**Alpaca Comparative Genomics: Recent Developments and Future Expectations**

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The alpaca was nominated and funded by National Human Genome Research Institute for whole genome sequence assessment as one of the representatives of the diversity observed in the mammalian radiation, and because of the strategic position of the camelid lineage at the base of the Artiodactyla radiation, which is the most successful group of herbivores with approximately 240 very diverse members. This order contains the majority of domesticated mammal species, including cattle, pigs, goats, and sheep, reindeer, and camelids, which consist of the dromedary camel of northern Africa and south-west Asia, the Bactrian camel of eastern Asia and the South American (new world) camels, with the wild guanacos and vicuñas and the domesticated llamas and alpacas. Most of the genetic resources developed for the alpaca will be directly applicability for all camelid species and will have important implications for many other vertebrates. A high quality draft sequence of the whole genome assembly has been completed and is available for preliminary scientific applications. Here I will provide an overall description of the assembly, discuss the implications of the results for further genomics research in both camelids as well as other mammals.

Camels offer numerous opportunities for important discoveries as research animals in the genomics era, including as models for human congenital defects, as a third of the over eighty congenital defects identified in camelids have similar inherited conditions in humans. Comparative genomics has become one of the keys to decoding the rapidly growing amount of genomic sequence that is being obtained, and of linking genetic variation with functional variations. The development of molecular tools for the camelids is also a crucial step in identifying genomic regions, and ultimately the genes and their functions, that are associated with phenotypic differences of economic interest, such as productivity traits. Identification of expressed genes and genetic markers that contribute to phenotypic variation in economically important traits would have a huge impact on improving the management of these species. In many of the poorest communities in the world, camelids are one of the few livestock species that can thrive in the regions harsh environmental conditions, and as such are among their most important assets and the mainstays of their economy. These animals provide income, food, and fertilizer and help sustain the community's health and environment. The benefits from the development of genetic tools to characterize camelids could eventually assist many of these communities.