Embryos and ancestors: Reconstructing gene regulatory networks and embryonic development in ancestral echinoids

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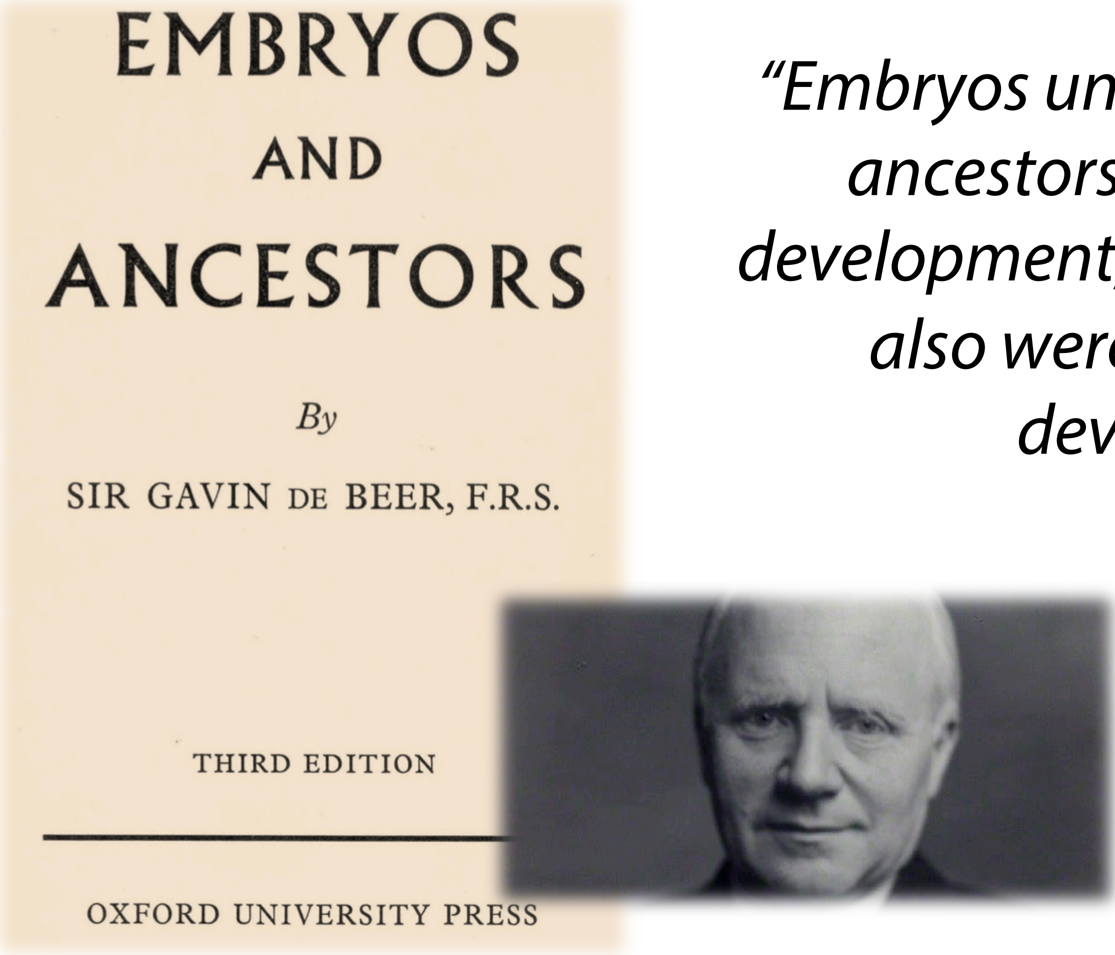

EMBRYOS
AND
ANCESTORS

By

SIR GAVIN DE BEER, F.R.S.

THIRD EDITION

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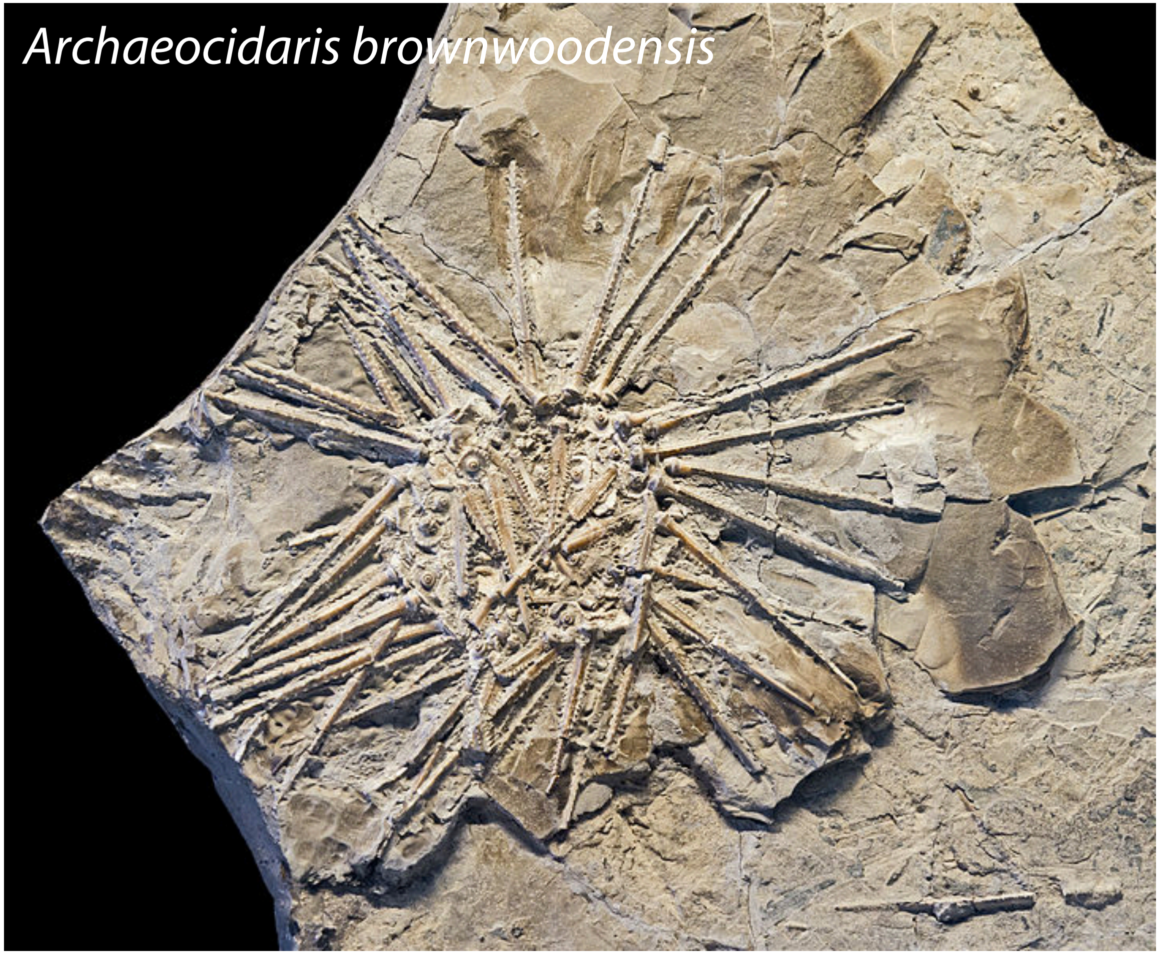
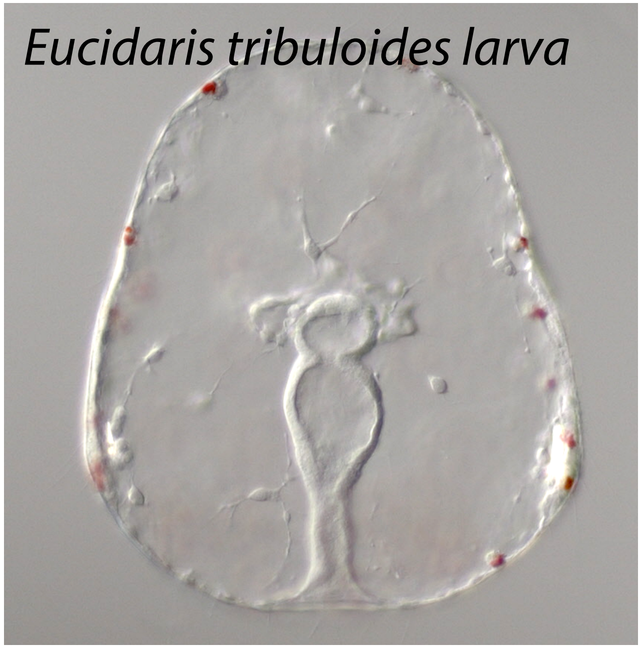
> *"Embryos undergo development; ancestors have undergone development, but in their day they also were the products of development."*
>
> *p. 1 (1940)*

Embryos and ancestors


Archaeocidaris brownwoodensis


Eucidaris tribuloides adult

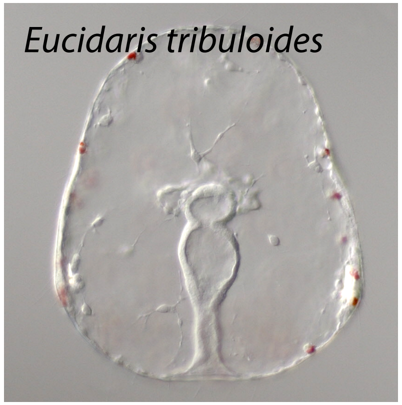

Eucidaris tribuloides larva

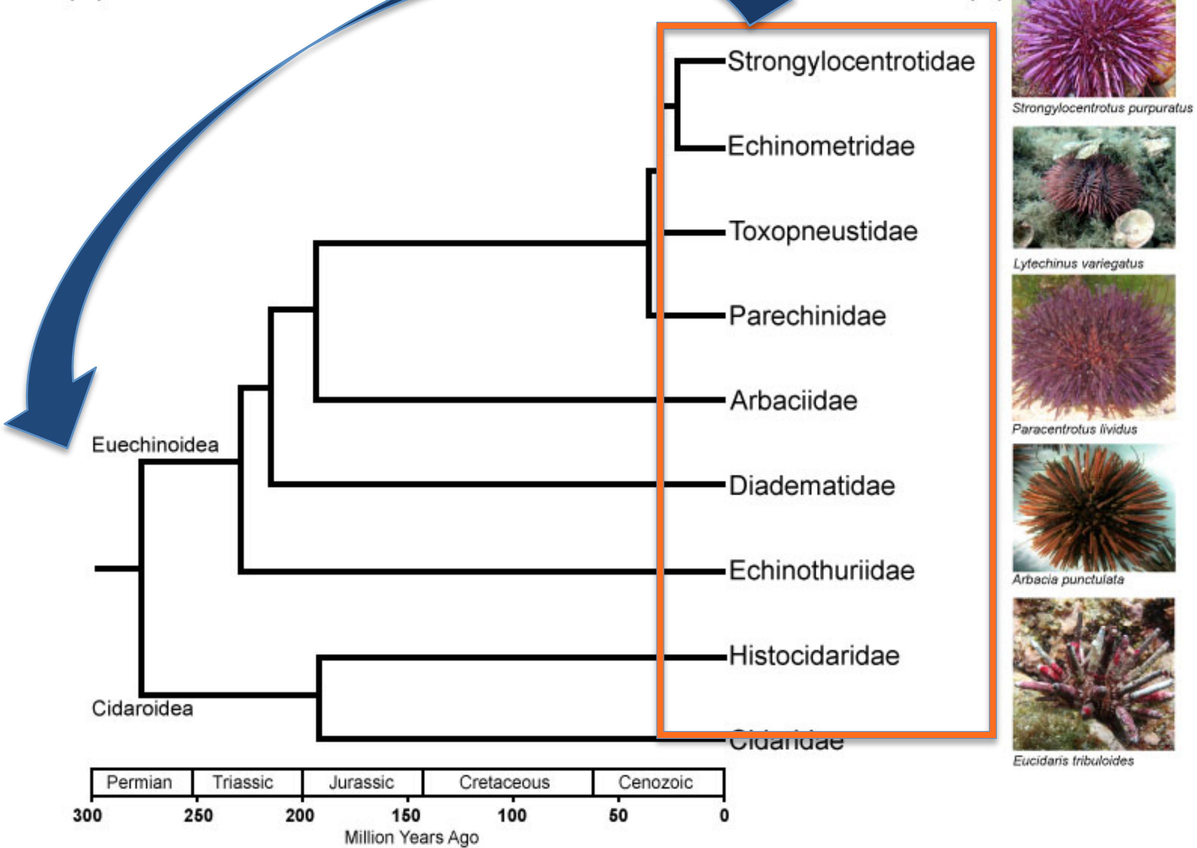
Motivating questions

- What can we say about the embryos and developmental programs of *Archaeocidaris spp.*?
- What kinds of data are at our disposal?
- Can we simultaneously investigate fundamental processes of development and evolution along the way?

Phylogeny of echinoids


Archaeocidaris sp.


Eucidaris tribuloides

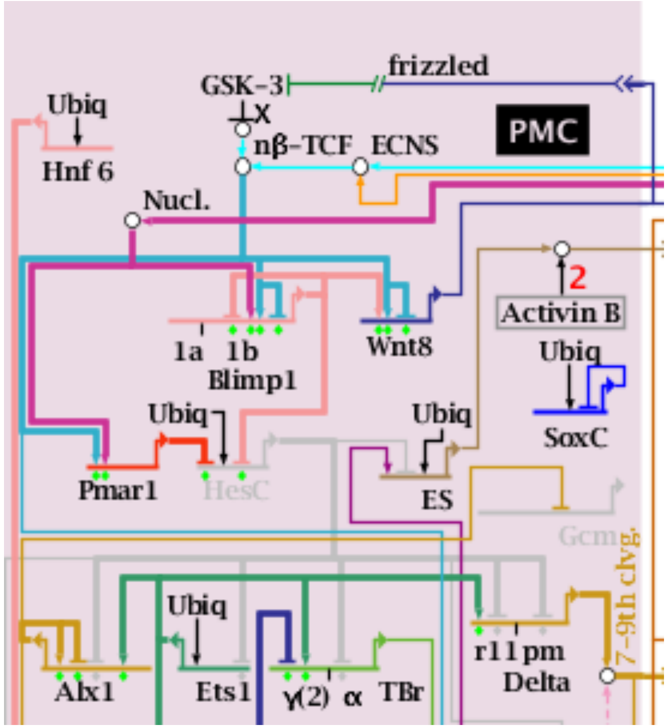


What kinds of data can we collect to make inferences about ancestral embryos?

- *Developmental modes*
  - larval life strategies, e.g. direct v. indirect development
- *Cell lineages*
  - clade-specific novelties, e.g. larval skeleton, larval pigment, etc.
- *Gene families*
  - Gene loss, sub- and neo-functionalization of duplicated genes, etc.
- *Gene regulation*
  - Gene regulatory networks (linkages, circuits), regulatory states (spatial localization of gene products), etc.

→ Common to all of these datasets is the importance of sampling numerous taxa

What is a gene regulatory network (GRN)?



Gene Regulation

Protein products of genes (e.g., transcription factors, signaling cascades) regulate the production (transcription) of other genes

Gene Regulatory Network

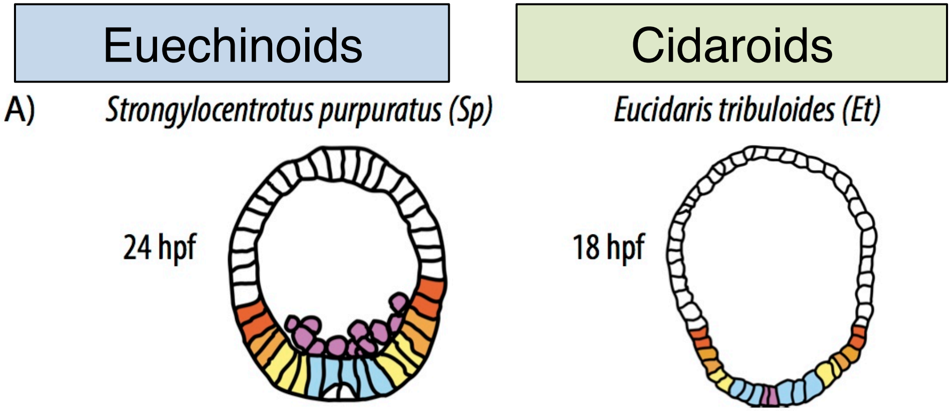
A wiring diagram representing the intricate, recursive regulatory circuitry of gene/protein interactions in the cell (or the embryo)

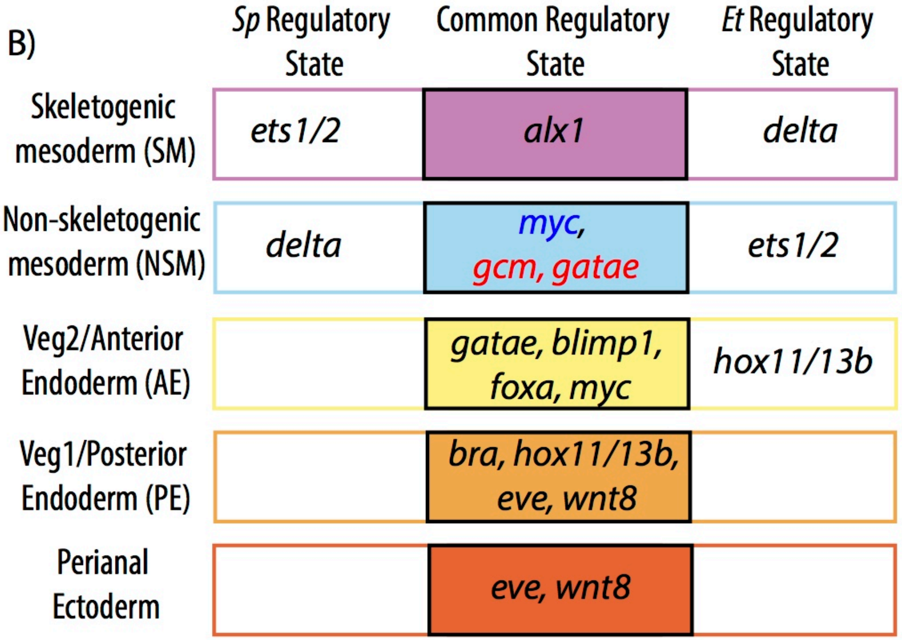
What is a regulatory state (RS)?

Regulatory State

-- The spatial output of gene regulatory networks in the embryo

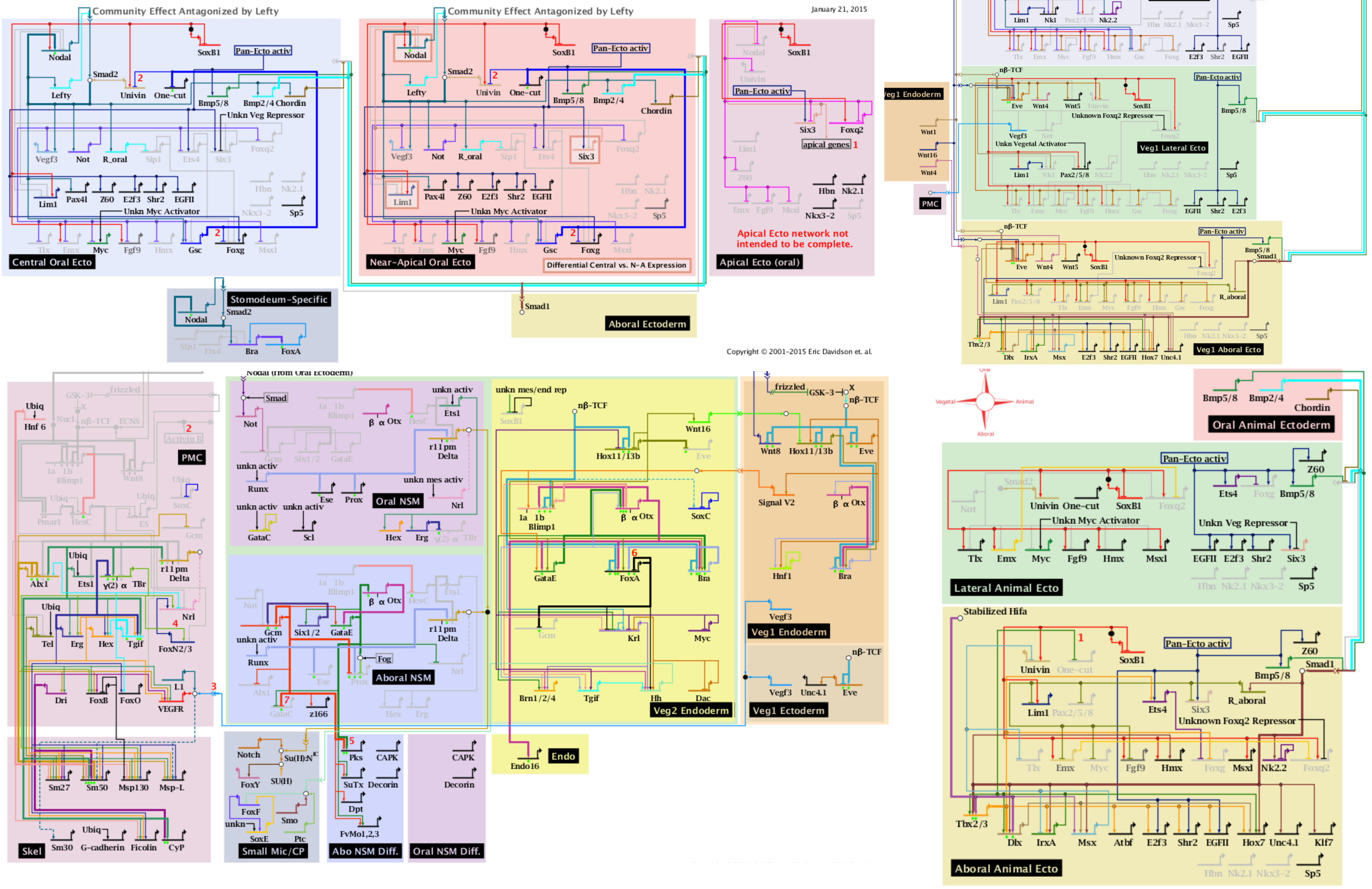
-- The total set of regulatory genes present in a given cell




B)

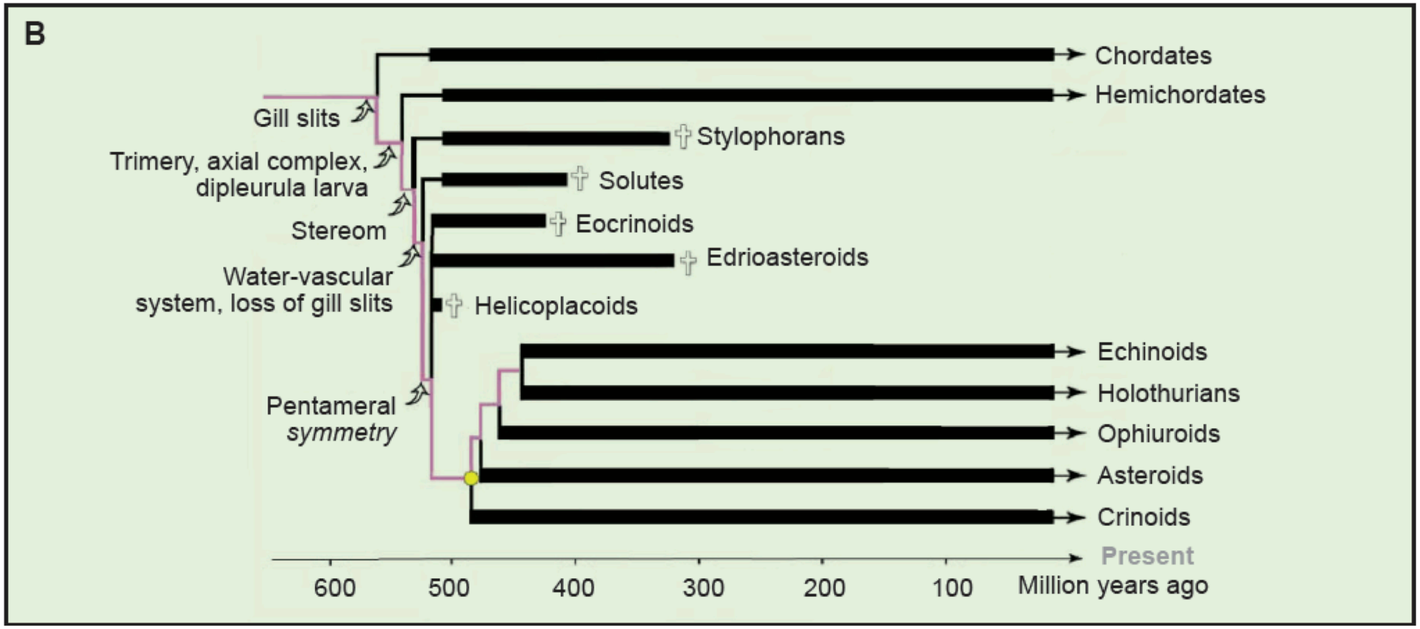
	Sp Regulatory State	Common Regulatory State	*Et* Regulatory State
Skeletogenic mesoderm (SM)	*ets1/2*	*alx1*	*delta*
Non-skeletogenic mesoderm (NSM)	*delta*	*myc,* *gcm, gatae*	*ets1/2*
Veg2/Anterior Endoderm (AE)		*gatae, blimp1, foxa, myc*	*hox11/13b*
Veg1/Posterior Endoderm (PE)		*bra, hox11/13b, eve, wnt8*	
Perianal Ectoderm		*eve, wnt8*	

Strongylocentrotus purpuratus Global GRN, 18-30 hpf (hours post fertilization)



January 21, 2015

Comparative analyses in echinoderms

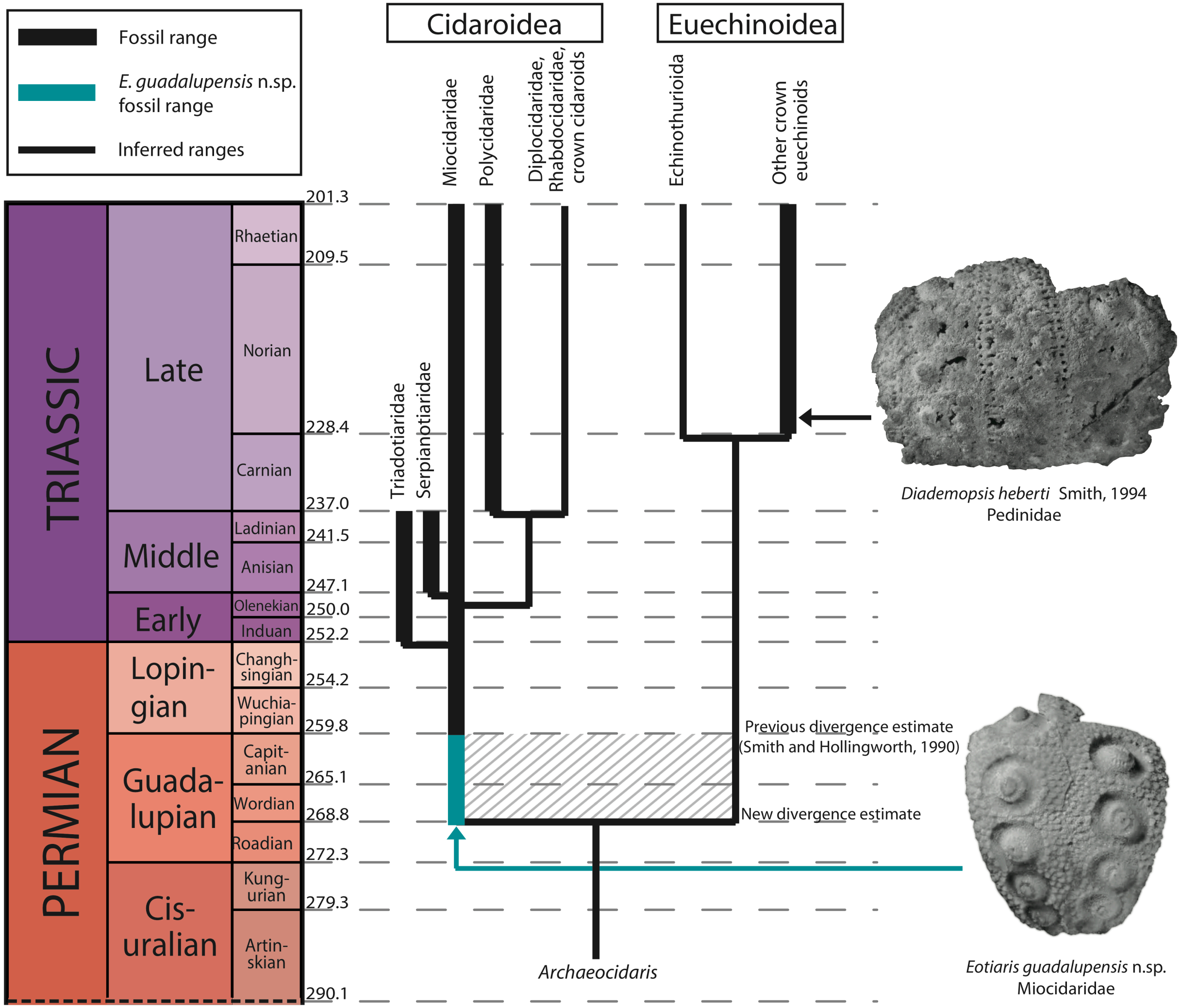


Bottjer et al. (2005)

→ Embryonic development of echinoid outgroups, e.g. asteroids, ophiuroids, holothuroids, afford polarity of developmental programs and modes

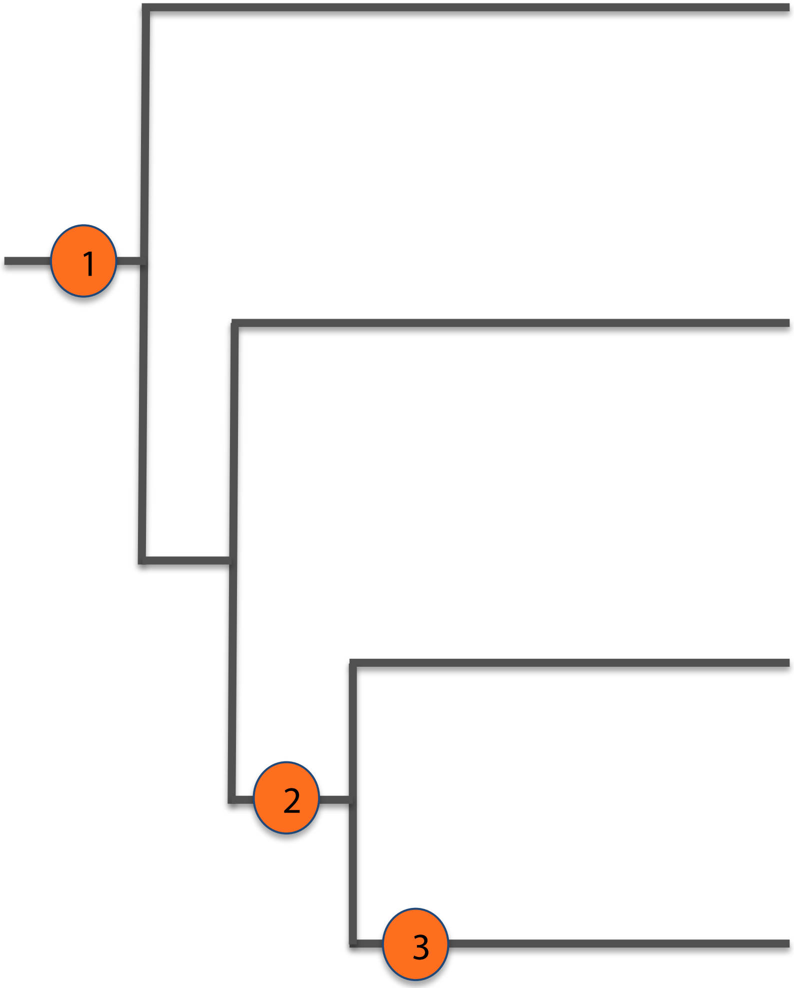
A good fossil record is a developmental evolutionary biologist's best friend

Accurate dating of echinoderm fossils combined with developmental studies of modern descendants reveals the tempo and mode of developmental evolution

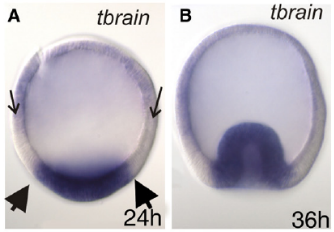


Thompson et al. (2015) Sci. Rep.

Expression of mesoderm-specific regulatory gene *tbrain* in echinoderms

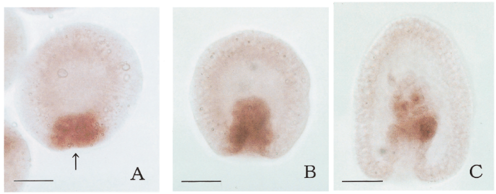


Asteroids
Endomesoderm



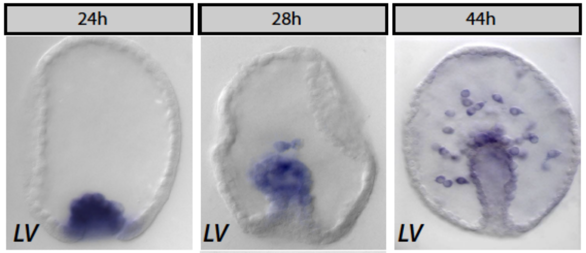
(Hinman and Davidson, 2007)

Holothuroids:
Endomesoderm

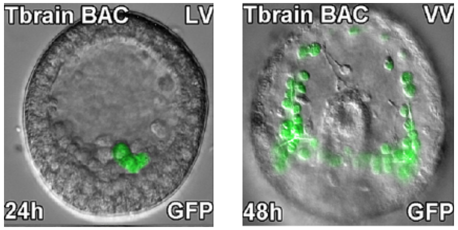


(Maruyama, 2000)

Cidaroids:
Mesoderm

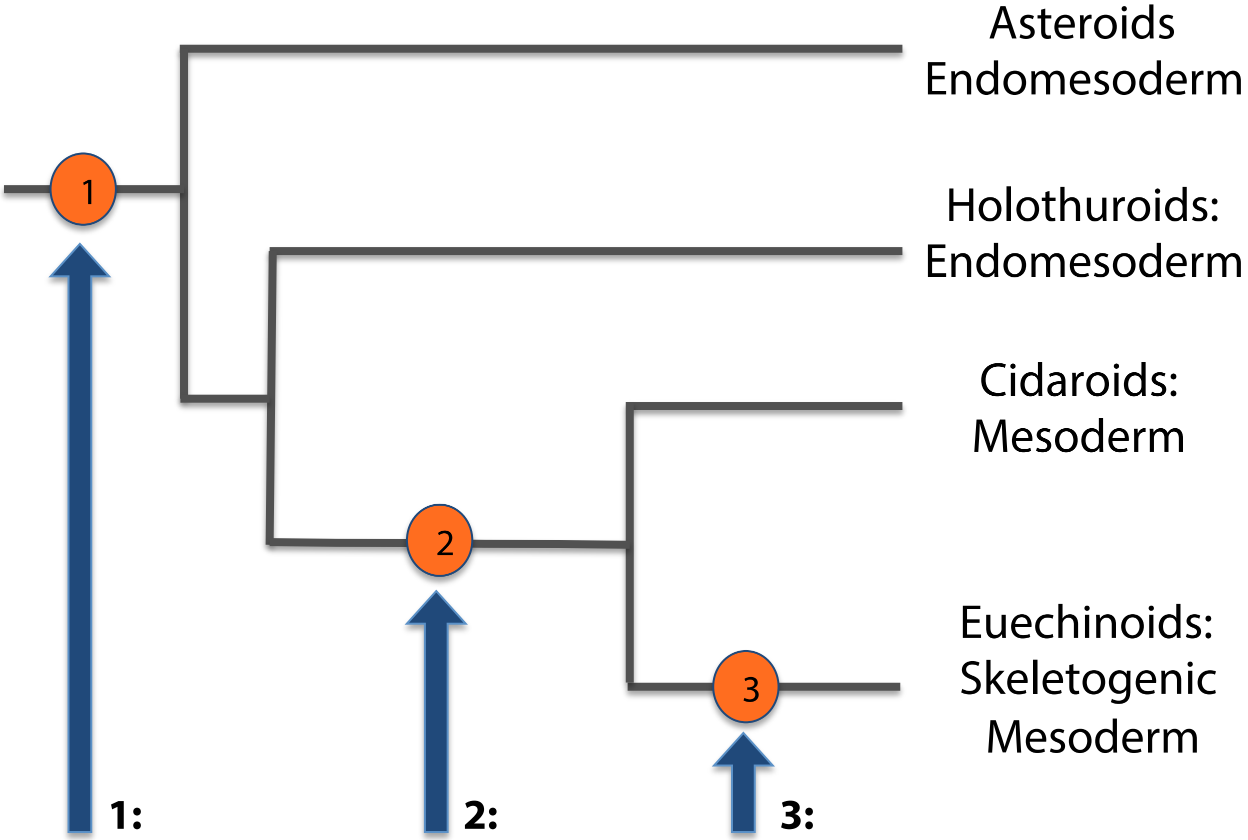


Euechinoids:
Skeletogenic
Mesoderm



(Wahl *et al*, 2009)

Dating deep-time developmental programs



Asteroids Endomesoderm

Holothuroids: Endomesoderm

Cidaroids: Mesoderm

Euechinoids: Skeletogenic Mesoderm

1: 480 mya (Jell, 2014) *Tbrain* is deployed in endomesoderm of eleutherozoa

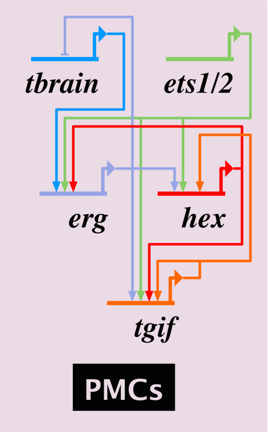
2: 268.8 mya (Thompson et al., 2015): *Tbrain* is deployed in mesoderm of echinoids

3: ~250-170 mya: *Tbrain* is deployed in skeletogenic mesoderm of euechinoids

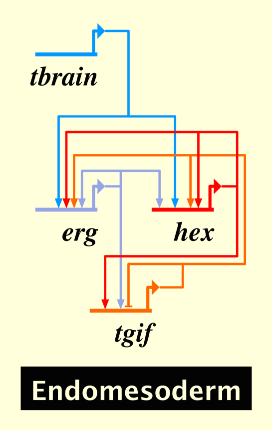
Divergence estimates based on fossil data allow us to make evolutionary statements about echinoderm developmental programs

A highly conserved mesodermal regulatory state in echinoderms

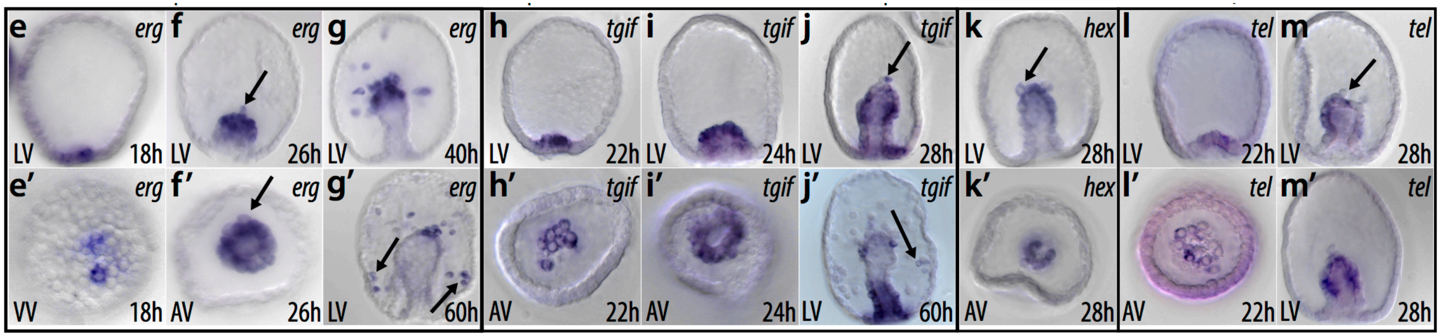
erg-hex-tgif
subcircuit in
euechinoids



erg-hex-tgif
subcircuit in
asteroids



erg-hex-tgif
subcircuit in
cidaroids



Erkenbrack et al. (2016) Dev Gen Evo

Reconstructing ancestral regulatory states in echinoderms and dating their appearance

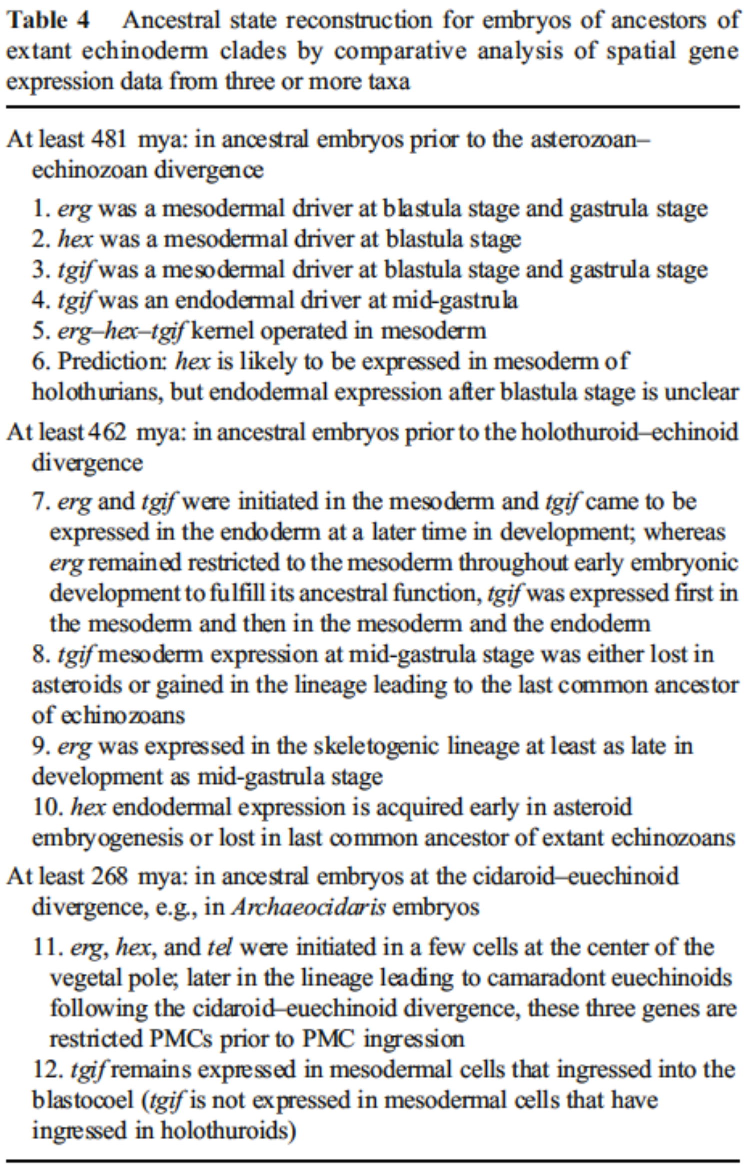


Table 4 Ancestral state reconstruction for embryos of ancestors of extant echinoderm clades by comparative analysis of spatial gene expression data from three or more taxa

At least 481 mya: in ancestral embryos prior to the asterozoan–echinozoan divergence

1. *erg* was a mesodermal driver at blastula stage and gastrula stage
2. *hex* was a mesodermal driver at blastula stage
3. *tgif* was a mesodermal driver at blastula stage and gastrula stage
4. *tgif* was an endodermal driver at mid-gastrula
5. *erg–hex–tgif* kernel operated in mesoderm
6. Prediction: *hex* is likely to be expressed in mesoderm of holothurians, but endodermal expression after blastula stage is unclear

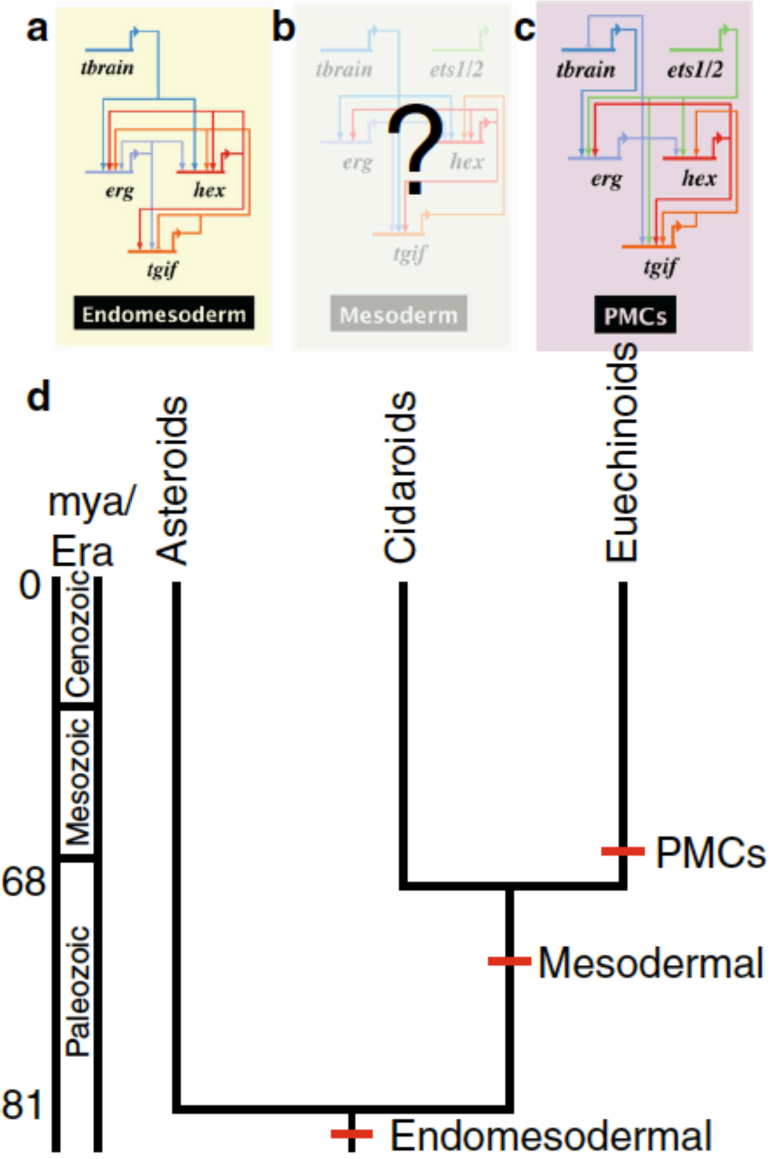
At least 462 mya: in ancestral embryos prior to the holothuroid–echinoid divergence

7. *erg* and *tgif* were initiated in the mesoderm and *tgif* came to be expressed in the endoderm at a later time in development; whereas *erg* remained restricted to the mesoderm throughout early embryonic development to fulfill its ancestral function, *tgif* was expressed first in the mesoderm and then in the mesoderm and the endoderm
8. *tgif* mesoderm expression at mid-gastrula stage was either lost in asteroids or gained in the lineage leading to the last common ancestor of echinozoans
9. *erg* was expressed in the skeletogenic lineage at least as late in development as mid-gastrula stage
10. *hex* endodermal expression is acquired early in asteroid embryogenesis or lost in last common ancestor of extant echinozoans

At least 268 mya: in ancestral embryos at the cidaroid–euechinoid divergence, e.g., in *Archaeocidaris* embryos

11. *erg*, *hex*, and *tel* were initiated in a few cells at the center of the vegetal pole; later in the lineage leading to camaradont euechinoids following the cidaroid–euechinoid divergence, these three genes are restricted PMCs prior to PMC ingression
12. *tgif* remains expressed in mesodermal cells that ingressed into the blastocoel (*tgif* is not expressed in mesodermal cells that have ingressed in holothuroids)

Erkenbrack et al. (2016) Dev Gen Evo



Erkenbrack et al. (2016) Dev Gen Evo

Going forward

Conceptual Toolkit

Integrating paleontological data and embryonic developmental data informs assumptions regarding the genomic and morphological alterations that must have occurred in lineages leading to modern taxa

Evolution of developmental programs

Interdisciplinary studies reveal the tempo and mode of evolution of genomically encoded developmental programs

More taxa, fewer problems

Comparative analyses of embryonic development and omics data of numerous taxa afford triangulation of evolutionary inferences and ancestral state reconstruction

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Liz Petsios
Feng Gao

Davidson Lab Members

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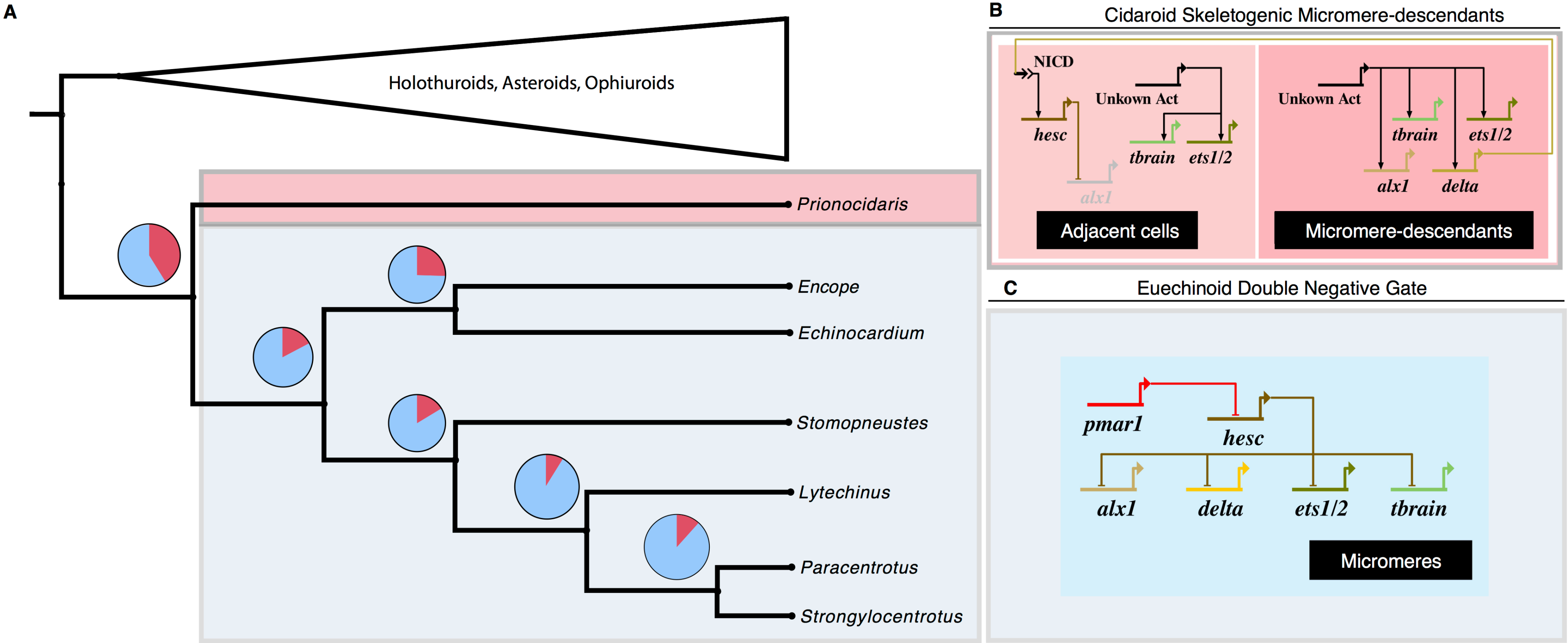
WARNING

Interdisciplinary Advertisement

I encourage paleontologists in the audience to reach out to developmental biologists!

Evolutionary inferences of the appearance of GRN circuitry

Comparative analyses of gene expression and knowledge of the fossil record revealed probability metrics for the appearance this developmental program



Thompson, Erkenbrack, et al. (In review) PNAS