Genes define the interaction of social amoeba and bacteria

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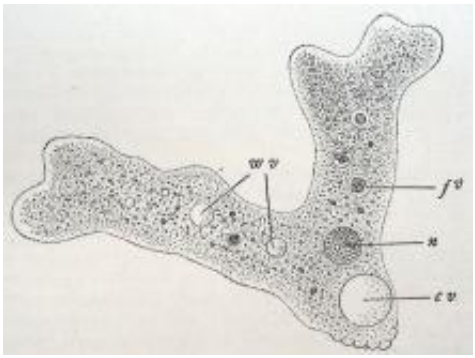

Amoeba Proteus, an animal consisting of a single naked cell, x 280 (From Sedgwick and Wilson's Biology.) Image: Wikimedia Commons

Amoeba eat bacteria and other human pathogens, engulfing and destroying them – or being destroyed by them, but how these single-cell organisms distinguish and respond successfully to different bacterial classes has been largely unexplained.

In a report in the journal *Current Biology*, researchers from Baylor College of Medicine use the model of the social amoeba – *Dictyostelium discoideum* – to identify the genetic controls on how the amoeba differentiate the different bacteria and respond to achieve their goal of destruction.

"No one has looked at the basic question of what happens when you put

the two classes of species together," said Dr. Adam Kuspa, professor in the department of biochemistry & molecular biology and senior vice president for research at BCM. "What does the amoeba do?"

The scientists, who included first author graduate student Waleed Nasser, did a genetic screen called a transcriptional profile, that identified sets of genes are active or expressed when interacting with two major classes of bacteria—gram negative and gram positive.

"The two kinds of bacteria are different in structure and biochemistry," said Kuspa, who is the corresponding author of the report. "We found that the *Dictyostelium* did differentiate between the different bacteria. In fact, it was shocking that nearly 800 different genes were activated when exposed to a kind of gram negative bacteria known as enterobacteria (*Klebsiella*)."

The researchers found 50 amoebal genes that were activated during growth on gram negative species of bacteria and 68 that were activated on gram positive species. The genes identified as active on gram positive bacteria were those most commonly defined as involved in metabolism. Those active on gram negative bacteria were most likely involved in degrading the cell wall, in particular one gene called alyL, which encodes an amoeba protein which likely acts as a lysozyme, an enzyme that breaks down bacterial cell walls. They also identified glucose-6-phosphate or a metabolite of it as signaling the presence of gram positive bacteria.

From that, said Kuspa, the question arises of whether this "barometer" of the presence of gram positive bacteria in the social amoeba might be conserved across evolution in humans.

"Might it be conserved in us?" he asked.

When the genome of the social amoeba was sequenced, Kuspa, colleague Dr. Gad Shaulsky, professor of molecular and human genetics at BCM, and others found that all amoeba are related. That means that what affects one kind of amoeba probably affects another.

"The second thing was that we found amoebae are more closely related to us than we thought," said Kuspa. Many of the proteins found in amoeba are conserved in mammals.

"We hope that what we learn from amoebae might be relevant to human immune systems," he said.

Others who took part in this work include Shaulsky, Balaji Santhanam, Edward Roshan Miranda, Anup Parikh Chris Dinh, Rui Chen and Blaz Zupan, all of BCM; and Kavina Juneja of Rice University and Gregor Rot of the University of Ljubljana in Slovenia. Zupan is also of the University of Ljubljana.

Provided by Baylor College of Medicine