Quantifying DNA damage in chromosome structure mutants

Julia Lo, Zac Bush, Libuda Lab

University of Oregon, Department of Molecular Biology

UNIVERSITY OF OREGON

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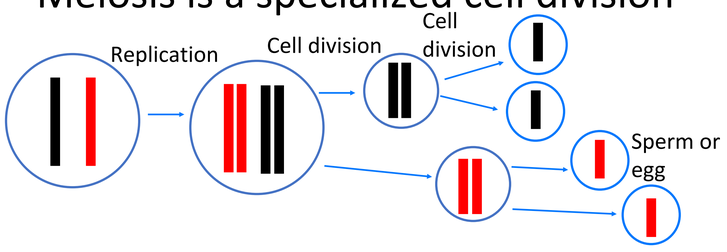
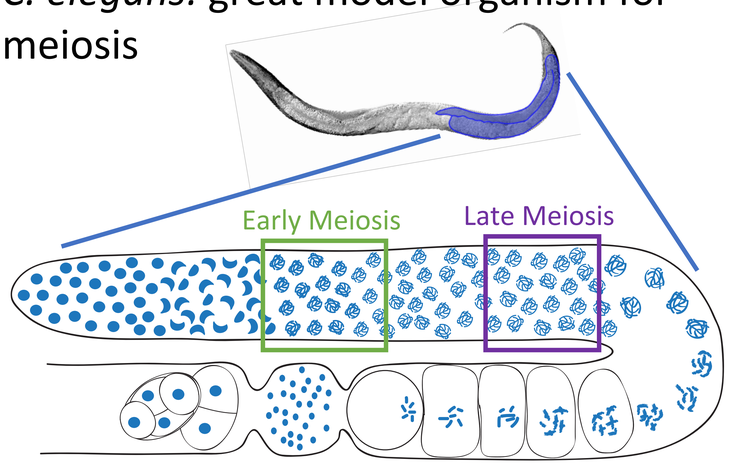
Meiosis is a specialized cell division



C. elegans: great model organism for meiosis



- Germline is a transparent pipeline of meiosis
- Quantified a marker of DNA damage in early and late meiosis

DNA is organized into chromatin

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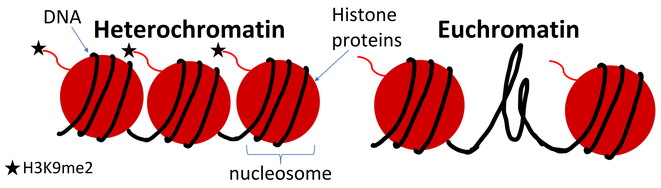
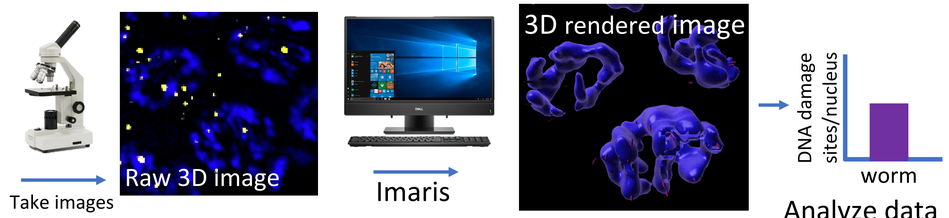
- Nucleosome = coiled DNA + histone
- Heterochromatin (tightly wound) = genes repressed
- Euchromatin (loosely wound) = genes expressed
- Histone modifications dictate chromatin state

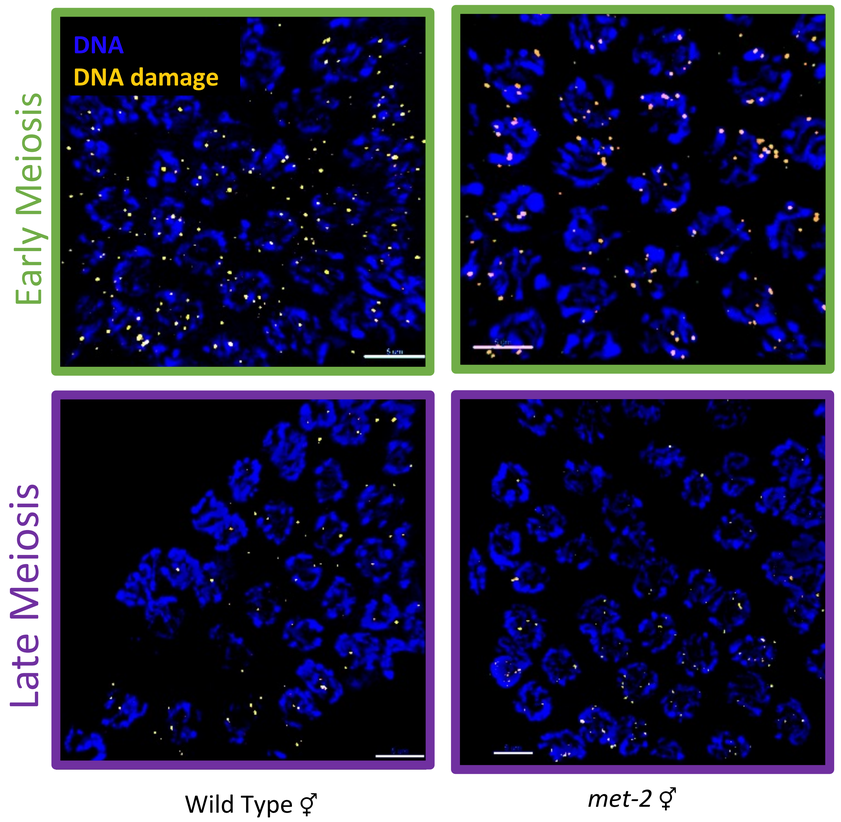


How does loss of a specific heterochromatic mark, H3K9me2 affect the DNA repair system?

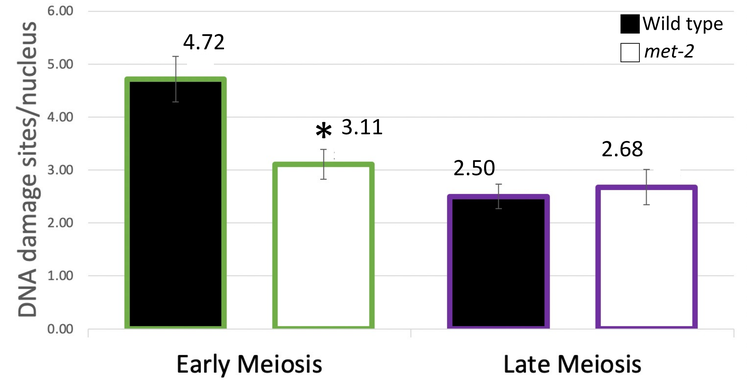
- *met-2* null mutant lacks the H3K9me2 mark
- Does loss of this mark create a more permissive repair environment?



met-2 mutant produces less DNA damage



Less DNA damage induced in *met-2* in early meiosis



*Mann-Whitney U Test: P<0.05
Number of gonads WT, *met-2*: 5, 5
# of nuclei, WT early meiosis, *met-2* early meiosis: 134, 120
# of nuclei, WT late meiosis, *met-2* late meiosis: 116, 217

H3K9me2 important for DNA damage induction

- *met-2* induces less DNA damage in early meiosis than WT
- *met-2* and WT have the same DNA damage in late meiosis

Future Directions

- Repeat study with higher sample size
- H3K9me2 surface creation
- DSBs in other chromatin mutants
- Look at other chromatin marks (ex. H3K9me3)

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