

Abstracts • Ctenopalooza Ctwo

Updated: 24-Aug-2026

TALK • 09:15 • Evolution & Phylogeny

Should the phylogenetic position of Ctenophora be controversial?

Nathan V. Whelan

The Ohio State University

Since the first Ctenopalooza, considerable advances have been made in dataset quality for resolving the phylogenetic position of Ctenophora. However, this has not resulted in scientific consensus. For instance, numerous papers have claimed to robustly determine that sponges are the sister lineage to all other Metazoa, only to be followed by passionate rebuttals and even retractions. A similar number of papers have claimed that the most likely sister lineage to other Metazoa are Ctenophora, albeit with less published rebuttals and no retractions that I am aware of. Nevertheless, the sheer number of studies claiming near certainty in differing phylogenetic placements of Ctenophora can give the sense that the issue is intractable or controversial. Here, I argue that the phylogenetic placement of Ctenophora should be uncontroversial. This argument rests on phylogenetic inference with recently generated datasets and decades of phylogenetic theory. Regardless of analytical method, analyses on datasets with a large number of choanoflagellates, ctenophores, and sponges result in phylogenetic hypotheses that place Ctenophora as the sister lineage to all other Metazoa. The time has come to embrace the certainty and focus using robust phylogenetic hypotheses to better understand non-bilaterian animals.

TALK • 09:30 • Evolution & Phylogeny

A Ctale of Ctwo Bumps: the Story of Ctenophore Protrusions

Joseph Ryan, Yuriy Bobkov, Leslie Babonis, Yuma Tani, Kogiku Shiba, Kazuo Inaba

Whitney Laboratory for Marine Bioscience, University of Florida

Many animals possess specialized sensory protrusions that transduce information from their environment. In ctenophores, the most conspicuous example is the elaborate sensory fingers of Leucothea. More enigmatic are the much smaller sensory papillae of the warty comb jelly, Mnemiopsis. Here, we use comparative transcriptomics, immunohistochemistry, electron microscopy, and calcium imaging to characterize and compare these two sensory structures. We identify striking molecular and morphological similarities that support the hypothesis that fingers and sensory papillae are homologous structures. However, despite these similarities, important differences remain, and the sparse, patchy distribution of these sensory protrusions across ctenophores makes their evolutionary origin difficult to infer. Regardless of their exact evolutionary history, these structures provide powerful models for understanding sensory processing in ctenophores, with broader implications for the origin and evolution of animal nervous systems.

TALK • 09:45 • Evolution & Phylogeny

A new un-ctenophore

Gustav Paulay, Claudia E. Mills, Larissa Frühe, Vincent Pieribone, F. Benzoni, Kevin Kocot

University of Florida

Ctenophores are predominantly pelagic animals that move using ciliary propulsion provided by ctenes. Two lineages have independently adopted a benthic lifestyle: the Platyctenea, comprising about one quarter of known living ctenophore diversity, and the lobate Lobatolampea tetragona. Platyctenes shed their ctenes after their larval stage, while Lobatolampea retains them. Despite their independent origins, both clades share numerous similarities, such as oral-aboral compression and widespread brooding. During a recent exploration of bathyal habitats around Palau, we discovered a new, benthic lobate ctenophore lacking ctenes, representing only the second known ctenophore lineage without these structures. These animals are dorsoventrally flattened, possess hypertrophied lobes bearing a frill of tentillae arising from the tentacular ridges, and lack auricles. Phylogenetic analyses of 18S rRNA sequences place the new taxon as sister to Lobatolampea, suggesting an apomorphic lineage that extends the benthic adaptations observed in Lobatolampea. We will present and discuss the morphology, phylogenetic placement, and ecology of this new remarkable ctenophore.

TALK • 10:00 • Evolution & Phylogeny

Uncovering the hidden diversity of Beroid Ctenophores in the World Ocean.

Nicholas Bezio, Steve Haddock, Dhugal Lindsay, Claudia Mills, Allen Collins

Smithsonian NMNH

Ctenophore systematics is on the precipice of a “golden age,” with recent methodological advancements now allowing many of the challenges in ctenophore systematics to be addressed directly for the first time in history. One such group at the forefront of these advancements is the small genus Beroe, comprised of strictly marine, gelatinous predators found worldwide across all marine ecosystems. Although only 12 valid names are recognized in the genus, recent years have seen the documentation of additional morphologies through scientific publications and citizen scientists' observations (iNaturalist), suggesting that species diversity within the genus remains incompletely documented. Here, we present the redescription of 11 of these 12 valid names and additionally provide the descriptions of 11 new species that fail to match any historical species account, with five species needing additional sampling. In particular, we found that what was described as *B. abyssicola* comprises five cryptic species, *B. cucumis* comprises six species, *B. forskalii* comprises five species, *B. gracilis* comprises three species, *B. mitrata* comprises four species, and *B. ovata* comprises a single species. Additionally, we show that the sister genus Neis Lesson, 1829, is a misidentified Beroe and is therefore a junior synonym. Furthermore, certain morphological traits, such as body compression and macrociliary tooth distribution, appear to show a clear phylogenetic signal, mapping into several monophyletic lineages within the Beroe phylogeny. These results demonstrate that not only is their untold diversity hiding within Beroe, as suggested by previous surveys and citizen scientists, but there is likely to be similar hidden diversity in other understudied marine taxa. We anticipate this redescription of Beroe to be a starting point for future systematics and taxonomic revision for not only Ctenophora but also the rest of the macro gelatinous zooplankton.

TALK • 10:15 • Evolution & Phylogeny

Euplokamis dunlapae and the ancestral ctenophore karyotype

D.T. Schultz, S.H.D. Haddock

Lehigh University

Most ctenophores have 13 chromosomes, but mertensiid ctenophores have 14. Comparisons across animals and non-animal holozoans show that the crown ctenophore karyotype is 14 chromosomes. Species with 13 chromosomes have a shared, derived fusion. Here, we characterize the stability of the ctenophore karyotype, and highlight this system as a model for chromosome evolution and the regulatory impacts.

TALK • 11:30 • Evolution & Phylogeny

The near (?) future of ctenophore taxonomy

Steven Haddock, Claudia Mills, Shannon Johnson, and others depending on the species

MBARI

POSTER + LIGHTNING TALK • 16:30 • Evolution & Phylogeny

The ctenophores Hormiphora and Pleurobrachia are the same but different.

Shannon B. Johnson, Claudia E. Mills, Jacob R. Winnikoff, Darrin T. Schultz, Sanna Majaneva, Anela Choy, Anik Grearson, and Steven H.D. Haddock

MBARI

The ctenophore family Pleurobrachiidae includes the genera Hormiphora, Pleurobrachia, and Pukia. They are pelagic and live in all regions of the world ocean, usually within the top few hundred meters of water. We used morphology and fragments of 18S and 28S rRNA, nuclear Histone-3 (H3) and mitochondrial Cytochrome-C-oxidase-subunit-1 (COI) to estimate phylogenies among all available members of the Pleurobrachiidae. Two results reshape the group's taxonomy. First, Hormiphora californensis nests within the genus Pleurobrachia, rendering Pleurobrachia paraphyletic. We therefore reclassify H. californensis as Pleurobrachia californensis. Second, we found at least four new species of Hormiphora in the tropical Pacific that fall outside of Pleurobrachia. These species form a monophyletic clade that is sister to Pleurobrachia plus Pukia, and include Hormiphora sp. GoC+HI, Hormiphora sp. Moorea+HI, Hormiphora HI and Hormiphora sp. GoC. One of the species inhabits the Gulf of California and Hawaii, one inhabits Tahiti and Hawaii, one is restricted to Hawaiian waters and one is restricted to the Gulf of California. In addition to the findings that reshape the taxonomy of Pleurobrachiidae, we uncovered the evolutionary dynamics of the family through population genomic analyses of selected species. Despite overlapping ranges and similar life histories, P. bachei and P. californensis rarely co-occurred and differed in dispersal. Pleurobrachia californensis was collected mainly with trawl nets and remotely operated vehicles between 100-500m, and P. bachei was mostly found from 0-20m while blue-water SCUBA diving. Pleurobrachia californensis showed relatively uniform population structure throughout their range apart from a divergent population collected near the Galápagos Islands, whereas we found population subdivision within P. bachei over the same range. Pleurobrachia pileus showed additional subdivision unrelated to geography. These contrasting patterns of gene flow and speciation make the Pleurobrachiidae a clear example of divergent evolution among morphologically similar species.

FEATURED • 11:00 • Neurobiology & Sensory Biology

One Animal, Many Problems for Neurobiology

Pawel Burkhardt

Michael Sars Centre (University of Bergen)

Ctenophores continue to challenge some of the most fundamental assumptions in neurobiology. Their nervous systems combine molecular novelty with unconventional cellular organization, including lineage-specific neuropeptides, a syncytial subepithelial nerve net, and a highly organized aboral sensory complex. I will present recent findings from our work on ctenophore neuropeptide signaling and discuss how divergent peptide repertoires may contribute to sensory processing and behavioral coordination. I will further examine the organization of the syncytial nerve net and its implications for neuronal individuality, signal propagation, and circuit architecture. Finally, I will discuss new insights into the cellular and ultrastructural organization of the aboral organ, a central sensory structure that integrates locomotory and environmental information. Together, these findings provide an opportunity to rethink long-standing ideas about the evolution, architecture, and functional principles of nervous systems.

TALK • 12:00 • Neurobiology & Sensory Biology

The organization of the tentacle of adult Mnemiopsis is not what you think!

Anthony Moss and Gen Dong

Auburn University

The organization of the tentacular structures of adult Mnemiopsis is elucidated by very careful light microscopy methods. We show that the tentacle, previously misidentified as a vestigial cydippid tentacle, is actually made up of myriad tentilla arranged as a fan-shaped structure. Each tentillum in the food groove connects directly to the aboral end of the tentacular bulb, contradicting earlier models. Cryosectioning and lesion experiments define the origin and migration of tentilla, while videography reveals muscular fan swaying that bilaterally distributes them. Tentilla can be recycled via entrapment in the transport groove and redirected to the mouth. This updated model provides for an improved understanding of tentillar growth, distribution, transport and recycling within the feeding apparatus.

FEATURED • 09:00 • Neurobiology & Sensory Biology

Cilia, Circuits, and Behavior in Ctenophores

Kei Jokura

National Institute for Basic Biology

TALK • 11:45 • Cell & Developmental Biology

Cytoplasmic Polyadenylation Is an Ancestral Hallmark of Early Development in Animals

Labib Rouhana, Allison Edgar, Fredrik Hugosson, Valeria Dountcheva, Mark Q. Martindale, and Joseph F. Ryan.

Understanding the origin and evolution of mechanistic innovations for control of gene expression is integral to evolutionary and developmental biology. Cytoplasmic polyadenylation is the biochemical extension of polyadenosine at the 3'-end of cytoplasmic mRNAs. This process regulates the translation of specific maternal transcripts and is mediated by the Cytoplasmic Polyadenylation Element-Binding Protein family (CPEBs). Genes that code for CPEBs are amongst a very few that are present in animals but missing in nonanimal lineages. We have conducted phylogenetic analyses of CPEBs, and our results show that CPEB1 and CPEB2 subfamilies originated in the animal stem lineage. Our assessment of expression in the sea anemone, Nematostella vectensis (Cnidaria), and the comb jelly, Mnemiopsis leidyi (Ctenophora), demonstrates that maternal expression of CPEB1 and the catalytic subunit of the cytoplasmic polyadenylation machinery (GLD2) is an ancient feature that is conserved across animals. Furthermore, our measurements of poly(A)-tail elongation reveal that key targets of cytoplasmic polyadenylation are shared between vertebrates, cnidarians, and ctenophores, indicating that this mechanism orchestrates a regulatory network that is conserved throughout animal evolution. We postulate that cytoplasmic polyadenylation through CPEBs was a fundamental innovation that contributed to animal evolution from unicellular life.

FEATURED • 14:00 • Cell & Developmental Biology

Morphogenesis of the cydippid-to-lobate transition

Yinghui Wang, Elias Joseph, Orianna Duh, Phillip M. Barden, Allison Edgar

New Jersey Institute of Technology

Some ctenophores undergo dramatic morphological transitions to the body plan as they grow while others undergo minimal morphogenetic changes. The relationship between these changes and other life stage transitions is unclear. We have developed a morphometric approach to describe the cydippid-to-

lobate transition in the ctenophore *Mnemiopsis leidyi*. We find multiple inflection points during this ontogenetic process. Furthermore, we find that limiting the analysis to persistent structures, i.e. those that are present in both the cydippid and lobate stages, does not eliminate these distinct morphostage groupings. The analyses are also robust to plane of measurement and body size, suggesting that they may be extended to other species in the future.

TALK • 14:30 • Cell & Developmental Biology

Reconstructing cell-type specification in *Mnemiopsis* from scRNAseq timecourse

N. Padillo-Anthemides, Y. Bobkov, F. Hugosson, B. Foster, M.Q. Martindale, K. Inaba, R. Bacher, J.F. Ryan

University of Florida

Ctenophores, as the sister lineage to all other animals, offer a unique window into the ancestral regulatory logic of cell type specification. Despite their phylogenetic significance, cell-type specification programs in ctenophores remain largely uncharacterized. To address this, we performed single-cell RNA sequencing on over 23,000 cells from *Mnemiopsis* embryos across eleven timepoints between 4- and 24-hours post-fertilization, reconstructing transcriptional trajectories and cell state transitions during early embryogenesis using URD. These data provide insight into the cell types, regulatory patterns, and germ-layer specification in *Mnemiopsis*.

TALK • 14:45 • Cell & Developmental Biology

The curious case of *Mnemiopsis leidyi*: first evidence of reverse development in Ctenophora

Joan J. Soto-Angel, Pawel Burkhardt

Department of Natural History, University of Bergen

Reverse development, defined as the reversal of ontogeny through the transformation of a mature individual into a preceding life-history stage, has long been considered an exceptionally rare phenomenon restricted to a few cnidarian species. Here, we demonstrate that the lobate ctenophore *Mnemiopsis leidyi* is capable of undergoing complete reverse development from the sexually mature lobate stage to an early cydippid morphology. Reverse development was induced experimentally through prolonged starvation or physical injury, followed by a low feeding regime. Individuals undergoing reversal progressively reabsorbed lobes and auricles, regenerated functional tentacles, and recovered the characteristic morphology of cydippid stages. These findings represent the first documented case of reverse development in Ctenophora and considerably expand the phylogenetic distribution of this phenomenon within Metazoa. Given the pivotal phylogenetic position of ctenophores as one of the earliest-diverging animal lineages, the results suggest that developmental plasticity and ontogenetic reversal may have deeper evolutionary roots than previously recognized. Beyond establishing *M. leidyi* as a promising model for investigating the cellular and molecular mechanisms underlying reverse development, this work raises fundamental questions regarding the evolution of animal body plans, developmental trajectories, and the origins of life-cycle flexibility across Metazoa.

TALK • 15:15 • Cell & Developmental Biology

Molecular components of ctenophore comb plates

Mio Kosaka, Yu Sato, Ke Jokura, Kogiku Shiba, Kazuo Inaba

University of Tsukuba

We newly identified three additional comb plate components in *Bolinopsis mikado*: BmBTBD19, CTENO78, and BmODF3-like. All three proteins exhibited distinct compartmentalized localization patterns. BmBTBD19 was localized to the proximal region, whereas CTENO78 and BmODF3-like were localized to the distal region, consistent with the localization patterns previously reported for CTENO64 and CTENO189, respectively. BmODF3-like, a protein homologous to Outer Dense Fiber Protein 3 (ODF3), a component of the mammalian sperm flagellum, was of particular interest. BmODF3-like was found in both the comb plate and the dome cilia of the apical organ. Morpholino (MO)-mediated knockdown of BmODF3-like resulted in the disappearance of both structures in larvae, demonstrating that this protein is essential for the formation and/or maintenance of both comb plates and dome cilia.

TALK • 15:00 • Cell & Developmental Biology

Building a molecular atlas of the ctenophore comb plate

Kazuo Inaba, Miguel Leung

Hubrecht Institute, Royal Netherlands Academy of Arts and Sciences

Cilia are microtubule-based molecular assemblies that diverse eukaryotic cells use to propel themselves through fluid environments. The most elaborate cilia known in nature are found in the ctenophore comb plate, where thousands of millimeter-long cilia bundle into large, iridescent swimming paddles. How is this elaborate organelle constructed from individual protein components at the molecular scale? Here, we report our preliminary efforts to resolve the molecular architecture of native comb plate cilia using cryo-electron microscopy (cryo-EM). Our reconstructions reveal that comb plate microtubules are stabilized by a highly complex network of proteins, rivaling the elaborate networks seen in the mammalian sperm flagellum. Our data further provide a first glimpse into the three-dimensional organization of the compartmenting lamellae, a ctenophore-specific structure that bundles neighbouring cilia. We are currently working to identify individual protein components and assembling these data into a molecular atlas of this remarkable structure.

POSTER + LIGHTNING TALK • 16:05 • Posters & Lightning Talks

Characterization of novel ctenophore photoproteins using transcriptomics and biochemical approaches

Lena Vincent, Isabelle Santiago, Anik Grearson, Steve Haddock

MBARI

POSTER + LIGHTNING TALK • 16:10 • Posters & Lightning Talks

Combing the deep: what ctenophores can teach us about deep sea cell membranes

Anik Grearson, Jacob Winnikoff, Itay Budin, Steven Haddock

MBARI / UCSC

TBD

POSTER + LIGHTNING TALK • 16:15 • Posters & Lightning Talks

Opsins in Ctenophores

Natasha Picciani, Steven Haddock

MBARI

POSTER + LIGHTNING TALK • 16:20 • Posters & Lightning Talks

Environmental zinc causes a highly specific hatching defect in ctenophores

Elias Joseph, Yinghui Wang, Orianna Duh, Allison Edgar

New Jersey Institute of Technology

Our lab has identified a highly specific and penetrant developmental phenotype arising from environmental zinc exposure in the ctenophore *Mnemiopsis leidyi*. Zinc-exposed embryos fail to hatch. Detrimental levels of zinc can occur in water that contacts zinc-containing plumbing components. Since ctenophores are abundant and ecologically significant zooplankton, this finding may have ecosystem-level consequences for zinc pollution as the phenotype occurs far below the level of zinc currently deemed hazardous.

POSTER + LIGHTNING TALK • 16:25 • Posters & Lightning Talks

The 9 stages of Mnemiopsis

Anthony Moss

Auburn University

The cellular activities leading to the repair of a bisected canal are described.

POSTER + LIGHTNING TALK • 16:35 • Posters & Lightning Talks

Ctenophore's molecular response to hypoxia

Pedro G. Suzuki, Antonio C. Marques, Mark Q. Martindale.

Universidade de São Paulo

Paleontological and molecular analyses show that animals most likely have originated in the Neoproterozoic era, before the main earth atmosphere oxygenation events. However, little is known regarding the adaptations the first animal ancestors had to these conditions, especially given the prevalence of aerobic metabolism in animals. Ctenophores are ideal models for this study given their ancestral position in the metazoan phylogeny and described ability to thrive under hypoxic conditions in the wild and in laboratories. Interestingly, ctenophores (and also sponges) lack the complete canonical HIF-signalling pathway, the main hypoxia signalling pathway in metazoans. Through transcriptomic analyses on the species *Mnemiopsis leidyi*, this study aims to describe the molecular mechanisms underlying the ctenophore's seeming adaptation towards hypoxia as well as the evolutionary conservation of said mechanisms across metazoan evolution.

POSTER • 16:45 • Posters & Lightning Talks

Characterizing gene expression during gastrovascular canal development in Mnemiopsis leidyi

Jason S Presnell, Nicasio S Jurani, Allie M Graham

University of Kansas

Ctenophores possess a unique gastrovascular canal system that serves as the site of nutrient transport and uptake, yet the molecular and cellular programs associated with canal development and function are understudied. To gain a better understanding of canal system organization, we carried out a developmental transcriptomic analysis during paragastric canal morphogenesis in *Mnemiopsis leidyi* and examined expression of candidate digestive gene families. In addition, differentially expressed genes were mapped to annotated cell types from a previously published single-cell RNA-sequencing dataset. We identified genes associated with proteolysis, lipid metabolism, lysosomal activity, and nutrient transport using protein domain homology-based approaches and characterized their expression during paragastric canal development. We also found that different classes of digestive-associated genes exhibited distinct patterns of expression across annotated scRNA-seq cell types. Ongoing in situ hybridization experiments are being carried out to examine the spatial expression patterns of candidate genes during canal development. These results provide an initial molecular framework for understanding the development and functional organization of the ctenophore gastrovascular system.

POSTER • 16:45 • Posters & Lightning Talks

Prey sensing

Mariana Rodriguez-Santiago and Kei Jokura

Colorado State University

Prey sensing is a complex behavior that requires very fast and accurate relay of external sensory cues to motor circuits that generate movement. Beroe are active predators that locate prey using chemical cues, but the cellular circuitry underlying this sensory response remains unknown. We used detailed behavioral analysis and live calcium imaging to characterize chemosensory responses in *B. cucumis*. Prey-conditioned water triggered increases in swimming speed and changes in trajectory, quantified via DeepLabCut tracking of statocyst position, body contractions, and lip micro-movements. To identify responsive cell types, we loaded excised lips with Fluo8-L-AM and imaged calcium dynamics before and after exposure to prey chemical cues. Epidermal cells showed elevated calcium signal in response to prey cues, and a subset of macrocilia exhibited a localized — but non-propagating — calcium increase. These results provide a first step toward mapping the sensorimotor circuit driving predatory behavior in ctenophores.

POSTER • 16:45 • Posters & Lightning Talks

Assessment of presence and diet of ctenophores in Nantucket

Valeria Dountcheva, Labib Rouhana

University of Massachusetts Boston

Ctenophores are known to be voracious predators. However, the distribution and ecological impacts of ctenophores are not fully understood. In this study, the presence, regional distribution, and diet of ctenophores in the island of Nantucket were assessed from Spring to Fall in the year 2025. The species of ctenophores that is most prevalent in the island was found to be *Mnemiopsis leidyi*, both in formal surveys and in reports by citizen science. *M. leidyi* was observed at highest seasonal abundance during the month of October. The *M. leidyi* population throughout Nantucket was found to be largely homogenous, with only one of 24 samples varying in its COI allele sequence. Furthermore, ctenophores were detected in higher numbers at the Town Docks, and less often or absent at more internal locations in the Head of the Harbor. No correlation was found between ctenophore abundance and water temperature or salinity during the period of this study. However, ctenophores were most abundantly detected when nutrient availability was highest, as assessed by nitrogen and phosphorous levels. The diet of ctenophores in Nantucket was assessed by Third-Generation DNA sequencing of gut contents and found to be largely composed of arthropods and sponges, with algae becoming a component of their diet at times of highest ctenophore density. These findings provide a baseline description of ctenophore presence in the region and shed light on potential ecological impacts of these extensive predators.

POSTER • 16:45 • Posters & Lightning Talks

Spontaneous Rhythmic Electrical Activity in Mnemiopsis leidyi

Gen Dong, Anthony Moss

Auburn University

We investigated the electrical activity in the tentacular apparatus of the lobate ctenophore *Mnemiopsis leidyi*, using extracellular suction-electrodes. We detected spontaneous rhythmic signals in the adult tentacular apparatus fan (iScience 2026) and tentilla, where they appeared as recurring burst events with rhythmic temporal organization. We observed rhythmic paired-burst, multi-burst, and single-burst signals, as well as arrhythmic activity.

Simultaneous recordings from the tentacular fan and associated tentilla showed temporally correlated events, suggesting coordinated electrical activity across different parts of the tentacular apparatus. The largest signals were recorded near the aboral end of the tentacular bulb, where tentilla are anchored. Lesion and isolation experiments showed that rhythmic activity persisted in isolated fan-region preparations, supporting a local origin. Spontaneous signals were also detected from epithelial and aboral-region preparations, suggesting that multiple electrically active regions could contribute to the wave activity. Larval tentacles showed weaker and less organized spontaneous activity. These results provide the first evidence for spontaneous rhythmic electrical activity in the adult tentacular apparatus of *M. leidyi* and are contra the 'silent until stimulated' activities of *Pleurobrachia pileus*, which displayed rhythmic bursting activity only when stimulated by prey and electrical stimulation within the tentacular axons (Phil. Trans. R. Soc. Lond. B, 1993) but otherwise are quiet when slowly swimming. Our results suggest that electrically active rhythmic oscillator systems are inherent in ctenophores and are critical to coordination of the behavior of these organisms.

TALK • 10:15 • Immunity & Genomics

Expansion of the C1A cysteine peptidase family plays dual roles in development and innate immunity in the ctenophore *Mnemiopsis*

Gracie Scheve, Ingrid Miranda Perez, Lauren Vandepas, Kevin H. Wong, William E. Browne

University of Miami

Peptidases of the C1A, or papain, family are known to have a broad range of functions across the tree of life, including both protein degradation and cleavage-dependent protein activation in the lysosome-endosome system, processing of antigens by immune cells, modification of extracellular matrix proteins, stress response, and key roles in programmed cell death. Protease cleavage assays and transcriptional analyses of *Mnemiopsis* cells suggest that canonical C1A cathepsin homologs are differentially expressed in ctenophore immune phagocytes; HCR-in situ hybridizations across embryogenesis reveal differential expression of cathepsin homologs in the developing endoderm. To assess the extent of the ctenophore C1A repertoire, I performed HMMER searches on *Mnemiopsis*, *Bolinopsis*, and *Hormiphora* proteomes that revealed a large lineage-specific expansion within this gene family. Analyses in *Mnemiopsis* suggest significant association of cathepsin C1 expansion paralog expression with the development of cell types and tissues unique to the ctenophore lineage including colloblasts, muscle, sensory cells, and mucosal cells. We hypothesize that the diversification of the C1A papain protease family may have paralleled the development of novel cell types in the ctenophore lineage.

TALK • 09:45 • Immunity & Genomics

From hidden homology to antimicrobial function: saposin-like peptides in *Mnemiopsis* phagocytes

Ingrid Miranda Perez, Gracie Scheve, Kevin H. Wong, Antoni Luque, Cynthia Silveira, William E. Browne

University of Miami

The ctenophores comprise an early-diverging lineage of animals that provide a useful system for exploring the evolution of metazoan innate immune effectors. In *Mnemiopsis leidyi*, phagocytic immune cells respond to bacterial challenge with significant gene expression changes, however many highly expressed genes remain poorly annotated. I combined phagocyte-enriched single-cell RNA-seq with structure-informed protein language models, UMAP-based manifold learning, profile searches, and AlphaFold3 predictions to identify remote homology among uncharacterized highly expressed immune-cell genes. This AI-guided workflow prioritized MlePSAP1, a gene strongly upregulated in pathogen-challenged phagocytic cells and predicted to encode two mature saposin-like peptides, SAP1a and SAP1b. I will present the computational discovery of these candidate effectors, molecular dynamics simulations, ongoing functional validation, molecular dynamics simulations, and antimicrobial assays. This work links ctenophore cell biology, protein annotation, and antimicrobial peptide function, providing a path from hidden immune-cell expression to experimentally testable molecules.

TALK • 10:00 • Immunity & Genomics

Structural and functional properties of the complete reference genome for the MV31 laboratory strain of *Mnemiopsis leidyi*

Steven S. Plotkin, William E. Browne, Matt R. K. Peng, Pranav Garg, Charlotte Barclay, Gabriel Dall'Alba

University of British Columbia Vancouver

As a likely earliest-branching lineage of the metazoan tree, ctenophores provide a powerful system for studying the origins of animal multicellularity. We report a complete telomere-to-telomere genome assembly comprising 203 Mb across 13 chromosomes, with 15,760 annotated genes. Syntenic organization suggests the presence of proximal regulatory elements, and supports the placement of ctenophores as the sister group to all other metazoans. Gene architecture includes deeply nested structures exceeding 10 levels, extensive isoform diversity, and unusually high intron-exon counts. Repetitive elements--mostly class I LTR retrotransposons and class II DNA transposons--make up nearly half of the genome. In contrast to earlier reports, all major developmental signaling pathways (Wnt, TGF- β , Hedgehog, Notch, and FGF) are represented, albeit with reduced gene repertoires. Single-cell transcriptome profiling reveals several key developmental regulators with differential expression during the earliest stages of embryogenesis. This work was partially supported by a seed grant from the Center of Evolutionary Science, Caltech.

TALK • 09:30 • Immunity & Genomics

Early diversification of metazoan molecular immune defense programs and immune-competent cells informed by *Mnemiopsis* gene expression and cell behavior

Lauren E. Vandepas, Kevin H. Wong, Ingrid Miranda Perez, Gracie Scheve, William E. Browne

University of Miami

Innate immune responses are critical for maintaining organismal homeostasis and mediating a range of self/non-self recognition functions. Understanding the evolution of cell types that mediate self/non-self recognition and response is essential for understanding the origins of metazoan multicellularity. Among core innate immunity functions, phagocytosis represents a deeply conserved physiological mechanism shared across the majority of extant eukaryotic lineages and is deployed by many innate immune cell types in metazoans. We mapped single-cell RNAseq from whole animals and isolated phagocytic cells to an annotated, strain specific, T2T *Mnemiopsis* genome to identify genes preferentially expressed in cells competent for microbial phagocytosis. We identify multiple distinct phagocytic cell types including specialized innate immune cells. Comparative cross phyletic single-cell RNAseq analyses of gene expression highlight the early establishment of distinct phagocytic/highly endocytic cell types and processes in the metazoan lineage, suggesting an early diversification of metazoan innate immune cell states and cell types.

TALK • 11:00 • Ecology, Taxonomy & Natural History

The Rhythm of the Ocean

Jeff Milisen

Kona Honu Divers

The Kona coast provides a rare opportunity to maintain one of the only long-term monitoring datasets of epipelagic communities. This observational record of 160 taxa and accompanying abiotic conditions has been maintained during weekly blackwater dives since 2021. This dataset has been

designed to observe those creatures that go unnoticed but play a pivotal role in our ocean ecosystem. Phenological relationships with Enso index, lunar cycle, seasonality, current speed, and many others will be modeled and discussed. In addition, we will look at shifting trends in taxa.

TALK • 11:15 • Ecology, Taxonomy & Natural History

Highly impactful predation of oceanic ctenophores - What's their secret?

Sean Colin, Jack Costello, Brad Gemmell, Mande Holford, Kelly Sutherland

Lobate ctenophores are often numerically dominant members of oceanic epipelagic and midwater ecosystems. Despite this prevalence, little is known about their trophic ecology. Multiple co-occurring species are frequently found in these ecosystems and appear to feed similarly, using feeding currents that entrain prey. Through novel, non-invasive gut content analyses of five co-occurring lobate and cestid ctenophores (*Eurhamphaea vexilligera*, *Ocyropsis crystallina*, *Bolinopsis vitrea*, and *Cestum veneris*), we found that these ctenophores ingest an average of 32 prey per hour, with some species consuming more than 50 prey per hour. At these rates, lobate and cestid ctenophores feed at levels comparable to their highly impactful coastal relative, *Mnemiopsis leidyi*, and are likely among the most influential planktonic predators in the open ocean. Hydrodynamic and predator-prey analyses of lobate and cestid ctenophores feeding in situ revealed that their predatory success is largely attributable to the hydrodynamics of their feeding currents and high capture efficiencies. Recent work reveals that ctenophore mucus contains neurotoxins that incapacitate prey. In conjunction with sensory scanning, these neurotoxins likely lead to the high ctenophore capture efficiencies. These findings indicate that epipelagic ctenophores represent a powerful guild of planktonic predators whose combined impacts may play a far greater role in shaping material cycles across broad regions of the open ocean than previously recognized.

FEATURED • 13:30 • Ecology, Taxonomy & Natural History

Ctenophore diversity

Claudia E. Mills

Friday Harbor Laboratories, University of Washington

TALK • 11:30 • Culturing & Aquaculture

Smells Like Ctene Spirit

MacKenzie Bubel & Tommy Knowles

Monterey Bay Aquarium

We will summarize our techniques for culturing multiple species of ctenophores.

TALK • 11:45 • Culturing & Aquaculture

Creation of a mobile oxygen minimum zone holding system for deep sea midwater species

Evan Firl

Monterey Bay Aquarium

Over the past 8 years the Monterey Bay Aquarium has designed complex life support systems to safely house deep-sea jelly species. After years of design and testing, optimal design and operational strategies were developed leading to the opening of the Into the Deep exhibition in 2022. A dual gas-membrane system was designed to remove dissolved oxygen via vacuum from seawater while simultaneously dosing minimal quantities of CO₂ via a gas solenoid distribution system to maintain safe pH and dissolved oxygen levels as well as maintaining temperature parameters of deep-sea jellies living in and around the Oxygen Minimum Zone. The next stage for improvement was the redesign of a mobile and portable low-oxygen holding system that could function at sea for multi-day collection expeditions aboard the research vessel David Packard. In 2025 design, construction, and implementation of the "M.O.M.Z." (Mobile Oxygen Minimum Zone system) was completed. This was the first time a mobile and portable low-oxygen system had been able to function to the same capacity as our large-scale permanent exhibit and holding systems. The M.O.M.Z. was designed to be portable, modular, functional in high seas, and capable of meeting all seawater parameters required for safe habitation of deep-sea jelly species. The successful implementation of the M.O.M.Z. aboard the David Packard has allowed for the collection and holding of sensitive deep-sea jelly species on multi-day collection expeditions including *Lampocteis cruentiventer*, *Red x*, *Tiburonia granrojo*, *Aulacoctena* sp., and *Pandea rubra*. Future efforts aim to add holding tanks to directly hold animals within the sealed system and to optimize holding for larger jelly and cephalopod species.

TALK • 12:00 • Culturing & Aquaculture

Cteno Ctube: Closing the Life Cycle of Leucothea in Culture

Wyatt Patry

TALK • 14:00 • SciComm & Outreach

Swim Down: Finding Neurodivergent Identity in the Depths

Lilianna Watson, illustrations by Freya Hammar

Monterey Bay Aquarium

Swim Down is a digital graphic novel about a neurodivergent teenager's underwater journey through the Monterey Submarine Canyon that reveals her sensory differences as powerful adaptations. The narrative explores how Mari's sensitivities to light, noise, and touch relate to deep-sea darkness, acoustics, and pressure—with a special appearance by ctenophore *Lampocteis cruentiventer*. Video: <https://youtu.be/YBN6BOVhzww?si=ZrefUWSa2kJvsV6Y>

TALK • 14:15 • SciComm & Outreach

Increasing Public Engagement with Ctenophores through Art and Outreach in the Salish Sea

Jamie Andersen M Fields

Despite ctenophores being abundant, widely distributed, visually interesting, and scientifically notable, they've received far less public attention than many other marine invertebrates. In online spaces, ctenophore misinformation is common, even on reputable websites. This has led to a limited and flawed public perception of these incredible animals. My personal mission has been to improve public knowledge and appreciation of ctenophores through art, experiential outdoor learning, pop-up aquarium events, social media, and community science. My efforts have been met with community enthusiasm, leading to recurring programming by The Salish Sea School, Friends of the San Juans, and Rosario Beach Marine Lab. I will discuss these efforts, community outcomes, and goals to leverage these results towards community science ctenophore monitoring in the Salish Sea.

TALK • 14:30 • SciComm & Outreach

Integration of STEAM concepts for ctenophore visibility and outreach

Kip Howell

Friday Harbor Laboratories

Ctenophores are ecologically important components of marine ecosystems, yet they often remain underrepresented in public outreach due to their fragile nature, seasonal occurrence, and challenges associated with display and observation. As part of my artist residency at Friday Harbor Laboratories (FHL), I periodically initiated dock lighting sessions, inviting students and visitors to showcase local ctenophore diversity through the integration of scientific observation and visual art. Regular dock-lighting sessions were conducted to collect and take photo documentation of several phyla including ctenophores, providing opportunities for students and visitors to observe living specimens and engage in discussions about ctenophore biology, ecology, and biodiversity. Concurrent plein air painting demonstrations translated these observations into accessible visual representations, creating additional pathways for public engagement. The residency spanned the University of Washington spring quarter 2026, allowing repeated observations of seasonal shifts in ctenophore occurrence, particularly among the genera *Pleurobrachia*, *Bolinopsis*, and *Euplokamus*. By combining scientific field observations with artistic interpretation, this project demonstrates how STEAM approaches can enhance the visibility of gelatinous marine organisms, promote informal science education, and broaden public engagement with marine research.

POSTER + LIGHTNING TALK • 14:45 • SciComm

Braiding Science & Story: Connecting People to Ocean Science Through Digital Media

Calista Kerba

POSTER + LIGHTNING TALK • 14:50 •

Science and Discovery: A Human Story

Marika Pinsonneault

MBARI
