

UC SANTA BARBARA

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PROTOZOAN CHOSEN FOR GENOME SEQUENCING, RESULTING FROM PROPOSAL BY UC SANTA BARBARA PROFESSOR

A protozoan that has been studied by a University of California, Santa Barbara scientist for the past 46 years has been assigned high priority for genome sequencing by the National Human Genome Research Institute (NHGRI).

Called Tetrahymena, the single-celled organism split off from an ancestor in common with humans about two billion years ago. Yet it carries many of the same genes as humans, and therefore can be used to understand the function of many human genes.

Small as it is, Tetrahymena has about 30,000 genes, a similar number as humans. It reproduces quickly, doubling in numbers every two hours, which makes it inexpensive and easy to study. The organism is a ciliate, and uses tiny cilia, like hairs, to propel itself.

Eduardo Orias, research professor of genomics in the Molecular, Cellular and Developmental Biology Department at UC Santa Barbara, submitted a white paper to the NHGRI, on behalf of and with contributions from the international ciliate research community. He also consulted with the Whitehead Institute/MIT Genome Center. This

resulted in Tetrahymena being chosen as a high priority genome for sequencing.

Orias began his study of Tetrahymena in 1956, when he was a graduate student at the University of Michigan, and has been working on it virtually ever since. For several years now his research group at UCSB has been doing genetic and physical mapping of the organism.

Studies of Tetrahymena have made major contributions to genetics and cell biology. For example, scientists used this organism to study the structure of telomeres (ends of chromosomes) and the telomerase enzyme, which has profound importance in cancer and aging.

Sequencing of Tetrahymena will have many benefits, including informing the biology of the causative agent of malaria and other related protist pathogens of great medical or agricultural significance.

Orias, who is the coordinator of the International Tetrahymena Genome Project, will collaborate in the analysis of the genome sequence and will facilitate the exchange of information and expert advice between the Tetrahymena research community and the sequencing center.

Rat and mouse genome sequencing is approaching completion. In addition to Tetrahymena, NHGRI has chosen (in alphabetical order) chicken, chimpanzee, fungi (various species), honey bee and sea urchin for the next round of sequencing.

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About UC Santa Barbara

The University of California, Santa Barbara is a leading research institution that also provides a comprehensive liberal arts learning experience. Our academic community of faculty, students, and staff is characterized by a culture of interdisciplinary collaboration that is responsive to the needs of our multicultural and global society. All of this takes place within a living and learning environment like no other, as we draw inspiration from the beauty and resources of our extraordinary location at the edge of the Pacific Ocean.