Understanding the mechanics of tail grasping in seahorses using a parametrized computer model

Seahorses are intriguing fishes for several reasons, one being their prehensile tail. Syngnathid fishes, to which seahorses, pipefish, seadragons and seahorses belong, are characterised by a body armour of bony plates. They form a serially articulated system that encloses the vertebral column and its musculature. In the ancestral condition, as in pipfish, the tail is straight with limited flexibility, and mainly used for steering (pectorals and dorsal used for swimming). During evolution, the tail became modified into a grasping apparatus multiple times independently within the syngnathid family. Less known than the seahorse prehensile capabilities, pipefishes also show different morphologies related to grasping performance. To better understand the structural basis of tail grasping mechanics, a parametrized model of the seahorse tail was developed. By combining multibody dynamics analysis with finite element analysis, we analysed the implication of partial contribution of epaxial and hypaxial muscles, versus ventral median muscle, as well as that of the bony plate geometry. Natural bending postures, as observed in living seahorses, can be obtained up to some degree. The analyses showed particular relations between morphology and bending kinematics. Using this seahorse model, functional implications of evolutionary changes in in syngnathid tails can be further analysed, as well as to develop biomimetic designs of serially articulated systems that meet particular application demands.

99.8 PRESNELL, JS*; SCHNITZLER, CE; BROWNE, WE; University of Miami, FL, National Human Genome Research Institute, NIH, Bethesda, MD; j.presnell@umiami.edu

Klf/Sp transcription factor family expansion, diversification, and innovation in the Unikonta

The Krüppel−like factor (Klf) gene family consists of two groups of transcription factors, Klf and Specificity protein (Sp) factors. Klf/Sp proteins bind GT box and GC−rich DNA sequences associated with gene regulatory regions through a highly conserved DNA binding domain (DBD) composed of three C−terminal C2H2 zinc fingers (KLF−DBD). Members of the Klf gene family influence transcription via interactions with other transcription factors, cofactors, chromatin remodeling factors, and transcriptional machinery components. These protein−protein interactions are mediated by an array of transactivation domains typically found N−terminal of the KLF−DBD. Collectively the Klf/Sp genes play key roles in a variety of critical biological processes including cell proliferation, stem cell maintenance, embryonic development, and tissue differentiation and they have been implicated in a number of human diseases and cancers. Many Klf/Sp genes have been characterized in a handful of bilaterian lineages, however very little is known about the Klf gene family in non−bilaterians and virtually nothing is known outside of the metazoans. We identified and characterized the complete Klf/Sp gene complement from the genomes of 14 lineages spanning the Unikonta. We also examined the phylogenetic distribution of transactivation domains associated with the Klf gene family. Within the Metazoa, the expansion of the Klf gene family transactivation repertoire is strongly associated with the expansion of cell type complexity. Our results indicate that expansion of the Klf gene family is paralleled by transactivation domain diversification via both the acquisition of pre−existing ancient domains as well as by the appearance of novel domains exclusive to the Klf gene family.

98.3 PRICE, E.R.*; CAVIEDES−VIDAL, E.; KARASOV, W.H.; University of Wisconsin−Madison, Universidad Nacional de San Luis; eprice2@wisc.edu

Mechanistic correlates of paracellular nutrient absorption in protein specialists

Water−soluble nutrients (e.g., glucose and amino acids) can be absorbed across enterocytes via protein−mediated transport, or paracellularly through the tight junctions between enterocytes. Previously we demonstrated that absorption of arabinose (a nutrient−sized paracellular probe) was higher in intact insectivorous bats (Tadarida brasiliensis and Myotis lucifugus) when compared to insectivorous rodents. This phenomenon can also be observed in isolated intestines: in intestinal perfusions, arabinose clearance was higher in intact insectivorous bats (Tadarida brasiliensis and Myotis lucifugus) when compared to intact insectivorous rodents when compared on a nominal surface area basis. This implies that bats have either more tight junctions per nominal surface area (for example via longer villi) and/or bats have leakier tight junctions (perhaps achieved via differential expression of the proteins that form the tight junctions). We investigated these mechanistic correlates using histological examination of intestines and by measuring gene expression of several Claudin proteins. Supported by NSF Award 1025886.