Aquaculture industry may benefit from water mold genome study

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(Phys.org) —An Oregon State University scientist and partners borrowed some technology from the Human Genome Project to more clearly identify the genes used by a type of water mold that attacks fish and causes millions of dollars in losses to the aquaculture industry each year.

Researchers compared the fish and plant pathogens to clearly identify the genes involved. By better understanding how these pathogens invade animals, the aquaculture industry can develop more effective control methods, such as improved vaccines and fungicides, researchers said.

The water mold belongs to a group of more than 500 species of fungus-like microorganisms called "oomycetes" that reproduce both sexually and asexually. Oomycetes, close relatives of seaweeds such as kelp, are serious pathogens of salmon and other fish. This is a particular problem in regions of the world where trout and salmon are raised, including the Pacific Northwest, Scotland and Chile.

Brett Tyler, professor and director of the Center for Genome Research and Biocomputing in the OSU College of Agricultural Sciences, led a project that mapped the entire genome of an oomycete species known as Saprolegnia parasitica. This is the first time these methods have been applied to water mold pathogens of fish.

The pathogen causes a disease called saprolegniosis, characterized by visible grey or white patches of mycelium on skin and fins that can also transfer into the muscles and blood vessels of fish. The potato late blight pathogen that caused the great Irish famine of the 1840s is a relative of S. parasitica. While saprolegniosis can't affect humans, relatives of S. parasitica can.

People around the world now get more protein from fish than from beef, Tyler said. As natural fish stocks decline, farmed fish are more vital to fulfill increasing global demand. But farmed fish are also more prone to disease because of crowding, which can spread to wild fish.

"Developing new, environmentally sustainable ways to reduce fish disease will cut down on the use of chemicals on fish farms, while also protecting wild fish, such as salmon, found in the rivers of the Pacific Northwest," Tyler said.

Key findings of the research include:

- S. parasitica can rapidly adapt to its environment through changes to its genes, allowing it to spread to new fish species or overcome fungicides.
- S. parasitica contains an enzyme that can actively suppress a fish's initial immune response, leaving it less able to defend against initial stages of infection.
- Plant pathogens can change the physiology of their hosts by using special enzymes that suppress plant immunity, while animal oomycetes have developed different enzymes, proteins and toxins that enable infection of fish.
- S. parasitica has more enzymes involved in adaptation than humans, allowing it to recognize and quickly adapt to a wide variety of environments.
- S. parasitica is vulnerable to an antifungal agent called a chitin synthesis inhibitor, contrary to previous beliefs that animal-damaging oomycetes did not contain any chitin.

More information: The study was published in the journal *PLOS Genetics* at www.plosgenetics.org/article/i … journal.pgen.1003272

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