

USDA NIFA Grant “Breeding climate-smart beef cattle”

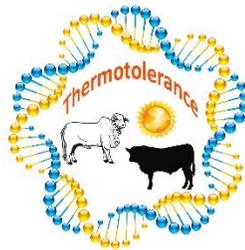
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Project Overview

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Climatic stress is a major limiting factor of production efficiency in beef cattle in tropical and subtropical environments and in dairy cattle throughout most of the world. This stress is expected to increase due to climate change. More than half of the cattle in the world are maintained in hot and humid environments, including about 40% of beef cows in the US. Substantial differences in thermal tolerance exist among breeds and among animals within breeds indicative of opportunities for selective improvement. For example, *Bos indicus* cattle exhibit increased resistance to many environmental stressors relative to *Bos taurus*, but tend to have slower growth, lower fertility and poor meat quality as they have not been as intensively selected for these traits as specialized *Bos taurus* breeds. Use of genomic tools to produce an animal with superior ability for both thermal adaptation and food production represents an energy-efficient sustainable approach to meet the challenge of global climate change.

Overall goal: Our *long-term goal* is to develop the knowledge and tools the cattle industry needs to increase tolerance to heat stress, while simultaneously allowing for increased efficiency of production, reproduction, and meat quality. The strategy we propose is to reveal the genetic architecture of traits defining thermal tolerance using *Bos indicus* influenced cattle. A population of Brangus (Brahman x Angus) cattle will be used in this project. In comparison to straight *Bos taurus* populations, we expect that the frequency of genetic variants controlling thermal tolerance will be high in these indicine-influenced populations due to the length of time since divergence of the two subspecies, natural adaptation to different environments, and exposure to artificial selection of different intensities and with different objectives. The *aims of this project* are to discover genetic variants responsible for thermal tolerance and use this knowledge to develop genomic tools for marker-assisted selection (MAS) to improve thermal tolerance in cattle populations at risk of exposure to heat stress. In addition, the maturation of technologies for gene editing means that thermotolerance genes can be rapidly introduced into beef and dairy cattle breeds. Development of “the cow of the future” will be realized through use of genomic selection within breeds and through application of gene editing technologies that allow genetic variants conferring thermal tolerance to be rapidly incorporated into non-adapted breeds. Introduction of alleles for thermal tolerance into the elite germplasm of a specialized breed productively superior but poorly adapted to tropical environments offers a powerful new approach to address the challenges of climate change and develop climate-smart productive cattle for a future hotter world.



Supporting objectives:

Objective 1. Identify QTL associated with regulation of body temperature during heat stress and estimate the accuracy of using these QTL for MAS to improve thermal tolerance. Frequent body temperature measurements, skin temperature and perspiration rate in free ranging cattle will be recorded during heat stress on 2,000 Brangus heifers genotyped with the 250K functional SNP chip. These replacement heifers will be subsequently exposed to synchronized AI and fertility data at first calving will be recorded. Phenomics for thermal tolerance and genomic data will be integrated to identify chromosomal regions associated with regulation of body temperature. We will estimate the accuracy of genomic prediction and define a sufficient reduced SNP set to be used in a MAS program.

Objective 2. Analyze the mutational landscape and identify causal genetic variants underlying thermal tolerance. Functionally annotated genes will be assigned to markers associated with thermal tolerance in Objective 1 to transition from naïve to informed genomic prediction. Functionally-enriched gene networks will be developed to identify major drivers and pathways controlling thermal tolerance. Transcriptomic information on animals with extreme body temperature will be integrated to identify gene functions and interactions relevant for thermal tolerance and potentially not described by current bovine functional data base. Subsequently, we envision subjecting genomic regions of interest to targeted-sequencing to identify causative mutations with the long-term goal of using gene editing to introduce the mutation in thermally-susceptible breeds. Additionally, public whole-genome sequences data generated for the bovine genomics community, such as the 1000 Bull Genomes project, will be used to confirm and validate our causal variants.