

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.

Gene expression is required for nearly all aspects of life. Unlike most viruses and bacteria, which can encode many proteins in a single messenger RNA (mRNA) molecule, most eukaryote genes are expressed with only one protein being expressed from each mRNA. In rare cases called 'dicistronic genes', eukaryotes are thought to translate a second open reading frame (ORF) using special structured 'folds' in the mRNA called 'internal ribosomal entry sites' (IRES). IRES elements have been shown to interact with and recruit the ribosome directly to the downstream ORF. Despite numerous examples of viral IRES sequences, there are few consistent patterns that are common to all IRES elements, making them difficult to predict. With the identification of over 50 cDNA-verified dicistronic gene annotations in the fruitfly, it is has become clear that dicistronic genes are more abundant than previously thought. With more examples of dicistronic genes and the completion of over 15 insect genomes, it is now possible to use comparative genomics to gain insight into dicistronic gene evolution and conserved IRES elements. A greater understanding of dicistronic genes and RNA regulatory structures may provide insights into how viruses hijack the cellular machinery and may aid in production of industrially or medically relevant proteins. Training in comparative genomics will also give involved students a useful skill set to apply to other biological projects relevant to the state of California.