Meiotic cell cycle progression and its connection to genome evolution

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Main points of presentation

- The meiotic cell cycle
- The meiotic checkpoint network (MCN)
- Our work on meiotic cell cycle progression in Arabidopsis
- Consequences of defective cell cycle progression in meiosis
- How unreduced gametes may affect genome evolution

Different cyclins oscillate once in a cell cycle with CYCAs expressed from S phase to G2 or M phase



Meiosis vs. mitosis





\leftarrow S phase and G₂ phase

Prophase I

Adapted from Subramanian and Houchwagen, Cold Spring Harb Prospet Biol, 6: a016675, 2014

Outcomes of defective meiotic cell cycle progression

- Animals: cell death without completion of meiotic cell cycle progression
- Yeasts: cell cycle arrest or switching to mitosis if conditions are right
- Plants: delayed cell cycle progression but progressing through meiosis

Meiotic cell cycle progression is regulated by the meiotic checkpoint network (MCN)

- MCN consists of a smaller number of proteins that are highly connected
- MCN functions in both normal meiotic cell cycle progression and in response to defects in prophase I
- The key components of the network are evolutionarily conserved
- Different outcomes of defective meiotic cell cycle progression suggest variation in the architecture of the MCN in different organisms
- Currently little is known about the components and architecture of the MCN in plants

Dependent relationships established by the MCN



Subramanian and Houchwagen, Cold Spring Harb Prospet Biol, 6: a016675, 2014

Table 1. MCN proteins and their homologs									
Mammals	S. cerevisiae	C. elegans	S. pombe	Drosophila	Arabidopsis	Function			
Signaling pro	oteins								
ATR	Mec1	ATL-1	Rad3p	Mei-41	ATR	PI3 ^a kinase-like kinase			
ATM	Tel1	ATM-1	Tel 1 p	Atm	ATM	PI3 kinase-like kinase			
RAD9A, Rad9b	Ddc1	HPR-9	Rad9p	Rad9A, Rad9B	-	PCNA ^b -like clamp (9-1-1			
RAD1	Rad17	MRT-2	Rad1p	Rad1		PCNA-like clamp (9-1-1 complex)			
HUS1 HUS1B	Mec3	HUS-1	Hus1p	Hus1	-	PCNA-like clamp (9-1-1 complex)			
CHK1	(Chk1)	CHK-1	Chk1p	(Grp)	_	Protein kinase			
CHK2	Rad53 Mek1	CHK-2	Cds1p Mek1p	Mnk	-	Protein kinase with FHA ^c domain			
Several	Cdc5	PLK-2	Plo1p	Polo	_	Protein kinase			
HORMAD1 HORMAD2	Hop1	HTP-1 HTP-2 HIM-3	Hop1	_	ASY1	Chromosomal HORMA- domain proteins			
SYCP3	Red1?	HTP-3?	Rec10?	C(2)M?	ASY3?	Chromosome axis component			
Several	Sir2	SIR-2	Sir2p	Sir2	SRT1 SRT2	NAD-dependent deacetylase			
TRIP13	Pch2	PCH-2	_	Pch2	_	AAA ⁺ -ATPase ^d			

Subramanian and Houchwagen, Cold Spring Harb Prospet Biol, 6: a016675, 2014

Our work on meiotic cell cycle progression in Arabidopsis

- The function of the ARABIDOPSIS SKP1-LIKE1 (ASK1)
- The function of the TARDY ASYNCHRONOUS MEIOSIS (TAM)

How was the work started?

Formation of double gametophytes and dyad meiotic products in *tam-1*



Magnard et al. Plant Physiol, 127: 1157-1166, 2001

Question:

Do dyads result from precocious cytokinesis or slower cell cycle progression?

Comparison of meiotic stages in two consecutive buds in both WT and *tam-1* plants



Magnard et al. Plant Physiol, 127: 1157-1166, 2001

Dynamics in number of microspores per meiotic product during development



Conclusion

Male meiotic cell cycle progression in *tam-1* is slower than in the WT; TAM is required for the normal pace of cell cycle progression during male meiosis



Identification of *TAM* by map-based cloning: CYCA1;2, an A-type cyclin, complemented *tam-1* meiotic defect



Further characterization of *tam-1* revealed that TAM primarily functions in pachytene



a, leptoene; b, zygotene; c, pachytene; d in WT, diplotene to early tetrads; d in *tam*, diplotene to early dyads

Examine stages in two anthers in the same bud at two time points





b, zygotene; c, pachytene; d in WT, diplotene to early tetrads; d in *tam*, diplotene to early dyads; e, early dyads to early tetrads

Conclusion

TAM regulates the progression of pachytene and meiosis II.

Overexpression of *TAM* results in the production of the same meiotic products as in the loss-of-function *tam* mutants



Chromosome thread thickness is differentially affected in *TAM*-overexpression lines and *tam* mutants



Pericentromeric heterochromatin regions tend to cluster in *tam* mutants but not in *TAM*-overexpression lines



ASY1 subcellular localization is differentially affected in *tam* mutants and *TAM*-overexpression lines



Hypothesis

Either the different meiotic defects or a common defect such as missing ASY1 on the chromosomal axes triggers the MCN in the *tam* mutants and *TAM*-overexpression lines, leading to the production of the same abnormal meiotic products.

Arabidopsis mutants in which the MCN is potentially activated based on the presence of meiotic products of dyads and triads

Protein	Function	Dyads	Triads	Tetrads	Polyads
ASK1	Ubiquitin ligase/cell cycle progression, synapsis	Yes	Yes	Yes	Yes
DMC1	Single-strand DNA invasion	Yes	Yes	Yes	Yes
DYAD/SWI1	Novel protein/meiotic progression	Yes	Yes	Yes	No
SDS	Cyclin/meiotic progression	Yes	Yes	Yes	Yes
TAM/CYCA1;2	Cyclin/meiotic progression	Yes	Yes	Yes	Yes
AESP	Separase/against nonhomologous centromere aggregation	Yes	Yes	Yes	Yes
DUET/MMD1	PHD finger protein/meiotic progression	Yes	?	No	No
OSD1	APC inhibitor	Yes	Yes	Yes	No
AtPS1	Forkhead –associated domain/spindle orientation in meiosis II	Yes	Yes	No	No
ТОР3а	DNA topoisomerase IIIα/resolution of Holliday junctions	Yes	No	No	No
RMI1	Resolution of Holliday junctions	Yes	No	No	No

The *tam-2* null allele produces unreduced gametes that lead to genome duplication in the next generation



Wang et al., Genesis, 48: 254-263, 2010

Evidence for genomic instability in the third generation of *tam-2*



Wang et al., Genesis, 48: 254-263, 2010

Evidence for dramatic ploidy reductions and genomic instability in the fourth generation of *tam-2*



Plants with different baseline ploidy levels in the fourth generation of *tam-2*.

Ploidy	2x	Зx	4x	6х	7x	8x
Plant family						
1 (n=8)	1		2	4	1	
2 (n=7)		1	1	2	1	2
3 (n=7)			2	5		
4 (n=6)					1	5
5 (n=12)		1	1	2	6	2

n is the number of plants examined.

An artificial hexaploid line also exhibits genomic instability



Upper left: diploid wild type. Others: plants from an artificial hexaploid line.

Progeny from an artificial octaploid line also exhibits genomic instability



Uppermost: octaploid parent. Other two: progenies from the parent

Evidence for an unusual mechanism for the dramatic ploidy reduction



Chromosome missegregation and spore budding in male meiosis. (a, b) Artificial octaploid, showing tetrads with one containing a small extra cell with DNA (arrows). (c–f) Dyads in the third-generation tam-2, containing small extra cells (thick arrows), spore budding (thin arrows), and micronuclei (arrowheads).



Nuclear size and number in pollen. (a) Artificial octaploid. (b) Second-generation *tam-2*. (d-h) All from a thirdgeneration *tam-2*. (e-g) Different focal planes of the same pollen grain.

MCN may be activated by multiple mechanisms to generate unreduced gametes in nature

- Mutations such as *tam*—autopolyploidy
- Hybridization between distant species—allopolyploidy
- Environmental factors such as low temperature--autopolyploidy

Characteristics of octaploid plants that possibly contribute to genome evolution

- Octaploid plants produce progenies of dramatically reduced ploidy and possibly greatly altered genome composition
- Greatly reduced fertility of octaploid plants and their progeny are subject to out-crossing
- Genome changes will be either lost due to sterility or fixed in just a few generations

Acknowledgements

OSU

Yixing Wang Ajay Jha Brian Hercyk

PGEC

Sophia Chen Jean-Louis Magnard Michele Leary Sheila McCormick

The Samuel Roberts Noble Foundation Hwa-Soo Shin

Rujin Chen

The John Innes Center John Doonan

University of Birmingham Chris Franklin

Funding

USDA University of California The Samuel Roberts Noble Foundation Oklahoma State University Underwood Fellowship, BBSRC, UK Oklahoma Center for the Advancement of Science and Technology