Yeast biology yields insights into human knowledge expansion

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How does human knowledge expand over time? Intriguing as the question is, it's not easy to investigate, due to the difficulty of measuring knowledge and its spread.

But by analyzing three decades of discoveries about baker's yeast---an organism that has been extensively studied for insights into the workings of genes and proteins---University of Michigan researchers have revealed some interesting patterns in the proliferation of scientific understanding. Their findings, published online March 20 in the open-access journal *PLoS Computational Biology,* suggest ways of making scientific endeavors more productive.

In recent decades, scientists have significantly furthered their knowledge of yeast biology by studying interactions among the organism's 6,000 or so genes. By the end of 2007, more than 73,000 gene-gene interactions in baker's yeast (*Saccharomyces cerevisiae*) had been discovered and documented in some 5,400 publications authored by 11,238 researchers.

In the current study, Jianzhi "George" Zhang, an associate professor of ecology and evolutionary biology, and his former graduate student Xionglei He, now at Sun Yat-sen University in Guangzhou, China used a technique known as temporal network analysis to explore the explosive growth of this field of research.

Perhaps the least surprising finding was that the growth of knowledge about yeast biology has been exponential and that it shows no signs of

slowing down.

"That's what people had believed, and our study confirmed it," Zhang said. However, the analysis did debunk one popular belief among yeast researchers: that the rate of discovery increased even more dramatically after the yeast genome was deciphered in 1996.

"We didn't see anything unusual around 1996," Zhang said. "The growth of knowledge continued increasing exponentially; there was no sudden jump or slow-down."

More surprising was a finding that emerged when Zhang and He looked at the productivity of individual researchers involved in yeast studies. Although research in the life sciences is increasingly done in large teams, "we found that scientists who engage in large collaborations tend to have smaller contributions per scientist than those who work in smaller groups," Zhang said. Could that be because large groups typically include many junior scientists, whose productivity is lower than that of more established researchers? Zhang and He thought so at first, "but when we considered senior authors only, we still found lower productivity," said Zhang, who believes that large group collaborations are simply less efficient than small teams.

The researchers also wanted to know whether yeast biologists tend to study "important" genes---those that later are found to be essential for yeast growth---before less influential genes. They found that to be the case. However, Zhang says this is not because scientists have some sixth sense that leads them to the most significant study subjects; it's probably because important genes have more obvious effects, so researchers notice them before genes with more obscure effects.

In addition, Zhang and He found that researchers tend to focus on determining properties of previously-discovered genes rather than

probing newly-discovered genes. This could be because the risks are smaller and the rewards greater for following up with familiar subjects, but the overall result is that "discovery is conservative," Zhang said. "So maybe that's something we should avoid."

Whether these findings about yeast research apply to the spread of knowledge in other fields is an open question, but if any of the same trends are operating, the ramifications for the advancement of science are profound, Zhang says. "The patterns we observed certainly indicate that these behaviors will slow down innovation."

Source: University of Michigan (news : web)

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