Camelid Genetics and Reproductive Biotechnologies

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The public profile of the alpaca (Vicugna pacos) increased significantly as it became a more common agricultural species around the world and the focus of more intense modern breeding techniques and of genomic studies. The alpaca is 1 of 7 camelids that together occupy some of the world’s most arid ecosystems and which have had large beneficial impacts on the human cultures in these areas. Today, wild bactrian camels (Camelus bactrianus) and domestic bactrian camels (Camelus dromedarius) primarily inhabit Central and South Asia and the Middle East, whereas wild guanaco (Lama guanicoe) and vicuña (Vicugna vicugna) inhabit parts of South America along with domestic llamas (L. glama) and alpacas (Franklin 2011).

The alpaca was domesticated from the wild vicuña 6000–7000 years ago in the Central Andes by a hunter–gatherer society that selected for docile animals with fine hair (Marín et al. 2007). Alpacas, as well as llamas (which were domesticated most likely from guanacos), were important to ancient Andean civilizations (Wheeler 2012). Today, alpaca husbandry is most commonly practiced in association with llamas and introduced sheep and is the principal agricultural use of the extensive areas of high altitude, natural pasture in the Andean altiplano, where crop agriculture and successful raising of other domestic animals have proved unfeasible. Most of the world’s alpacas are in Peru, typically in regions with high poverty and economic marginalization, making the role of the alpaca especially important because of their significant contributions to local indigenous economies. The animals provide meat, wool, fuel, transportation of goods, and an important source of cultural identity. The alpaca is especially coveted for its soft, fine-diameter, lightweight, and warm wool, used for luxurious blankets, sweaters, and cloth.

Starting in the early 1980s, alpacas were exported from Chile, Bolivia, and Peru to Australia, New Zealand, the United States, Canada, and Europe, where small industries developed. Although the camelids are currently a minor agricultural species in these areas, their potential impact and importance is significant because of their ability to thrive in a variety of environments.

The alpaca is the first camelid for which whole genome sequence information and a comprehensive genome map have been developed publically. The genome was sequenced using a female alpaca named “Carlotta” (AHFN-0088) by the Genome Institute, Washington University School of Medicine in St. Louis, MO, with funding provided by the National Human Genome Research Institute, National Institutes of Health. The latest version of the assembly is Vicugna pacos (alpaca) v. 2.0. (http://www.ncbi.nlm.nih.gov/genome?term=alpaca). Already the alpaca has served as a reference for the other domestic and wild camels for a broad range of comparative genomic studies. As has happened with the published genomes of several other domestic species (including cattle, pig, horse, dog, cat, and chicken), the alpaca genome and related resources are also assisting research efforts in related species, such as the endangered wild Bactrian camel, and are fostering the integration of genetic approaches in the management and husbandry of domesticated camels, particularly in Eurasia and North Africa.

In anticipation of the completion of the alpaca genome, the second Camelid Genetics and Reproductive Biotechnologies meeting was held on 16–18 September 2011. Geneticists, reproductive scientists, veterinarians, and breeders from the Middle East, Australia, South America, and the United States convened to exchange information on developments in camelid science and husbandry. A major goal of the conference was to provide the unique opportunity to interact across these diverse disciplines and international institutions. Advances in camelid research and applied management will depend on such multifaceted scientific enquiry spanning diverse fields of population and evolutionary genetics, comparative genomics, epidemiology, immunology, wildlife ecology, veterinary medicine, and computer science.

Talks presented at the meeting covered a wide range of topics, from candidate disease genes to the genetic basis of wool color to regional population histories. The 4 papers published in this issue provide examples of the range of research that can benefit from increased camelid genomics resources. They include data from a bactrian camel genome, a description of the genetic inheritance pattern of an important alpaca phenotype, the development of cytogenetic tools for camelids, and the linkage of a reproductive disorder in alpaca with a mutant autosomal chromosome.

Relative to other important agricultural species, camelid genomic tools have been emerging slowly. However, the potential for the development and use of these tools is large, and the alpaca genome project is providing a firm launching
pad for future camelid genomic research. As a world community, camelid researchers and managers have the opportunity to bridge traditional political, cultural, and economic barriers to international camelid research and can use multidisciplinary approaches to improve the health, welfare, and management of domestic and wild camelids.

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References

