

Podcast Interview: Tetsuto Miyashita

PNAS: Welcome to Science Sessions. I'm Paul Gabrielsen. Hagfish are one of the uniquely odd wonders of the natural world. They're jawless, boneless, and are well known for their voluminous production of slime. In the same way that hagfish can tie themselves in knots to slip away from predators, they have slipped in and out of classification in the tree of life. Genetic evidence suggested that hagfish are related to lampreys in a group that split off very early from the rest of the vertebrates. Anatomical evidence suggested hagfish sit outside of the vertebrate lineage entirely. In a recent PNAS paper, Tetsuto Miyashita and his colleagues describe a fossil that changes the entire discussion and present a revised phylogeny, or evolutionary history, of hagfish that enables a fresh look at the earliest ancestors of all vertebrates. Miyashita, of the University of Chicago, describes his first-hand experience with living hagfish.

Miyashita: I also worked on hagfish for several years in marine lab, just on the west coast of Vancouver Island, Canada. I trapped them and brought them back to the lab and looked at their anatomy. People talk a lot about slime with hagfish, right? Hagfish slime is basically a lot of protein fibers that trapped seawater within. It's a bag of water. If you take the hagfish slime and squeeze it, you can squeeze the water out from the slime. What's remaining is what looks like a cobweb of spiders.

PNAS: Hagfish are an example of what Miyashita calls the "long branch problem" in taxonomy. We can observe living species; the tips of evolutionary branches. But with a fossil record that's far from complete, the length of each branch and its connections are virtually unknown.

Miyashita: Of course, there are many ways to solve this problem. You can get more genetic sequences and have this giant dataset of molecular data, but you can also look at the anatomy of living and also fossil vertebrate animals and reconstruct that evolutionary history. The fundamental problem is that the molecular data and the morphological, or anatomical data, usually don't agree with each other. They each have internal biases in how variations accumulate over geological time.

PNAS: Miyashita says resolving that conflict is critical to defining the entire group of vertebrates.

Miyashita: About 550 million years ago, or before that point, there was an animal that sits right at or right before the split between the lineage that gives rise to lampreys and another that gives rise to most of what we know as the vertebrate animals. Now, to reconstruct this hypothetical ancestor, we use the next branch down. If there is another branch that came before this ancestor, if there was another split in the branch that gave rise to animals we know, in this case hagfish, then we can use hagfish to reconstruct the entire history of the common ancestry between those two splitting events. If hagfish truly fell out of the vertebrate group, then we can use hagfish to define what was primitively present in that common ancestor. But if hagfish and lampreys form a natural group, that they share the common ancestor that the rest of us didn't, then we can't

really use the hagfish to inform that ancestor. By shifting the position of the hagfish branch, we have a really different view of what the common ancestor should look like.

PNAS: The fossil that would clarify this dilemma came from a Cretaceous-age limestone quarry in Lebanon, discovered by amateur paleontologists. It's shaped like an eel, but without any preserved bones. Phil Currie, from the University of Alberta, happened to see the fossil at the Tucson Mineral Show.

Miyashita: He took a photograph of that specimen and came back to Edmonton and showed me that photograph. My immediate reaction to it was: this is looking like a hagfish, but if it's a hagfish, it's probably too good to be true. The hagfish fossil record is almost nonexistent.

PNAS: With the fossil acquired by the Black Hills Institute of Geological Research, Miyashita and his colleagues went to work scanning its anatomy.

Miyashita: Eventually, after synchrotron scanning, we found the chemical evidence of the slime glands. This fossil had this series of bag-like structures that looks like gills, in a series of them. But these gill pouches are not really anywhere close to the head. They were sitting in the mid-portion of the trunk. Now, this is a really unique character for hagfish. This can't be anything other than hagfish. But it took a lot more detailed research into the morphology of this fossil to get confidence that yes, these are gill pouches and, hold on, yes, there are also slime glands, and here are barbels that they have, those tentacle things at the front end of their head. So we know that the branch extends all the way back at least 400, 500 million years, it's just that we didn't have much to fill in that huge gap, and now we have one important data point that looks pretty much like living hagfish from 100 million years ago. At least by this time, all of these structures have evolved. It's the calibration point.

PNAS: The fossil supported genetic evidence that lampreys and hagfish form a natural group together. That group branched off very early on from the line of ancestry that leads to every other living vertebrate lineage, from sharks to frogs to snakes to us.

Miyashita: Now we can move on to the next stage. Our paper provided an intriguing possibility or intriguing interpretations of how we go about this. There are assemblages of extinct jawless vertebrate lineages from the Paleozoic era. They have the bony skeleton. And our phylogenetic analysis puts some of them, in this case anaspids, closer to the lampreys and hagfish than to the rest of the vertebrates. It raised a number of intriguing possibilities, like maybe lampreys and hagfish had an ancestor that had a bony skeleton, but they simply lost it.

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