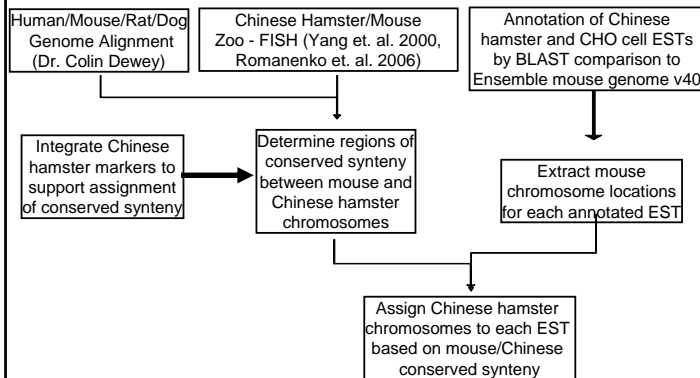


Chinese Hamster Orthology Map and Chromosome Scaffold

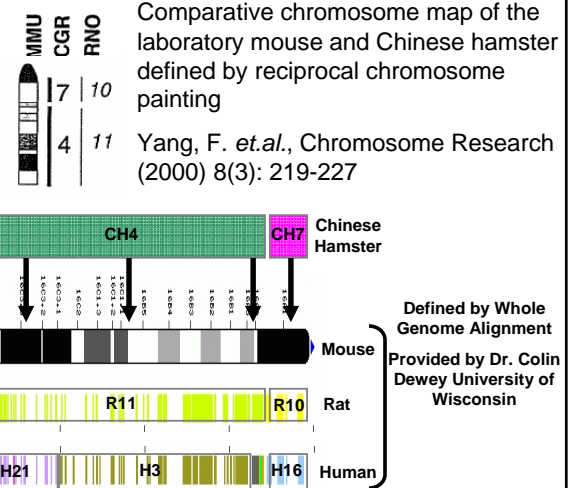
Defining Regions of Conserved Synteny Between Chinese Hamster and Other Sequenced Genomes

Flowchart of Chromosome Mapping



Construction of an Orthology Map

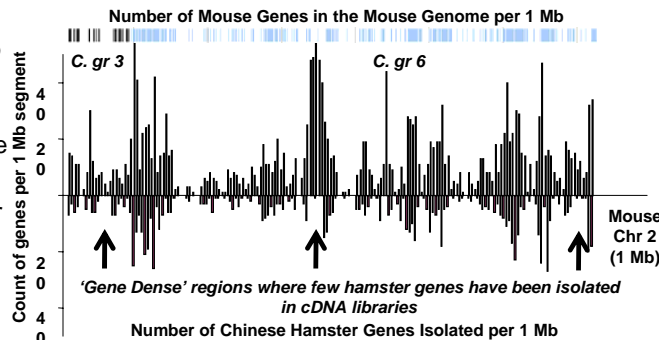
- Zoo-FISH (reciprocal chromosome painting) was used to define regions of conserved synteny between mouse and Chinese hamster
- Whole genome alignment was used to assign the genomic locations (in bp) to junctions between chromosomal rearrangements
 - The locations of breakpoints in chromosome structure are conserved among mammals
- Marker genes from literature were used to confirm the assigned conserved regions



A Genomic Context for Data Analysis

Analysis of Transcribed CHO Genes

- X-axis: Each bar represents a contiguous 1 Mb region mouse chromosome 2
- Y-axis (positive): The bar height is the number of known genes in the 1 Mb region of the mouse genome
- Y-axis (negative): The bar height is the number of unique genes isolated from CHO cell line cDNA libraries
- Comparison of 'gene dense' and 'gene sparse' regions can identify large chromosomal regions not actively expressed in CHO cells



Acknowledgements

We acknowledge the support of the members of the Consortium for Chinese Hamster Ovary Cell Genomics



http://hugroup.cems.umn.edu/CHO/cho_index.html

We thank the Minnesota Supercomputing Institute and the Center for Computational Genomics and Bioinformatics for computational resources and support