

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

Isolating the cow genome

ArticleInfo		
ArticleID	:	3960
ArticleDOI	:	10.1186/gb-spotlight-20010118-02
ArticleCitationID	:	spotlight-20010118-02
ArticleSequenceNumber	:	31
ArticleCategory	:	Research news
ArticleFirstPage	:	1
ArticleLastPage	:	2
ArticleHistory	:	RegistrationDate : 2001-01-18 OnlineDate : 2001-01-18
ArticleCopyright	:	BioMed Central Ltd2001
ArticleGrants	:	
ArticleContext	:	130592211

Jonathan B Weitzman

Email: jonathanweitzman@hotmail.com

Inbreeding is thought to cause reduced genetic variation and [diminished viability](#). In the January 18 [Nature](#), Visscher *et al.* studied the genome of a viable herd of cows, [Chillingham cattle](#) (*Bos taurus*), that have lived as an isolated inbred herd for over 300 years in the north of England (*Nature* 2001, **409**:303). Visscher *et al.* analyzed 13 of the Chillingham animals (the breed totals just 49 animals) and scored for 25 polymorphic microsatellite markers. They report that the herd is remarkably homozygous, with only one marker displaying heterozygosity. The authors suggest that any deleterious alleles have been purged from this population and that the Chillingham herd may make a useful contribution to [bovine genome](#) studies.

References

1. Conservation genetics.
2. *Nature*, [<http://www.nature.com/nature/>]
3. The Wild White Cattle of Chillingham, [<http://www.whitepark.org.uk/chillingham.htm>]
4. Bovine Genome Database , [<http://bos.cvm.tamu.edu/bovgbase.html>]