

EXECUTIVE SUMMARY [NON-CONFIDENTIAL, NON-TECHNICAL ABSTRACT FOR PUBLIC INFORMATION OR PROGRAM PROMOTION]: State in layman's terms the application's broad, long-term objectives and specific aims, making reference to the potential public benefits of the project relevant to California. Do not include proprietary or confidential information. This may be distributed before the funding decision has been finalized.

The public-funded genome projects have focused on “model” organisms such as humans, dogs, and mice and are providing a wealth of biological information. The benefits of these projects are waiting to be tapped by other disciplines including evolutionary biology, and more specifically, molecular systematics. Characterization of similar genes that are found in humans, dogs, and mice can now be expanded to include the examination of these genes in “wild” species; such species are not traditionally used in laboratory studies. In addition to providing ever-increasing knowledge about evolutionary relationships among all organisms, e.g., “The Tree of Life”, this knowledge can be funneled back to provide additional background information for the pharmaceutical sciences, drug development/pharmacogenomics, medicinal chemistry, and vaccine development. In this study, three mammalian groups, shrews/moles, chipmunks, and hares will be examined and approximately 6 different genes will be analyzed in all three groups. Genes characterized from human and mice will be examined in these “wild” species using the previous knowledge gained from the genome projects. The similarity of these genes, found in such diverse species, will provide valuable information about genome structure, gene evolution, and genetic relationships among different mammals. Ultimately, this will contribute to a better understanding of evolution and of our own organs.