## Executive Summary

**This proposal seeks to analyze the effects of the pollutant stressor selenomethionine (SeMet), singly and in combination with methyl mercury (MeHg), temperature, and salinity stresses on the biochemistry, physiology, and overall fitness of different life stages of sturgeon. Because white sturgeon (Acipenser transmontanus) and green sturgeon (Acipenser medirostris) both occur in the San Francisco (SF) BayDelta this study will focus on both species. Our proposal aims at better understanding the mechanistic basis for bioaccumulation of SeMet and MeHg, and unraveling key elements of the molecular response to such pollutant stresses in sturgeon. This proposal represents a collaborative effort by four experienced UC Davisbased laboratories and CDFG in Stockton. The research team has excellent prerequisites for addressing key areas that are of primary concern to CALFED using an innovative and modern approach, and utilizing the power of combining stateoftheart expertise in multiple areas of science. This collaborative effort is expected to yield more useful and comprehensive information than would have been possible by five individual proposals. Furthermore, the proposed collaboration streamlines procedures by allowing efficient sharing of expertise, personnel, equipment, and supplies. Our proposed research will significantly enhance the depth of knowledge about the stress biology of sturgeon and allow further development of life history models by performing a series of integrated tasks. These tasks will test the overall hypothesis that specific stress proteins in combination with biochemical, cellular, and physiological parameters a) indicate exposure of sturgeon to specific types and defined combinations of stresses and b) allow us to deduce molecular mechanisms and biological processes of stress adaptation in sturgeon. We will breed sturgeon and obtain samples from laboratory acclimation experiments and obtain biopsies from wild sturgeon in the field. Using these samples we will quantify the toxicokinetics, bioaccumulation, and chronic toxicity of selenium when present alone or in combination with MeHg in the diet. Moreover, we will quantify effects of chronic exposure to dietary SeMet stress, singly and in combination with MeHg, salinity, and temperature stresses on swimming performance, resting metabolism, and hematology. Furthermore, we will identify novel bioindicators and entire proteome signatures and biochemical pathways affected by the stressors outlined above. These 'stress-signatures' will be compared to the proteome of sturgeon biopsies obtained in the field to deduce exposure history in field specimen. Finally, we will construct tissue microarrays (TMAs) from sturgeon tissues to enable robust, stressor-specific, and high-throughput bio-monitoring field assays in the future. This was a significant weakness in existing programs, which will be addressed directly by our proposed approach. By knowing the proteins and biochemical pathways associated with stressful levels of selenium, mercury, salinity, and temperature we can identify physiological functions that are affected by such stresses in endangered fish species such as sturgeon. Knowledge of physiological functions, in turn, is essential for modeling the impact of future environmental changes on the SF BayDelta ecosystem as a whole.**