

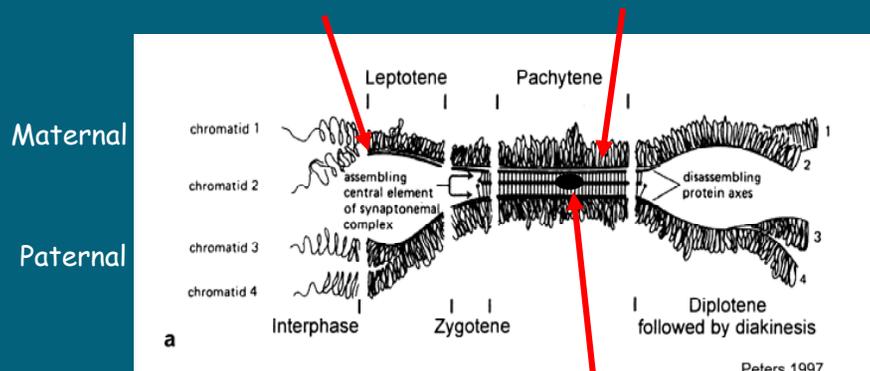
Meiotic crossover control is related to cohesin proteins in tomato

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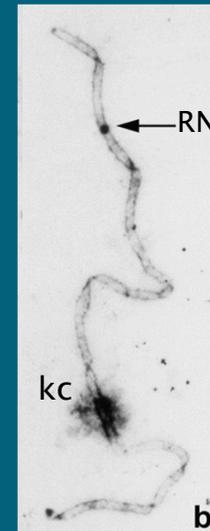
Meiotic Recombination

1. Crossovers are closely linked with synapsis (synaptonemal complex - SC)
2. Recombination nodules (RNs) mark crossover sites and future locations of chiasmata.
3. Crossovers are tightly regulated - number and location.
4. How is crossing over controlled? Link between synapsis and crossing over.

Axial element = Lateral element



Recombination nodule



Stack and Anderson
1986 AM. J. Bot.



Tomato



Synapsis:

AE/LEs = Cohesin proteins

Meiotic
cohesion
complex { SMC1
SMC3
SCC3
REC8/SYN1 -
Meiosis-specific

Crossovers: MLH1

- mismatch repair protein
- interference pathway of CO
- present in ~70% of RNs from tomato

(Lhuissier et al. 2007)



WT Tomato SC spread

Tomato *as1* mutants:

- *Spontaneous mutation, very low fertility*
- *Meiosis-specific, recessive, monogenic*
- *Asynaptic (ave. 25% of WT SC length)*

wild-type

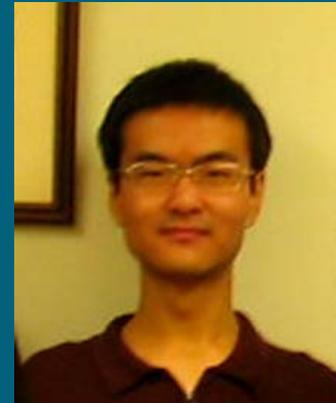


as1/as1

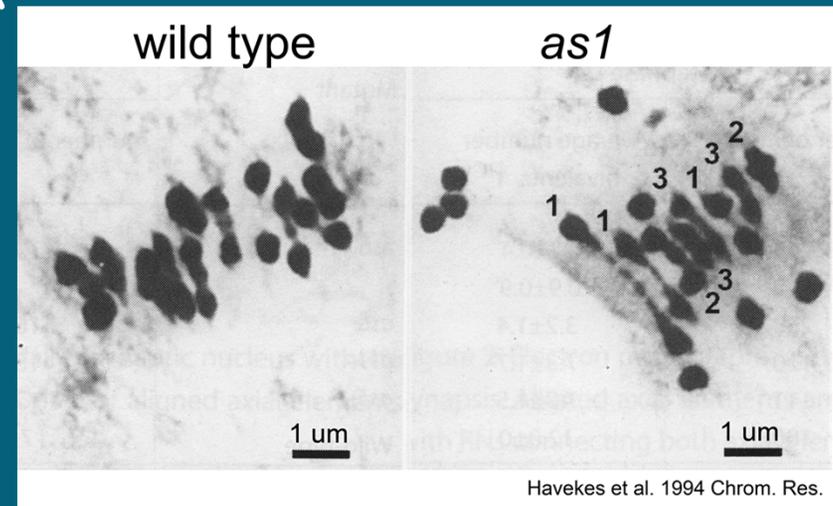
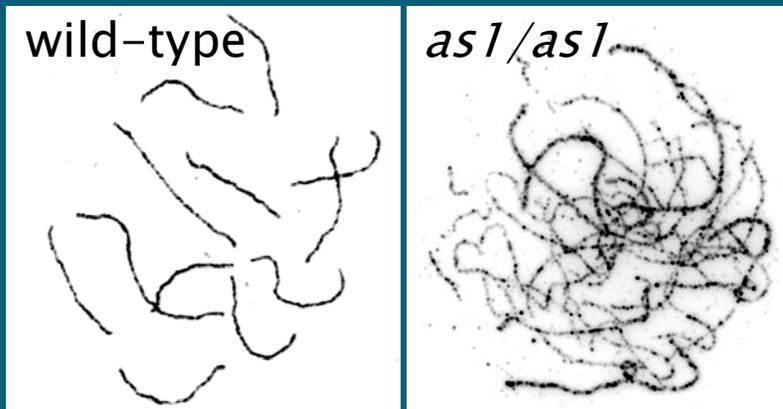


Tomato *as1* mutants:

- Spontaneous mutation, very low fertility
- Meiosis-specific, recessive, monogenic
- Asynaptic (ave. 25% of WT SC length)
- Chiasmate bivalents and univalents at metaphase I
- Genetic linkage maps (Soost 1951; Moens 1969)
 - expect reduced CO due to asynapsis
 - near normal CO levels *
 - higher frequency of double CO*



Joe
Qiao



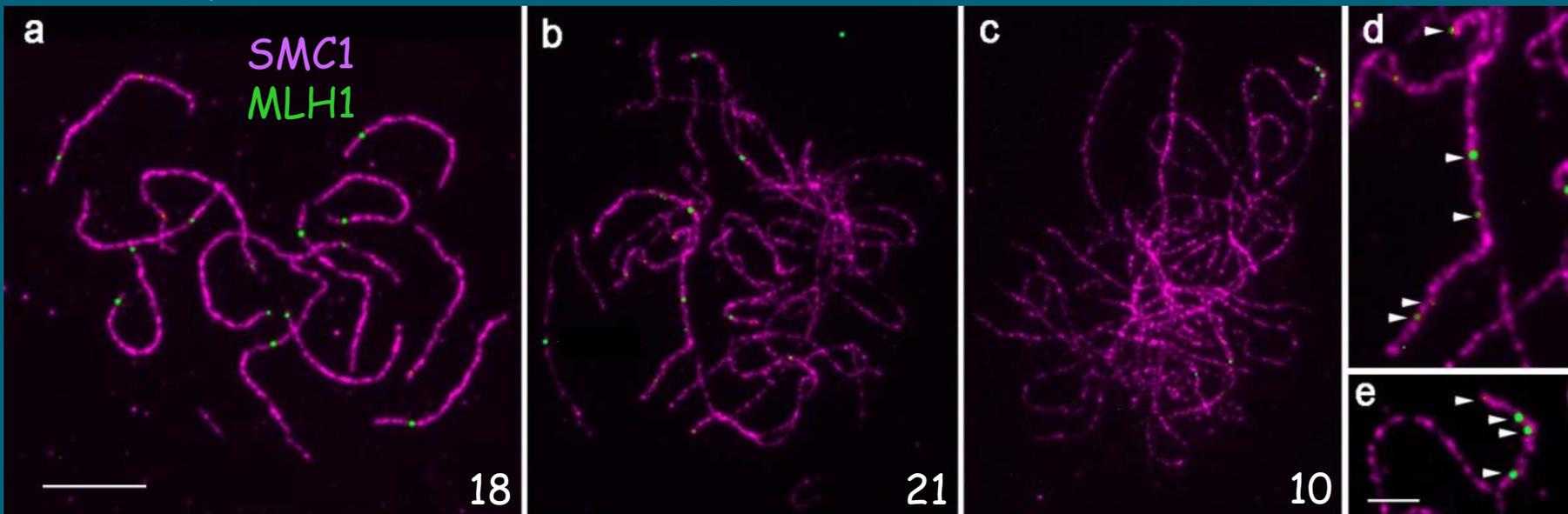
Havekes et al. 1994 Chrom. Res.

MLH1 focal patterns & synapsis

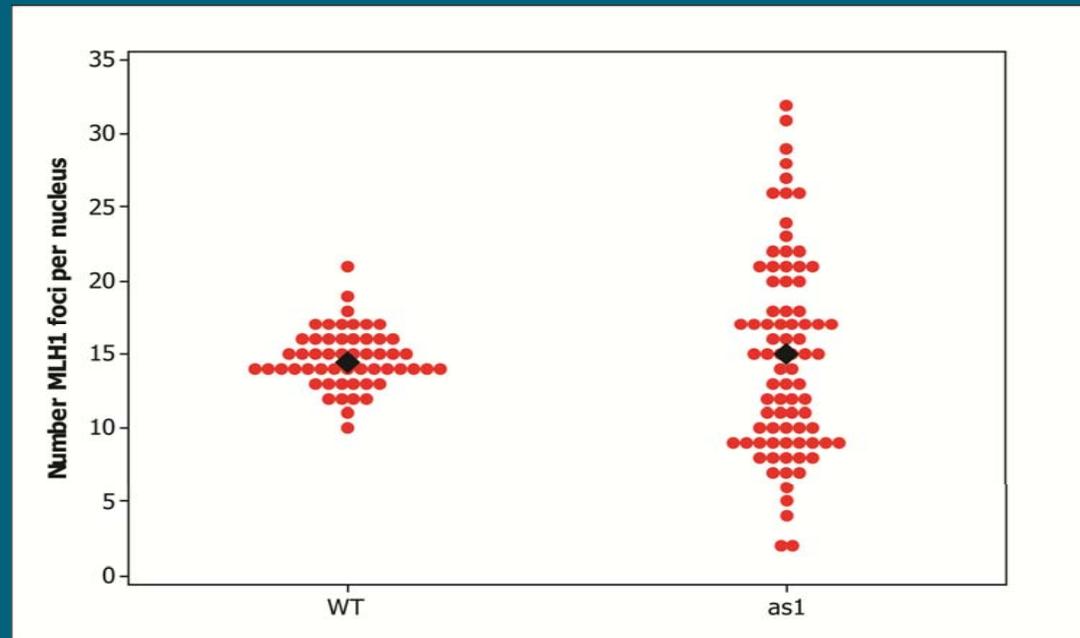
WT

asl

asl



MLH1 foci: frequency and distribution

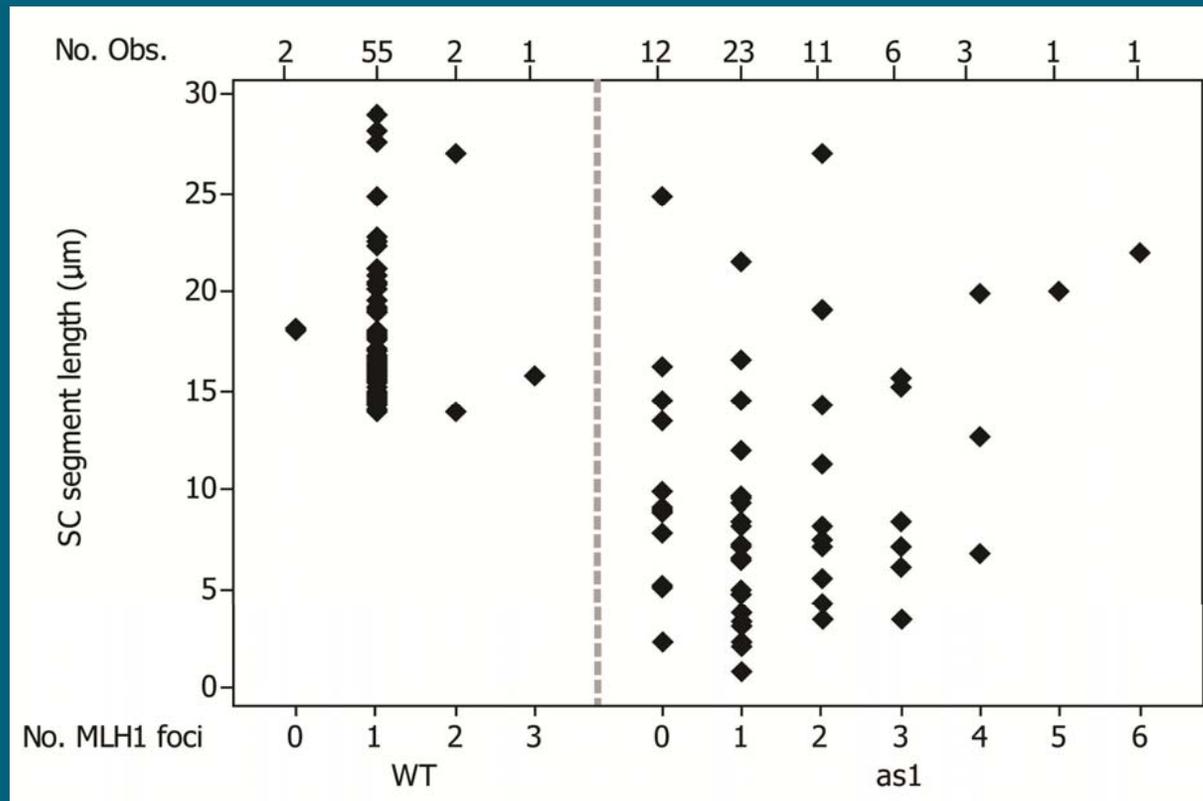


Ave. number MLH1 foci per nucleus:

WT: 15.2 (n = 74)

as1: 14.8 (n = 81)

$P > 0.2$



Ave # MLH1 foci per μm SC

WT = 0.06

as1 = 0.15

$P < 0.001$

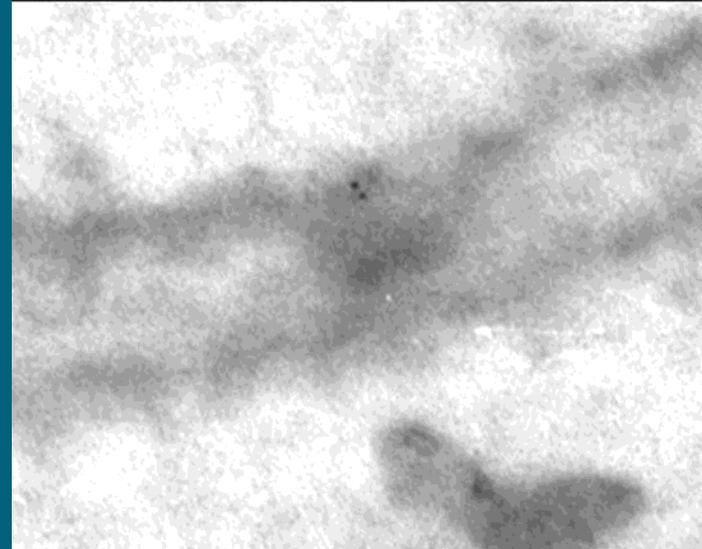
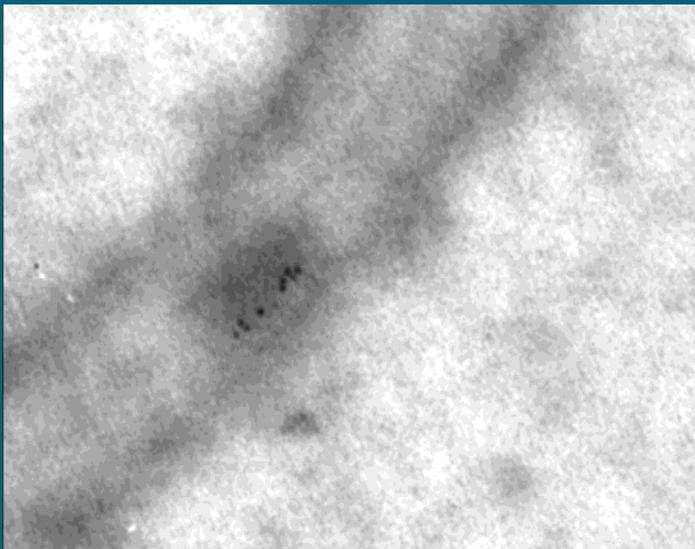
Ave. interfocus distance

WT = 11.5 μm

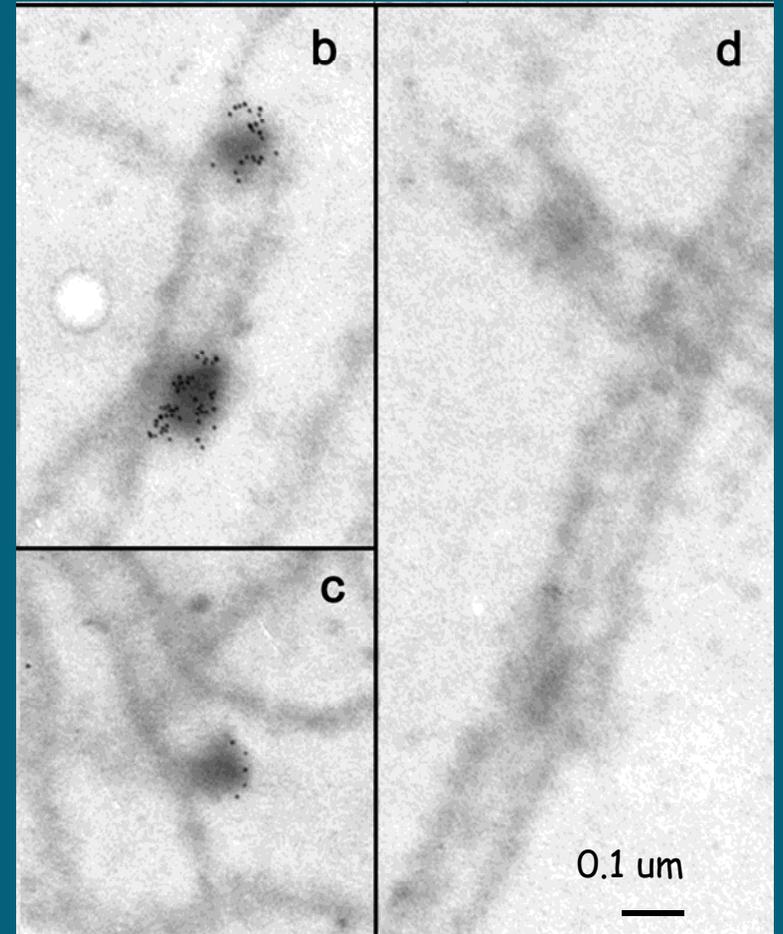
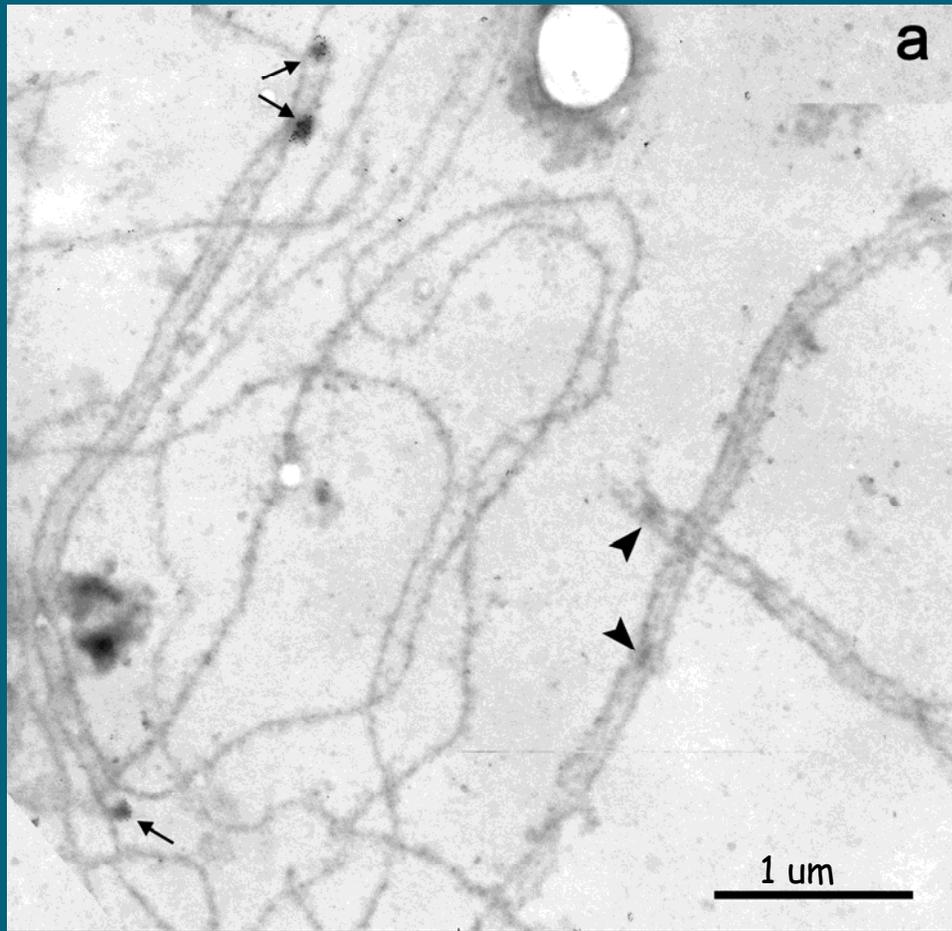
as1 = 3.3 μm

$P < 0.001$

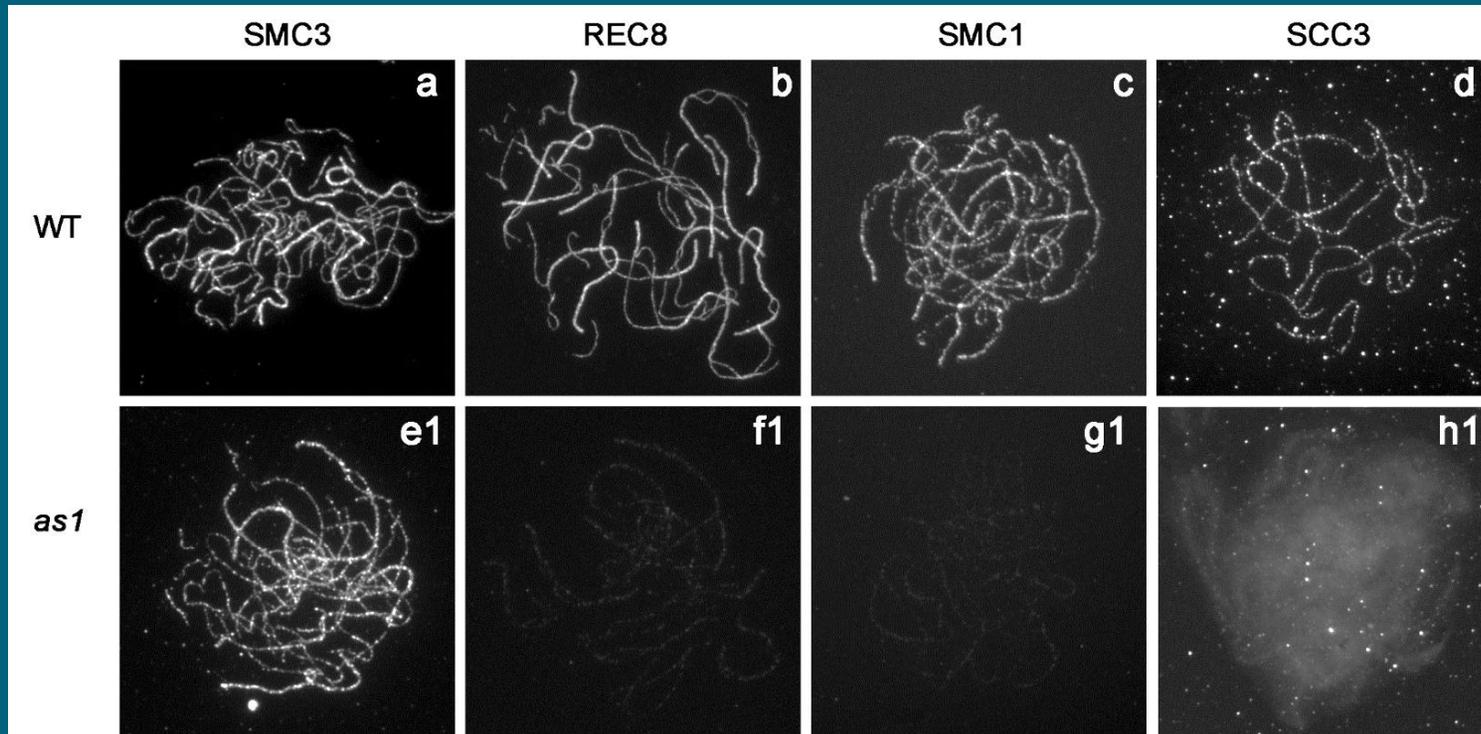
Wild-type tomato - MLH1 immunogold



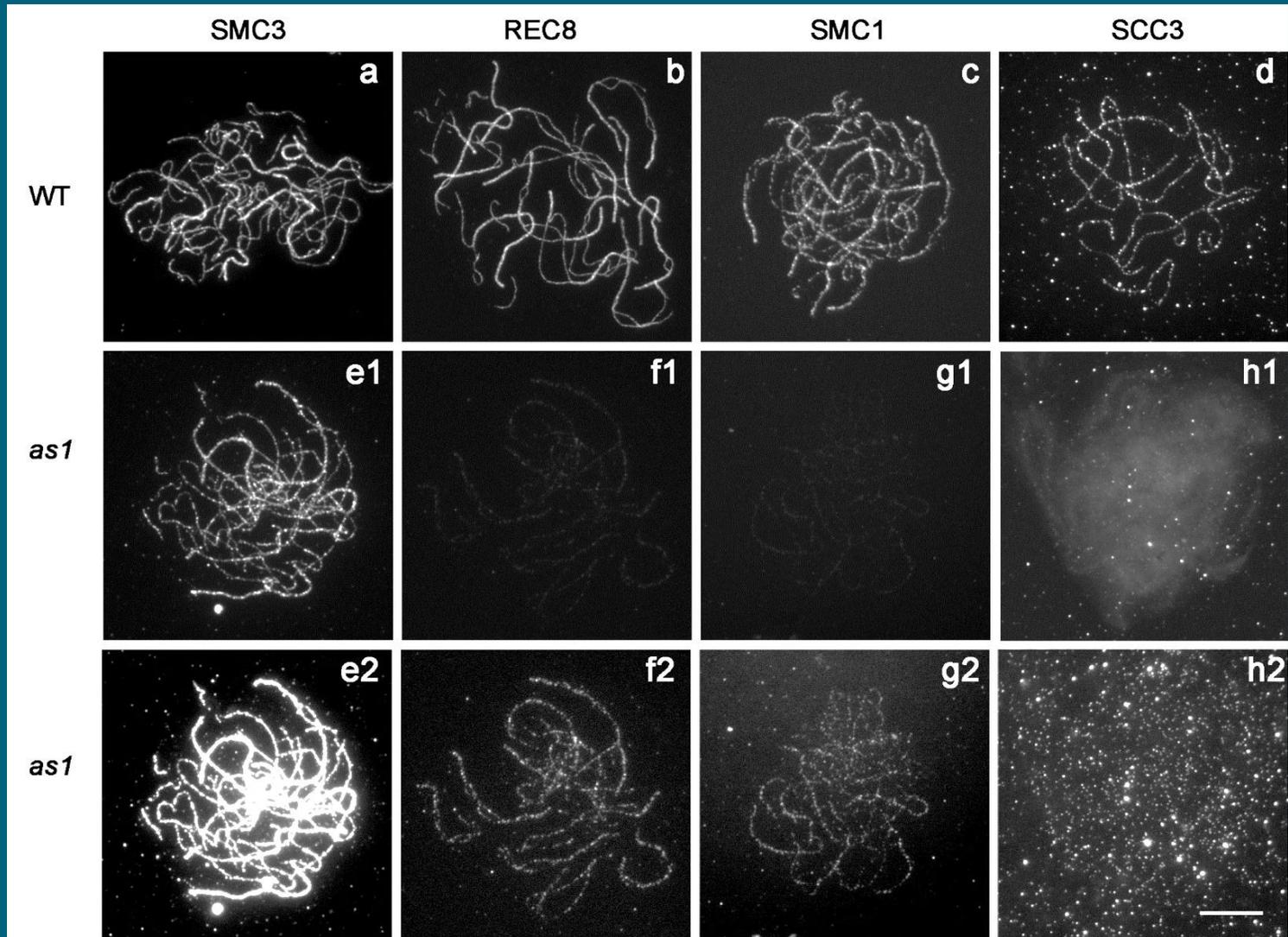
asl - MLH1
immunogold



Immunolabeling of cohesin proteins SMC3, REC8, SMC1, SCC3



Immunolabeling of cohesin proteins SMC3, REC8, SMC1, SCC3



Total AE/LE length is significantly **longer** for *as1* than WT or a different asynaptic mutant (*asb*)

Ave. total AE/LE length (μm)

WT = 505 ± 53

asb = 556 ± 46 ; $P > 0.17$

as1 = 812 ± 87 ; $P < 0.001$

The *as1* mutant differs from WT:

1. Asynapsis.
2. Altered MLH1 (crossover) pattern:
 - Increased number of MLH1 foci per unit length of SC (~ chiasmate bivalents, "normal" CO levels, increased double COs).
 - High frequency of SC segments with no MLH1 foci (~ univalents).
3. Altered cohesin immunolabeling:
 - Reduced immunolabeling for 3 of the 4 cohesins in AE/LEs.
4. Altered chromosome axis compaction (longer than WT or *asb*).

as1 mutant - Chromosome axis structure, synapsis, and crossover control are all closely linked in plants.

as1 mutant affects AEs (cohesin proteins - directly or indirectly) with impacts on SC formation and crossover control.



Acknowledgements:

Joe Qiao - Colorado State Univ.
Hildo Offenberg - Wageningen U.

Christa Heyting - Wageningen U.
Christine Mezard - Versailles
Chris Makaroff - U. Miami, Ohio

National Science Foundation