# FINAL REPORT

## Improving the Alpaca Genome Sequence Assembly

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**RESULTS: Researchers improve accuracy and contiguity of alpaca reference genome.**

Morris Animal Foundation-funded researchers at Texas A&M University worked to improve the existing assembly and annotation of the alpaca genome, filling in critical information gaps. Genome assembly and analysis for alpacas and other camelids is lagging behind other domestic species. This has hampered efforts to search for genetic abnormalities associated with diseases and congenital disorders in these animals.

Genome assembly refers to the final product produced after taking large numbers of DNA fragments, sequencing them, and assembling them into the correct order to reconstruct the entire DNA map of an individual. This creates a type of genome assembly library or instruction map – a critical research tool that helps scientists discover DNA mutations associated with diseases and inherited disorders. Discovery of genetic mutations then allows researchers to develop diagnostic tests as well as new prevention and treatment strategies.

The team successfully characterized almost 19,000 functional genes. This improved tool will be invaluable for discovering underlying genetic factors and causes of diseases. The team already discovered genetic links to minute chromosome syndrome, a condition responsible for reproductive problems and anatomic defects in alpacas.

A more detailed assembly of the alpaca genome will ultimately benefit all camelid species, from domesticated llamas to the critically endangered wild Bactrian camels found in the Gobi Desert of China and Mongolia. The updated alpaca sequence assembly is essential for the study of genetic diseases and disorders in related species as well as an important tool in conservation genetics for species survival programs.

**Thank you to the Llama Association of North America for supporting this study!**