

# Project launched to study evolutionary history of fungi

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The University of California, Riverside is one of 11 collaborating institutions that have been funded a total of \$2.5 million by the [National Science Foundation](#) for a project focused on studying zygomycetes – ancient lineages of fungi that include plant symbionts, animal and human pathogens and decomposers of a wide variety of organic compounds.

Zygomycetes, used in numerous industrial processes and fermentation of foods, are thought to be among the first terrestrial [fungi](#). Symbiotic associations with zygomycetes may have facilitated the origin of land plants. Zygomycetes also represent one of the earliest origins of multicellular growth forms in fungi. Their filamentous growth is in the form of the tube-like cell growth that characterizes species of fungi like bread and fruit molds.

Called the Zygomycete Genealogy of Life ([ZyGoLife](#)), the project is funded for four years, starting Jan. 1, 2015. Jason Stajich, an associate professor of plant pathology and microbiology, is the principal investigator of the project.

"Despite zygomycetes' critical ecological roles and importance to human civilization, they remain understudied and their evolutionary relationships are still not well understood," Stajich said. "This is likely a result of some of the difficulty in culturing many of the species, but also because, in general, too few researchers have been studying them."

Zygomycetes can be challenging to grow in the lab when some are

parasites of other organisms including amoebae, insects, plants, or other fungi, making it harder to study the fungus alone. Identification of some species by examination under a microscope can also be difficult, requiring expert training for distinguishing among species groups.

"Some of the groups are difficult to isolate, but when we look carefully there is fantastic diversity found in perhaps the most unexpected places like the digestive tracts of insects and small freshwater crustaceans," Stajich said. "When culturing fungi from the environment many of these zygomycetes do not grow well, or as fast as other fungi, so they may not be as readily identified."

ZyGoLife aims to resolve the evolutionary relationships through integration of numerous types of data, including genome sequencing and analyses, discovery and description of zygomycete fossils, development of enhanced tools for detecting zygomycetes in the environment, and state-of-the-art bioimaging. In addition, the project will develop educational resources for schools and the general public to highlight the importance of this poorly known group of fungi including expansion of [Encyclopedia of Life](#) pages about these fungi.

"We have limited understanding of the relationships between species in this part of the fungal tree of life," Stajich said. "As these have been understudied lineages, a careful and focused effort on sampling all of the lineages to determine how they are related is the first step in understanding the evolutionary history of the fungi.

Stajich explained that by resolving these earliest branches in the fungal genealogy scientists can study what the likely characteristics of ancestral fungi were, and determine what traits emerged first and were necessary as part of the transitions of life from aquatic to terrestrial ecosystems.

"We can use ZyGoLife to understand the order of particular growth and

morphology traits like fruiting bodies and the presence of separating emerged first, which ones emerged multiple times, and use genomic tools to understand when the genes that might underpin these traits evolved," he said. "We can use this information to understand processes like how did filamentous growth emerge. The white fuzzy mold you can see on your strawberries left on the counter for too long is often caused by a species of *Rhizopus*, a zygomycete. The fuzzy part you see are the millions of filaments of the fungus. Understanding the evolution of genes important in filamentous growth can help establish when and how this process evolved."

Besides UC Riverside, the following institutions are collaborating on ZyGoLife: Oregon State University, The University of Michigan, Arizona State University, University of British Columbia, University of Kansas, Boise State University, Duke University, University of Florida, University of Ottawa and Bacterial Foodborne Pathogens & Mycology Research Unit of the USDA-ARS in Peoria, Ill.

At UCR, Stajich's group will be performing genome sequencing to generate approximately 25 new genomes of zygomycetes focusing on three groups that include free-living and parasites of insects, plants, and other fungi. This project will generate at least 100 new zygomycete genomes to be analyzed by the team to determine the relationships between these fungi.

The Stajich lab will also host visiting students and postdocs from the other teams to provide training in bioinformatics and evolutionary genomics in fungi. In addition, members of his lab will travel to collaborators' labs for training in microscopy, methods for dating fungal fossils, and training in zygomycete identification and taxonomy. The lab at UCR will be spearheading genome sequence analysis to better establish the family tree of fungi from these lineages and disseminating data into genomic databases like [MycoCosm](#) of the Joint Genome

Institute of the U.S. Department of Energy and [FungiDB](#).

Currently, Stajich and his colleagues are completing project planning to finalize the roles in data collection and analyses, recruiting members to their labs, developing and sharing culturing protocol and a website for the project to coordinate how samples will be shipped out from the stock center to their labs, and other preparation work.

As part of the project, Stajich and his colleagues will update the [Encyclopedia of Life](#) website pages with more detailed information on zygomycetes. The researchers will also be putting together teaching modules to make teaching about these groups of fungi easier with images and explanations of the [evolutionary relationships](#) and importance of these fungi in industry and agriculture.

"Our hope is to help train the next generation of mycologists for work on zygomycetes through this project," Stajich said. "The teams will develop skills in genomics, evolutionary biology, imaging and taxonomy to study these groups of fungi."

The [project website](#) will provide access to research results and data, laboratory protocols, and educational materials will be dissemination.

This new project builds upon work Stajich's lab has been doing to [sequence 1000 fungal genomes](#)— a project that received support from the Joint Genome Institute.

UCR will receive \$715,000 of the \$2.5 million funding for the project. This amount includes subawards UCR will make to collaborators at Duke University and Boise State University.

"Our first steps in this [project](#) will be obtaining live cultures from fungal culture collections in the United States and worldwide to begin genome

sequence and bioimaging data collection," Stajich said.

Provided by University of California - Riverside

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