EXECUTIVE SUMMARY [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. Molecular analyses of natural populations provide valuable insights into the social lives, movement patterns and evolution of marine mammals, from the individual to the population and higher taxonomic levels. This information is particularly important for its application to the effective management of endangered species. The markers of choice for molecular studies in marine mammals during the last decade, however, can be inadequate for certain species and questions, and posses significant analytical and technological limitations. In genetic studies of humans and model organisms, single nucleotide polymorphisms (SNPs) are rapidly becoming the most widely used marker, since they can be used for a wide range of applications. They are abundant and widespread throughout the genome and they evolve in a way consistent with simple mutation models, which permits a larger analytical simplicity. Furthermore, the recent development of technology that has accompanied whole genome sequencing projects greatly facilitates the discovery, genotyping, and analysis of SNPs, with reduced efforts and costs in the long term. The development and testing of screening techniques and reagents will provide a powerful new tool to elucidate stock boundaries where traditional markers may fail to do so. A publicly available list of markers and protocols will enable any interested researcher to access the information, thus permitting their use on a wide variety of marine mammal studies which, ultimately, will result in the better management and conservation of these organisms.