

Second generation of alpaca radiation hybrid map: use of high-throughput genotyping.

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First generation of alpaca radiation hybrid (RH) map was developed in 2007 with support of Alpaca Research Foundation and had 428 markers (371 type I (coding genes) and 57 type II (microsatellites)). Higher-resolution RH maps were constructed for two alpaca chromosomes by assigning additional 50 markers to chromosome 16 and 60 markers to X-chromosome. On average there were 10 markers per chromosome. However, the number of markers on the RH map was still quite low and there were some significant gaps.

To find an efficient way to bring RH map of alpaca to higher level of resolution and to enrich it with markers we have tested several high-throughput genotyping technologies. In total the number of markers was increased approximately five times in comparison with the original map. All three approaches (homologous and non-homologous Illumina SNP-chip technology, custom designed GoldenGate assay) yielded significant number of mapped markers.

We used custom alpaca SNP chip (767 SNPs total) and 529 SNPs produced good quality signal on RH panel. We also report here the use of 50K Bovine SNP chip to map markers on non-homologous genome of alpaca. We discovered that about 4% of cow SNPs produce high quality signal suitable for mapping on alpaca RH. To ensure even spacing of the markers on the map we additionally designed custom Illumina GoldenGate assay. Using multiple cross-species whole-genome sequence comparison we designed 1560 oligo pool based on 2X alpaca genome assembly, and low coverage hamster sequence. About 90% of these markers produced reliable genotypes on RH panel.

The second-generation RH map is currently being developed with those new markers obtained through highly efficient methods of high-throughput genotyping. Present number of markers and even spacing along the whole chromosome complement makes current RH map a useful tool to aid alpaca genome assembly.