto the chromosomes slightly earlier than AtMSH4. Furthermore, during synopsis in zygotene, AtMSH4 does not seem to remain on regions of chromosomes that have synapsed, as indicated by colocalization studies with ZYP1.

The importance of AtMSH4 in recombination, particularly crossover formation, was demonstrated by the analysis of atmsh4 mutant and RNAi lines (Higgins et al., 2004). These plants have dramatically reduced fertility, producing only 7% of the normal number of seeds, and defective in bivalent formation. The mutant meiocytes have a small number (1.55) of chiasmata per cell, compared the normal ~10 per cell. In addition, the remaining crossovers in the atmsh4 mutant are distributed randomly, indicating that Arabidopsis, like the budding yeast, also has a genetically separate pathway for interference-insensitive crossovers, which do not require the function of the AtMSH4 gene (Higgins et al., 2004). Although juxtaposed chromosomes are observed at pachytene in light microscopic images, TEM analysis of chromosome spreads indicate that SC formation is not complete, with regions of desynapsed chromosomes, suggesting AtMSH4 is involved in promoting synopsis.

The analysis of the AtMSH4 gene provides direct evidence for an interference-sensitive pathway of crossover formation in Arabidopsis. It is likely that other genes are also needed for this pathway. In yeast, the MER3 gene is also required for this pathway. Is there an Arabidopsis MER3 homolog that is necessary for crossover formation? Two recent studies have demonstrated that this is indeed the case (Chen et al., 2005; Mercier et al., 2005). Chen et al. (2005) identified a gene that is preferentially expressed in the Arabidopsis anther at the time of meiosis and found that it is expressed in meiocytes more than other tissues in the developing anther. This gene was named ROCK-N-ROLLERS (RCK) for the meiotic chromosome behavior.

Figure 12. Male meiosis I in the wild type and ptd mutants. Shown are DAPI images from wild-type (A-E), ptd-1 (F-J), ptd-2 (K-O) cells. A, B, K, zygotene. C, D, L, pachytene, wild-type and ptd cells appear similar. C, H, M, diakinesis, showing a clear contrast between 5 bivalents in the wild type and 10 univalents in ptd mutants. E, J, O, metaphase I. Unlike the 5 bivalents in the wild-type, the ptd cells have one bivalent (arrow) and 8 univalents. This figure is modified from Figure 4 of Wijeratne et al. (2006).
caused by mutations in this gene. The analysis of the full-length RCK cDNA indicates that the predicted gene structure from the genomic sequence has a number of errors, resulting in a putative protein with a wrong sequence. The newly obtained sequence revealed that RCK is a highly similar to MER3, with three conserved domains.

Several T-DNA insertional lines were available for the RCK gene, and analysis of four insertional rck mutants
A Molecular Portrait of Arabidopsis Meiosis

This study in Arabidopsis has identified a potential key player in a step after the Holliday junction. Nevertheless, a recent or animals have not uncovered a gene specific involved in this process (Wijeratne et al., 2006). Using microarray analysis with RNAs from immature Arabidopsis anthers and other tissues, a number of putative meiotic genes were identified. One of these, At1g12790, was annotated as being similar to bacterial DNA ligases and is expressed in the anthers at approximately the time of meiosis. This gene was named as PARTING DANCERS (PTD) for its meiotic phenotypes (see below). RNA in situ hybridization experiments indicate that PTD is expressed in the floral meristem, the male and female meiocytes, and other tissues. Analysis of two independent T-DNA insertion lines in the PTD gene indicates that the mutants are normal in vegetative and flower development, but have reduced fertility. Reciprocal crosses indicate that both male and female fertility are affected in the ptd mutants.

An examination of pollen development quickly established that male meiosis is abnormal in the ptd mutants (Wijeratne et al., 2006). Further investigation using DAPI-stained chromosome spreads indicate that the ptd meiocytes exhibit normal meiotic chromosome morphologies from the onset of meiosis I through pachytene, forming juxtaposed chromosomes detected as “thick threads” (Figure 12). However, at diakinesis, the numbers of bivalents in the mutants are clearly reduced, though not absent, with an average of about 2.7 (ptd-1) or 1.8 (ptd-2) bivalents per cell, instead of the normal 5. Therefore, ptd mutants could not maintain the normal number of bivalents. TEM analysis further revealed that indeed the SC is formed in the ptd meiocytes, indicating that synopsis is not affected by the ptd mutations (Figure 13). Again using a social dance as a metaphor for the meiotic homolog interactions, the homologs in the ptd mutants initially dance in pairs, able to pair, juxtapose, and synapse, but then separating from each other prematurely. Thus the mutants were named “parting dancers.”

The ptd mutant phenotypes are rather similar to those of the atmsh4 and rck/atmer3 mutants (Higgins et al., 2004; Chen et al., 2005; Mercier et al., 2005), suggesting that PTD might also be important for crossing over via the interference-sensitive pathway. This hypothesis was tested by investigating the distribution of the remaining chiasmata in ptd-1 and ptd-2 meiocytes (Figure 14) (Wijeratne et al., 2006). Unlike the wild-type chiasma distribution, which deviated dramatically from the Poisson prediction (Figure 1A), the distribution of the residual chiasmata among cells in ptd-1 and ptd-2 mutant alleles (Figures 14B and C) were very similar to the predicted Poisson distribution. Furthermore, distributions of chiasmata per single chromosome are very different between the wild type (Figure 14D) and the ptd mutants (Figures 14E and 14F). Therefore, the chiasma remaining in the ptd mutants appear not to be sensitive to interference, indicating that PTD is important for the interference-sensitive pathway.

Figure 14. Distribution of chiasmata in wild type, ptd-1 and ptd-2. A-C, chiasma distribution per meiocytes. D-F, chiasma distribution per chromosome. Black lines and closed circles indicate observed distributions whereas gray line and closed squares represent predicted Poisson distribution. A and D, the observed distributions of the chiasma in the wild-type cells and on the wild-type chromosomes, respectively. B, C, E and F, the observed distributions of the chiasma in mutant cells and on mutant chromosomes are close to the predicted Poisson distributions. This figure is Figure 5 of Wijeratne et al. (2006), with permission from Mol. Biol. Cell.
Although ptd mutants are similar to the atmsh4 and rck/atmer3 mutants in terms of reduction of chiasmata and bivalents and the distribution of the remaining chiasmata, ptd mutants differ from atmsh4 and rck/atmer3 mutants in one critical aspect, the formation of complete SC in the ptd mutants (Wijeratne et al., 2006). In other words, the onset of meiotic defects in ptd is later than that in the atmsh4 and rck/atmer3 mutants, suggesting that PTD acts downstream of AtMSH4 and RCK/AtMER3. It is possible that PTD may function after the formation of the double Holliday junctions, for example, by promoting their resolution. As mentioned earlier, late recombination nodules are correlated with crossing over and in Arabidopsis, RCK/AtMER3 is involved in the formation of late recombination nodules. Therefore, the ptd mutants were examined in detail for the formation of recombinational nodules using serial TEM sections. At both mid-pachytene and late pachytene, the ptd mutant meiocytes have similar numbers of late recombination nodules to that in the wild-type, with associated normal appearing SCs. Therefore, late recombination nodules are formed at normal levels, indicating that PTD is not required for this step in the recombinational pathway and supporting the idea that PTD acts downstream of AtMSH4 and RCK/AtMER3.

Clearly, PTD defines a critical step in the meiotic recombination pathway. What clues might its sequence provide in terms of the mechanisms of its actions? The PTD gene encode a 250 amino acid protein that has a putative rice homolog, OsPTD, with 63% amino acid sequence identity and 78% similarity over a 223-aa region, as well as putative homologs in other plants. Therefore, PTD represents a conserved function in plants, suggesting that its homologs in others may also have a similar meiotic function. Moreover, PTD shares low levels of sequence similarity in its C-terminal region to several DNA repair/recombination proteins, including ERCC1 from mammals, RAD10 from S. cerevisiae, the UvrC subunit of the ABC exonucleases in bacteria, and a bacterial NAD-dependent DNA ligase (Wijeratne et al., 2006). The level of sequence similarity is between 24 and 36% identity (45-58% similarity) over a region of up to 80 amino acids; therefore, it is unlikely that PTD has the same function as these proteins, although there may be some resemblance in biochemical activities. The ptd mutant phenotypes and the PTD protein sequence suggest that PTD may act to facilitate the resolution of the double Holliday junction, by cutting and/or ligating DNA. Furthermore, it is possible that PTD acts to resolve the double Holliday junction in favor of crossing over, rather than non-crossing over.

Relationship among Pairing, Synapsis, and Recombination

In meiotic prophase I, homologs pair and become juxtaposed; the SC is formed between homologs, and recombination also involve the same homologs. In addition, these processes occur during overlapping time periods and must be carefully coordinated and intimately coupled. However, the relationship between these processes is not always the same among different organisms. In yeast, synopsis and recombination are interdependent and closely coupled. In particular, genetic studies strongly support the idea that SC is dependent on the initiation of recombination by DSBs. On the other hand, in C. elegans and Drosophila, recombination, but not synopsis, is dependent on DSBs, indicating a different relationship in these invertebrate animals (Keeney et al., 1997; Dernburg et al., 1998; McKim et al., 1998; Peoples et al., 2002). The analysis of Arabidopsis genes provides direct evidence for the close relationship between pairing, synopsis and recombination in plants.

In plants, pairing is largely homology dependent; similarly, recombination necessarily relies on homology. From the above discussion of the phenotypes of several mutants defective in recombination, it is more than plausible that pairing and early recombination share the same molecular machinery. SPO11 induces DSBs, which allow homolog verification between homologs. RAD51 is important for DSBs repair; therefore, it is reasonable that early RAD51 foci mark DSBs. Analysis in maize wild-type and mutant meiocyte have led to the proposal that early DSBs allow homology search for homolog pairing (Franklin et al., 2003; Pawlowski et al., 2003; Pawlowski et al., 2004). It has been shown that RAD51 is part of some early meiotic nodules in lily (Anderson et al., 1997) and that recombination nodules may be involved in pairing and synopsis (Anderson et al., 2001; Anderson et al., 2004). The analysis of the Arabidopsis AtRAD51 gene provides genetic support for its role in homolog pairing and/or juxtaposition (Li et al., 2004). Furthermore, the phenotypes of atrad51c and atrxcc3 mutants also support the function of these genes in both DSBs repair and pairing. It is known that early RAD51 foci, thus DSB sites, are more numerous than recombinational crossovers in maize and Arabidopsis (Franklin et al., 1999; Higgins et al., 2004). Therefore, most of SPO11-induced DSBs are probably generated to allow pairing, which involved base-pairing of DNA from two non-sister chromatids. After homology has been established, most of the DSBs are repaired without exchange of flanking sequences (crossing over), whereas a small fraction of DSBs remain to form crossovers and chiasmata, which maintain bivalent. This hypothesis predicts that all genes needed for the generation and repair of DSBs are also
important for pairing, and that pairing is correlated with repair of DSBs, or gene conversion. In addition to AtSPO11-1, AtRAD51, AtRAD51C, and AtXRCC3, AtMRE11, and AtRAD50 are also required for early recombination steps. Although details of homolog pairing in the atmre11 mutant meiocytes are not available, the pachytene phenotypes are consistent with a pairing and/or synapsis defect. Further analysis of atmre11 and other mutants to fully investigate their pairing properties is needed to verify the above proposed direct coupling of DSB repair and pairing.

The interdependence of synapsis and recombination in plants is very well supported. Although synapsis was not directly observed in the atspo11-1 mutant, the atspo11-1 mutant phenotypes is consistent with synapsis being SPO11-dependent (Grelon et al., 2001). Furthermore, analysis using TEM on synapsis in the atrad51-1 and atrad51c-1 mutants (Li et al., 2004; Li et al., 2005) argue strongly for a close relationship between recombination and synapsis, similar to that in yeast. Moreover, the atmsh4 and rck/atmer3 mutants are also defective in synapsis. During normal meiosis, it is likely that DSBs are

Figure 15. Spindle structures in wild-type and atk1-1 male meiocytes. The microtubules (green) were visualized with anti-tubulin antibodies; DNA was stained with DAPI and the false red color was generated using Photoshop. A-D, I-L, wild-type. E-H, M-P, atk1-1. A and E, prophase I, with perinuclear microtubules. B and F, metaphase I; the atk1 spindle is unfocused at the poles. C and G, anaphase I, showing abnormal chromosome segregation in the atk1 cell. D and H, telophase I. I and M, prophase II. J and K, metaphase II, with multiple mini-spindles in the atk1 mutant. L and O, anaphase II. L and P, telophase II, with more than 4 nuclei in the mutant. This figure is Figure 5 of Chen et al. (2002).
the sites of early recombination nodules. In addition, a subset of DSBs might be the sites for loading SC proteins, as supported by the analysis of ZYP1 foci, which initially number in 20-25 (Higgins et al., 2005). This can explain why in the absence of SPO11-1 induced DSBs, synopsis is defective. AtDMC1 is required for bivalent formation, indicating a critical role in crossover formation. However, unlike AtRAD51, AtRAD51C, and AtXRCC3, AtDMC1 does not seem to be required for DSBs repair, suggesting that it may have a more specialized function for processing those DSBs targeted for crossover formation. It is possible that these DSBs correspond to late recombination nodules that require AtMSH4 and RCK/AtMER3, and that facilitate the loading of ZYP1. However, the localization of ZYP1 in atmsh4 meiocytes indicates that AtMSH4 is not required for early loading of ZYP1 (Higgins et al., 2005). It is not known what effect rck/atmer3 mutations might have on ZYP1 localization to the chromosomes.

**Chromosome Separation and Segregation**

The elaborate process of prophase I involving homolog pairing, synopsis and recombination results in formation of the bivalents at diakinesis. The purpose of this highly complex and tightly controlled "meiotic dance" is to make sure that homolog segregation at anaphase I is accurate. However, bivalent formation is not sufficient for proper segregation. Before the homologs can separate, the bivalents need to move to the metaphase plate, located at the center of the meiotic spindle. This process depends on a

![Figure 16: Wild-type and atk1-1 male meiosis. A.-D., I., J., L., wild type; E.-H., K., M.-T. atk1-1. A. and E. zygotene, B and F. pachytene, C and G. diplotene. D and H. diakinesis. Mutant cells during prophase I seem normal. I and M. metaphase I, the position of bivalents are not normal in the atk1-1 cell, with one bivalent (arrow) located slightly away from the equator; three others (arrowheads) are not aligned in parallel. K and N, metaphase I to anaphase I transition in atk1-1, showing asynchrony in homolog separation (arrows). J and O, anaphase I; in atk1-1 meiocytes, some pairs of homologues are misaligned (arrowheads in K and O). L and P, telophase I; atk1-1 has uneven chromosome segregation. This figure is modified from Figure 4 of Chen et al. (2002).](https://bioone.org/journals/The-Arabidopsis-Book)
properly assembled spindle and other spindle associated functions. Following the alignment of bivalents along the equatorial plane of the spindle, sister chromatid cohesion along chromosomal arms must be removed via the proteolytic degradation of specific cohesin subunits, to allow homolog separation at the onset of anaphase I. Subsequently in anaphase I, the newly separated homologs are pulled by the forces of the spindle microtubules towards the two spindle poles.

The meiotic spindle provides the force for chromosome movement and is critical for normal chromosome segregation. During meiosis I, the spindle forms at prometaphase I into a bipolar structure (Franklin and Cande, 1999). In Arabidopsis, a mutant (atk1, for Arabidopsis thaliana kinesin1) was found to have greatly reduced male fertility and mutant meiocytes form abnormal meiotic spindles (Chen et al., 2002). The atk1 mutant meiotic spindles have unfocused poles, with disorganized microtubules (Figure 15). In addition, bivalents in mutant meiocytes fail to align at the metaphase I plate perfectly, with some bivalents seemingly lagging behind in their movement to the metaphase I plate (Figure 16). Therefore, a normal-shaped spindle may be needed to facilitate the alignment of the bivalents. The atk1 mutant meiocytes also exhibit slightly asynchronous homolog separation (Figure 16). It is possible that uniform homolog separation requires an even distribution of microtubule forces from a properly formed spindle. The ATK1 gene is the same gene as the previously cloned KATA gene, which encodes a kinesin protein (Mitsui et al., 1993; Liu et al., 1996; Chen et al., 2002). ATK1 has a predicted C-terminal motor domain and is highly similar to the Drosophila NCD and budding yeast KAR3 proteins; both NCD and KAR3 are important for meiotic and/or mitotic spindle morphogenesis (Hatsumi and Endow, 1992; Roof et al., 1992). Therefore, ATK1, NCD and KAR3 are structurally and functionally conserved proteins.

Figure 17. DNA breaks in mmd1 microsporocytes detected by the TUNEL assay. A-D, wild type cells showing DNA (red), each with an inset in the upper right-hand corner showing no signal detected for DNA breaks (green). E-H, Chromosomes in mmd1 cells; I-L, DNA breaks in the same mmd1 cells as in E-H, respectively. A, diakinesis. B, prometaphase I. C, G and K, metaphase I. D, H and L, anaphase I. E and I, early diakinesis. F and J, late diakinesis. Chromosomes in mmd1 cells are labeled with TUNEL starting at late diakinesis. Bar = 10mm. This figure is modified from Figure 4 in Yang et al. (2003b).
important for meiotic spindle assembly. The abnormal unfocused spindle in the atk1 mutant is also similar to that of the maize mutant dv (divergent spindle) (Staiger and Cande, 1990).

Both ncd and kar3 mutants also have mitotic defects (Hatsumi and Endow, 1992; Roof et al., 1992; Endow et al., 1994). ATK1 is also expressed in vegetative and floral organs, suggesting that it may also have a mitotic function. Careful examination of mitotically dividing cells of the atk1 mutant revealed that the mitotic spindle is also affected and mitosis is prolonged in the mutant (Marcus et al., 2003); however, the spindle defect is not severe enough to cause gross developmental abnormalities (Chen et al., 2002). The mild defect in mitotic cells might be due to functional redundancy, because Arabidopsis has another gene, ATK5, which encodes a protein highly similar to ATK1, with an overall 83% amino acid sequence identity to ATK1. Both ATK1 and ATK5 proteins can bind to and move along microtubules in vitro (Marcus et al., 2002; Ambrose et al., 2005), suggesting that they have very similar functions. Whether they indeed have redundant in vivo functions will be determined by genetic studies.

At the metaphase I/anaphase I transition, the separation of homologs requires the resolution of sister chromatid cohesion. In Arabidopsis, it is not clear how cohesins are removed. Alternatively, the ask1 mutant is defective in chromosome separation and segregation at anaphase I (Yang et al., 1999). In ask1 meiocytes, some chromosomes remain associated when they are pulled by the spindle and become stretched. In addition, the forces of the spindle also seem to cause chromosome fragmentation. The failure of chromosome separation then results in grossly uneven chromosome distribution. Cytokinesis then produces abnormal number of microspores contain abnormal amounts of DNA. ASK1 encodes a homolog of the SKP1 protein (Yang et al., 1999), which is a critical component of SCF complexes (for SKP1, cullin/CDC53, F-box protein) (Zhang et al., 1995; Bai et al., 1996; Connelly and Hieter, 1996; Peters, 1998). As discussed before, the SCF complexes are E3 ubiquitin-protein ligases that control a number of biological processes by targeting specific proteins for degradation by the 26S proteosome (Zheng et al., 2002). The chromosome behavior of the ask1 mutant meiocytes suggests that an ASK1-containing SCF ubiquitin ligase is involved in the removal of the cohesin complex along chromosomal arms. Recently, it was found that the ASK1 protein accumulates during early prophase I, primarily at leptotene to pachytene, at levels higher than those at other stages (Wang and Yang, 2005), suggesting that the effect of ask1-1 mutation on chromosome separation might be indirect consequence of an early function of ASK1. In addition, the reduction of ASK1 function in the ASK1/ask1-1 heterozygous plants is associated with an increase in the rate of recombination, suggesting that ASK1 negatively regulates recombination (Wang and Yang, 2005). Further investigation is needed to understand the role of ASK1 and SCF complexes in meiosis.

In addition to ASK1, Arabidopsis has 20 other SKP1 homologs; among these, ASK2 is most similar to ASK1 in sequence and expression patterns (Zhao et al., 2003b; Kong et al., 2004). However, the fact that ask1 is completely defective in male meiosis, resulting in total male sterility, indicates that ASK2 is not able to fulfill the required function. ASK2 is expressed at a level lower than that of ASK1; therefore, it is possible ASK2 is not expressed sufficiently for the male meiotic function. Alternatively, the ASK2 protein might be different from ASK1 in sequence, such that ASK2 is not able to interact with other proteins as well as ASK1. These ideas were tested using transgenic plants overexpressing ASK2 (Zhao et al., 2003a); when ASK2 is overexpressed in the ask1 mutant background, the meiotic defects are partially corrected and the plants are partially fertile. However, the fact that these plants are still partially defective indicates that the ASK2 protein is functionally distinct from ASK1. This idea is further supported by the phylogenetic finding that ASK1 and ASK2 are members of separate clades which each have representatives of many plants (Kong et al., 2004). Therefore, ASK1 and ASK2 are not equivalent in male meiosis, although they do have redundant functions during embryo and seedling development (Liu et al., 2004).

### Meiotic Progression: Potential Regulators

To ensure the success of a complex process such as meiosis, it is necessary to control the timing and sequence of various meiotic events. For example, chromosome condensation and sister chromatid cohesion are regulated by protein phosphorylation (Wei et al., 1998; Suja et al., 1999; Wei et al., 1999; De Souza et al., 2000). In yeast and nematode, the mitotic histone H3 phosphorylation is controlled by the balanced activities of both a protein kinase (pp1/Aurora) and a phosphatase (Glc7/PP1) (Francisco and Chan, 1994; Francisco et al., 1994; Hsu et al., 2000). Furthermore, it was shown that the maintenance of sister-chromatid cohesion in maize is correlated with phosphorylation of histone H3 (Kaszas and Cande, 2000), suggesting a role in the regulation of sister chromatid cohesion. Another study indicates that dissociation of sister chromatid cohesion in maize is correlated with phosphorylation of the Xenopus XSA1/Scc3p cohesin subunit (Losada et al., 2000). Furthermore, purified cyclin B-CDK has been shown to phosphorylate XSA1 in vitro and reduce its ability to bind DNA or chromatin (Losada et al., 2000). These results together suggest that phosphorylation of several
proteins, at least in part mediated by cyclin-CDK, may be involved in the separation of sister chromatids.

Cyclins and CDKs were originally discovered as factors promoting the maturation of frog oocytes (MPF). In yeast, cyclins and CDKs (cdc2 from S. pombe and CDC28 from S. cerevisiae) play pivotal roles in controlling the mitotic cell cycle (Futcher, 1991; Nasmyth, 1993; Murray, 1994; Reed, 1996). In addition, they also function in regulating meiosis. For example, Cib1, Cib3, and Cib4 regulate events just before meiosis I (Grandin and Reed, 1993) and also meiosis II (Dahmann and Futcher, 1995). Moreover, the mitotic S-phase cyclins Clb5 and Clb6 are also required for the meiotic S phase (Dirick et al., 1998; Stuart and Wittenberg, 1998). Furthermore, Clb5 and Clb6 also seem to be important for the meiotic prophase I, including synopsis and recombination (Smith et al., 2001); however, the fact that these proteins are required for pre-miotic S phase makes it different to determine whether the Clb5/Clb6 function in prophase I is direct. In mouse, the cyclin A1 is specifically expressed in the testis and mutant mice are male sterile and defective in male meiosis (Liu et al., 1998a). In the mutant, male meiosis arrests before metaphase I, with desynaptic chromosomes, and then undergo programmed cell death. Cyclin-CDK also plays critical roles in regulating sister chromatid cohesion during mitosis. Cyclin-CDK mediated phosphorylation regulates the activity of the APC E3 ubiquitin ligase, thereby controlling the timing of cohesin removal (Heo et al., 1999; Zachariae, 1999).

In Arabidopsis, a screen for fertility defects among a transposon insertional population identified a mutant with greatly reduced fertility (Azumi et al., 2002). This mutant was named solo dancers (sds) because meiotic chromosomes progress through prophase I largely as individuals, unlike the wild-type chromosomes, which undergo prophase I as pairs following homolog pairing. The sds mutant meiocytes are defective in homolog pairing/juxtaposition and recombination, resulting in greatly reduced bivalent formation. The sds mutant phenotypes are nearly identical to those of atspo11-1 and atdmc1 mutants, suggesting that SDS is required for the SPO11-dependent pathway for meiotic recombination. At the same time, in contrast to the atrad51, atrad51c, or atrxxc3 mutants, the sds mutant meiocytes do not have fragmented chromosomes, suggesting that the sds mutant cells either do not have SPO11-induced DSBs or are able to repair the DSBs. In addition, sds mutant meiocytes exhibit premature partial separation of sister chromatids, suggesting a possible role in regulating cohesion. In situ hybridization experiments indicate that SDS is specifically expressed in male and female meiotic cells; in addition, SDS encodes a putative novel cyclin, which is phylogenetically distinct from other cyclins (Azumi et al., 2002; Wang et al., 2004a). It is likely that SDS activates one or more CDKs to regulate protein activities via phosphorylation, thereby coordinating multiple meiotic events, including pairing, synopsis, recombination, and possibly sister chromatid cohesion.

In addition, the Arabidopsis tardy asynchronous meiosis (tam) mutant is abnormal in the timing of meiotic divisions, resulting in the formation of intermediate structures such as dyads, which are not produced by wild-type meiosis (Magnard et al., 2001). In particular, in cells entering metaphase I or metaphase II, there is a clear indication of asynchronous meiosis (Magnard et al., 2001). Therefore, TAM may control the entry into metaphase, as further supported by the fact that the tam mutation is in the gene encoding the cyclin A CycA1,2 (Wang et al., 2004b). Using a GFP fusion, it was observed that TAM/CycA1,2 is present at its highest level at pachytene, becoming undetectable at diakinesis and subsequent meiotic stages, suggesting it regulates later stages of meiosis indirectly, presumably via the targets of TAM/CycA1,2-activated phosphorylation (Wang et al., 2004b). The function of TAM/CycA1,2 and the mouse cyclin A1 (Liu et al., 1998a) in meiosis suggests that plants and animals may share conserved aspects of the control of meiotic progression. Despite the asynchronous meiosis, the tam mutant is still fertile; therefore, it is possible that mutant screens for a reduction of fertility might have missed mutants that have altered meiotic timing but are fertile.

Another possibility for the small number of mutants in meiotic progression is that meiotic progression may share regulators with the mitotic cell cycle and mutations in such genes might have severe defects in mitotic growth, preventing their recovery as meiotic mutants. For example, the Arabidopsis homolog of the yeast CDC45 gene is expressed in floral buds; a reduction of CDC45 expression using an RNAi construct resulted in fertility defects (Stevens et al., 2004). Phenotypic characterization of these RNAi lines indicates that polyads instead of tetrads were formed from meiosis and nonviable pollen grains were produced. Furthermore, meiotic chromosomes in the RNAi transgenic plants are fragmented at late prophase I and the fragmentation becomes more severe at metaphase I and anaphase I. In yeast, CDC45 regulates mitotic DNA replication (Zou and Stillman, 1998, 2000), suggesting that CDC45 in Arabidopsis may regulate the pre-miotic DNA replication; a defect in DNA synthesis provides an explanation for chromosome fragmentation during meiosis.

Another potential Arabidopsis regulator of meiosis was discovered by two independent studies, called MALE MEIOTIC DEATH1 (MMD1) or DUET (Reddy et al., 2003; Yang et al., 2003b). Mutations in the MMD1/DUET gene cause severe defects in the progression of meiosis and the
inability to produce any normal microspores. In prophase I, the mmd1 mutant meiocytes appears normal up to diakinesis (Yang et al., 2003b). Subsequently through telophase II, mutant male meiocytes have chromosome fragmentation and cytoplasmic shrinkage; suggesting that the cells are undergoing programmed cell death. In addition, these mutant cells have positive TUNEL signal, indicating the presence of many DNA breakage in the chromosomes (Figure 17). The mmd1 mutant meiotic cells die before cytokinesis, resulting in a failure to produce any microspores. The mmd1 mutant was caused by a Ds transposon insertion just downstream of the ATG codon, resulting in a likely null allele (Yang et al., 2003b). In situ hybridization experiments indicate that MMD1 is preferentially expressed in the meiocytes. The predicted MMD1 protein contains a C-terminal PHD finger domain. PHD fingers are cystein-containing domains, some of which have been shown bind other proteins, DNA, or RNA (Aasland et al., 1995; Kennison, 1995; Coscoy and Ganem, 2003; Reddy et al., 2003; Yang et al., 2003b). The duet mutant has a milder phenotype than that of the mmd1 mutant, with delayed meiotic cytokinesis that often results in dyads (two spores) instead of tetrads (Reddy et al., 2003). The duet microspores usually proceed with one or two mitotic divisions, and then undergo cell degeneration. The duet mutation is also caused by a Ds insertion, which is approximately 500 amino acid residues downstream of the N-terminus and just upstream of the PHD finger. It is possible that the duet allele can produce a truncated protein that is partially functional. It is worth noting that in most plant meiotic mutants, the abnormal meiocytes do not undergo programmed cell death, unlike the meiotic mutants in animals. Therefore, the phenotypes of the mmd1 mutant are rather unusually for a plant meiotic mutant, and may suggest a general regulatory function of the MMD1 gene. The hypothesis that MMD1 is a general regulator, rather a promoter of a specific meiotic event, is also supported by the lack of specific meiotic chromosomal defects in pairing, juxtaposition, synapsis, or segregation in the mmd1 mutant.

Another potential regulatory gene was uncovered by the mutants ms5 and tdm1, which are male sterile and defective in male meiosis (Chaudhury, 1993; Ross et al., 1997). Detailed phenotypic analysis of tdm1 revealed that the mutant cells undergo meiosis I and II in a way similar to the wild-type cells; however, meiosis II is followed by an abnormal third division without a new round of DNA replication, resulting in the formation of polyads of 5-8 abnormal spores. Therefore, MS5 normally regulates the completion of meiosis II by presenting another division. The T-DNA insertional ms5-2/tdm1 mutation was used to clone the MS5 gene (Glover et al., 1998), which is a member of a gene family conserved in plants, including multiple members in Arabidopsis and rice. The MS5 protein sequence is novel; although it has limited similarity to a synaptonemal complex protein from rat, it is not clear what the physiological significance of this similarity is, as the ms5 mutant does not seem to have any defect in synapsis or other abnormal chromosomal behavior during prophase I.

**Meiotic Cytokinesis**

At the end of meiosis II, four clusters of chromosomes are formed and they become four new nuclei. Cell membranes and wall materials are then transported to the space between these nuclei and cytokinesis occurs to generate four haploid microspores. Using immuno-electron microscopy and electron tomography, Otegui and Staehelin (2004) showed that meiotic cytokinesis entails the formation of a distinctive post-meiotic-type cell plate. The formation of the post-meiotic cell plates depends on the function of mini-phragmoplasts and occurs simultaneously throughout the divisional plane. Presumably, vesicles carrying materials for cell plate are transported along microtubules of the mini-phragmoplast by microtubule associated motor kinesins. Fusion of these vesicles results in a tubular network, which fuses at its periphery with the plasma membrane, prior to the formation of the cell plate.

The Arabidopsis stud (std) and tetraspore (tes) mutants were found to have similar phenotypes and subsequently shown to be allelic (Hulskamp et al., 1997; Spielman et al., 1997). In the std/tes mutant meiocytes, meioses I and II proceed normally, but cytokinesis is defective and cell wall formation is incomplete. Consequently, a single microspore is formed with four nuclei that are partially separated by incomplete walls and a single cytoplasm. The abnormal microspore is able to continue through pollen development. In normal pollen development, the microspore first divides asymmetrically to form a large vegetative cell and a small generative cell, which is then internalized to be surrounded by the vegetative cells. The generative cell divides again inside the vegetative cell to form two sperm cells. During std/tes mutant pollen development within the large abnormal microspore, the four nuclei divide separately. The result is a very large pollen grain with four vegetative nuclei and up to eight sperm cells. Upon pollination, the large pollen grain produces a single pollen tube, allowing the fertilization of one ovule, resulting in greatly reduced male fertility (Hulskamp et al., 1997).

The TES/STD gene has been cloned using a mapped-based cloning strategy and it encodes a kinesin with an N-terminal motor domain (Yang et al., 2003a). The TES protein is most similar to two closely related tobacco kinesins, NACK1 and NACK2 (64% and 58% identity over the entire proteins, respectively), that are required for cell plate
such as AtSPO11-1, AtDMC1, and SDS, that are readily depends on not only single-copy meiosis-specific genes, it is already indicated by a number of genes, meiosis ing not only plant meiosis, but also meiosis in general. As Arabidopsis as an excellent model system for understand ing the BRCA2 genes. It is likely that future efforts will greatly expand the ranks of this second category of genes important for meiosis.

While currently available tools are invaluable in understanding meiotic gene functions, additional technology need to be developed. Meiosis in Arabidopsis is usually analyzed using chromosome spreading, which may distort mutant phenotypes, including exaggeration and loss of some details. In maize, meiotic chromosomes can be observed in three-dimensional images using deconvolu-

Concluding Remarks

The development of cytological tools for Arabidopsis by pioneers of plant meiosis has opened the door for the molecular genetic investigations of the meiotic machinery. Efforts by a number of laboratories over the last decade have identified key genes important for processes from early prophase I to meiotic cytokinesis, not only demonstrating conservation of gene functions between yeast and plants, possibly also with vertebrate animals, but also uncovering novel aspects of a molecular portrait of Arabidopsis meiosis. These studies have firmly established Arabidopsis as an excellent model system for understanding not only plant meiosis, but also meiosis in general. As it is already indicated by a number of genes, meiosis depends on not only single-copy meiosis-specific genes, such as AtSPO11-1, AtDMC1, and SDS, that are readily discovered by forward genetics or examined using reverse genetics, but also requires genes that are functionally redundant or are also essential for mitotic growth, including the BRCA2 genes. It is likely that future efforts will greatly expand the ranks of this second category of genes important for meiosis.

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