

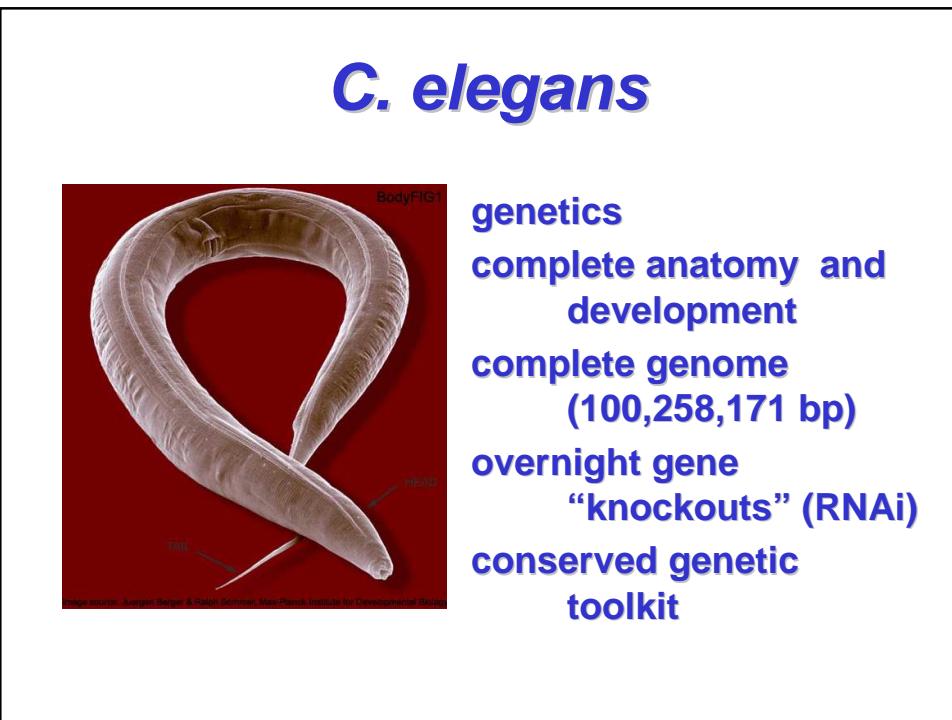
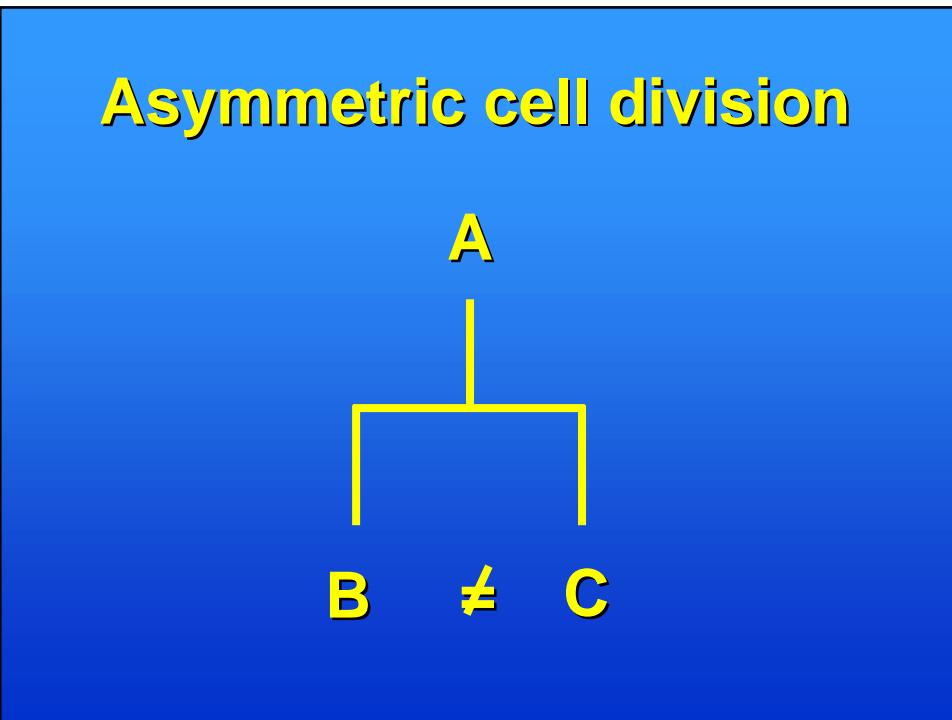
Developmental Switches and Gene Regulatory Networks in the Most Completely Described Animal, the Nematode *C. elegans*

Developmental switches and gene regulatory networks in the most completely described animal, the nematode *C. elegans*

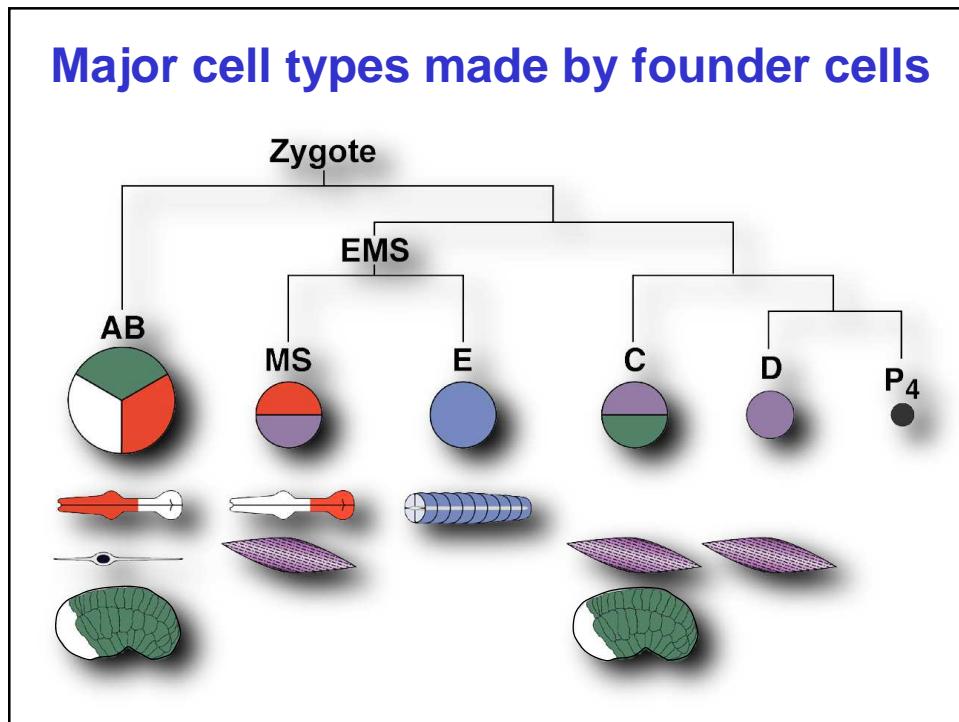
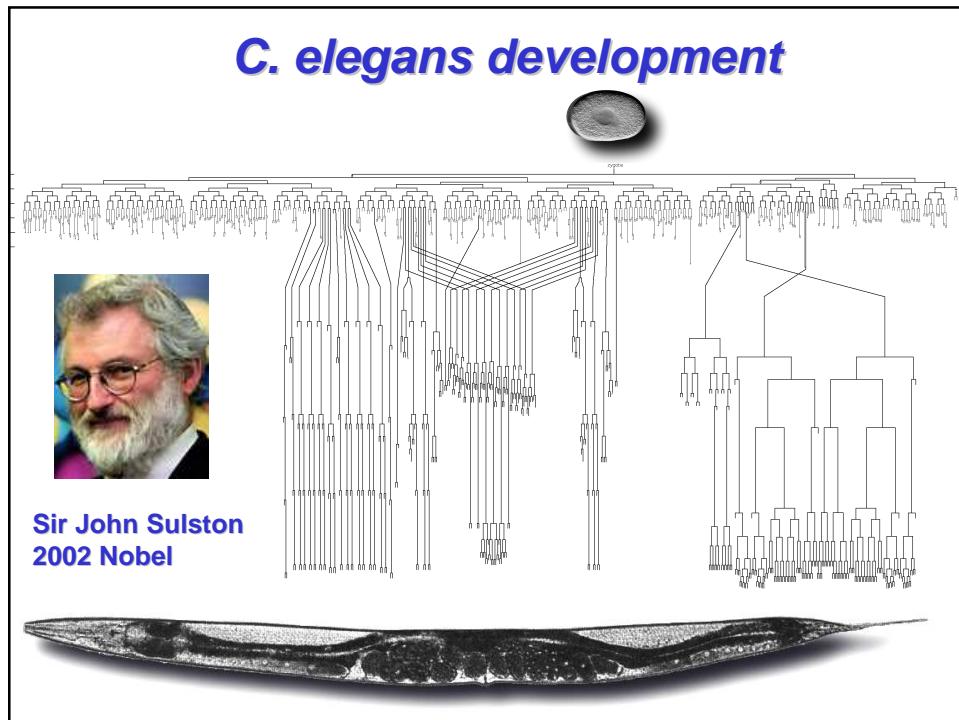
**Joel Rothman
UC Santa Barbara**

**Generating developmental diversity:
Symmetry breaking**

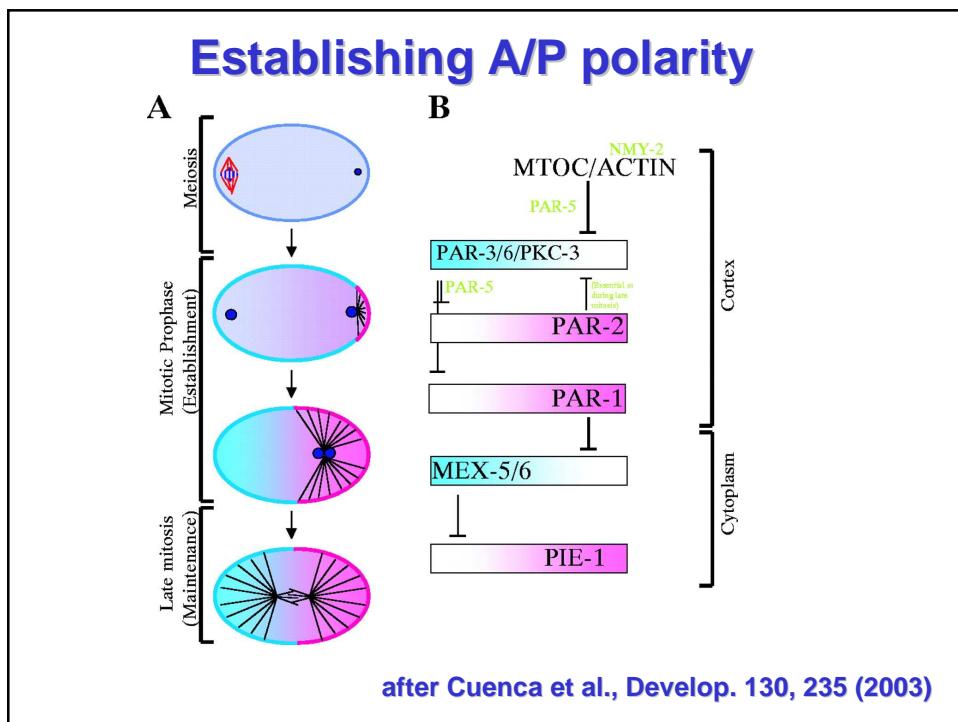
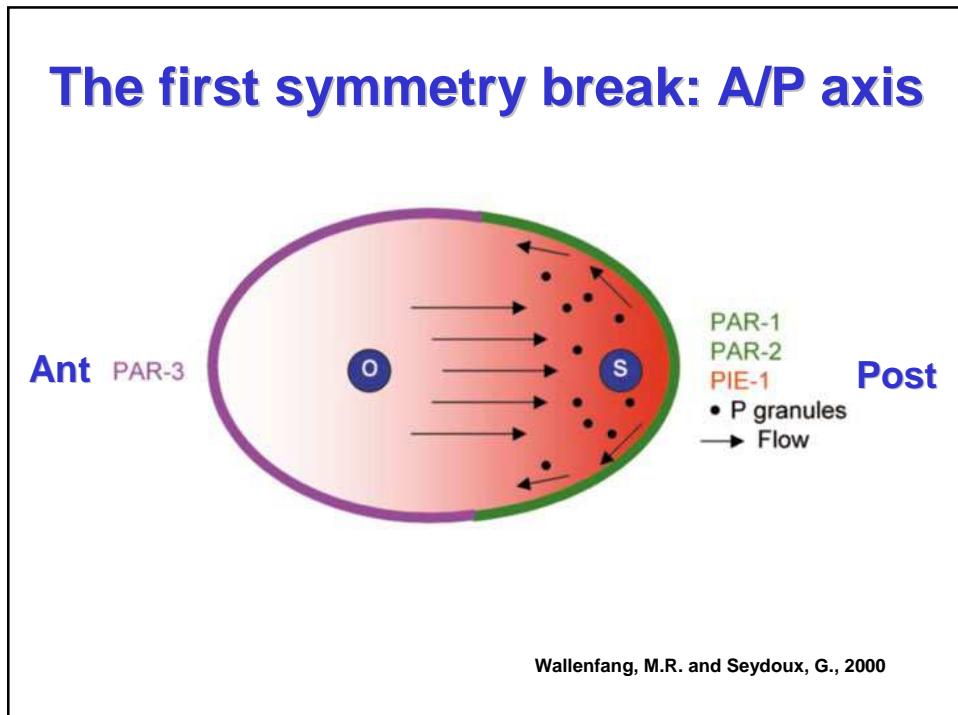
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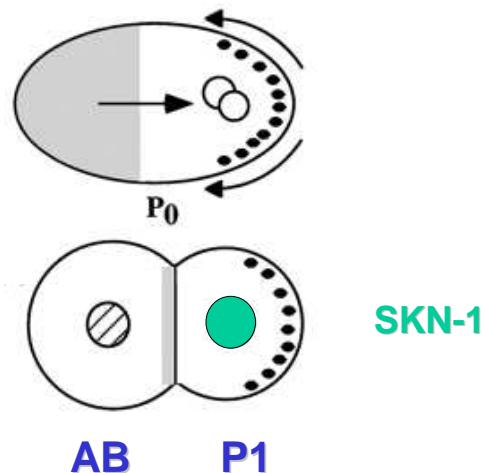


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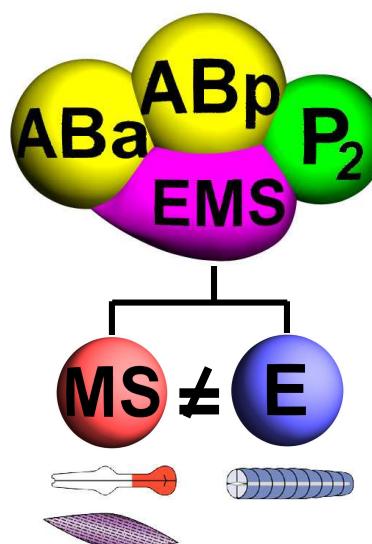


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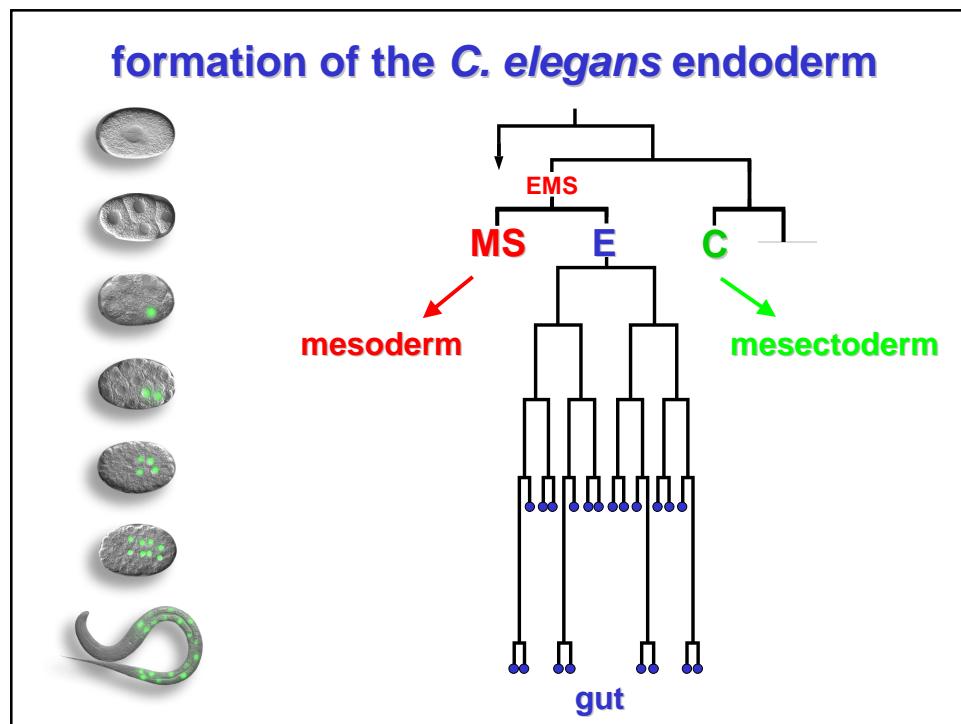
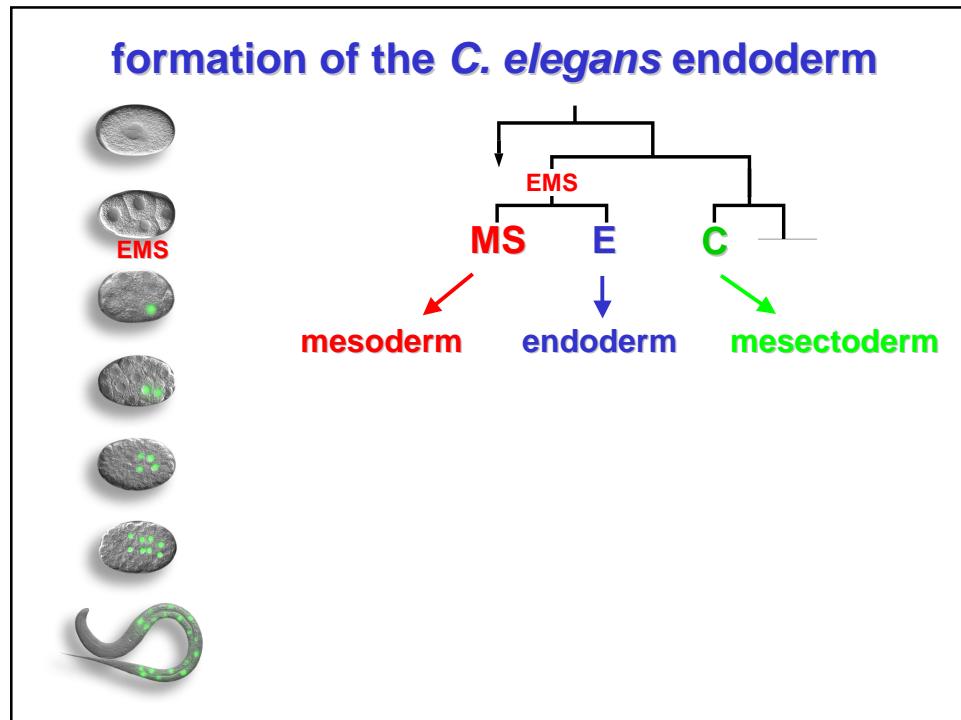
Asymmetric first division



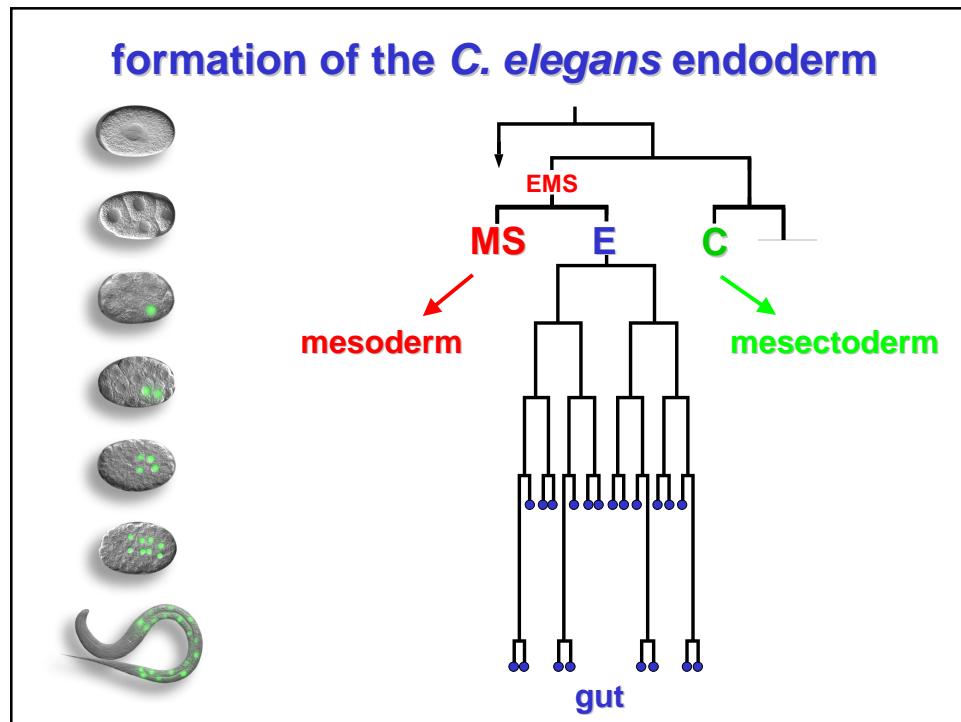
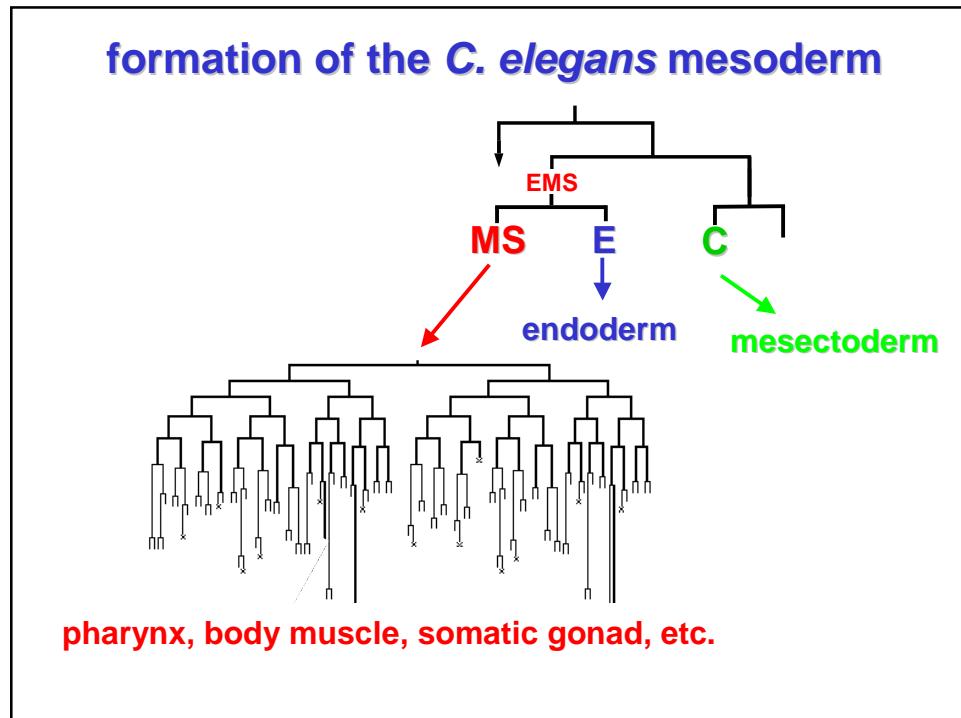
Asymmetric cell division



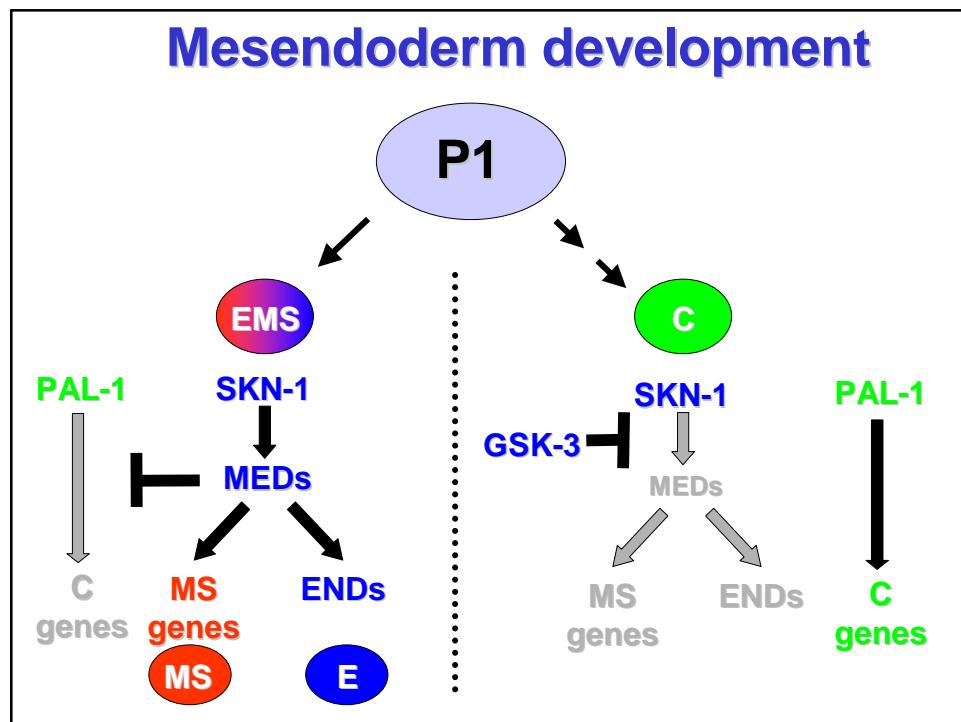
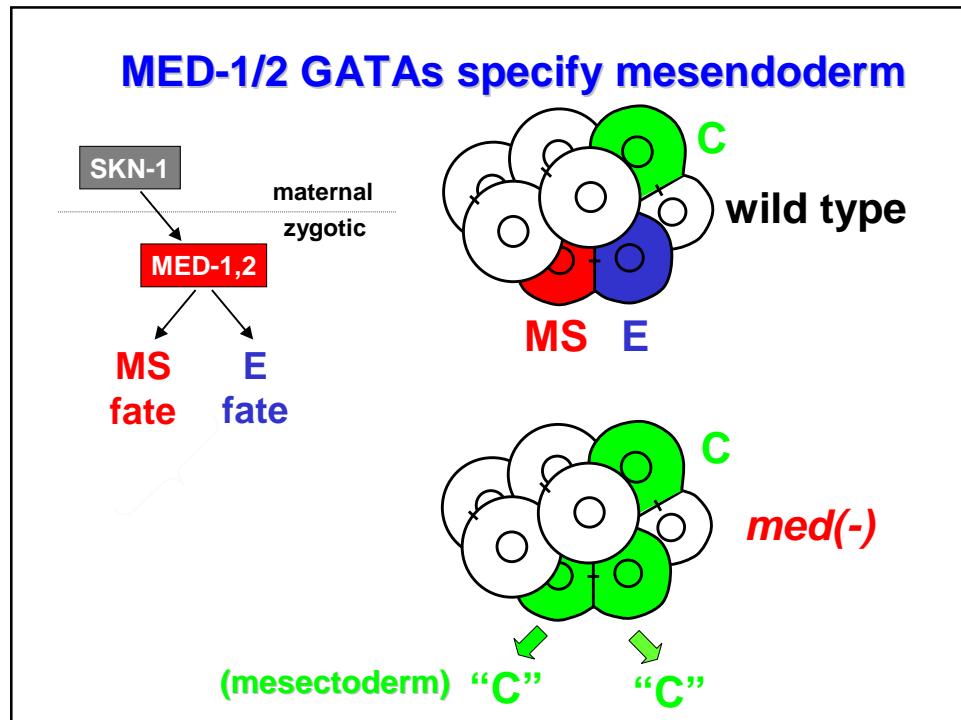
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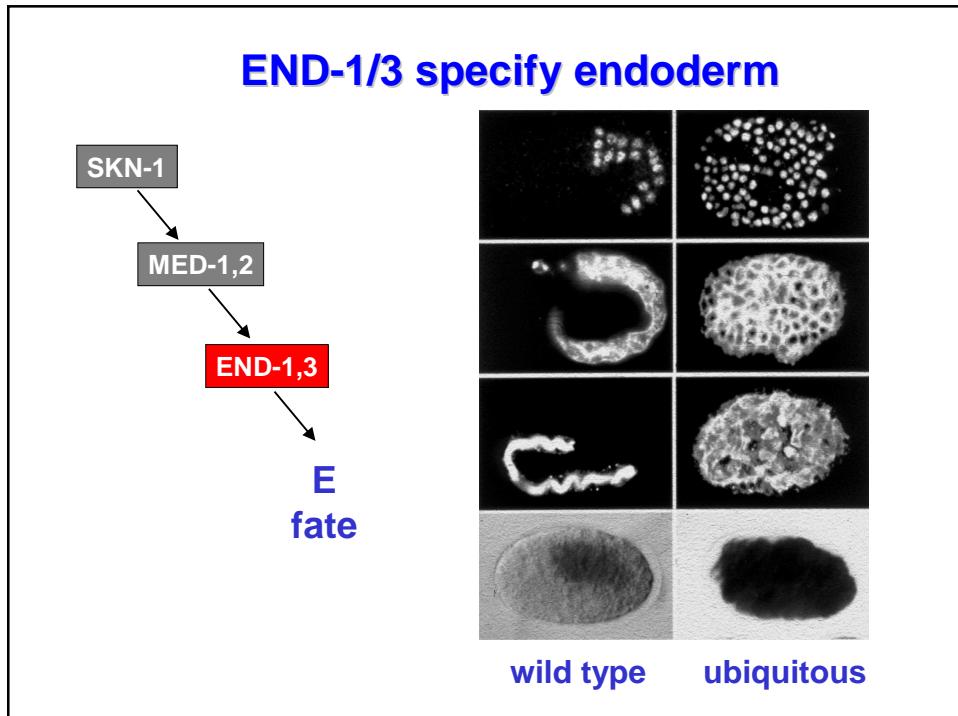
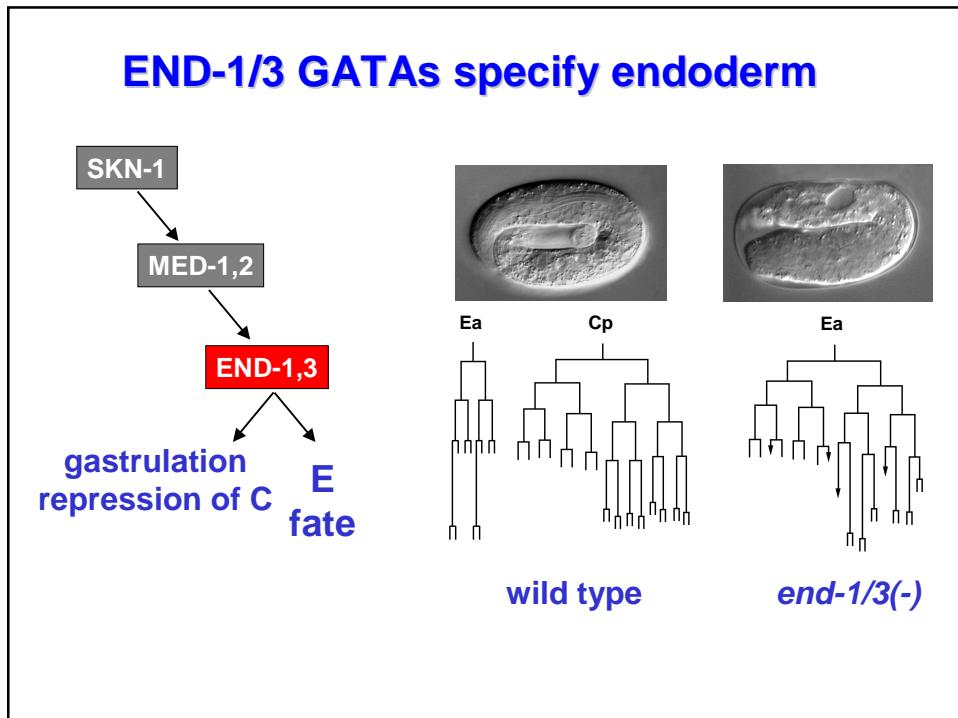
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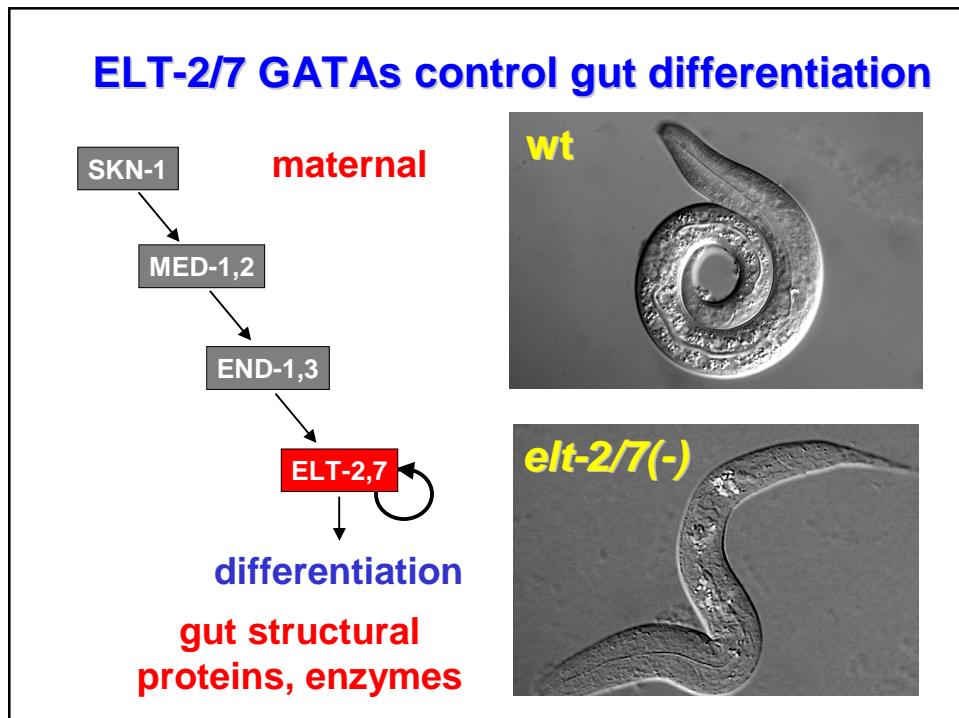
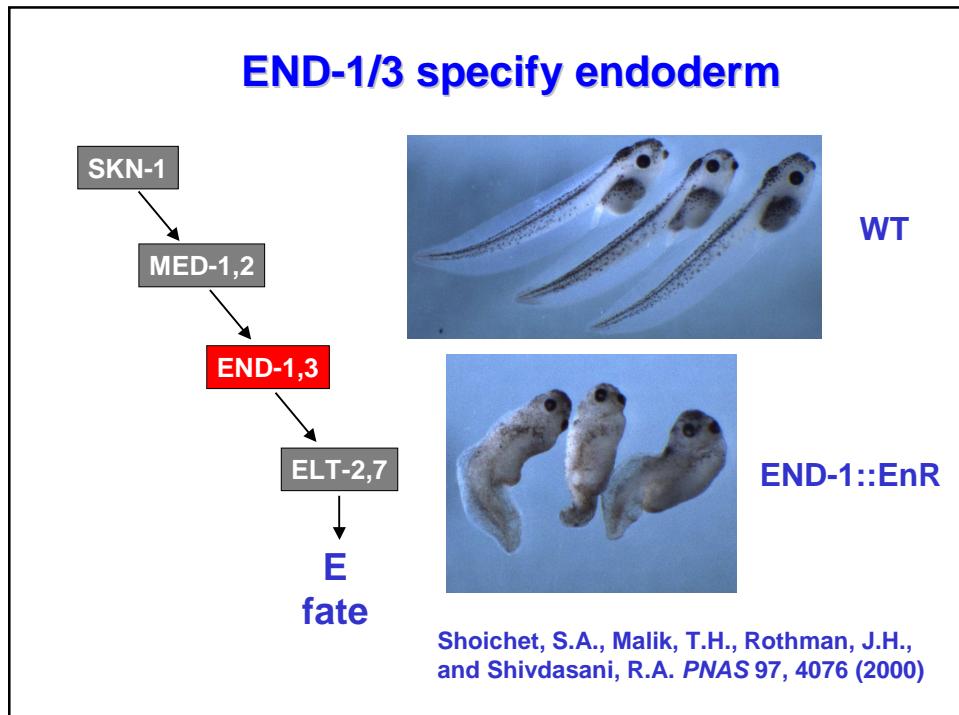
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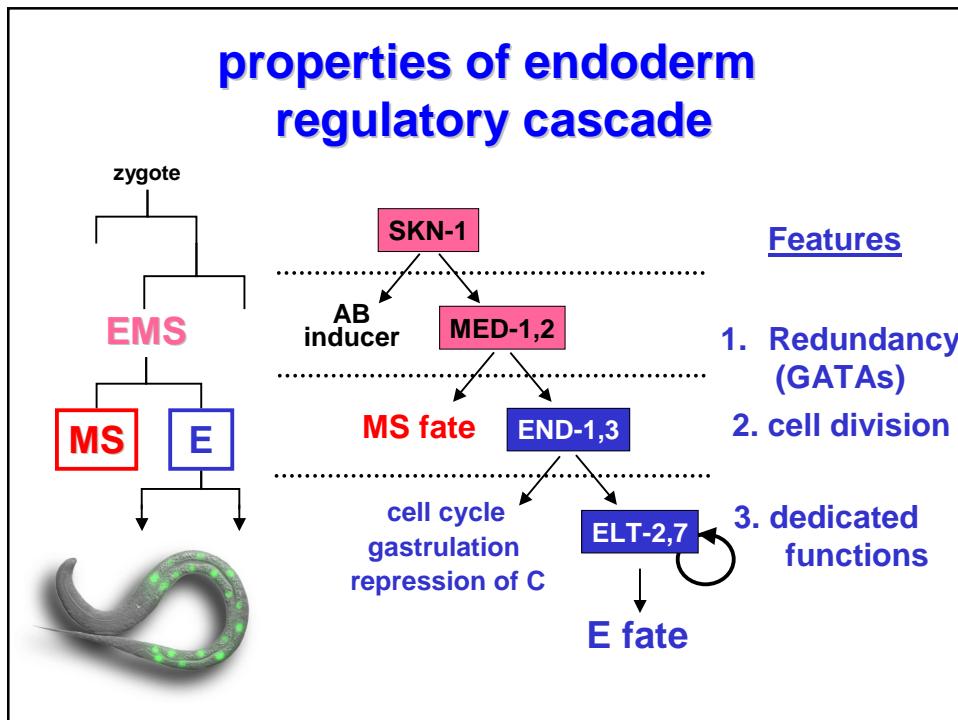
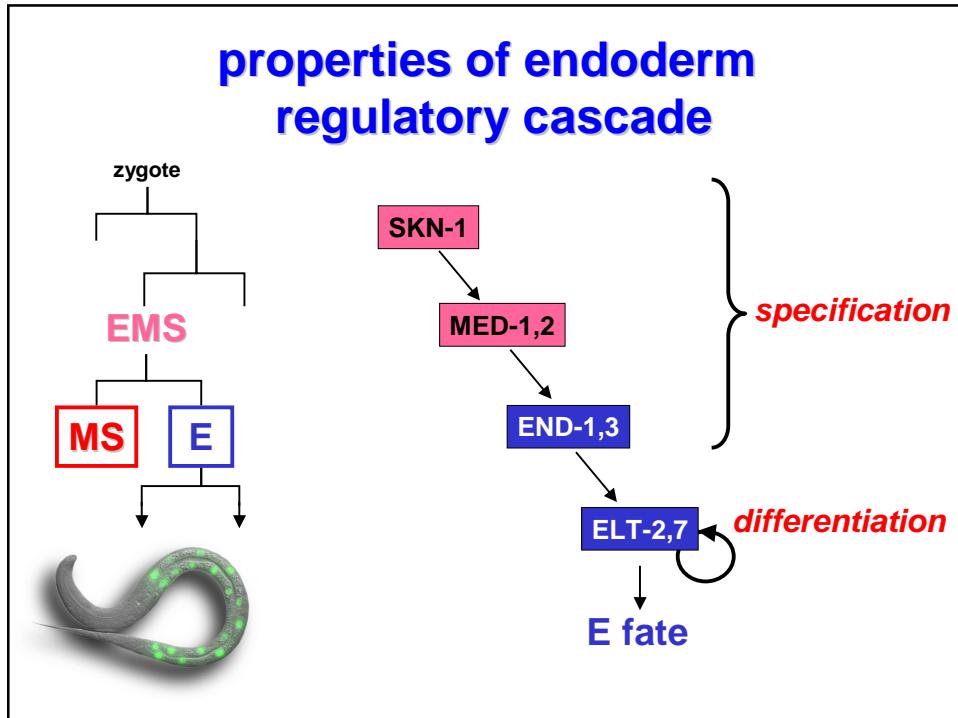
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Developmental Switches and Gene Regulatory Networks in the Most Completely Described Animal, the Nematode C. Elegans

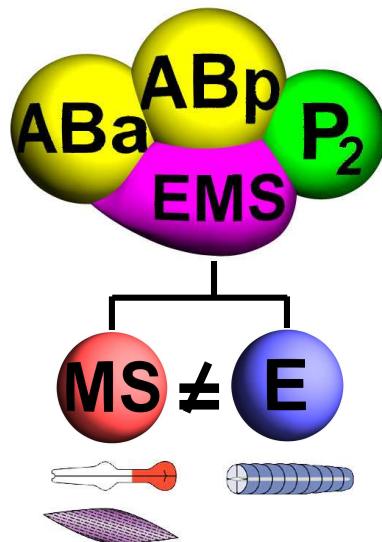


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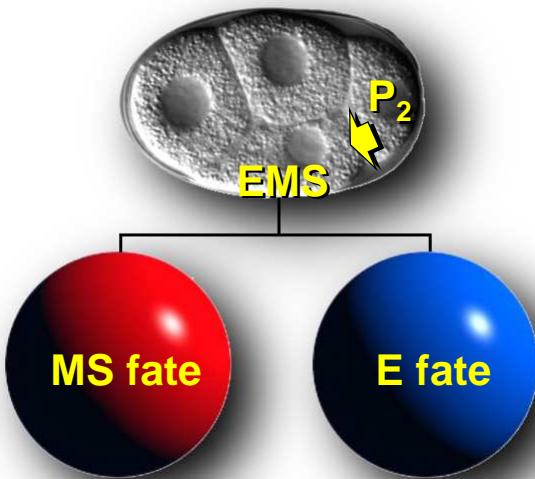


Developmental Switches and Gene Regulatory Networks in the Most Completely Described Animal, the Nematode *C. Elegans*

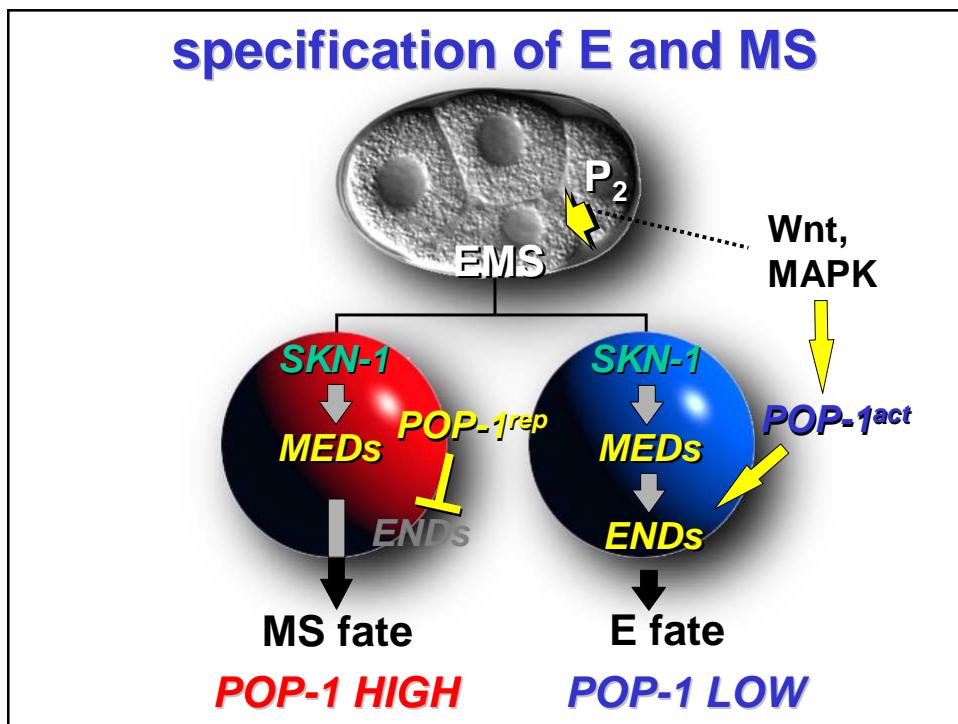
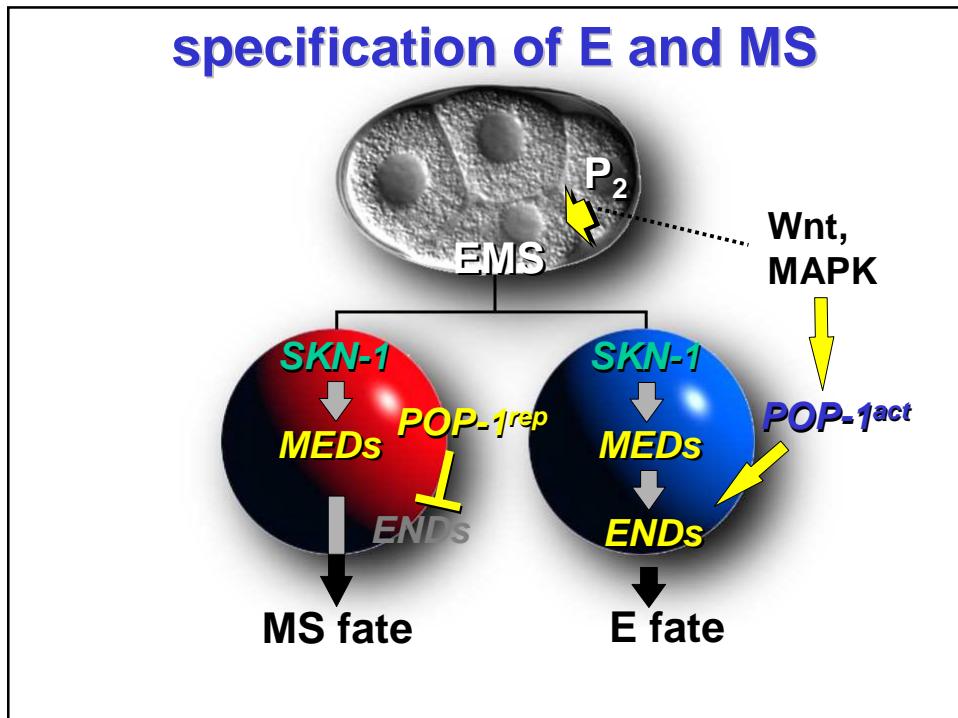
Asymmetric cell division



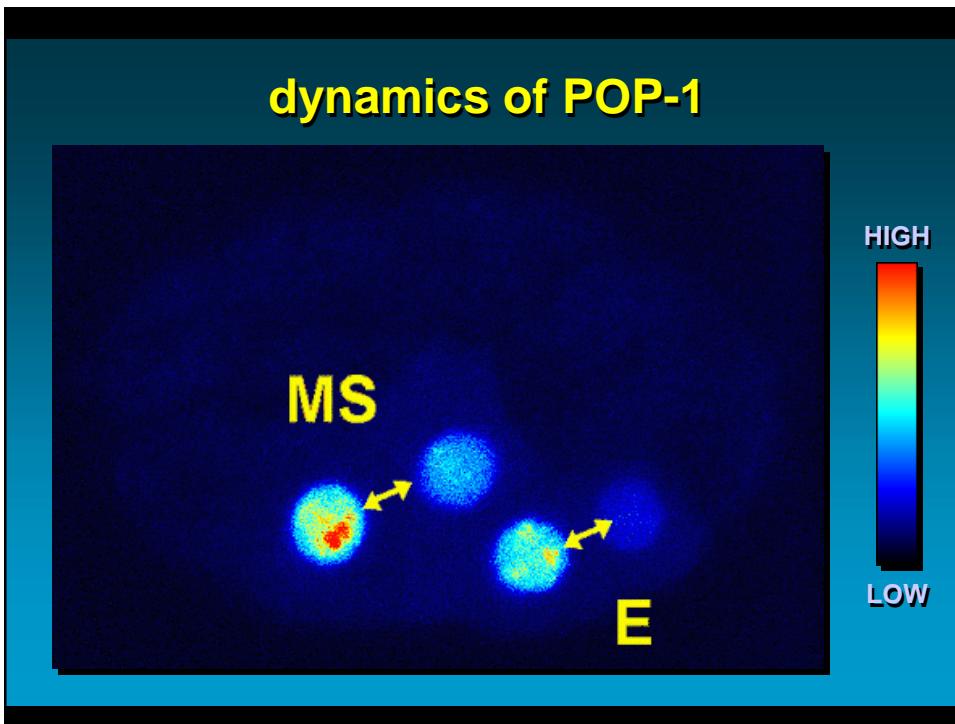
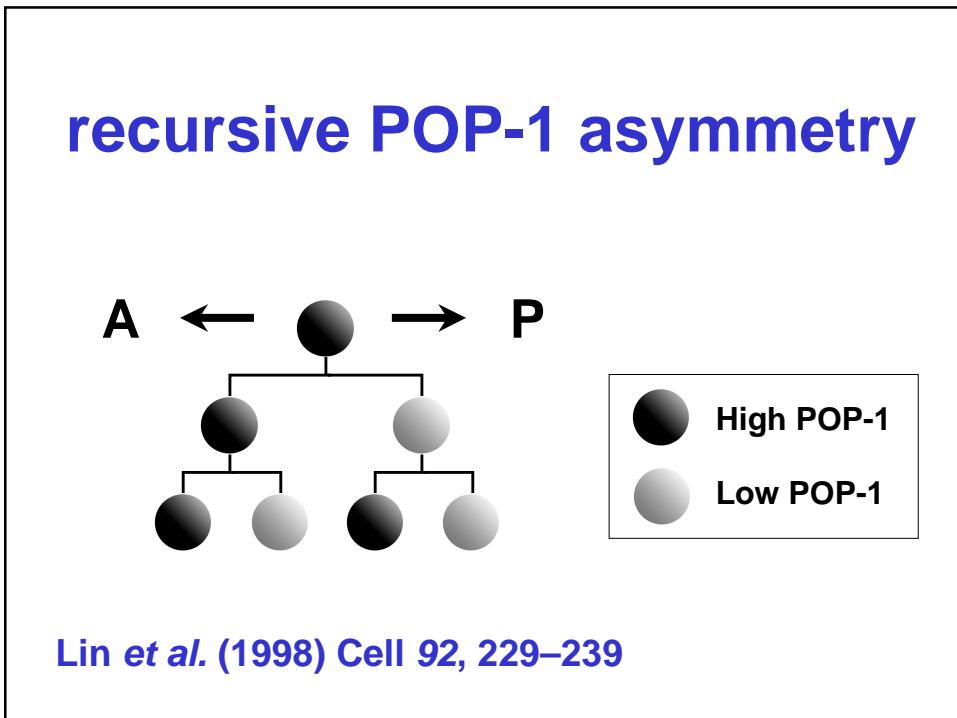
P₂ induces E fate



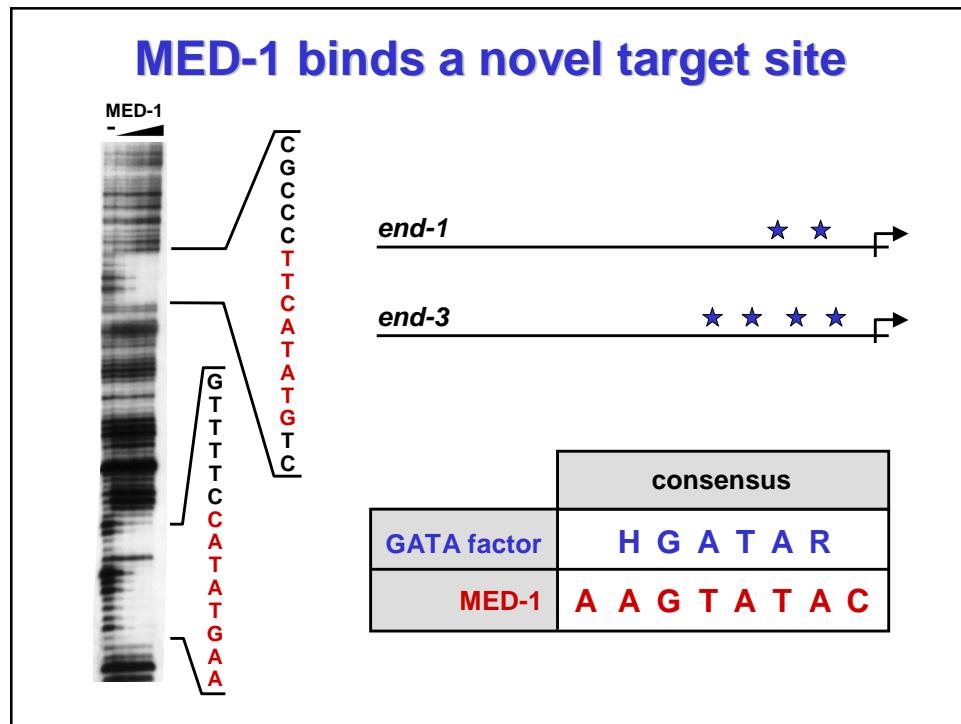
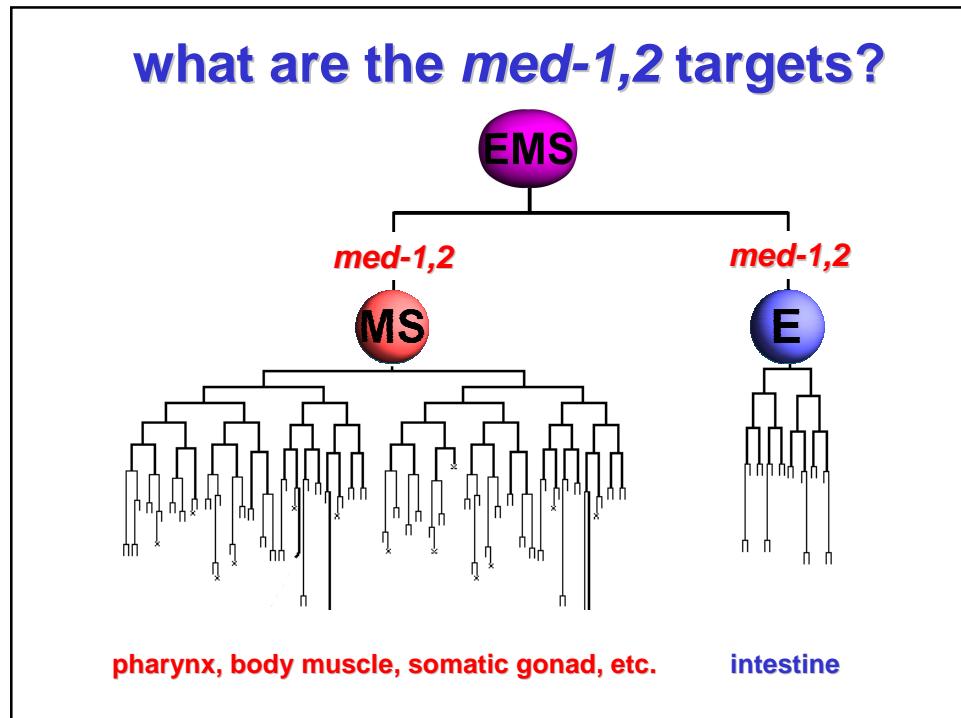
Developmental Switches and Gene Regulatory Networks in the Most Completely Described Animal, the Nematode C. Elegans



Developmental Switches and Gene Regulatory Networks in the Most Completely Described Animal, the Nematode *C. Elegans*

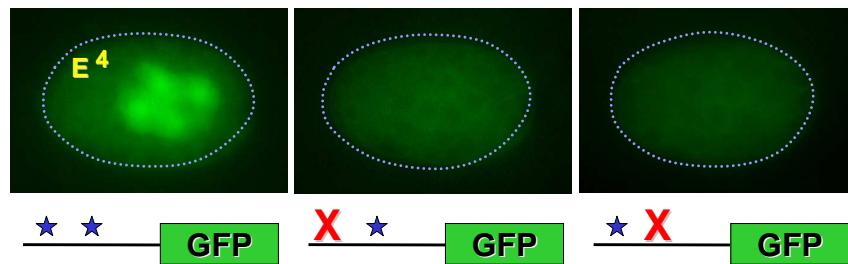


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GTATA sites are required for *end-1* expression



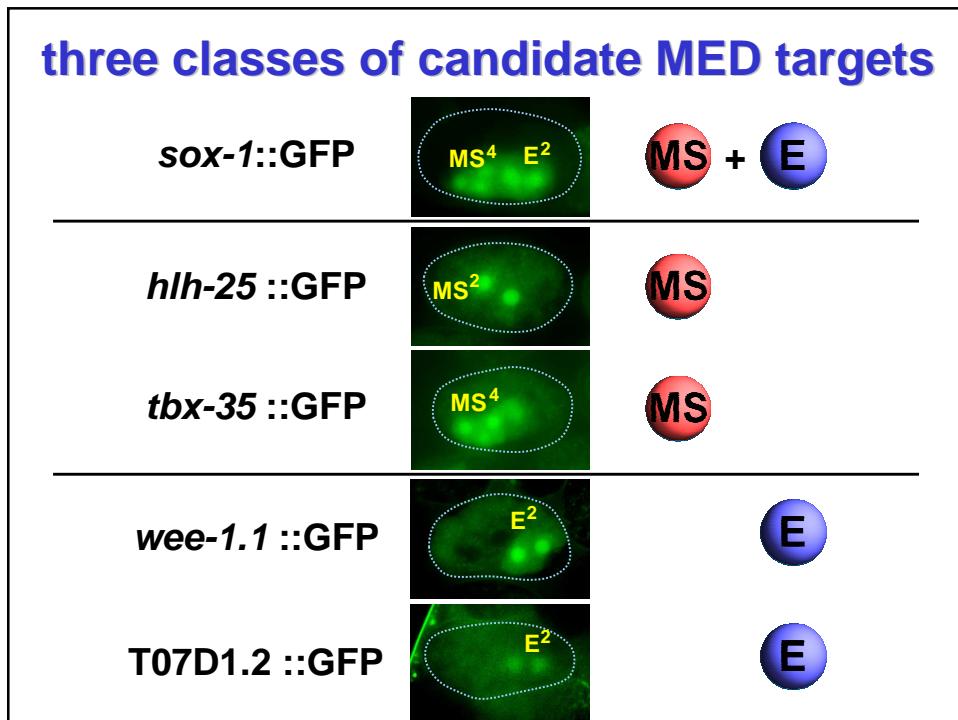
genomic search for MED targets

query with WormEnhancer:

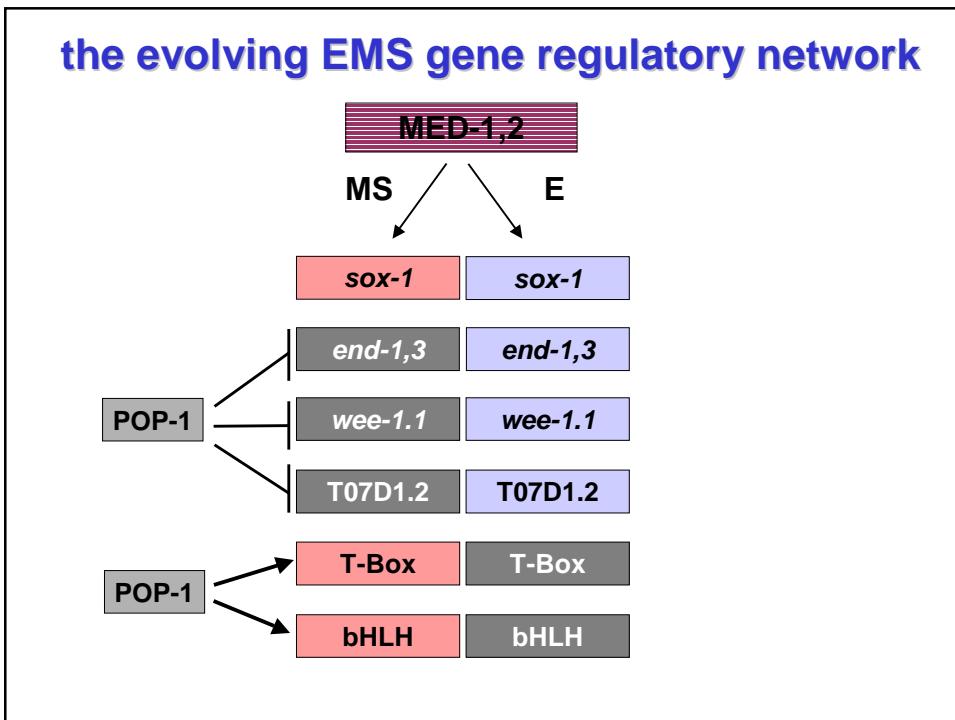
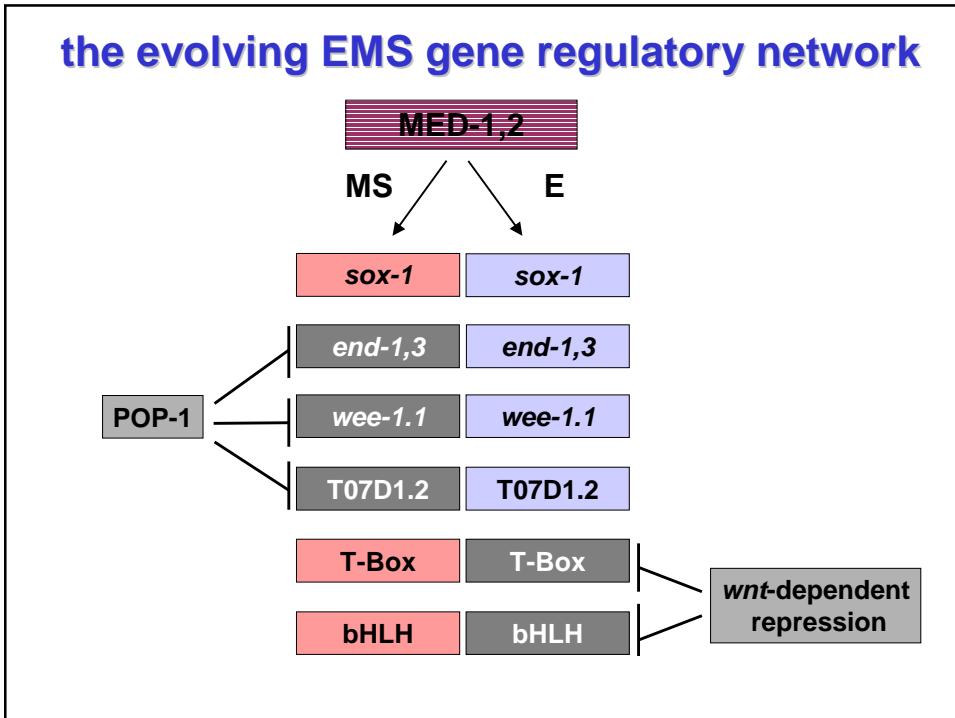
[A A G T A T A C] N₂₅₋₁₀₀ [A A G T A T A C]

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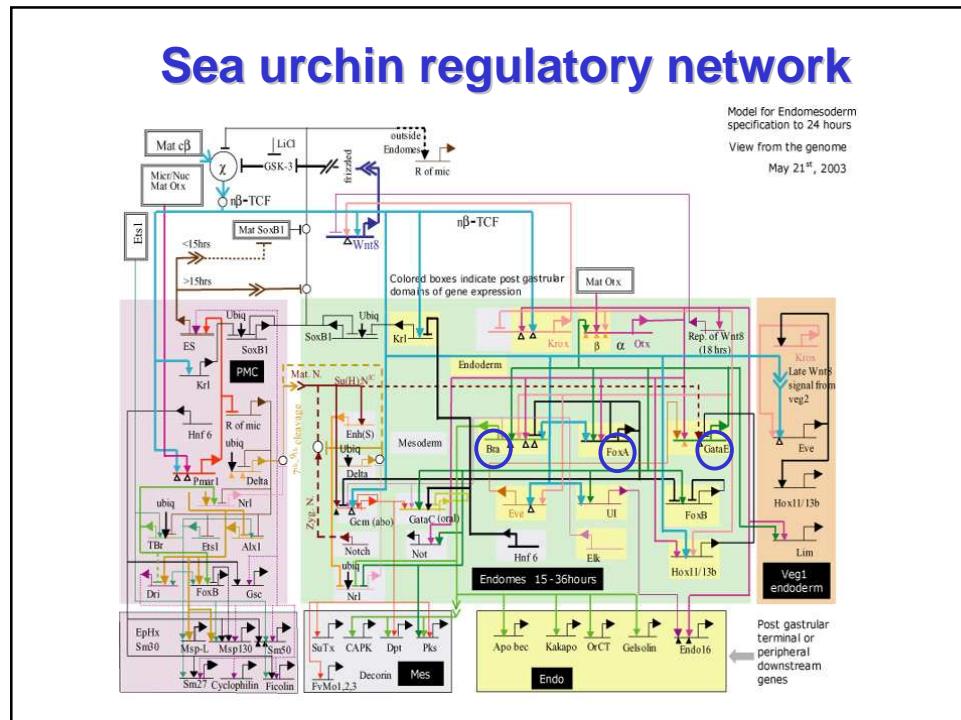
putative MED targets			
A A G T A T A C	N ₂₅₋₁₀₀	A A G T A T A C	
gene	product	MED sites	
F58E10.2	<i>end-1</i>	★ ★	
F58E10.5	<i>end-3</i>	★ ★ ★ ★	
F35H8.7	<i>wee-1.1</i>	★ ★ ★	
<i>ceh-20</i> /F31E3.2	homeobox	★ ★	
F58G4.4	LAG-2-like	★ ★	
C32E12.5	Sox family (HMG)	★ ★ ★	
ZK849.2	RCC1	★ ★	
T07D1.2	unknown	★ ★	
ZK177.10, ZK177.1	T-box/unknown	★ ★ ★ ★ ★ ★ ★ ★	
T11A5.5	oxygen transport	★ ★ ★	
C17C3.7, C17C3.10	bHLH (2)	★ ★	
B0303.8, 9	unknown	★ ★ ★ ★	



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