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Differential Transport Across the Surf Zone of Reflective and Dissipative Shores as a Determinant of Larval Supply

We determined whether differences in water exchange across the surf zone on dissipative and reflective shores regulates larval supply to intertidal populations. We surveyed zooplankton daily for one month relative to physical conditions inside and outside the surf zone at a dissipative and reflective beach near Monterey, California. Larvae of some species completed development nearshore while larvae of other species migrated offshore and back. Concentrations of zooplankters were much greater outside than inside the surf zone at the reflective beach, indicating that the surf zone may block onshore transport. Barnacle cyprids were an exception, suggesting that ontogenetic changes in larval behavior may facilitate penetration of the surf zone. In contrast, zooplankters were 1 to 2 orders of magnitude more concentrated inside the surf zone of the dissipative beach. Settlement of barnacles on rocks at both beaches was low, and settlement of sand crabs, *Emerita analoga*, was abundant only on the dissipative beach. Different hydrodynamics of surf zones at dissipative and reflective beaches together with larval behavior may play a major role in regulating larval supply along the West Coast.

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Genomic Bases for Independent Origins of Neurons and Complex Brains: New Insights from RNA−seq and genomic sequencing of basal metazoans, basal deuterostomes and molluscs

The origin of neurons and complex centralized brains are two major evolutionary transitions in the history of animals. How many times might complex brains and neurons have evolved? Monophyly (e.g. the presence of a centralized nervous system in urbilateria) vs polyphyly (multiple origins by parallel centralization of nervous systems within several lineages) are two historically conflicting scenarios to explain such transitions. To reconstruct the parallel evolution of nervous systems, genomic and metabolomic approaches have been implemented to probe enigmatic neurons of basal metazoans (including 8 ctenophores) and basal deuterostomes, as well as 23 species of gastropod and cephalopod molluscs (including Nautilus, Sepia, Loligo, Octopus). 1) Recent phylogenomic and cladistic analysis of RNA−seq data suggests that complex brains may have independently evolved at least 9−11 times within different animal lineages. Indeed, even within the phylum Mollusca cephalization might have occurred at least 5 times. 2) Cladistic, genomic and metabolomic analyses imply that neurons themselves evolved more than once (e.g. Ctenophores vs other animals). Emerging molecular data further suggest that at the genomic level neural specification might have been achieved by changes in expression of just a few transcriptional factors not surprising since such events might happen multiple times over 700 million years of animal evolution. Ancestral polarized secretory cells were likely involved in coordination of ciliated locomotion in early animals, and these cells can be considered as evolutionary precursors of neurons within different lineages. Under this scenario, the origins of neurons can be linked to adaptations to stress/injury factors in the form of an integrated regeneration−type cellular response with secretory signaling peptides as early neurotransmitters.

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Sexual dimorphism in the Gray Wolf (Canis lupus): specialization for male−male competition or for male provisioning?

Sexual selection theory predicts that male mammals will be more specialized for physical competition than females. Specialization for aggression, however, may result in functional conflicts with locomotor demands. Characters associated with locomotor economy include long, gracile limbs that reduce the cost of transport by increasing stride length and decreasing the energy required to swing the limbs. In contrast, specialization for aggression appears to result in stout bones and large distal muscles with high mechanical advantage that increase force available to strike or manipulate opponents. Gray wolves (*Canis lupus*) are highly cursorial animals, traveling immense distances to locate and run down prey. Gray wolves also aggressively defend territory through direct competition and kill much larger, highly dangerous prey species. Because both sexes actively participate in these activities, a low level of musculo−skeletal sexual dimorphism is expected. However, males often lead in aggressive encounters with conspecifics and, for a period during the mating season, must kill prey without the assistance of the dominant female to provision her and their young. Thus, male wolves may exhibit a higher degree of morphological adaptation associated with aggressive activities. To assess sexual dimorphism in three distinct subspecies of gray wolves, a series of skeletal metrics were taken from fresh cadavers and museum specimens. All measures were size−corrected and analyzed to detect relative differences in size and shape. Males were found to have broader skulls, more robust limb bones, and higher muscle mechanical advantages than females, suggesting that males are more highly specialized for physical aggression. However, results for each subspecies differed substantially, likely reflecting differences in selective pressures on pursuit versus handling capabilities based on prey size.

S8−1.4 MORROW, C.C.*; REDMOND, N.E.; PICTON, B.E.; ALLCOCK, A.L.; SIGWART, J.D.; MAGGS, C.A.; Queen's University Belfast, NMNH, Smithsonian Institution , National Museums Northern Ireland, Dept. of Zoology, Ryan Institute, National University of Ireland Galway; *christinemorrow@gmail.com*

Molecular phylogenies support homoplasy of multiple morphological characters used in the taxonomy of Heteroscleromorpha (Porifera: Demospongiae)

The most recent attempt to produce a stable classification of sponges was based solely on morphological characters (*Systema Porifera* Hooper & van Soest, 2002) and incorporated the cladistic analyses of van Soest et al., 1987 & 1990; de Weerdt, 1989 and Hooper, 1990 & 1991. The current study uses sequence data from 18S rDNA; 28S rDNA and CO1 barcoding fragment combined with morphology to justify the resurrection of Axinellida Levi, 1973. The abandonment of Axinellida and the establishment of Halichondrida *sensu lato* to contain Halichondriidae, Axinellidae, Heteroxyidae and a new family Dictyonellidae was based on the hypothesis that it was more parsimonious to assume that an axially condensed skeleton evolved independently in four separate lineages than to assume that asters (star shaped spicules); acanthostyles (club−shaped spicules with spines) and sigmata (C−shaped spicules) each evolved more than once (van Soest et al., 1990). Our resulting molecular trees are congruent and contrast with the morphology based trees of van Soest et al., 1990. The results show that axially condensed skeletons, asters, acanthostyles and sigmata are all homoplasious or alternatively that some may be ancestral but lost in certain lineages. We use the molecular trees presented here as a basis for re−interpreting the morphological characters within Heteroscleromorpha.