Highlight—Lowly Sea Cucumber Leads the Evolutionary Race

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If prizes were awarded for genetic diversity and rapid-fire evolution, tunicates would be stars among animals. These quiet, filter-feeding chordates, also known as “sea squirts,” usually make their home attached to rocks on the sea floor. Their lifestyle might be tame, but these jellied animals are the genetic equivalent of magical shape shifters, capable of rapidly evolving and holding, new research suggests, one of the highest known population sizes.

In Genome Biology and Evolution (Tsagkogeorga et al. 2012), Georgia Tsagkogeorga, from Queen Mary University in London, and Vincet Cahais and Nicolas Galtier, both from the University of Montpellier in France, examine the genomic variation of tunicates, Ciona intestinalis specifically.

After sequencing eight individuals’ transcriptome, a collection of messenger RNAs in the cell, the researchers analyzed how individuals of the same species differed from each other, and how members of one species differed from other species. Their goal? To know why proteins of some metazoans—multicellular animals with differentiated tissues—evolve rapidly and some more or less stagnate for eons.

“Just more mutations—spontaneous genetic changes?” asks Galtier. “Or perhaps more efficient adaptation—selected genetic changes?”

Tunicates provide an ideal study animal: a typical fast-evolving animal lineage and a close living relative of the vertebrate lineage.

“Working on tunicates allowed us therefore for the first time to investigate the population genomics of a typical fast evolving taxon,” said primary author Tsagkogeorga, a postdoc at the School of Biological and Chemical Sciences. “And to adopt a comparative point of view with respect to the slowly evolving vertebrates.”

They find that C. intestinalis both randomly changes its DNA and retains advantageous alterations, both mutating and evolving, that is, at faster rates than vertebrates. For Herve Philippie, from the University of Montreal, the exploration of mutation rate was the most interesting aspect of the article.

“We generally think about the selective causes and have a strong tendency to forget the neutral, mutational causes,” he says. “For instance, I think that all the improvements in the models of sequence evolution that have been implemented successfully to improve phylogenetic accuracy are directly motivated by selectionist reasons. The mutational aspect is simply ignored.”

No single factor rules a species’ mutation rate. The environment, how much oxygen or ultraviolet light it is exposed to, plays a role. However, so too does the organism’s biochemistry. Some organisms replicate with fewer errors to their DNA. Some are better able to detoxify their cells. A species’ natural history and selection pressures can also play a role.

Researchers have known for years that some lineages evolve speedily—tunicates, nematodes, and rodents outpace vertebrates, cnidarians, and primates, respectively.

“But we do not know very well why these fast-evolvers are fast,” said Nicolas Galtier, one of the article’s co-authors. “The key here was to take a population genetic approach to this problem, which allowed us to disentangle the various forces—mutation, selection, genetic drift—that control the evolutionary rate.”

One of the challenges in this study, says Galtier, was that they are among the first to use next-generation sequencing technology for population genetics. As an appendix, they publish a new method they have developed to analyze the next-generation data and distinguish variation from sequencing errors.

The variation that they found, it turns out, is enormous. They estimate that comparing the DNA sequences between two random C. intestinalis individuals would reveal a difference once every 18 base pairs. Considering that two random humans would vary only once every thousand base pairs, we seem positively bland by comparison. Not only bland but also behind the times. Tsagkogeorga et al. calculate that a tunicate’s per-year mutation rate is two to six times higher than a vertebrate’s.

Some researchers within the field were excited to see the new data but questioned the authors’ conclusions.

“They are broadening the whole genome polymorphism data set,” said Marie Nydam, a postdoctoral research associate at University of California–Santa Barbara. “This is a really important data set for many researchers.”

Nydam, however, believes the findings should be treated cautiously.

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“The introduction got me excited, but I’m not confident in their methods and therefore their results. … I am concerned about the error models used for SNP (single nucleotide polymorphism) and genotype calling.”

The authors stand behind their use of statistics, making it clear, they say, that the study employs a new methodological approach. “We keep thus comparing both M1 and M2 models [two error models used] throughout the paper, because we believe it is essential to discuss how these models behave when applied on real data, and how sensitive population genomic inference is based on model selection.”

Also, with their results based on genetic information from only eight individuals, the numbers presented are still a first look. Both the authors and their colleagues would like to see their data set strengthened, both by using larger numbers of individuals and more species.

“We make a strong assumption,” Galtier says, “which is that the evolutionary processes we observe in just one species have applied to the whole tunicate lineage during hundreds of millions of years. Obviously our results will be reinforced—or perhaps challenged?—by characterizing additional tunicate species the same way as we did here.”

**Literature Cited**

Tsagkogeorga G, Cahais V, Galtier N. 2012. The population genomics of a fast evolver: high levels of diversity, functional constraint and molecular adaptation in the tunicate *Ciona intestinalis*. Genome Biol Evol., Advance Access published June 28, 2012, doi:10.1093/gbe/evs054

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