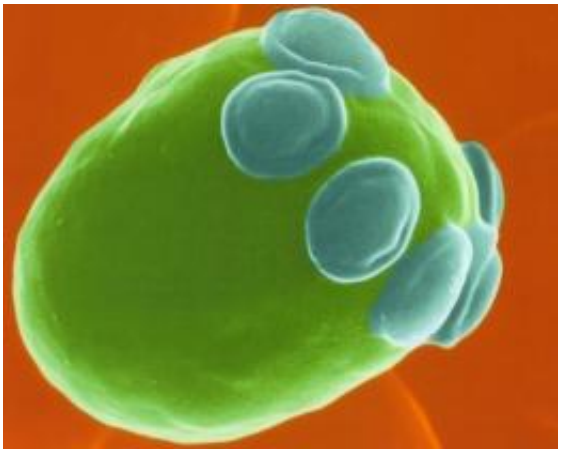
A new type of genetic variation could strengthen natural selection

February 17 2010



A colorized scanning electron microscope image of a single cell of Sacchromyces shows the budding scars in blue where the cell has reproduced asexually. Image: ASM MicrobeLibrary

(PhysOrg.com) -- The unexpected discovery of a new type of genetic variation suggests that natural selection - the force that drives evolution - is both more powerful and more complex than scientists have thought.

"We have discovered that natural selection can act not only on whole organisms and individual genes, but also on gene networks," says Antonis Rokas, assistant professor of biological sciences at Vanderbilt University and senior author of the paper reporting the discovery published online on Feb. 17 in the journal *Nature*.

This finding may help explain how some organisms, including bacterial pathogens, maintain high levels of diversity and adapt rapidly to new stresses.

Working with colleagues at the University of Colorado School of Medicine (UCSM) and the Universidade Nova de Lisboa in Portugal, Rokas found that a close relative of brewer's yeast, Saccharomyces kudriavzevii, exists in two very different states: one that can efficiently digest the sugar galactose and one that cannot. Galactose is a natural sugar found in milk and many fruits and legumes. The variant found in Portugal that consumes galactose uses a network of six genes to convert the sugar into energy. What is surprising is the fact that a variant found in Japan that cannot process galactose has nevertheless preserved a non-functional version of the network of galactose genes for millions of years.

"This level of genetic divergence is normal between distantly related species, like human and mouse. Instead, we find it being maintained within a single species of yeast," says coauthor Mark Johnston from UCSM.

Normally, natural selection and recombination work jointly within an individual species to actively maintain a single version of the genes that perform critical functions or that give organisms a competitive advantage. However, this has not happened with the galactose genes in S. kudriavzevii. When the scientists compared the genomes of the Japanese and Portuguese populations of the yeast, they were surprised to find that the divergence between the galactose genes was a hundred times greater than the divergence between the two genomes as a whole. This indicates that the two states have co-existed for millions of years, which the scientists conclude is convincing evidence that the two have been actively maintained by natural selection.

There is one type of natural selection, called balancing selection, which actively maintains different versions of an individual gene in a gene pool. The classic example is sickle cell anemia. Individuals who inherit the sickle cell variant of the hemoglobin gene from both parents have impaired red blood cells and shortened life expectancy. However, those who receive a sickle cell gene and a normal hemoglobin gene have an increased resistance to the parasite that carries malaria, giving them an advantage wherever malaria is present.

"All the cases of balancing selection that have been identified so far, like sickle cell anemia, involve a single gene," says Rokas. "What is unusual about our case is that we are talking about a network of genes, one that is dispersed throughout the yeast genome."

A number of scientists are looking for examples of balancing selection, but they are focused on single genes. Until researchers begin looking for this type of selection in gene networks, it is not be possible to determine whether it is a rarity or a fundamental process.

One place to look for this new form of selection is among pathogens, many of which have lifestyles very similar to that of yeast: They have very large populations and self-fertilize most of the time, reserving sexual reproduction for periods of high stress. Selection acts most powerfully in large populations and self-mating makes it easier to maintain alternative states that are difficult to sustain.

Specific candidates are the single-cell parasites that cause malaria and the tropical skin disease leishmaniasis. "This is exactly the type of life cycle that we expect to allow for the maintenance of this type of complex genetic variation," says coauthor Chris Todd Hittinger from UCSM.

If this new type of selection is providing a competitive advantage to even

one human pathogen, identifying it could prove important. "We are currently in a war with pathogens and we are loosing the battle. So every advantage we can get in understanding how pathogens adapt could be significant," says Rokas.

More information: www.nature.com/nature/index.html

Provided by Vanderbilt University