DEPARTMENT OF BIOLOGY | UNIVERSITY of WASHINGTON

Biology Seminar

By: Dr. Jennifer Ruesink

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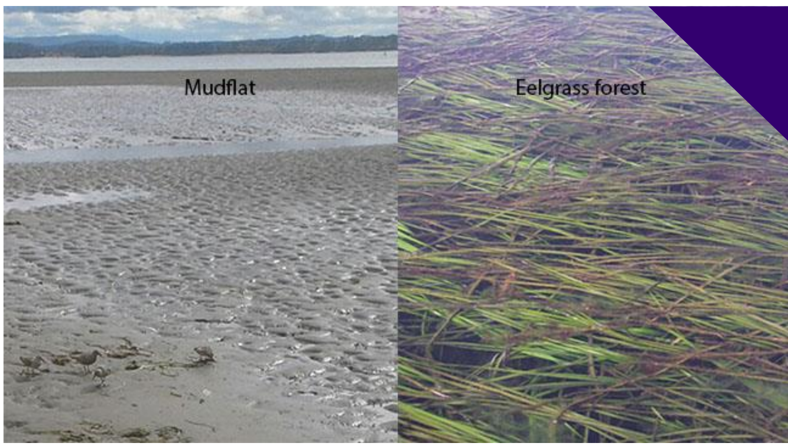
Response and effect traits in a phenotypically-variable marine foundation species



Monday, October 07, 2019 | 12:00pm
HCK 132 Refreshments at 11:45am

Eelgrass (*Zostera marina*) is a flowering plant in shallow soft sediments along all northern temperate coasts, where it is an indicator of water quality and energy, and plays a strong ecological role in food webs and shoreline stabilization. Within a single species, it exhibits extraordinary phenotypic variation: adult body size spans an order of magnitude; and life history ranges from annual populations where all plants flower and die each year, to perennial populations where >95% of shoots derive from clonal branching. This phenotypic variability lends itself to the ecological framework of response and effect traits to unravel both why its phenotype varies, and whether that variation matters for its ecological role. For response traits, taller plants tend to occur in calm conditions, fine-grained sediments, and deeper water depths, and reciprocal transplant studies revealed rapid remodeling and phenotypic plasticity. In contrast, life histories were largely fixed for transplants of seedlings and vegetative shoots. We are currently exploring whether the importance of source population for flowering stems from genetic distinction or cues very early in the life cycle. For effect traits, our state-wide sampling of fish and decapods revealed that eelgrass provides a seasonally-variable habitat, most distinct in its associated species relative to unvegetated habitats in summer. Looking ahead, these empirical data on response and effect traits will inform management decisions about source populations for restoration and methods for food production co-located with eelgrass, as well as better define the role of foundation species in supporting complex socio-ecological systems.

Seminar Speaker Host: David Perkel

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Biology Seminar

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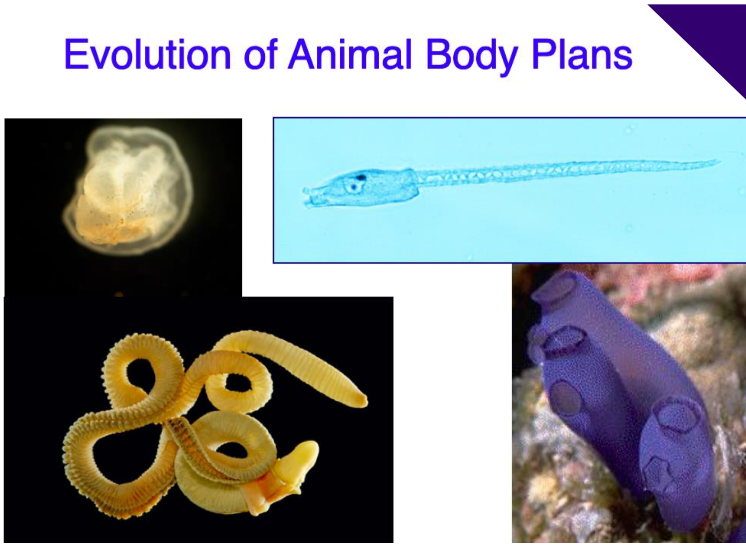
Evolution, Development and Regeneration of the Chordates



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Transcriptomic and genomic data offer exciting new approaches to examine the genetic networks underlying the origin and evolution of the chordate body plan. The Swalla lab currently has two distinct lines of investigation. In the first, microevolution project, we study two closely related tunicate species with very divergent larval body plans—the tailed ascidian *Molgula oculata* and the tailless *M. occulta*. We have sequenced the genomes and analyzed developmental transcriptomes for both species and the hybrid embryos and have shown that the muscle genes and tyrosinase pigment genes are pseudogenes in the tailless *M. occulta* species, but in some cases, the mutated transcripts are found in the transcriptomes. We also study the larger question of the evolution of the chordate body plan. This involves analyzing genomic and transcriptomic changes across phyla to infer ancestral body plans. Some hemichordate and tunicate species are also capable of regeneration, and we are looking for the genetic networks underlying these processes in an effort to understand the evolution and development of regeneration.

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