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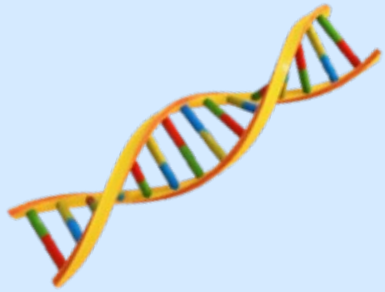
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ANOTHER STEP UP THE PHYLOGENETIC HILL

Assessing the viability of macrosynteny as a
phylogenetic trait in Lophotrochozoa

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Supervised by Torsten H. Struck & James F. Fleming

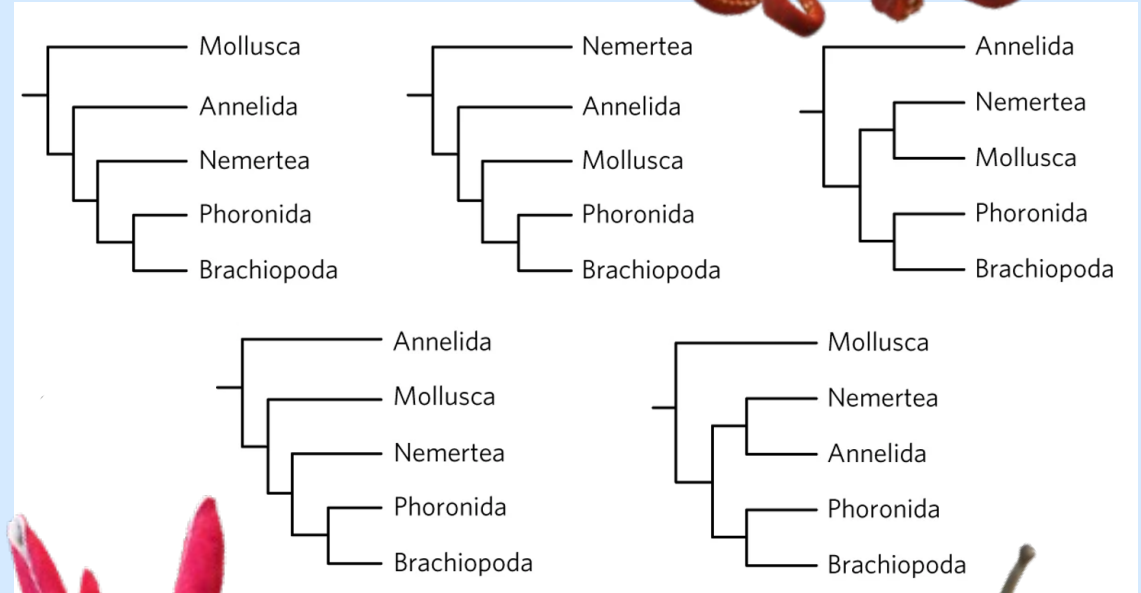




LOPHOTROCHOZOA

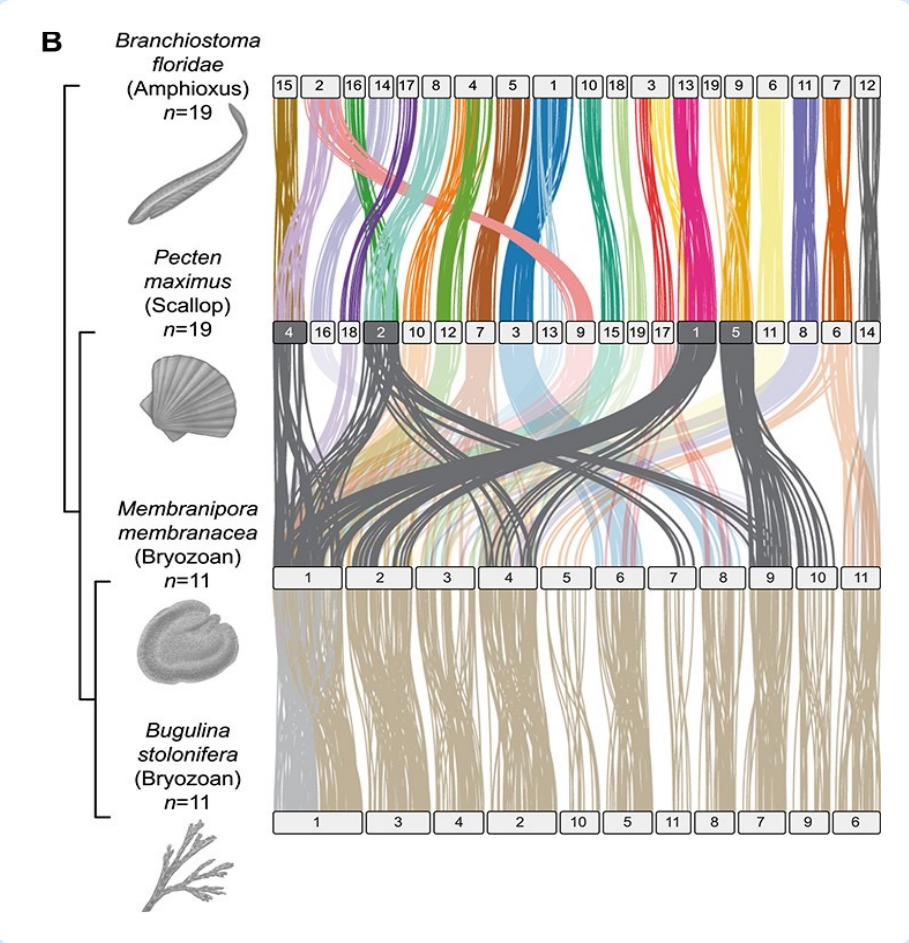


- Who are they?
- Finding the “true” lophotrochozoan tree – impossible?
- Prone to problems
 - Compositional heterogeneity
 - Long branch attraction
- Chronically underrepresented
 - 5% of data, ~30% of marine life

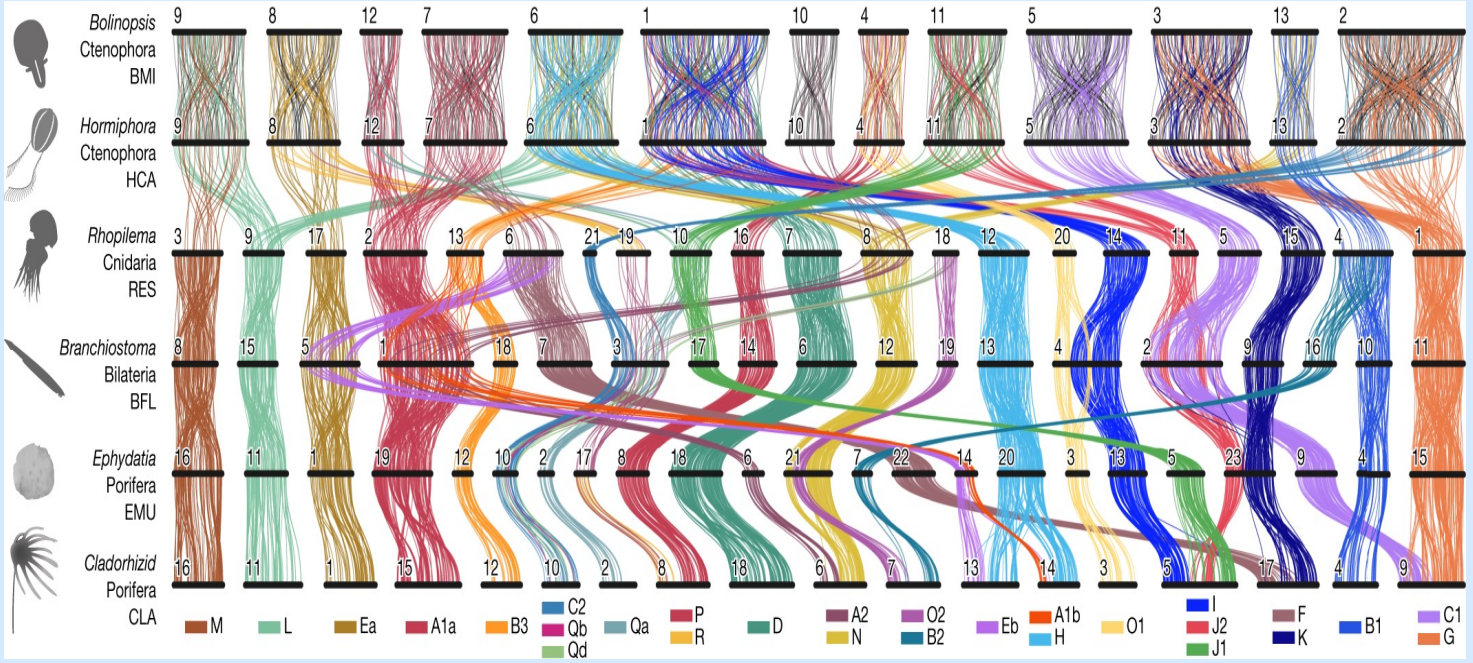




MACROSYNTENY



Gene linkage across species Renwick, 1971





THUS FAR



- Repeat previous experiments
 - Schultz et al., 2023
- Data collection
 - NCBI, EMBL-EBI, InvertOmics




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Ancient gene linkages support ctenophores as sister to other animals

[Darrin T. Schultz](#) , [Steven H. D. Haddock](#), [Jessen V. Bredeson](#), [Richard E. Green](#), [Oleg Simakov](#)  & [Daniel S. Rokhsar](#) 

Phylum	#	Phylum	#
Annelida	39	Entoprocta	1
Arthropoda	1	Gastrotricha	5
Brachiopoda	3	Mollusca	54
Bryozoa	7	Nemertea	7
Chaetognatha	2	Phoronida	1
Cycliophora	1	Platyhelminthes	13



NEXT STEPS



- Identification of macrosyntenic regions
 - BlastP, statistical analysis
- Ortholog identification
 - MAFFT, Synphoni
- ODP – Oxford Dot Plot analysis
- Barcelona
 - Deep-Time Evolution lab
- Writing!
 - Hope for a robust analysis of the viability of synteny
 - Hope to shed light on internal phylogeny of Lophotrochozoa



Dr. Jesus Lozano Fernandez



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THANK YOU FOR LISTENING!

