

PublisherInfo		
PublisherName	:	BioMed Central
PublisherLocation	:	London
PublisherImprintName	:	BioMed Central

Comparing cows with humans

ArticleInfo		
ArticleID	:	3789
ArticleDOI	:	10.1186/gb-spotlight-20001005-04
ArticleCitationID	:	spotlight-20001005-04
ArticleSequenceNumber	:	226
ArticleCategory	:	Research news
ArticleFirstPage	:	1
ArticleLastPage	:	2
ArticleHistory	:	RegistrationDate : 2000-10-05 OnlineDate : 2000-10-05
ArticleCopyright	:	BioMed Central Ltd2000
ArticleGrants	:	
ArticleContext	:	130591111

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Comparative genomics is emerging as a powerful approach for assessing the similarities and differences between species. In the September *Genome Research* Band *et al.* compare cows and humans to generate mapping information about the bovine genome (*Genome Res* 2000, **10**:1359-1368). The authors combined parallel radiation hybrid (RH) mapping analysis with express sequence tag (EST) sequence information and a bioinformatic methodology called COMPASS (comparative mapping by annotation and sequence similarity). They were able to create a whole-genome RH map with 768 cattle genes and 319 anchored microsatellite markers. Over 80% of these genes had human orthologs and the two genomes had at least 105 conserved chromosomal segments in common. The coverage of the cattle-human comparative map is predicted to be about 60%. These results provide a framework for future comparative studies. Clearly men and cows are more similar than they look.

References

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