Expected Outcome: Upon completion of Aim 1, we will have a synthetic understanding of the physiologic and genomics patterns associated with extreme dehydration, specifically with regards to osmoregulation and Solute carriers genes. These data will allow us to generate a list of genes, genomic regions, isoforms, and methylation states (putatively (predicted/expected/hypothecized) linked to the phenotype of interest. This list is critical, and will form the basis for AIM2, which will propose the development of a system where manipulation of specific genes is possible (e.g. the CRISPR/CAS9 transgenic system), thus moving the work from correlation to causation.

In addition, we aim to develop methods related to the study of isoforms using PacBio data as part of my long standing work in developing the de novo transcriptome assembler Trinity.

Potential Problems:

Though abundant preliminary data suggests that my hypothesis that genes in the Solute Carrier family are strongly linked to animals' ability to survive dehydration, the true power of the proposed approach lies in its ability to uncover all genomic changes that occur in response to dehydration. In the unlikely event that our original hypothesis is invalidated, we would turn to other genes whose expression/isoform diffs/mthylation is related to dehydration.

With regards to the experimental design and analytical methods,