



# THE WINN FELINE FOUNDATION

For the Health and Well-Being of All Cats

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## **Targeted Gene Mapping in Gaps of the Feline/Human Comparative Map**

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An improved map of the feline genome is desirable in order to give feline geneticists the necessary tools to identify and characterize genes causing disease in cats. By refining the comparative map linking the cat genome to the human genome, more diseases or traits can be linked to specific genes or their mutations.

The researchers designed primers from a database of roughly 4,000 testis, heart, and uterus expressed sequence tags (ESTs), and 80,000 traces from the feline 2X genome sequencing project. All sequences were repeat-masked and trimmed of low quality and vector sequence. The sequences were then compared to human and dog genome sequences. The researchers designed PCR primers for those markers that gave high scoring reciprocally best hits in the syntenic regions of the human and dog genome. They then selected 550 candidate primer pairs from the database that filled existing gaps in the feline-human comparative coverage on the latest feline radiation hybrid map.

These candidate primer pairs were ordered and pre-tested on a series of controls. Approximately 90% of the pairs – 493 – tested suitable for genotyping in the feline radiation hybrid (RH) panel, resulting in a large number of the holes in comparative coverage being successfully filled. Though 45 markers were not placed using the high-confidence threshold of LOD score of 8.0, these will be placed in their probable positions relative to the framework map that will be constructed from the loci assembled at LOD score of 8.0.

The researchers recently constructed a third-generation RH map of the cat genome in collaboration with scientists at the Laboratory of Genomic Diversity. This new map reveals that 96% of the 1793 total cat markers recently mapped have identifiable orthologues (genes derived from a common ancestor) in the canine and human genome sequences. The updated autosomal and X chromosome comparative maps identify 152 cat-human and 134 cat-dog homologous synteny blocks. Researchers constructed an enhanced comparative map relating the three genomes that provides 86% comparative coverage of the human genome and 85% comparative coverage of the canine genome.

The map provides a solid framework and comparative tool to aid in the identification of genes controlling feline phenotypes and the chromosomal assignment of feline contigs and scaffolds during assembly.

## **Glossary**

**Contigs:** a set of overlapping DNA segments from a single genetic source

**Expressed sequence tag:** a short strand of DNA that is a part of a cDNA molecule and can act as identifier of a gene

**LOD (logarithmic odds) score:** a statistical test used for linkage analysis; computerized LOD score analysis is used to analyze complex family pedigrees in order to determine the linkage between Mendelian traits (or between a trait and a marker, or two markers)

**Orthologues (orthologous genes):** genes in different species that are similar to each other because they originate from a common ancestor

**PCR (polymerase chain reaction):** A laboratory technique that can amplify the amount of DNA from a tiny sample to a large amount within a few hours

**Primer:** A short preexisting polynucleotide chain to which new deoxyribonucleotides can be added by the enzyme DNA polymerase

**Radiation hybrid (RH):** A hybrid cell containing small fragments of irradiated human chromosomes. Maps of irradiation sites on chromosomes for the human, rat, mouse, and other genomes provide important markers for investigation of traits and diseases.

**Scaffold:** a series of contigs in the right order, but not necessarily connected together continuously

**Synteny blocks:** Groups of genes occurring in the same order on chromosomes of different species

## **For further reading**

Murphy, W. J., B. Davis, et al. (2007). A 1.5-Mb-resolution radiation hybrid map of the cat genome and comparative analysis with the canine and human genomes. *Genomics* **89**(2): 189-96.

Murphy, W., A. Pearks Wilkerson, et al. (2006). Novel gene acquisition on carnivore Y chromosomes. *PLoS Genet* **2**(3): 0353-0363.

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