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

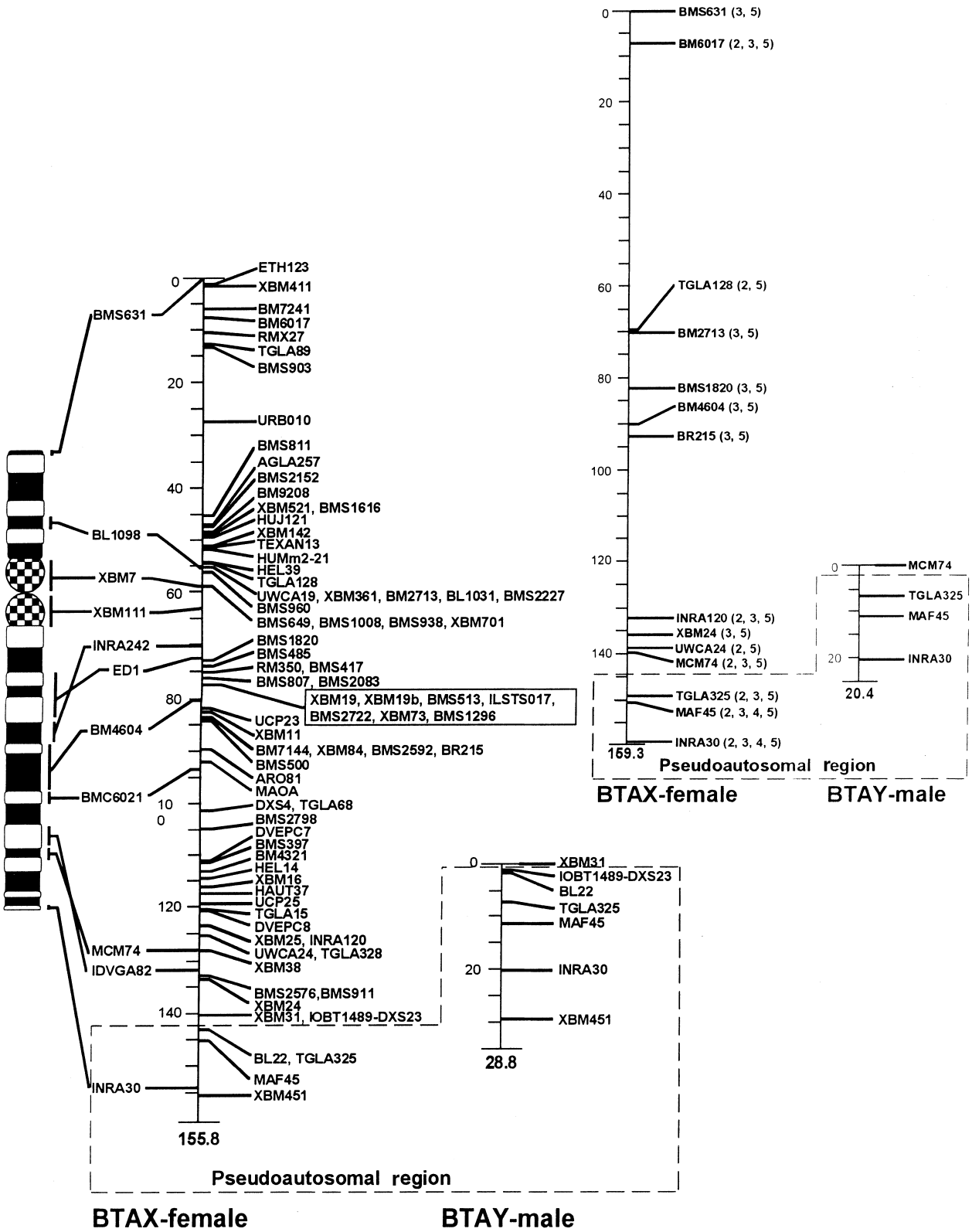
BMS631 (3, 5)
BM6017 (2, 3, 5)
TGLA128 (2, 5)
BM2713 (3, 5)
BMS1820 (3, 5)
BM4604 (3, 5)
BR215 (3, 5)
INRA120 (2, 3, 5)
XBM24 (3, 5)
UWCA24 (2, 5)
MCM74 (2, 3, 5)
TGLA325 (2, 3, 5)
MAF45 (2, 3, 4, 5)
INRA30 (2, 3, 4, 5)
159.3
Pseudoautosomal region
BTAX-female
BTAY-male
MCM74
TGLA325
MAF45
INRA30
20.4
ETH123
XBM411
BM7241
BM6017
RMX27
TGLA89
BMS903
URB010
BMS811
AGLA257
BMS2152
BM9208
XBM521, BMS1616
HUJ121
XBM142
TEXAN13
HUMm2-21
HEL39
TGLA128
UWCA19, XBM361, BM2713, BL1031, BMS2227
BMS960
BMS649, BMS1008, BMS938, XBM701
BMS1820
BMS485
RM350, BMS417
BMS807, BMS2083
XBM19, XBM19b, BMS513, ILSTS017, BMS2722, XBM73, BMS1296
UCP23
XBM11
BM7144, XBM84, BMS2592, BR215
BMS500
ARO81
MAOA
DXS4, TGLA68
BMS2798
DVEPC7
BMS397
BM4321
HEL14
XBM16
HAUT37
UCP25
TGLA15
DVEPC8
XBM25, INRA120
UWCA24, TGLA328
XBM38
BMS2576,BMS911
XBM24
XBM31, IOBT1489-DXS23
BL22, TGLA325
MAF45
XBM451
155.8
Pseudoautosomal region
BTAX-female
BTAY-male
XBM31
IOBT1489-DXS23
BL22
TGLA325
MAF45
INRA30
XBM451
28.8
BMS631
BL1098
XBM7
XBM111
INRA242
ED1
BM4604
BMC6021
MCM74
IDVGA82
INRA30

Figure 1 Comprehensive (left) and consensus linkage (upper right) maps of the bovine sex chromosomes are shown. Physical assignments for markers on the comprehensive map are denoted by line traces to a R-banded idiogram of BTAX. These assignments were either determined by Droegemuller and colleagues (*ED1*; personal communication) or were reported previously[8] (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). Except for *ED1*, all 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.

data containing a total of 32 919 marker genotypes. The number of informative meioses was larger than the number of marker genotypes, because male progeny in some data sets were scored by contributors as being hemizygous without supporting marker genotypes for loci beyond the PAR. Each data set was analysed independently using the TWOPOINT, FLIPS and CHROMPIC options. For the IBRP data set, independent analysis using CRIMAP detected male-specific recombination between markers located well beyond the PAR boundary of BTAY. To correct these aberrant calculations, marker genotypes for male progeny incorrectly scored as homozygotes were revised to a hemizygous state. All genotypic data were then combined into a single data set using the MERGE option. The consensus linkage groups were constructed using the BUILD option (LOD = 3.0) followed by analysis for best alternative orders by FLIPS5. For the comprehensive maps, additional markers were added to the consensus linkage groups using the BUILD option (LOD = 1.0) followed again by FLIPS5 analysis. Markers not positioned by this criteria were added using the ALL option. The FLIPS5 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. The marker genotypes generated for the locus listed as *sex* in these files represent artificial data used to denote the PAR boundary in the IBRP data set. This 'mock' locus was not used in these analyses.

Consensus map: Fourteen markers typed by more than one laboratory were used to produce consensus maps of the bovine sex chromosomes. The map of the BTAX was 159.3 cM in length and the map of BTAY was 20.4 cM (Fig. 1). The sex-averaged consensus map of the PAR was 20.1 cM (data not shown).

Comprehensive map: The analysis to produce a comprehensive map of BTAX included marker genotypes from 90 loci (Fig. 1). Two markers (*XBM19* and *XBM19b*) were haplotyped, because recombination between marker genotypes generated from these two different primer pairs flanking the same microsatellite locus was not detected. The lengths of the BTAX and BTAY linkage maps were 155.8 and 28.8 cM, respectively; while the sex-averaged map of the PAR was 25.8 cM (data not shown). The average interval was 1.73 cM, and the largest intermarker interval of 18.0 cM was found between *URB010* and *BMS811*. The marker order producing the highest log likelihood is presented. Based on this analysis, the PAR boundary of BTAY appears to be located in an estimated 1 cM marker interval between *XBM31* and *IOBT1489–DXS23*.

Markers *DIK090* and *HEL26* were excluded from the comprehensive map because of atypical inflation of the linkage group using either the BUILD or ALL options to position these loci. The *DIK090* was always placed to the centromeric end of the BTAXp, which inflated the BTAX linkage group by over 100 cM and suggested male recombination outside of the defined PAR. Placement of *HEL26* to the telomeric end of BTAXq expanded the BTAY linkage group by over 50 cM. Using TWOPOINT, the closest linkage for each marker was *DIK090* and *XBM19* (female LOD = 9.09 and rec. frac. = 0.04) and *HEL26* and *TGLA325* (female LOD = 12.45 and rec. frac. = 0.03). Recombinants for both markers need to be verified before these markers can be accurately placed on the maps.

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Characterization of equine microsatellite loci, *TKY102–TKY112*

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Source/description: Microsatellites were isolated from horse genomic library as previously described[1].

PCR conditions: The PCR cocktail consist of 10 ng horse genomic DNA, 0.2 μM each primer, 200 nM of each dNTP, 2.5 mM of $MgCl_2$, 1 U of *Taq* polymerase (Perkin-Elmer, Foster, CA, USA) in 20 μl.

Reactions were placed in a pre-heated thermal cycler (GeneAmp System 9600, Perkin-Elmer) and PCR was performed (10 min pre-denaturation at 95 °C; 30 cycles of 30 s at