

New organization brings together top researchers to sequence the genomes of invertebrates

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This is the logo for the Global Invertebrate Genomics Alliance. Credit: Global Invertebrate Genomics Alliance

Of the 1.9 million species of creatures that have been described on earth, more than 1.3 million are invertebrates. They have served as model organisms in many areas of biology.

There are many examples of the important role of invertebrates in science including sea urchins for developmental/cancer cell biology, the mollusks *Aplysia* and *Loligo* for neurobiology research, the fruit fly *Drosophila* for genetics, and the nematode worm *C. elegans* for cell line maturation, development and genetics. Studies using all of these have received Nobel Prizes.

Now, to learn more about these remarkable organisms, a cooperative consortium called the Global Invertebrate Genomics Alliance (GIGA) has been formed. The group will provide a network of diverse scientists to promote comparative genomics and bioinformatics research, on non-insect/non-nematode invertebrates.

William Browne, a biologist in the College of Arts and Sciences at the University of Miami, who works on the comb jelly *Mnemiopsis leidyi*, hopes his participation in GIGA will offer opportunities for interactions with a broader community of researchers delving into invertebrate genomics.

"The GIGA consortium lays the groundwork, for example, to take work on the genome of *Mnemiopsis* in our lab, and facilitate comparison of the results to work from other labs that are pursuing these same kinds of questions in different organisms," Browne said. "The hope is that syntheses of large scale genomic studies across many groups will improve, not only our understanding of the metazoan tree of life, but also illuminate repertoires of genetic diversity responsible for the present day diversity of animals."

Earlier this year, Jose Lopez, a professor of biology at Nova Southeastern University's Oceanographic Center, organized the inaugural workshop of expert invertebrate scientists to discuss the plausibility of, and long-term strategies for, sequencing the whole genomes of multiple, targeted invertebrate organisms.

"There's so much more we can learn from these animals if we come together to focus and coordinate our research efforts," Lopez said. "GIGA allows us to work collaboratively as we discover new and exciting details of invertebrate genomics."

Invertebrates display many unique and outlandish traits among animals:

- Some [invertebrates](#) are the longest-living animals on the planet, including *Lamellibrachia* tube worms (~250 years), Quahog clams *Arctica islandica* (maximum reported age 507 years), black corals (estimated 2,000 years) and the immortal *Hydra*
- Tardigrades ("water bears") can survive extreme temperatures (-150 °C to 150 °C), ionizing solar and galactic radiation, and even interplanetary vacuum
- Octopi not only have 8 arms, but also 3 hearts, as well as highly developed brains and visual systems
- Sponges represent one of the most ancient lineages of animals and, together with corals, produce the largest number of chemical "lead" molecular structures for discovery of novel pharmaceuticals
- Ctenophores, another ancient lineage of animals, possess a range of unique cell types and are the largest animals that use only cilia for locomotion

GIGA was partially inspired by the Genome 10K project, initiated by NSU's affiliate professor Stephen J. O'Brien, Ph.D. and colleagues, to sequence genomes from 10,000 vertebrate animals. The organization

held its inaugural workshop at Nova Southeastern University's (NSU) Oceanographic Center in March, 2013.

Workshop participants came from the U.S., China, and Europe and included more than 40 experts in invertebrate biology, genomics and systematics from several universities and institutions, such as the Smithsonian Institution, Scripps Oceanographic Institute, Harvard and Brown, as well as biotech industries (Life Technologies, PacBio and BioNanoGenomics). In-depth discussions to develop the consortium's framework were hashed out in breakout groups: such as which specific genomes to prioritize for sequencing, what DNA or RNA sequencing platforms are optimal, standards for collections and sample preparations, and where to specify a particular invertebrate taxon's place on the evolutionary Tree of Life. Also discussed were nascent policies on data submittal, access and sharing within the GIGA consortium.

Primary funding for the workshop to kick-start GIGA was generously awarded by the American Genetic Association, publisher of *Journal of Heredity*. The momentum of the workshop has carried on, leading to the creation of an NSU-hosted website (Giga-cos.org), more international collaborations (i.e. the GIGA symposium at next summer's Society for Molecular Biology and Evolution - SMBE – in Puerto Rico) and the white paper published in the current issue of *Journal of Heredity*. This article further showcases GIGA's main goals, ongoing projects, and recommended experimental standards and policies.

Provided by University of Miami

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