

DNA: Detailed Explanation

DNA analysis as a powerful tool to guide the conservation of the original Texas Longhorn breed. DNA results help guide breeders as they select animals that contribute to the future of the breed and prevent its extinction.

By late 2019 the Cattlemen's Texas Longhorn Registry (CTLR), had assembled over six hundred genotypes from conservation Texas Longhorns using Single Nucleotide Polymorphisms (SNPs). Individual animals were analyzed by placing their results along a linear scale that compared them to other breeds and distinguished breed influences by a percentage of influence from the various breeds and branches of cattle origins (indicine, Iberian, Northern European, and African). The CTLR also used a separate mitochondrial DNA analysis that tracked influences that come from the maternal side, and a similar separate analysis of the Y chromosome of males that tracks the paternal side. These two can both track any introgression from influences foreign to the traditional breed.

These analyses were then all combined to derive a proportion of an individual animal's genetic makeup that comes from the different bovine breed origins. The percentage that falls within the conservation Texas Longhorn can then be used to drive breeding and conservation decisions. In addition to helping assign animals into the traditional Texas Longhorn conservation breeding group, the results also validate the parentage of the animal by matching it to its sire and dam. This assures that pedigrees are accurate, which is essential for managing the breeding of a rare breed. In most breeds the error rate in breeder-assigned sires averages 15%. DNA validation removes this source of errors and guarantees that all animals have accurate pedigrees and can contribute to meaningful conservation breeding programs.

Neogen/GeneSeek reports a 100K SNP map that is interpreted by a software analysis developed for the Cattlemen's Texas Longhorn Registry. The results assign an indicine percentage to each individual. Explanation of the origin of indicine percentage is in the research article *New World cattle show ancestry from multiple independent domestication events*.
<https://www.pnas.org/doi/10.1073/pnas.1303367110>

Up until 2023, The University of California-Davis performed an analysis of microsatellites that was capable of identifying in males, percentages of introgression of 17 breeds; 13 common Taurine English/Continental breeds and 4 Indicine; African Sanga/Middle East/India Zebu breeds. The UC Davis report for both males and females includes the percentage of genetics grouping with conservation Texas Longhorn cattle and/or the percentage an animal groups with hybridized horned cattle. Y-chromosomes haplotypes in males are associated with specific regions (Y1 northern Europe and British Islands, Y2 Iberian Peninsula and Southern Continent, Y3 Zebu (all humped cattle), and reveal percentage of introgression of any of the 17 breeds on file. *Bos taurus* (includes all European cattle) or *Bos indicus* (includes all Zebu or Indian cattle), mtDNA lineages are classified according to major *Bos taurus* families (haplogroups T1, T1a, AA (or T1c), T2, T3, Q) and *Bos indicus* families (I1, I2). Results to expect for conservation Texas Longhorn cattle are rankings of 80% or greater with conservation control group.

Less than 1% of Hereford, Shorthorn, Angus, British White, and Zebu are not uncommon in conservation Texas Longhorn cattle. Low percentages reflect historic introgression from the 1800s and early 1900s. Animals possessing markers found only in Iberian breeds with 0% introgression of other referenced breeds do exist. In combination with 90+% conservation genetics, these animals are considered elite. Many conservation Texas Longhorn bulls possess a Y-haplotype indicating historic admixture of Hereford, Shorthorn or Angus due to the introduction of those breeds in 1885 to west Texas. Read an article from 1920 in The American Hereford Journal.

<https://www.ctlc.org/wp-content/uploads/2023/01/Herefords-in-West-Texas.pdf>

Cattle gathered along coastal regions possessed historic admixture of Nelore and Gyr; Zebu breeds that were imported to the US in the 1885 to become the foundation of the American Brahman breed.

We must accept less than 1% admixture from other breeds as part of the evolution of the Texas Longhorn breed. We do not consider introgression from other breeds introduced in the last sixty years to be natural evolution. Animals possessing greater than 1% of other detectable breeds are excluded from conservation status. We have learned by experimentation offspring can be 'bred up' from parents possessing unacceptable genotypes, when one grandparent possessed conservation genetics, the calf has a 50/50 chance of inheriting the conservation alleles or the hybrid alleles. For this reason, we include eight bulls that fall below our minimum acceptable range of 80% conservation score. These are available for experimentation in effort to increase diversity but are not guaranteed to produce an offspring that will be acceptable for CTLR registration.

