



**CALIFORNIA STATE SCIENCE FAIR
2011 PROJECT SUMMARY**

Name(s) Katie S. Shao	Project Number 31062
Project Title Evolutionary Genetics: An Investigation into the Light-Absorbing Property of Variants of Bacteriorhodopsin	
<p style="text-align: center;">Abstract</p> <p>Objectives/Goals The objective is to determine if protein sequence variations seen in families of evolutionarily derived bacteriorhodopsins (bR) confer structural and functional change, and to see whether such variations could be useful for bR-based device engineering.</p> <p>Methods/Materials Sequences of bR from 33 species of haloarchaea were obtained and used to construct a phylogenetic tree in order to express evolutionary relationship to Halobacterium salinarum (NRC-1), and a sequence alignment was made to examine patterns of genetic variation. bR from several species of haloarchaea were then chosen based on their genetic dissimilarity to NRC-1, cloned into SD23 strain of halobacteria, purified, and measured for their light absorbance peaks.</p> <p>Results Spectroscopy of cloned wild type bR from Haloarcula marismortui shows that it absorbs optimally at a slightly higher energy level (~548 nm of wavelength of light) compared to NRC-1 (at ~568nm), and sequence analysis suggests a correlation between ~15 key residue variations in H.marismortui to its left-ward shift in absorbance peak. Further examination of the sequence alignment reveals "blocks" of conserved amino acids that are responsible for distinctly characterizing 9 species of bR, H.marismortui included, as a clade of the bR phylogram.</p> <p>Conclusions/Discussion bR from Halobacterium salinarum (NRC-1) remains one of the most well-studied of all wild type bRs. This comprehensive study of the genetic relationship of many wild type bRs compared to NRC-1 shows that within the bR phylogram, there exists four new clades, each characterized by several distinct residues, that separate 19 species of bR from NRC-1 on an evolutionary genetic level. Further data show that amino acid substitutions in H.marismortui, representative of one clade, are potentially responsible for the shift in its absorbance peak, suggesting functional variation associated with genetic variation between clades as well. Such knowledge of the residue light absorption correlation presents the possibility of using alternate species of bR as the substrate for bR-based applications involving photosensing properties.</p>	
Summary Statement Investigating whether a genetic variation in bR corresponds to a change in its optimum light-absorption.	
Help Received Used lab equipment at UC Davis under the supervision of Dr. Facciotti; printed poster from BME center	