Applying cutting-edge technology for reproductive control in bivalves

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Managing expectations: this talk has no data

Outline

- Reproductive control in aquaculture
 - Approaches to sterility
 - Ploidy manipulation
 - Germ cell elimination
- Identification genes involved in germ cell development in bivalves
 - Single-cell RNA Sequencing

Why is sterility desirable in aquaculture?

- Improved growth
- Year-round marketability
- Blackboxing of selectively bred lines
- Minimize genetic impact of selectively bred stocks on natural populations
- Escapement is less of a threat when culturing non-native species

Current approach to reproductive control: Ploidy manipulation

- Triploid bivalves have 3 chromosome sets (instead of 2)
- Effectively sterile because they can't complete meiosis
- Challenges:
 - Takes a long time to develop selected lines (10 years!)
 - Triploids can exhibit compromised performance in the field

Alternative approach: Elimination of germ cells

What are germ cells?

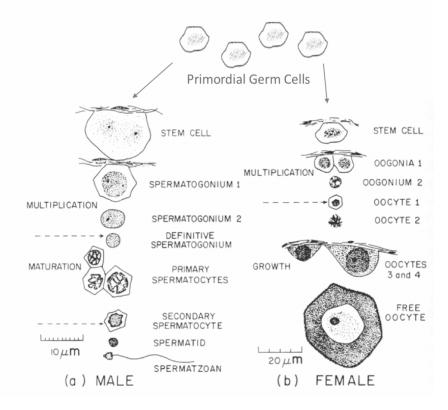
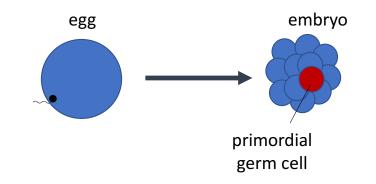
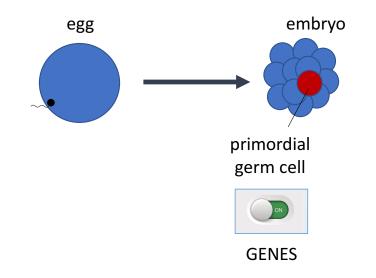
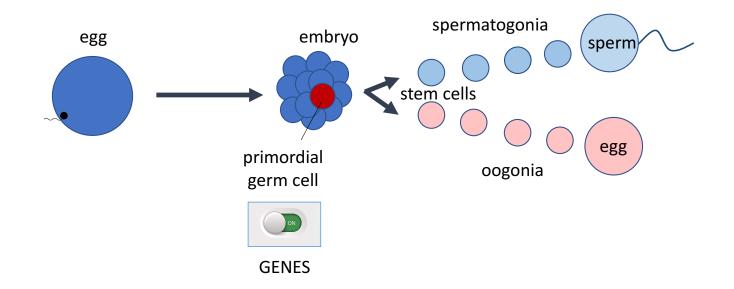


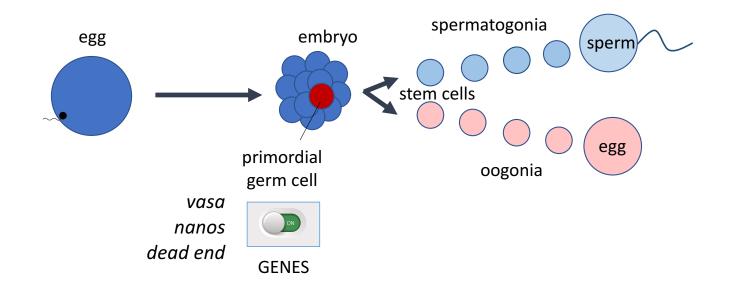
Image modified from (Sastry, 1979)



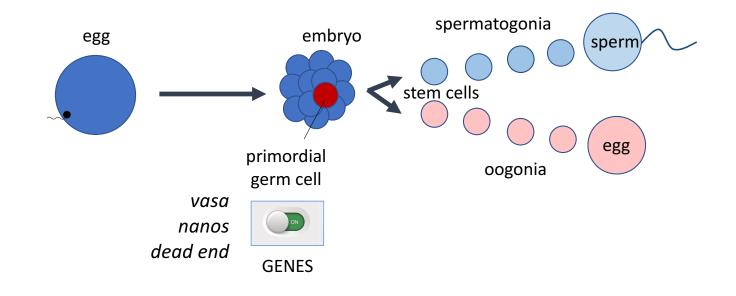




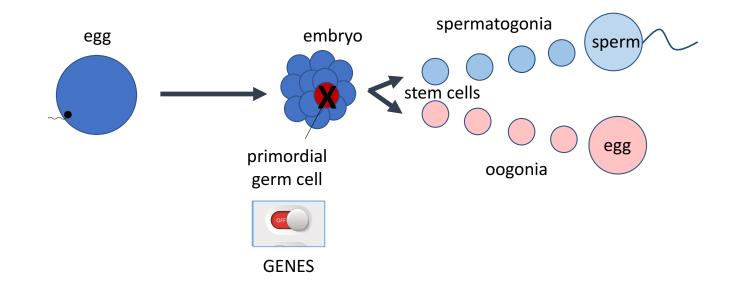




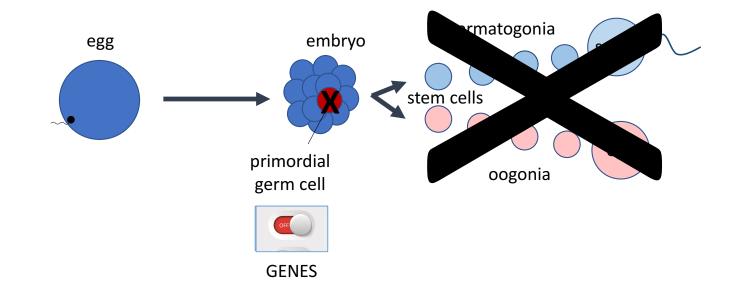
How are germ cells eliminated?

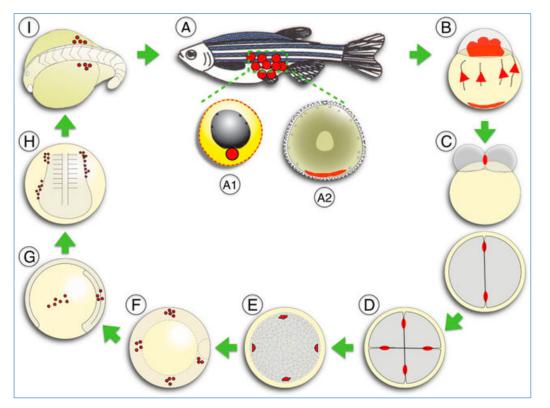


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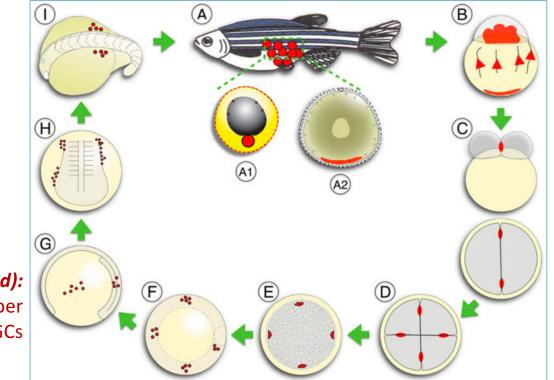


How are germ cells eliminated?





Doesch 2014; Critical reviews in biochemistry and molecular biology

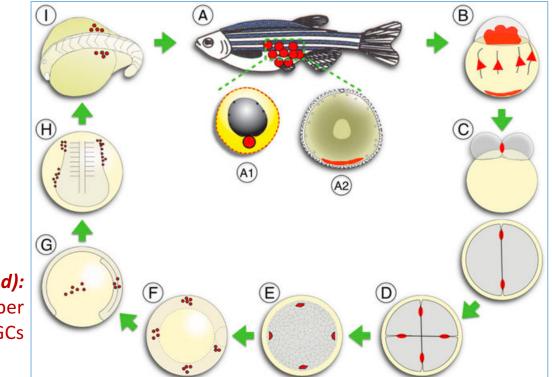


Dead end (dnd): important for proper migration of PGCs

Doesch 2014; Critical reviews in biochemistry and molecular biology

morpholino: short synthetic RNA; turns off a specific gene (temporarily)

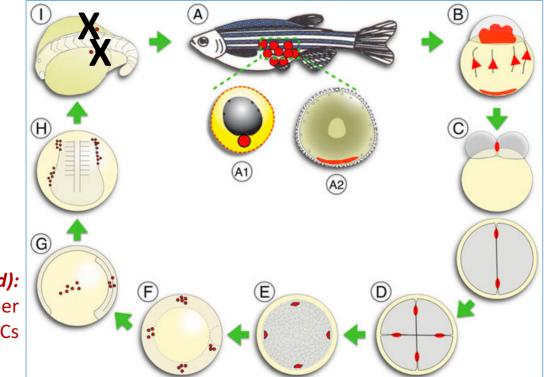
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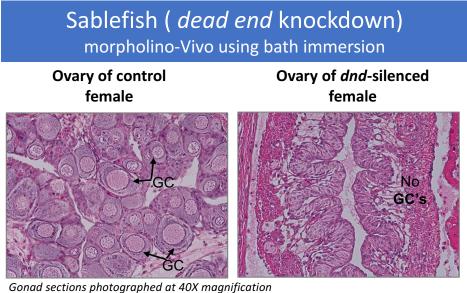
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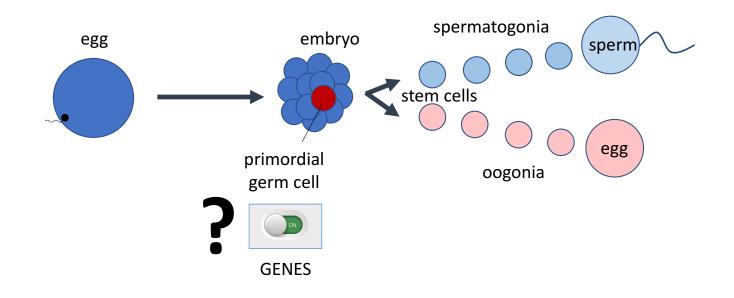


Doesch 2014; Critical reviews in biochemistry and molecular biology



GC = germ cell; dnd = dead end gene

Adam Luckenbach (NWFSC) Ten-Tsao Wong, Yoni Zohar (University of Maryland)



RNA-Seq: Whole transcriptome sequencing to quantify RNA of a biological sample

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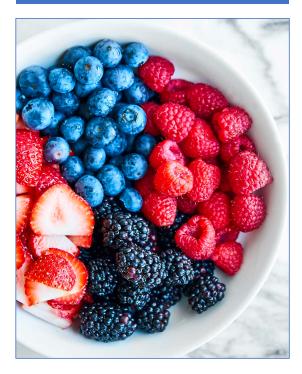
Bulk RNA-Seq

RNA-Seq: Whole transcriptome sequencing to quantify RNA of a biological sample

Bulk RNA-Seq



Single-cell RNA-Seq



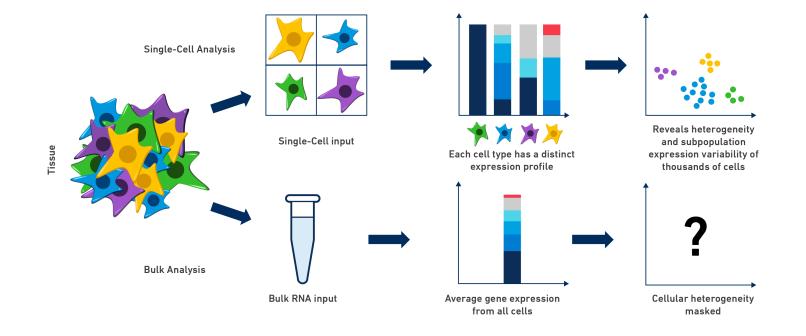


Image: 10x Genomics website

- 1. Dissociate tissue to single cell suspension
- 2. Prepare cDNA libraries of single cells
- 3. Sequencing on high-throughput sequencer (Illumina)

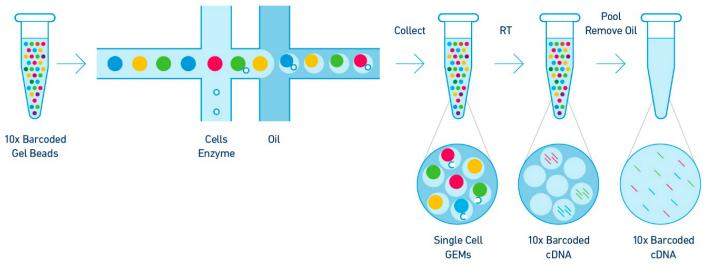
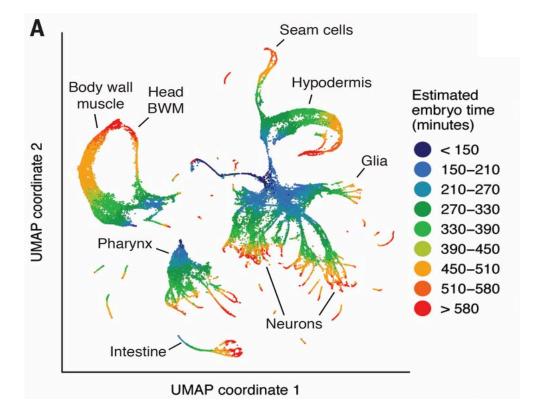


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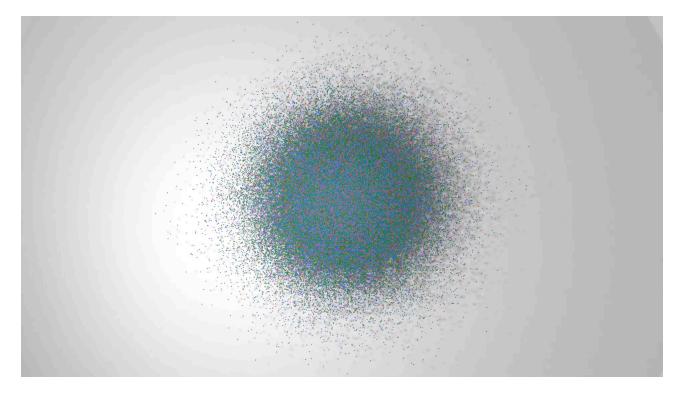
- Sequenced cells from all developmental stages of *C. elegans* to understand key mechanisms of cell fate decisions
- 86,046 cells were sequenced

Science	RESEARCH ARTICLES	
	Cite as: J. S. Packer <i>et al., Science</i> 10.1126/science.aax1971 (2019).	
A lineage-resolved molecular atlas of <i>C. elegans</i> embryogenesis at single-cell resolution		
Jonathan S. Packer ^{1*} , Qin Zhu ^{2*} , Chau Huvnh ¹ , Priva Sivaramakrishnan ³ ,	Elicia Preston ³ , Hannah Dueck ³⁺ ,	

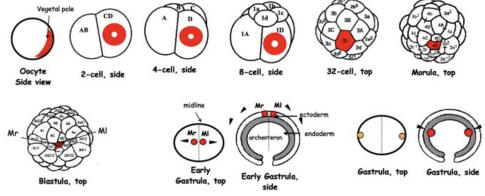
Jonathan S. Packer^{1,*}, Qin Znu^{-*}, Chau Huynn^{*}, Priya Sivaramakrishnan^o, Encia Preston^o, Hannan Dueck Derek Stefanik^{*}, Kai Tan^{3,5,6,7}, Cole Trapnell¹, Junhyong Kim⁴[‡], Robert H. Waterston¹[‡], John I. Murray³[‡]



Packer et al. 2019, Science

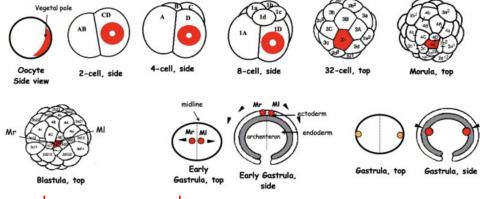


Movie: Cole Trapnell



red = *vasa* expressed

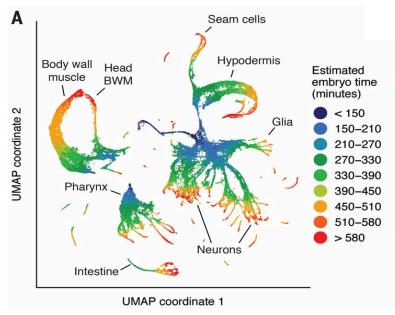
Fabioux et al. 2004, Biochem Biophys Res Commun.



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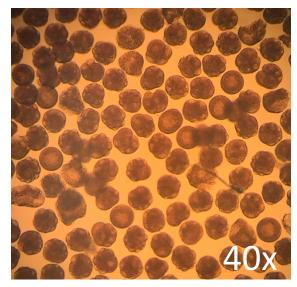
Fabioux et al. 2004, Biochem Biophys Res Commun.

Example trajectory analysis:

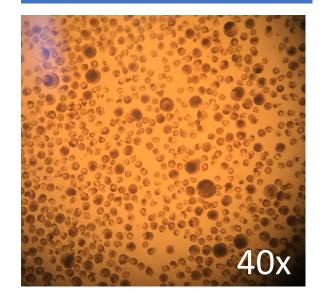


- Testing cell dissociation protocols
- Optimizing method for collection of multiple developmental stages
- Generate scRNA-Seq libraries and perform differential expression and trajectory analysis

Early cleavage embryos

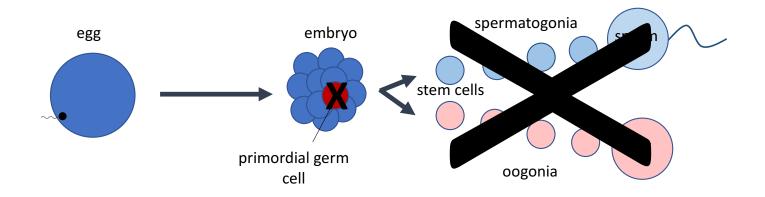


Post-dissociation



Expected outcomes

- Identify candidate genes involved in primordial germ cell formation in bivalves
- Future work will evaluate how silencing these genes impacts germ cell development
- Ultimately, developing a germ cell elimination protocol for bivalves will confer all the benefits of sterility while avoiding the challenges of ploidy manipulation



Acknowledgements

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Molly Jackson Beniot Eudeline Joanie Hendricks

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