

Camelids: From chromosomes to physical maps and back to chromosomes

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An essential component of the Alpaca Genome Project is the construction of a whole genome cytogenetic map. This includes physical assignment of genes and DNA markers to all alpaca chromosomes. Mapping is carried out by fluorescence *in situ* hybridization (FISH) using clones from the CHORI-246 alpaca genomic library. Currently, over 160 genes and ESTs have been assigned to 32 alpaca autosomes and the X chromosome. Over 60 of these genes are shared with the radiation hybrid map. The map i) effectively integrates the genome sequence, radiation hybrid and genetic linkage maps with physical chromosomes, ii) anchors unassembled sequences and assists and validates the genome sequence assembly, and iii) generates molecular markers for each alpaca chromosome, chromosome arm or region, thus clarifying current inconsistencies in chromosome nomenclature. This is of particular importance for alpaca clinical cytogenetics because the species is known for high diploid chromosome number ($2n=74$) and a 'difficult' karyotype. Last but not least: since alpaca is the only camelid with a prospective to have whole genome sequence information combined with a well-developed genome map and molecular-based chromosome nomenclature, the information will serve as a reference for all other camelids—domestic and wild.