food-deceptive orchids pollinated primarily by female bees, has also been shown recently [10]. Collectively, these data suggest that specificity and exploitation of male mating behavior provide higher male fitness for the plants through improved pollen export. Within *Gorteria*, some forms nevertheless rely mostly on pollination by food-seeking females, perhaps because it optimizes pollination success, the female component of reproductive fitness [6].

In *Gorteria*, pseudocopulation obviously evolved from food reward. In some forms, perhaps representing the intermediate evolutionary stage, simple petal spots only release inspecting-behavior by male insects, but no pseudocopulation [6]. Spots eliciting pseudocopulations are three-dimensional ornaments consisting of three types of specialized cells [11], with possible scent emission not yet investigated. The selective force leading to a continuous elaboration of petal spots is likely the pre-existing preference of males for female-like features. Sexual deception thus evolves under pre-existing bias of male pollinators selecting for different degrees of floral mimicry. As shown by Ellis and Johnson [6], *Gorteria* forms eliciting mating behavior in males are less attractive for females and vice versa, suggesting males and females have different preferences and thus select for different floral traits. The *Gorteria* systems shows that mimicry can evolve as a continuum, in which not all forms neatly fit into man-made categories of perfect resemblance between mimic and model. Examples for such imperfect mimicry are becoming more commonly known [16–18], and the evolutionary mechanisms through pre-existing bias better understood [19,20]. The new study by Ellis and Johnson highlights that pollination through male mating behavior can convey selective advantages and, further, that prerequisites of sexual floral mimicry are not limited to orchids. Nevertheless, orchids have evolved the most sophisticated examples of female-insect imitations, some being striking even to human eyes. But besides these textbook examples of sexual deception, a sharpened focus will likely unravel more subtle forms of sexual mimicry in various plant taxa in the future.

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Male Meiosis: Y Keep It Silenced?

What drives defective spermatocytes into apoptosis during mid-pachytene? A recent study identifies the first mid-pachytene 'killer' genes: two Y-linked transcription factors, the *Zfy1/2* gene pair, must be silenced to avoid apoptosis.

Attila Tóth and Rolf Jessberger

Successful reductional meiotic division and the generation of haploid gametes requires the formation of crossovers (COs) between homologous chromosomes (homologues, i.e. two pairs of sister chromatids) during the first meiotic prophase in most organisms, including mammals. Inter-homologue CO formation involves the active generation of DNA double-strand breaks (DSBs), which are repaired through recombination between the homologues. This happens within a prominent meiosis-specific chromatin structure, the synaptonemal complex (SC; reviewed in [1–5]).

To prevent formation of gametes with abnormal genomic content, gametogenesis must be blocked in spermatocytes that fail to form COs between all pairs of homologues and/or fail to repair DSBs. Indeed, for many decades researchers have noted that

mutant spermatocytes that fail in DSB repair or SC formation die at a specific stage of meiosis corresponding to mid-pachytene, which takes place in testis tubules at stage IV of the testicular epithelial cycle. However, genes responsible for stage IV apoptosis have not been identified. In addition, oocytes that bear the same mutations are not eliminated efficiently in mid-pachytene. Instead, in most mutants, oocytes undergo apoptosis soon after pachytene, and in some mutants they progress even further [6,7].

The molecular basis of the sex-specific meiotic prophase quality surveillance mechanisms have been at the center of a lively debate for a long time. It has been suggested that the sex differences in prophase surveillance mechanisms or checkpoints are connected to the distinct transcription status of sex chromosomes in wild-type oocytes and spermatocytes. Synapsed chromosomes are usually transcriptionally active, while unsynapsed chromosomes become silenced during pachytene. Except for a short region of homology, the Y and X chromosomes in spermatocytes cannot synapse, are silenced, and form a distinct male-specific chromatin structure, the sex body. In oocytes, the two X chromosomes synapse and remain transcriptionally active. Interestingly, common to most if not all of the meiotic mutants exhibiting stage IV apoptosis is the failure to fully synapse homologous autosomes in meiotic prophase I and the failure to effectively silence sex chromosomes in males. A prominent, perhaps the only, exception is in XYY spermatocytes, in which apoptosis occurs without apparent defects in DSB repair or autosomal synapsis but with defective Y chromosome silencing [5] (Figure 1). Therefore, it was suggested that spermatocyte progression beyond mid-pachytene requires efficient silencing of sex chromosomes [8].

How can sex chromatin silencing be linked to surveillance that monitors defects in DSB repair and SC formation? The ATR kinase, a pivotal DSB checkpoint kinase in somatic cells, is recruited to both DSB sites and to unsynapsed chromatin during meiosis [5]. Active ATR phosphorylates histone H2AX. Consequently, phospho-H2AX (γH2AX) accumulates on unsynapsed chromatin, which results in meiotic silencing of unsynapsed chromatin (MSUC). Upon full autosomal synapsis, ATR is restricted to unsynapsed sex chromatin, which is believed to cause their efficient silencing. Since the amount of silencing factors available in a cell is limited, recruitment of ATR activity to autosomes in DSB repair and SC mutants means less recruitment to sex chromosomes. Thus, meiotic sex chromosome inactivation (MSCI) becomes compromised and may fail to various degrees, depending on the extent of autosomal asynapsis [5]. A key prediction of the above model is that there must be 'killer' gene(s) on sex chromosomes, whose 'pathological' expression in mutant pachytene spermatocytes results in apoptosis.

As reported in this issue of *Current Biology*, Royo *et al.* [9] examined the 15 known Y-linked genes and identified two Y-encoded transcription factors, Zfy1/2, as stage IV killer proteins. What is the evidence? In several mutants there is a very strong correlation between pachytene expression of *Zfy1/2* and stage IV mid-pachytene apoptosis. The work of Royo *et al.* strongly suggests that in XYY male mice, in which the two Y chromosomes frequently synapse, and thus escape silencing, spermatocytes displaying synapsis of the Y chromosomes undergo stage IV apoptosis. Autosomal DSB repair and SC formation, however, appeared normal. Crucially, when the two Y-linked genes, *Zfy1* and *Zfy2*, are placed on autosomes, expression of these genes during pachytene triggers apoptosis. In contrast, males remain fertile when *Zfy1* and *Zfy2* are inserted as transgenes into the X chromosome, which is silenced during pachytene. Consistently, if the authors moved the extra Y chromosome in XYY males onto the distal end of the X chromosomes and thereby prevented Y–Y synapsis, MSCI was restored and the spermatocytes survived meiotic prophase. Having identified *Zfy1/2* as the only Y chromosomal killer genes, it still remains likely that there are also X-linked stage IV killer genes to be discovered, since Royo *et al.* [9] reported stage IV apoptosis in mutant mice where only X chromosome silencing is defective.

Stage IV apoptosis in males depends on neither defective DSB repair nor general autosomal SC failures, as Royo *et al.* [9] showed. Nevertheless, the identification of *Zfy1/2* as the first

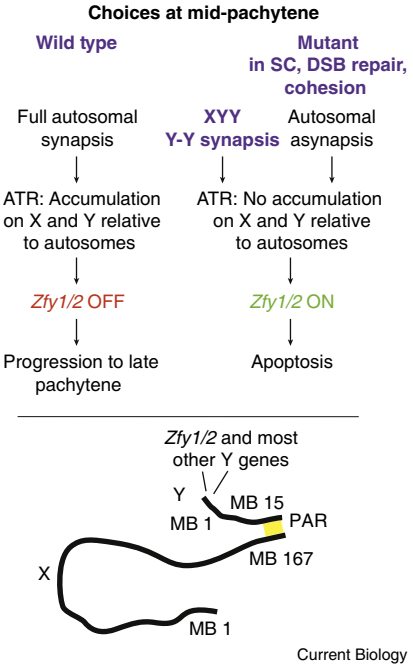

Figure 1. Pathway of spermatocyte stage-IV/mid-pachytene apoptosis.

Deficiencies in various processes (mutant, right) cause autosomal asynapsis. Asynapsed regions recruit ATR and partner proteins. These become limiting, do not accumulate as much on sex chromosomes anymore and therefore do not suffice for meiotic sex chromosome inactivation. This allows X and Y chromosome genes to be transcribed, among them the killer genes *Zfy1/2*. Y–Y synapsis has a comparable effect. *Zfy1* and *Zfy2* are silenced in wild-type spermatocytes (wild-type, left), which therefore survive. The pachytene sex chromosomes are shown in the lower part of the figure, with synapsis at their rather short (ca. 700 kbp; [13]) pseudo-autosomal region of homology (PAR) and the location of the *Zfy1/2* genes indicated (MB, megabase pairs).

stage-IV killer genes provides robust support for the idea that incomplete autosomal SC formation can trigger apoptosis through transcriptional up-regulation of sex chromosomes during stage IV. One important question is if there is a common mechanism underlying the female and male prophase surveillance pathways. If so, why are efficiency and timing of defective meiocyte elimination different in males and females? ATR activity is recruited to unsynapsed chromosome regions in meiocytes of both sexes by a still mysterious mechanism that likely involves elusive meiosis-specific proteins. Inappropriate silencing of essential genes on unsynapsed chromosomes

in females could trigger apoptosis at different times during prophase depending on which particular gene is silenced. However, MSUC at variable unsynapsed chromatin regions may be insufficient to explain the elimination of oocytes in many of the DSB and SC mutants. It is possible that both unrepaired DSBs and unsynapsed chromatin can trigger sustained ATR activation. High ATR activity might be incompatible with oocyte survival beyond the pachytene or diplotene stages, independently from its possible effect on gene expression.

The involvement of ATR in the detection of SC and DSB defects seems to be similar in males and females. This may pose the danger that a female-type meiotic prophase checkpoint response would trigger apoptosis in all spermatocytes due to lack of SC formation and delayed DSB repair on the X/Y pair in males. Thus, during the course of the evolution of sex chromosomes in mammals an alternative prophase surveillance mechanism had to emerge in males. It appears that the solution came in the form of a mechanism that acts at an earlier stage than the female checkpoint controls. This surveillance mechanism is exceptionally robust because elimination of defective spermatocytes does not depend on the function of proteins that are involved in the monitoring of essential meiotic processes, i.e. synapsis and DSB repair. Instead, the sensory mechanisms, in particular ATR activation, are required for progression beyond stage IV/mid-pachytene. It is likely that this male stage-IV death mechanism can be inactivated only by multiple mutations affecting redundant killer genes on the Y and X chromosomes, two of which have been identified by Royo *et al.* [9].

How do ZFY1/2 proteins kill? Gene duplication during evolution probably generated *Zfy1* and *Zfy2*, which encode very similar zinc finger-type transcription factors [10]. *Zfy1* is the mouse homolog of human *ZFY*, and there are other *ZFY* family members on the X chromosome (*Zfx*) and on autosomes (*Zfa*). The normal biological role of Zfy1/2 proteins remains elusive, although they are expressed during embryogenesis in somatic cells and primordial germ cells of the genital ridge, in meiosis before pachytene, and later in spermatids during spermiogenesis [11]. Thus, to understand how Zfy1 and Zfy2 kill, one must know the target genes regulated by them. Another question, perhaps even therapeutically relevant, concerns options to down-regulate *ZFY1/2* expression when that is considered pathological. Infertility in men affects about 5–7% of couples [10,12]. Among those patients are XYY males, which show very frequent Y–Y synapsis. It is not far-fetched to speculate that MSCI failure and *ZFY* expression causes or at least significantly contributes to azoospermia seen in these men.

Because *ZFY1* and *ZFY2* are expressed at various stages during germ cell development, they may have essential functions during gametogenesis. Thus, it is possible that the mid-pachytene surveillance mechanism cannot be inactivated without deleterious affects on gametogenesis, which would make this quality control mechanism inescapable during male meiosis.

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Bacterial Cytokinesis: FzlA Frizzes FtsZ Filaments for Fission Force

Most bacteria divide by assembling filaments of the tubulin-like protein FtsZ into a cytokinetic ring, which then constricts. A recent study suggests that *Caulobacter crescentus* uses a novel regulator, FzlA, to activate ring constriction by inducing helical bundles of FtsZ filaments.

Tushar K. Beuria and William Margolin*

The protein FtsZ is conserved in most bacteria, plant plastids, and many archaea, and is a structural homolog of tubulin that plays an important role in cell or organelle division [1]. Like tubulin, FtsZ assembles into polymers in the presence of GTP, which is hydrolyzed upon assembly. FtsZ does not form microtubules, but FtsZ protofilaments tend to interact laterally and form straight bundles when incubated with ionic or protein cofactors [2]. High-resolution imaging of *Escherichia coli* cells suggests that the dividing ring, called the Z ring, is