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Consensus and comprehensive linkage maps of bovine chromosome 17

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Introduction: Comprehensive linkage maps have been constructed with the purpose of integrating existing genetic data from several populations[1,2,4,9]. 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 bovine chromosome 17 (BTA17). Six laboratories contributed marker genotypes for analysis that tallied to 19 443 informative meioses generated from 41 marker loci. Eighteen loci were typed by at least two laboratories and 17 of these loci were used to construct a consensus linkage map. The sex-averaged consensus map covered 98.9 cM. All 41 loci were subsequently used to construct a comprehensive map. The sex-averaged comprehensive map was 103.8 cM. Average distance between loci in the comprehensive map was 2.53 cM.

Linkage analysis: Six genotype data sets generated from 58 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/), a Danish Holstein cattle population[7], the genome project of the German Cattle Breeders Federation (ADR)[8], the University of Illinois reference/resource families[6], the US Meat Animal Research Center reference population[5] and the Norwegian cattle map population[10]. The meioses numbers submitted by each laboratory were 859, 1017, 5406, 1983, 8300 and 1878, respectively. The number of marker loci submitted by each laboratory were 5, 5, 9, 12, 34 and 14, respectively. A total of 19 443 informative meioses from 38 microsatellite loci, two gene-associated polymorphisms, and an erythrocyte antigen type were represented in the combined data containing a total of 30 047 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) followed again by FLIPS5 analysis. Markers not positioned by this criteria were added to the linkage group using the ALL option. The FLIPS5 analysis was repeated until the best ordering 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: Sixteen of the 17 microsatellite markers and one erythrocyte antigen marker typed by two or more laboratories were used to produce a sex-average consensus map spanning 98.9 cM (Fig. 1). For the microsatellite marker *URB048*, a map position could not be determined using the criteria established for consensus map construction. This marker is positioned on the comprehensive map. The female map was 110.4 cM in length and the male map was 97.0 cM (data not shown).

Comprehensive map: Marker genotypes from 41 loci were analysed to produce a comprehensive map of BTA17 (Fig. 1). Two markers (*BMS2780* and *BMS2780b*) were haplotyped, because recombination between marker genotypes generated from these two different primer pairs flanking the same microsatellite locus was not detected. The length of the sex-averaged map was 103.8 cM (Fig. 1), while the female and male maps were 109.2 and 102.8 cM, respectively (data not shown). The average marker interval was 2.53 cM, and the largest intermarker interval of 8.7 cM was found between *RM323* and *BM1233*. The order producing the highest log-likelihood is presented.

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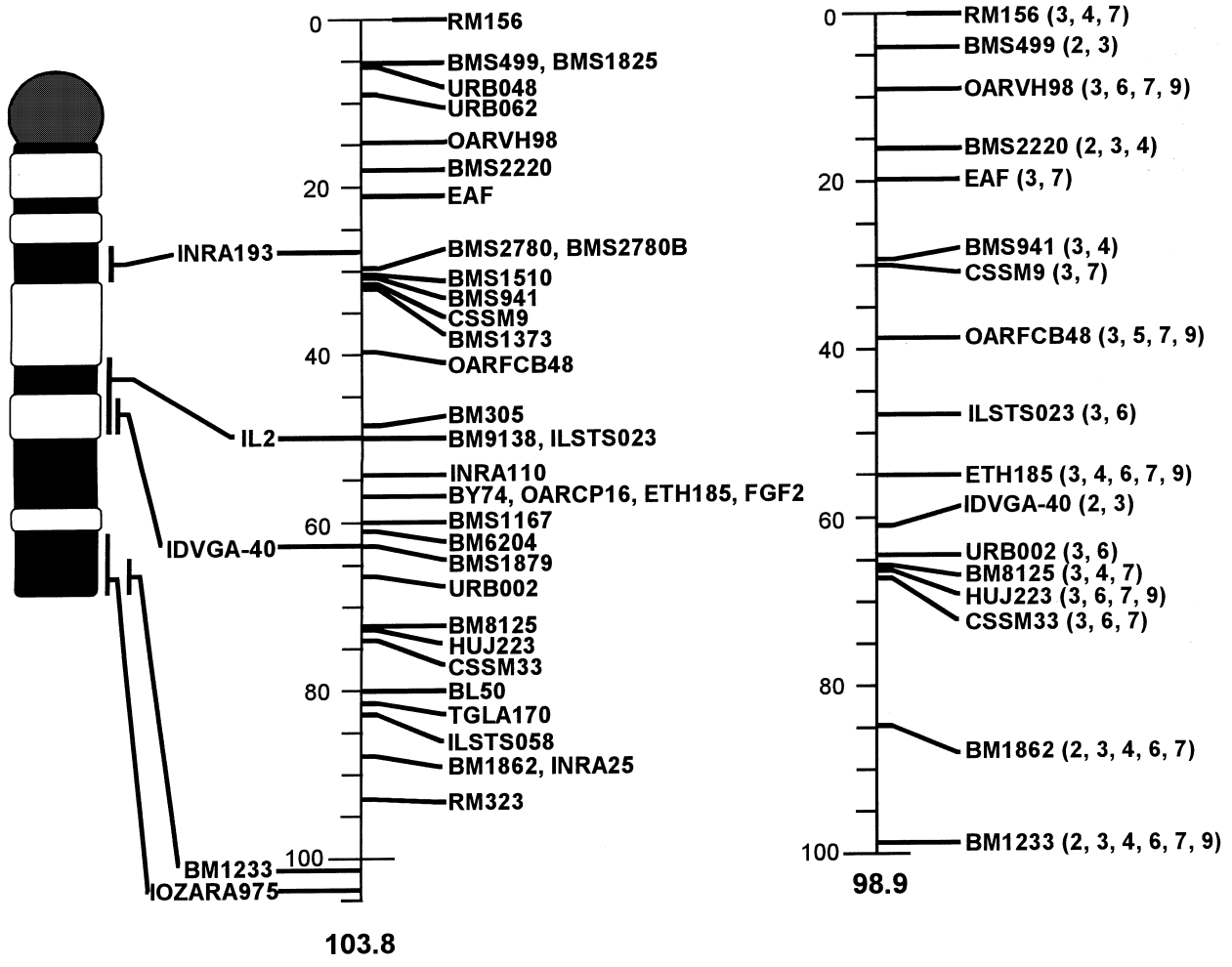

Figure 1 Sex-averaged comprehensive (left) and consensus linkage (right) maps of BTA17 are shown. Physical assignments for markers on the comprehensive map are denoted by line traces to a R-banded idiogram of BTA17. These assignments were either determined by Lopez-Corrales and colleagues (*INRA193* and *BM1223*; 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 (see superscript from author list where 2 = ‡ 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.

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