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*Bhanu P. Chowdhary, Terje Raudsepp, Srinivas R. Kata, Glenda Goh, Lee V. Millon, Veronica Allan, François Piumi, Gérard Guérin, June Swinburne, Matthew Binns, Teri L. Lear, Jim Mickelson, James Murray, Douglas F. Antczak, James E. Womack, and Loren C. Skow. April 2003. The First Generation Whole Genome Radiation Hybrid Map in the Horse Identifies Conserved Segments in Human and Mouse Genomes. **Genome Research** 13(4):742-751.*

Generating a composite genetic map of the horse could provide information on the location of various genes controlling traits important to the entire equine industry. These traits range from improved equine health and disease resistance to reproduction and perhaps even athletic performance.

The first major steps aimed at acquiring cross-the-board knowledge of the horse genome will be critical in understanding the molecular causes underlying various equine diseases and hereditary disorders. This will be crucial in developing diagnostic and prevention/therapeutics approaches for these problems.

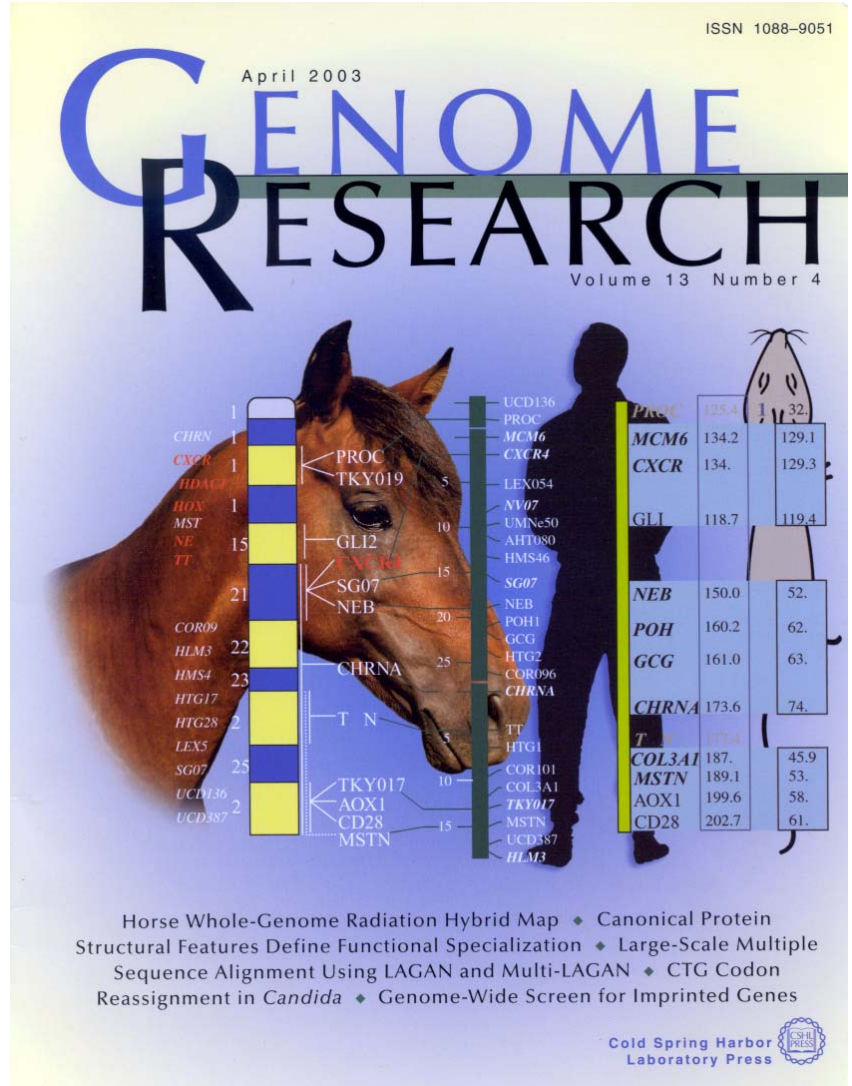
The 730 marker map (including genes and non-gene specific variable regions) generated in this study provides the first comprehensive framework gene map of the horse. It provides the most detailed genome-wide information to date on the organization and comparative status of the equine genome. Genetic markers were localized to all horse chromosomes including the X chromosome. On average, the mapped markers are distributed every 4 megabases of the equine genome - a significant improvement in resolution over previous maps.

The assembled comparison of 447 equine genes with the location of draft sequences of their human and mouse counterparts provides the most extensive horse-human and horse-mouse comparative map to date. It is expected that the foundation provided by this map will facilitate rapid, targeted expansion of the horse gene map and consequently, mapping and positional cloning of genes governing traits significant to the equine industry. Most importantly, it will be the source to move horse genetics from the laboratory into the realm of direct application.

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