Consensus and comprehensive linkage maps of bovine chromosome 25

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Introduction: Comprehensive linkage maps have been constructed with the purpose of integrating existing genetic data from several populations[1,2,4,8]. This workshop report, presented under the of auspices of the International Society for Animal Genetics (1998–2000), summarizes construction of consensus and comprehensive linkage maps for bovine Chromosome 25 (BTA25). Five laboratories contributed marker genotypes for analysis that tallied to 9668 informative meioses generated from 30 loci. Twelve loci typed by at least two laboratories were used to construct a consensus linkage map. The sex-averaged consensus map covered 69.9 cM. All 30 loci were subsequently used to construct a comprehensive map. The sex-averaged comprehensive map was 73.3 cM. Average distance between loci in the comprehensive map was 2.44 cM.

Linkage analysis: Five genotype data sets generated from 44 bovine pedigrees were submitted to the Beltsville Agricultural Research Center, Beltsville, MD, USA in a standardized format for analysis using CRIMAP V. 2.4[3]. Marker genotypes were submitted from the Canadian beef cattle reference herd (http://skyway.usask.ca/~schmutz/), the genome project of the German Cattle Breeders Federation (ADR)[7], the University of Illinois reference/resource families[6], the U.S. Meat Animal Research Center reference population[5] and the Norwegian cattle map

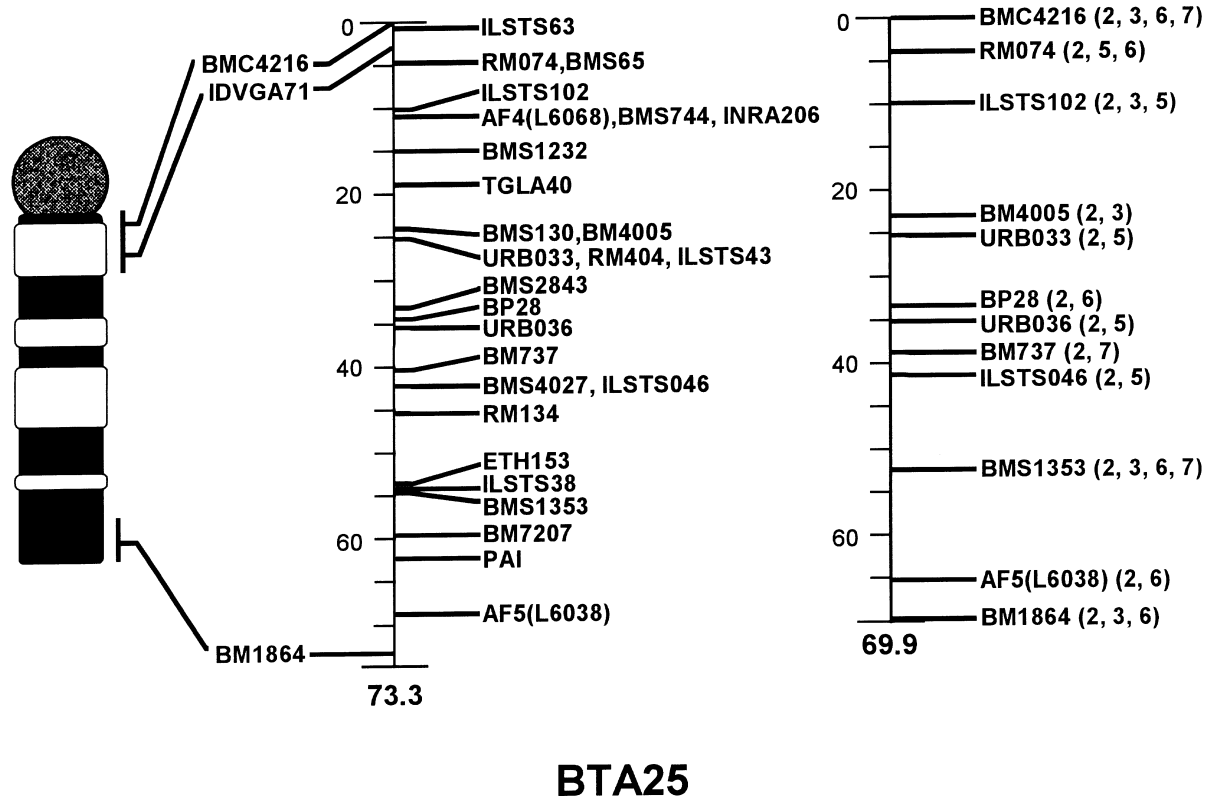

Figure 1 Sex-averaged comprehensive (left) and consensus linkage (right) maps of BTA25 are shown. Physical assignments for markers on the comprehensive map are denoted by line traces to a R-banded idiogram of BTA25. These assignments were either determined by Lopez-Corrales and colleagues (*BM1864*; personal communication) or were reported previously (see http://bos.cvm.tamu.edu/cgi-bin/mapviewer?species = cattle). Laboratories contributing marker genotypes to loci on the consensus linkage map are referenced by location from author address list † = 2, ‡ = 3, etc. Primer sequences and PCR amplification conditions can be found in the USDA-ARS MARC and ARKdb-cattle databases at http://sol.marc.usda.gov/genome/cattle/cattle.html and http://bos.cvm.tam.edu/arkdb/browsers/browser.sh?species = cattle, respectively.

population[9]. The meioses numbers submitted by each laboratory were 627, 2343, 972, 4577 and 1149, respectively. The number of marker loci submitted by each laboratory were 3, 5, 8, 23 and 10, respectively. A total of 9668 informative meioses from 30 microsatellite loci were represented in the combined data containing a total of 15 757 marker genotypes. Each data set was analysed independently using the TWOPOINT, FLIPS and CHROMPIC options. Genotypic data were then combined into a single data set using the MERGE option. The consensus linkage group was constructed using the BUILD option (LOD = 3.0) followed by FLIPS5 analysis to test alternative marker orders. For the comprehensive map, markers were added using the BUILD option (LOD = 1.0) again followed by FLIPS5 analysis. Markers not positioned by this criteria were added to the linkage group using the ALL option. The FLIPS5 was repeated until the best marker order was obtained. Map figures, number of meioses per marker (*.loc files), TWOPOINT and FIXED output files can be accessed at the http://aipl.arsusda.gov/maps.

Consensus map: Twelve markers typed by more than one laboratory were used to produce a sex-average consensus map spanning 69.9 cM (Fig. 1). The female map was 63.8 cM in length and the male map was 71.8 cM (data not shown).

Comprehensive map: Marker genotypes from 30 loci were analysed to produce a comprehensive map of BTA25 (Fig. 1). The length of the sex-averaged was 73.3 cM (Fig. 1), while the female and male maps were 64.0 and 75.4 cM, respectively (Data not shown). The average interval was 2.44 cM, and the largest intermarker interval of 8.4 cM was found between *RM134* and *ETH153*. The order producing the highest log-likelihood is presented.

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Consensus and comprehensive linkage maps of the bovine sex chromosomes

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Introduction: Comprehensive linkage maps have been constructed with the purpose of integrating existing genetic data from several populations[2,3,5,9]. This workshop report, presented under the of auspices of the International Society for Animal Genetics (1998–2000), summarizes construction of consensus and comprehensive linkage maps for the bovine sex chromosomes. Five laboratories contributed genotypes for analysis that totalled to 39 067 informative meioses generated from 92 marker loci. Fourteen loci typed by at least two laboratories were used to construct consensus linkage maps. The consensus map of the bovine X chromosome (BTAX) was 159.3 cM and the map of BTAY was 20.4 cM. The sex-averaged consensus map constructed from the meiotic pairing region between BTAX and BTAY, and denoted as the pseudo-autosomal region (PAR) covered 20.1 cM. The comprehensive maps were constructed using 90 of the 92 loci. The lengths of the BTAX and BTAY maps were 155.8 and 28.8 cM, respectively; while the sex-averaged comprehensive map of the PAR was 25.8 cM. Average distance between loci for BTAX was 1.73 cM.

Linkage analysis: Four genotype data sets generated from 28 bovine pedigrees were submitted to the Beltsville Agricultural Research Center, Beltsville, MD, USA in a standardized format for analysis using CRIMAP V. 2.4[4]. Sex chromosome marker genotypes were submitted from the genome project of the German Cattle Breeders Federation (ADR)[7], the International bovine reference population (IBRP)[1], the US Meat Animal Research Center reference population[6], and the Texas A & M Angleton families[10]. The meioses numbers submitted by each laboratory were 844, 7329, 13 642 and 17 252, respectively. The number of marker loci submitted by each laboratory were 2, 24, 67 and 21, respectively. A total of 39 067 informative meioses from 91 microsatellite loci and one gene-associated polymorphism were represented in the combined