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Translation of information between human and livestock gene maps using a deer interspecies hybrid mapping panel

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ABSTRACT

The burgeoning knowledge associated with the gene maps of humans and mice can provide key information for the identification of genes underlying production traits in livestock. In theory, it should be possible to translate information associated with a human chromosomal location to a chromosome location in sheep, cattle or deer. However, in practice, livestock gene maps often require more comparative links to make accurate translation possible. We have taken a novel approach to livestock comparative mapping by using an interspecies hybrid mapping panel to map both gene loci and sheep and cattle microsatellites. The panel comprises DNA from 346 1/4 Père David's deer (*Elaphurus davidianus*) 3/4 red deer (*Cervus elaphus*) backcross progeny of male F1 Père David's deer x red deer hybrids. We are using this deer mapping resource to relate the sheep, cattle and human gene maps and by mapping key markers from each.

Keywords: deer, interspecies, hybrid, comparative, gene map.

INTRODUCTION

Completion of framework linkage (or recombination) maps of the sheep and cattle genomes, (Bishop *et al.* 1994; Crawford *et al.* 1994) has facilitated identification of gene loci which influence productive traits in livestock. (Georges *et al.* 1995; Haley 1995; Goosen *et al.* 1997). However, even if such quantitative trait loci (QTL's) are localised to a specific linkage map interval, this interval will typically contain tens of millions of base pairs of DNA sequence and include hundreds of genes and control regions. Linking livestock genetic maps with "information rich" mammals such as humans and mice may provide key information on the genes in a particular map interval and narrow the search for the "production gene" responsible for a QTL. The Human Genome Project is making rapid progress toward mapping sequencing all of the estimated 100 thousand genes used in the construction of a mammal (Lewin 1987). In laboratory mouse, in addition to gene mapping, data is expanding exponentially on the effects specific mutations, and the expression patterns of genes during development. This data is available via the world wide web in a variety of public access databases, for example, the United States National Center for Biocomputing ENTREZ database (<http://www.ncbi.nlm.nih.gov>), The Genome Database (<http://gdbwww.gdb.org/gdb/gdbtop.html>), Mouse Genome database <http://www.informatics.jax.org>).

Comparative studies have shown the chromosomal arrangement of genes in livestock is very similar to humans. This is most graphically illustrated by chromosome painting studies in which genomic material from a single chromosome of one species is isolated and used to paint a chromosome spread from another species. Typically, each human chromosome paints 1-3 large segments of the ruminant chromosomes demonstrating considerable con-

servation in chromosome structure (Solinas-Toldo *et al.* 1995). In theory it should be possible relate human and mouse map information to livestock maps so that when a livestock QTL is identified all the human and mouse data relevant to this genome position can be down loaded and candidate "production genes" selected from the sequence and functional data. In practice, however, relating human data to the linkage maps used to identify QTL's has proved difficult. The primary reason for this that genes which are highly conserved, and therefore useful for relating genomes are typically not polymorphic. Conversely highly polymorphic genes which are useful for tracing the inheritance of traits, are typically not conserved widely among mammals. For example, of 231 markers on the framework sheep linkage map there were less than 20 genes with a comparative location in humans (Crawford *et al.* 1994).

THE INTERSPECIES HYBRID PANEL

We have generated an interspecies hybrid mapping panel to map both conserved gene loci and livestock microsatellites. The panel comprises DNA from 346 1/4 Père David's deer (*Elaphurus davidianus*) 3/4 red deer (*Cervus elaphus*) backcross progeny of male F1 Père David's deer x red deer hybrids (Tate *et al.* 1997). Because of the divergence between the parental species conserved genes can be rapidly mapped by linkage analysis (Tate *et al.* 1995). In addition, about 20% of highly polymorphic sheep and cattle microsatellite markers amplify specifically in the deer panel and can be mapped. A subset of 89 backcross animals from which large amounts of DNA has been extracted available from the authors as a international gene mapping resource (Tate *et al.* 1997).

Currently the deer map database contains 251 mapped loci, 145 of these are also mapped in humans, 93 in the