International system for cytogenetic nomenclature of domestic animals (1989)

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The Second International Conference on Standardization of Domestic Animal Karyotypes

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Historical introduction (P. Popescu)

This year is the 25th anniversary of the discovery of chromosome abnormalities in domestic animals. In 1964 Gustavsson and Rockborn reported in Sweden the first Robertsonian-like translocation in cattle, the 1;29 translocation, and Henrickson and Backstrom discovered the first heterozygous translocation in the pig. These two papers stimulated a renewed interest in livestock cytogenetics.

In the following years, many laboratories were established worldwide for the study of chromosome disorders in domestic animals. Considerable effort was also devoted to the accumulation and application of knowledge of the normal and abnormal chromosomes of livestock.

In the early seventies, the application of banding methods to domestic animal chromosomes produced different systems of cytogenetic nomenclature of the various species that resulted in confusion and indicated a need for standardization. For this reason, a small group of workers convened in Reading in 1976. The objective was to describe the G-band patterns in sufficient detail to permit the identification of individual chromosomes. The system proposed in the report of the Reading Conference was the basis for all subsequent descriptions of chromosome abnormalities and variants in domestic animals.

Since the Reading Conference, several other chromosome banding techniques were developed. The purpose of the Second Conference for Standardization of Domestic Animal Karyotypes was to standardize karyotypes with different banding techniques, which can be used for the description of chromosome abnormalities and for gene mapping.

Objectives

The objectives of this meeting were to update the standard karyotypes of cattle, goat, and sheep established at the first meeting in Reading and also of the improved karyotype recommended by Long (1985) for sheep; to correlate the G-banded and R-banded karyotypes and thereby establish standard karyotypes for R-banded chromosomes; and to establish a system of nomenclature for both band types along with schematic representations.

Cattle (*Bos taurus*)

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The extensive information available on the chromosomes of cattle facilitated general agreement on this species and all the objectives noted above could be achieved.

The G-banded standard karyotype established at the Reading Conference was confirmed and improved with the aid of the results obtained from prometaphase chromosomes. The numbering of the chromosomes follows completely that of the Reading classification. A standard GTG-banded karyotype for cattle is shown in Fig. 1.

Since the Q-staining method was the first one used to produce band patterns on chromosomes (Hansen, 1972), a QFQ-banded karyotype for cattle prometaphase chromosomes is included in this report (Fig. 2).

The results of the sequential GTG-RBA–banding technique applied to chromosomes of the same metaphase, developed by Di Berardino for cattle chromosomes (in preparation) made it possible to establish an unambiguous correlation between G-banded and R-banded chromosomes and to define the standard karyotype for cattle R-banded chromosomes. Figures 3 and 4 present standard RBA- and RBG-banded karyotypes for cattle.

Idiograms were constructed for both G- and R-bands, landmarks and regions were defined, and bands were numbered. As far as possible, landmarks were placed in positive or negative G-bands which constitute a distinct and recognizable element of the chromosome and which subdivide it into approximately equal regions containing at most nine bands.

The numbering of regions and bands is based on the International System for Human Cytogenetic Nomenclature (ISCN, 1985). In some cases, since the number of bands observed was not always the same according to the type of banding used, it was necessary to divide the bands into sub-bands. For example, in the R-band pattern of chromosome 3, the three sub-bands 33.1, 33.2, and 33.3 correspond to band 33 in the G-band pattern.

The idiograms (Fig. 5) were drawn using black and white for all euchromatic bands. Centromeric regions are crosshatched and are numbered p11 and/or q11. Their size is fixed arbitrarily as equal for all autosomes. The first euchromatic band is then numbered p12 or q12.

These schematic representations of chromosomes correspond approximately to 400 bands for either band type (410 G-bands, 404 R-bands).

The G- and R-banded chromosomes of cattle can be described as follows:

Chromosome 1. Four regions. **21 G-bands**: two negative central bands (31 and 33) separated by a positive band (32); a terminal negative band (45); a narrow dark telomere. **21 R-bands**: three prominent positive bands, two central (31 and 33), often joined, and one terminal band (45).

Chromosome 2. Four regions. **20 G-bands**: four positive bands (13, 15, 22, and 24) in the proximal half of the chromosome, 13 and 15 sometimes fused; four positive bands (34, 36, 42, and 44) in the distal half, 42 and 44 being more prominent; a negative telomere. **20 R-bands**: one prominent positive band (21) in the proximal half of the chromosome; three prominent positive bands in the distal half (41, 43, and 45); 43 and 45 often joined.

Chromosome 3. Three regions. **15 G-bands**: a positive subcentromeric band (12), two prominent central positive bands (24 and 32) separated by a large negative band (31). **17 R-bands**: a

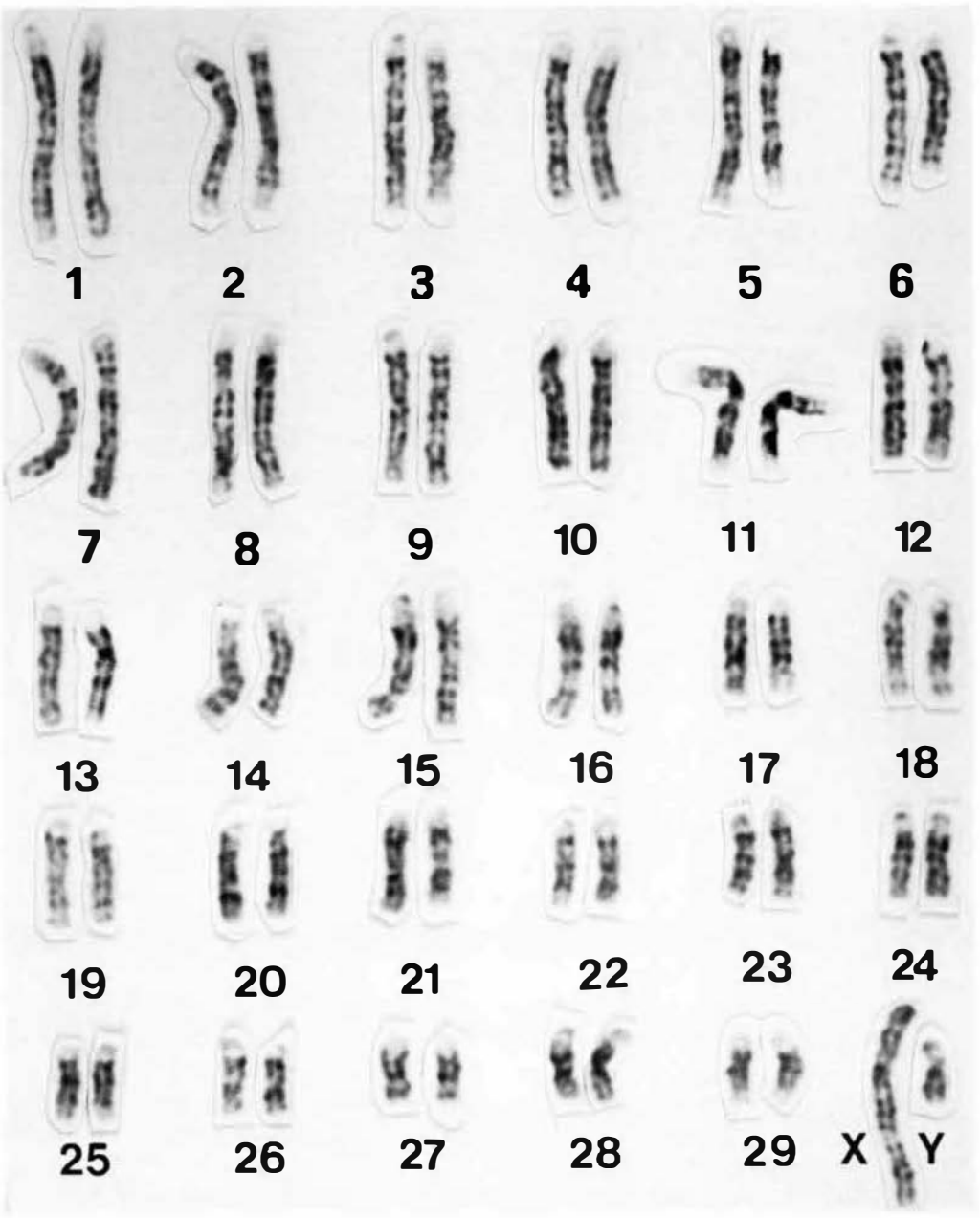


Fig. 1. Standard GTG-banded cattle karyotype. (Courtesy of D. Di Berardino.)

central prominent positive band (31) with two adjacent negative bands, one above (24) and one below (32, which is broader than 24).

Chromosome 4. Three regions. **19 G-bands**; four positive bands (12, 14, 16, and 18) in the proximal half of the chromosome with a large negative band (15) between bands 14 and 16; two prominent positive bands (21 and 31) separated by an additional small positive band (23) in the distal half of the chromosome. **19 R-bands**; a prominent positive band (15) in the proximal half of the chromosome; two negative bands (21 and 31) separated by a group of two positive bands (22 and 24) in the distal half; three positive terminal bands often joined.

Chromosome 5. Three regions. **15 G-bands**; two broad central negative bands (21 and 31) separated by a group of three positive bands (22, 24, and 26) equally distributed; a negative telomere. **15 R-bands**; three prominent positive bands: one proximal (21), one central (31), and one terminal (35), the latter resulting from the fusion of two sub-bands.

Chromosome 6. Three regions. **17 G-bands**; three positive bands (12, 14, and 21) equally distributed in the proximal half of the chromosome; the distal half resembles that of chromosome No. 4 with two positive bands (23 and 31) separated by a small positive band (25). **17 R-bands**; two prominent negative bands (21 and 31) divide the chromosome into three regions; three terminal positive bands close to each other, as in region No. 3 of chromosome No. 4.

Chromosome 7. Two regions. **13 G-bands**; two prominent positive bands: one proximal (21) and one distal (25), the latter broader than the former and containing two or more sub-bands; a negative telomeric band (28) not always visible. **13 R-bands**; one large prox-

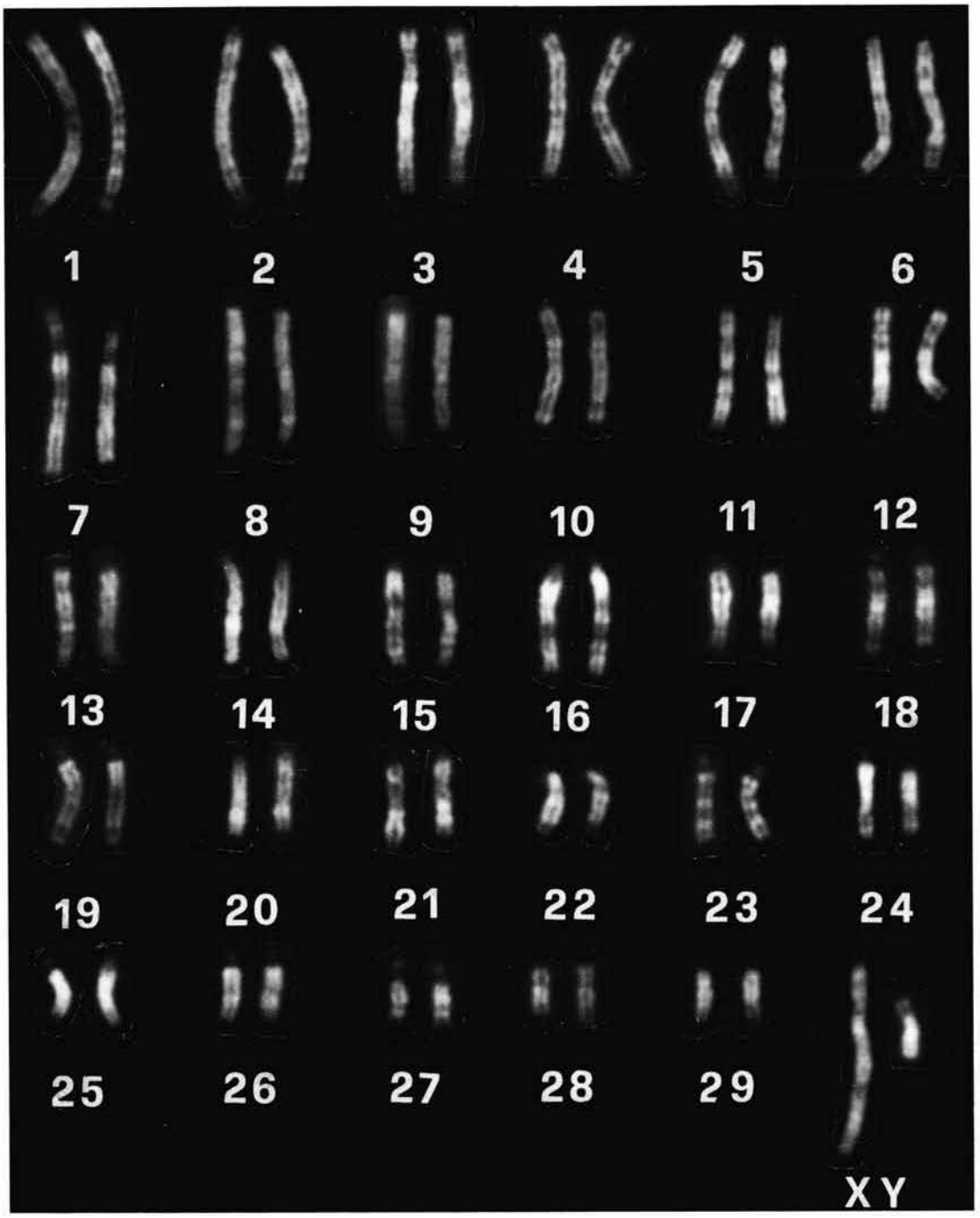


Fig. 2. Standard QFQ-banded cattle karyotype. (Courtesy of D. Di Berardino.)

imal positive band (15), two central prominent positive bands (22 and 24) followed by a large negative band (25), and two small terminal positive bands (26 and 28).

Chromosome 8. Two regions. **16 G-bands**: four positive bands (12, 14, 16, and 18) separated into two groups by a large negative band (15) in the proximal half of the chromosome; a prominent subterminal positive band (26). **16 R-bands**: a cluster of three positive bands (21, 23, and 25) in the distal half of the chromosome followed by a negative band (26) and a subterminal positive band (27); a negative telomere.

Chromosome 9. Two regions. **17 G-bands**; two proximal positive bands (12 and 14), one prominent central positive band (21), and two terminal positive bands (25 and 27). **17 R-bands**; a prominent central positive band (19) followed by a broad negative band (21) and two strong positive bands (24 and 26).

Chromosome 10. Three regions. **17 G-bands**; symmetrical pattern for regions No. 1 and 2: one subcentromeric positive band (12), four positive bands equally distributed (14, 21, 23, and 25); two prominent positive bands (31 and 33), a subterminal small positive band (35) in the distal part of the chromosome; a negative telomere. **19 R-bands**; symmetrical pattern for regions No. 1 and 2; two positive bands (13 and 15) often joined in the proximal half of the chromosome; a prominent subterminal positive band (34); a positive telomere.

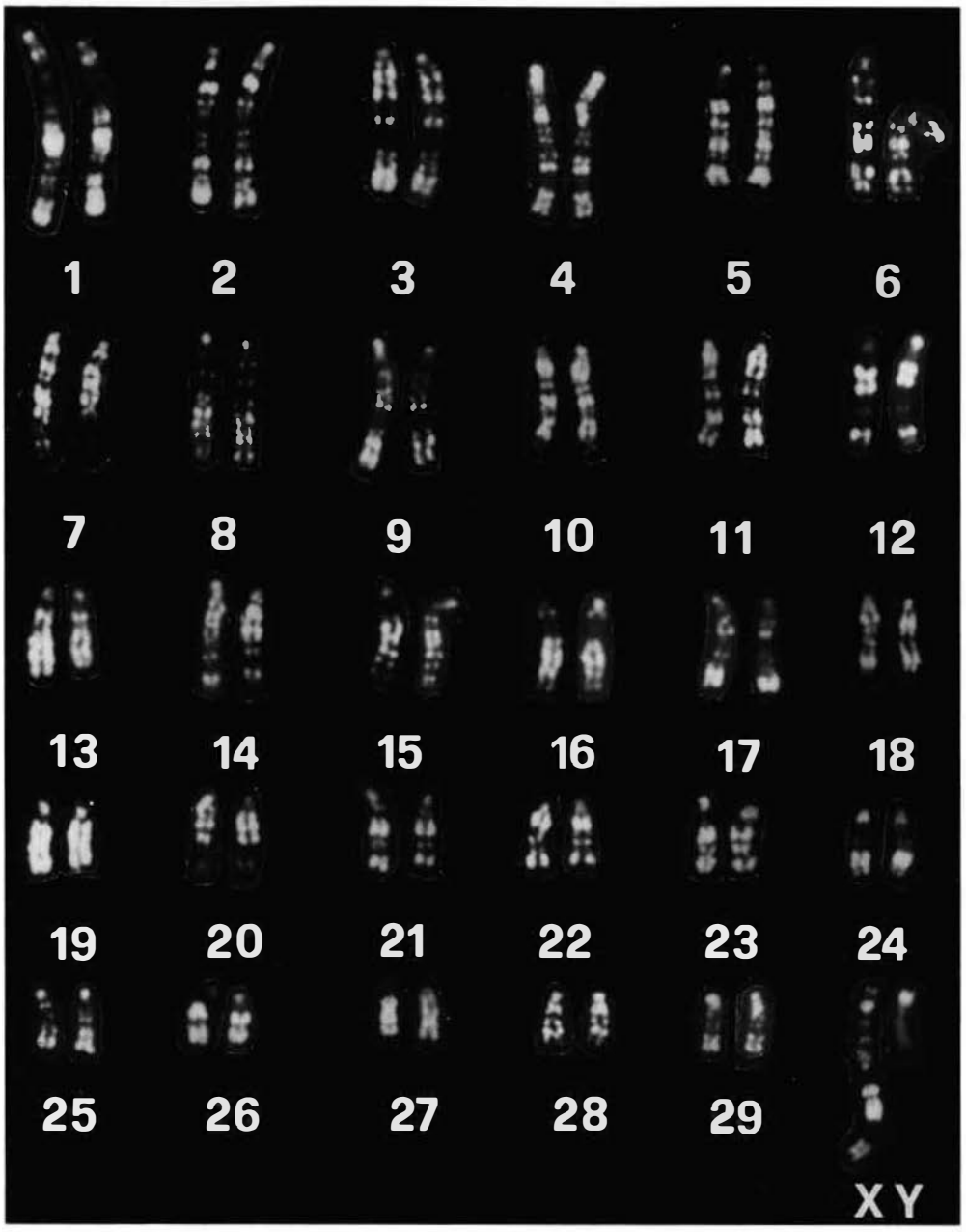


Fig. 3. Standard RBA-banded cattle karyotype. (Courtesy of D. Di Berardino.)

Chromosome 11. Two regions. **14 G-bands**; two prominent central bands (21 and 23); two positive bands (13 and 15) in the proximal part of the chromosome and two other positive bands (25 and 27) in the distal part: a negative telomere. **16 R-bands**; two broad central negative bands (21 and 23) separated by two small positive bands (22.1 and 22.3); threepositive bands (12, 14, and 16)usually joined in the proximal part of the chromosome and two prominent positive bands (24 and 28) in the distal part.

Chromosome 12. Two regions. **11 G-bands**; one prominent subcentromeric band (12) and two prominent positive bands (21 and 23) in the distal half of the chromosome. **11 R-bands**; a negative subcentromeric band (12) followed by two prominent positive bands (13 and 15) usually joined in the proximal half of the chromosome; two large negative bands (21 and 23) separated by a small positive band (22) in the distal half; a positive telomere.

Chromosome 13. Two regions. **11 G-bands**; a prominent subcentromeric positive band (12) followed by two positive bands (14 and 16) in the proximal half of the chromosome; two positive bands (21 and 23) separated by a wide negative band (22) in the distal half; a negative telomere. **11 R-bands**; a large negative subcentromeric band (12) and a strong positive band (13) in the proximal part of the chromosome; a cluster of three strong positive bands (17, 22, and 24) in the distal half.

Chromosome 14. Two regions. **15 G-bands**; four small positive bands (12, 14, 16, and 18) equally distributed in the proximal half of the chromosome; two prominent positive bands (21 and 23) in the distal half. **15 R-bands**; four positive bands (13, 15, 17,and 19)

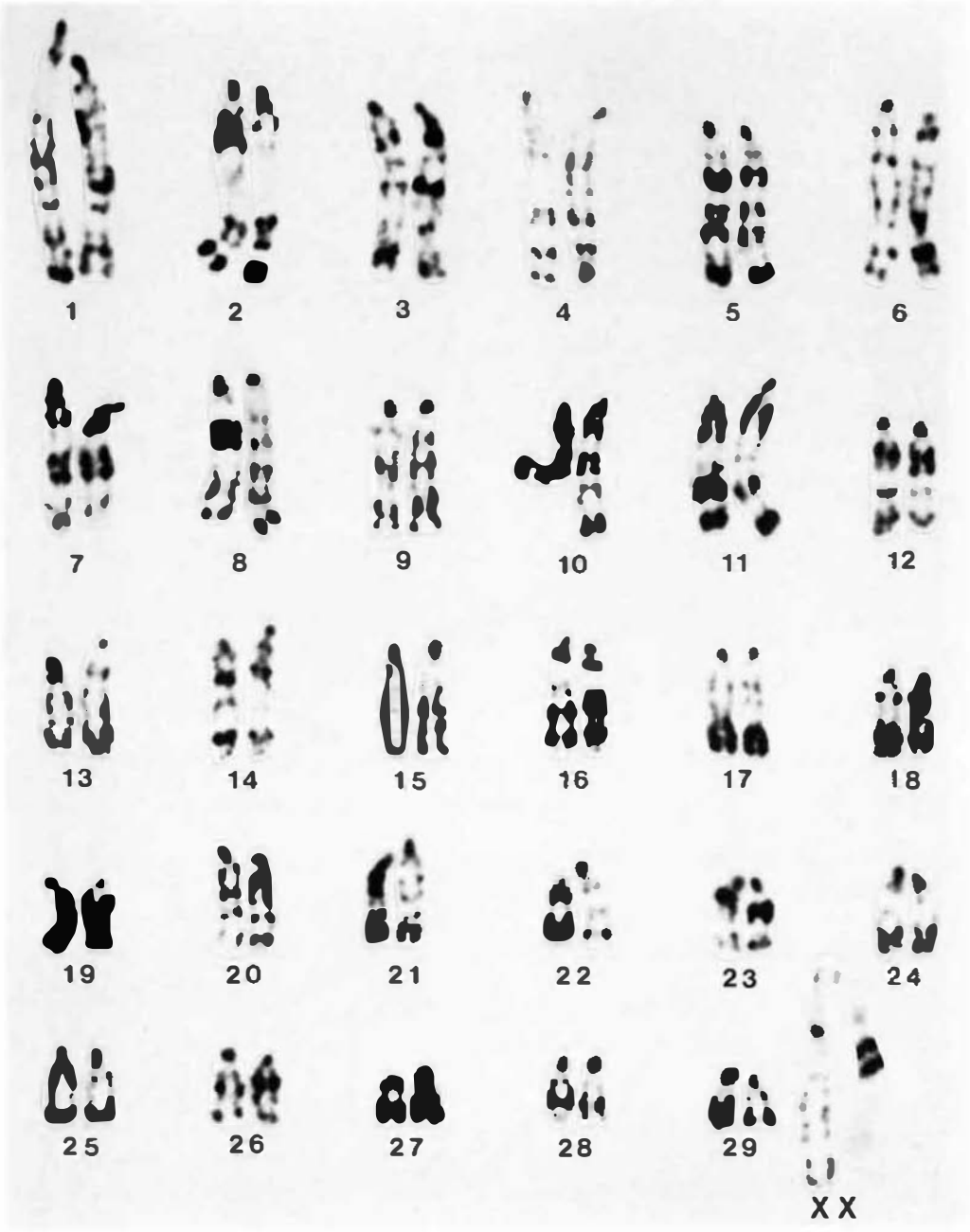


Fig. 4. Standard RBG-banded cattle karyotype. (Courtesy of H. Hayes.)

equally distributed in the proximal half of the chromosome; in the distal half: two large negative bands (21 and 23) separated by a small positive band (22), and a subterminal positive band (24); a positive telomere.

Chromosome 15. Two regions. **13 G-bands**: a prominent subcentromeric positive band (12) and a large negative band (21) in the proximal half of the chromosome; four equally distributed, positive bands (22, 24, 26, and 28) in the distal half; a negative telomere. **13 R-bands**: three positive bands (21, 23 and 25) clustered at the center of the chromosome; two smaller terminal positive bands (27 and 29).

Chromosome 16. Two regions. **12 G-bands**; a subcentromeric negative band (12) and three positive bands (13, 15, and 17) in the proximal half of the chromosome; a broad negative band (21) and two small positive bands (22 and 24) in the distal half; a negative telomere. **12 R-bands**; a subcentromeric positive band (12) followed by two broad negative bands (13 and 15) separated by a small positive band (14); four positive bands (16, 21, 23, and 25) usually clustered in the distal part of the chromosome.

Chromosome 17. Two regions. **11 G-bands**: two prominent central positive bands (21 and 23); a negative telomere. **11 R-bands**; two broad central negative bands (21 and 23) followed by two prominent terminal positive bands (24 and 26), usually joined.

Chromosome 18. Two regions. **11 G-bands**: symmetrical pattern with three central positive bands (14, 21, and 23), a subcentromeric positive band (12) and a subterminal positive band (25); a negative telomere. **11 R-bands**; symmetrical pattern with a prominent proximal positive band (13), two small positive bands

(15 and 22) at the center of the chromosome and a prominent terminal positive band (24); a positive telomere.

Chromosome 19. Two regions. **10 G-bands**; a subcentromeric positive band (12) followed by three small positive bands (14, 16, and 21) equally distributed; a positive telomere. **10 R-bands**; a subcentromeric negative band (12) followed by four broad positive bands (13, 15, 17, and 22) usually joined, thus giving the impression of one broad positive region.

Chromosome 20. Two regions. **11 G-bands**; a subcentromeric positive band (12) and two positive bands (14 and 16) in the proximal half of the chromosome; a prominent positive band (21) in the distal half is the main identifying feature of this chromosome; a negative telomere. **11 R-bands**; a subcentromeric negative band (12) and three positive bands (13, 15, and 17) usually clustered in the proximal part of the chromosome; a broad negative band (21) followed by two minor terminal positive bands (22 and 24) are the main identifying features of this chromosome.

Chromosome 21. Two regions. **11 G-bands**; two subcentromeric positive bands (12 and 14) close to each other, followed by two negative bands (15 and 17) separated by a small positive band (16) in the proximal part of the chromosome; two prominent positive bands (21 and 23) in the distal part; a negative telomere. **11 R-bands**; two subcentromeric negative bands (12 and 14) separated by a minor positive band (13) followed by two positive bands (15 and 17) usually joined into one broad band in the proximal half of the chromosome; two wide negative bands (21 and 23) separated by a small positive band (22) and a prominent terminal positive band (24) in the distal half.

Chromosome 22. Two regions. **9 G-bands**; similar to chromosome No. 23; a small subcentromeric positive band (12) followed by a broad negative band (13) separated into two sub-bands (13.1 and 13.3) by a minor positive sub-band (13.2); two positive bands; one central (21) and one subterminal (23); a negative telomere. **7 R-bands**; a small subcentromeric negative band (12) followed by a broad positive band (13); two central negative bands (21 and 23) separated by a small positive band (22); a broad positive telomere.

Chromosome 23. Two regions. **10 G-bands**; similar to chromosome No. 22; a prominent subcentromeric positive band (12) followed by two negative bands (13 and 15) separated by a small positive band (14); two strong positive bands: one central (21) and one distal (23); a positive telomere. **10 R-bands**; a prominent subcentromeric negative band (12) followed by two positive bands (13 and 15) often joined into one broad band; a central positive band (22) close to band 15; a prominent subterminal positive band (24); the central negative band (21) is less pronounced than the distal negative band (23); a negative telomere is usually not visible.

Chromosome 24. Two regions. **12 G-bands**; a subcentromeric negative band (12) followed by two positive bands (13.1 and 13.3) often joined; a central positive band (22); two small positive bands (24 and 26); a negative telomere. **10 R-bands**; a subcentromeric positive band (12) followed by a wide negative band (13); a small central positive band (21); two prominent positive bands (23 and 25) often joined in the distal half of the chromosome; a positive telomere.

Chromosome 25. Two regions. **9 G-bands**; a subcentromeric positive band (12) followed by two central positive bands (14 and 21) often joined; a small positive band (23) in the distal half of the chromosome; a negative telomere. **9 R-bands**; a subcentromeric negative band (12) followed by two small positive bands (13 and 15) in the proximal half of the chromosome; two prominent, usually joined, positive bands (22 and 24) in the distal half, with 24 broader than 22.

Table 1. Similarities between G-banding patterns of sheep and cattle chromosomes confirmed by the Jouy-en-Josas Conference

Sheep chromosomes numbered according to the recommendation of Long (1985)	Equivalent cattle chromosomes numbered according to the Reading recommendation
1	1 and 3
2	2 and 8
3	5 and 11
4	4
5	7
6	6
7	10
10	12
11	19
12	16
13	13
14	18
15	15
16	20
17	17
18	21
19[a]	23[a]
20[a]	22[a]
22	26
23	24
24	29

[a] For sheep chromosomes 19 and 20, the equivalent cattle chromosomes are different from those listed in the Reading proceedings because, in those proceedings, the descriptions of these two chromosomes were reversed as compared to the photographs.

Chromosome 26. Two regions. **7 G-bands**; two prominent positive bands: one subcentromeric (12) and one distal (22); negative telomere. **7 R-bands**; a wide subcentromeric negative band and two prominent positive bands (21 and 23) separated by a negative band (22).

Chromosome 27. Two regions. **10 G-bands**; a subcentromeric negative band (12.1) followed by three positive bands (12.2, 13, and 21) joined in more contracted preparations; a broad terminal negative band (22) and a subtelomeric positive band (23); a negative telomere. **8 R-bands**; a pronounced subcentromeric positive band (12) followed by three positive bands (14, 22, and 24) which tend to be joined in more contracted preparations.

Chromosome 28. One region. **9 G-bands**; a subcentromeric positive band (12), two prominent central positive bands (14 and 16); a small subtelomeric positive band (18). **9 R-bands**; three positive bands: one proximal (13), one central (15) and one prominent subterminal (17); a positive telomere.

Chromosome 29. One region. **9 G-bands**; two proximal positive bands (12 and 14) often joined; a central positive band (16); a small subterminal positive band (18); a negative telomere **9 R-bands**; two small positive bands (13 and 15) in the proximal half of the

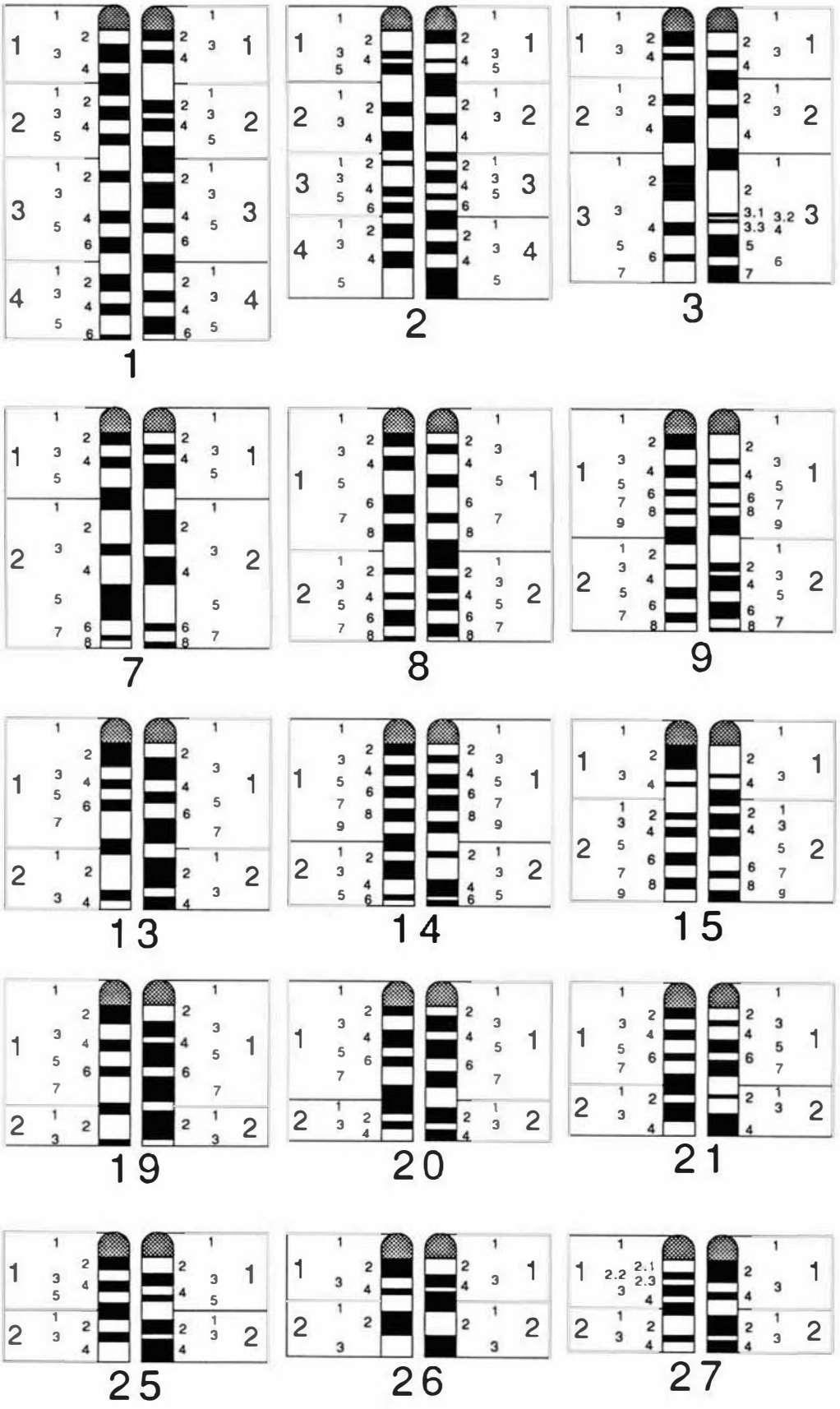
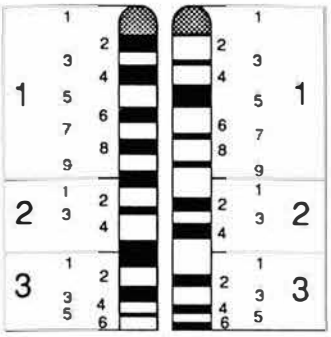


Fig. 5. Diagrammatic representation of G-bands (left) and R-bands (right) of cattle chromosomes.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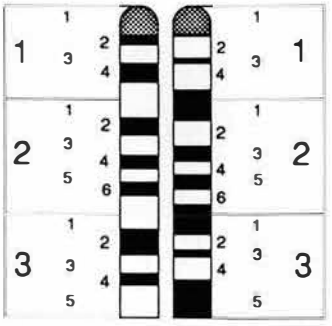
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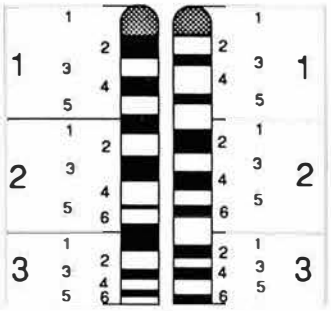
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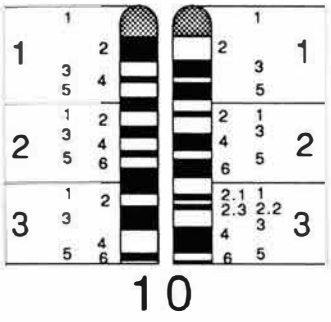
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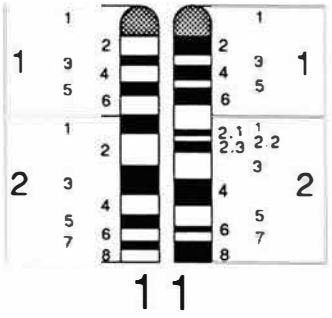
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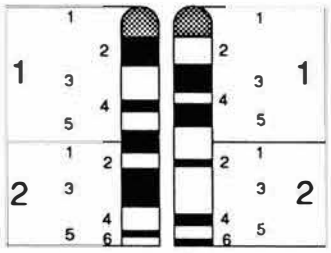
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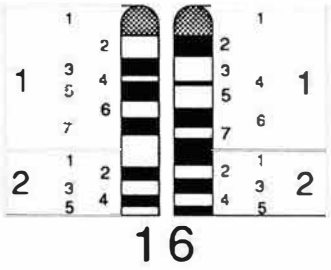
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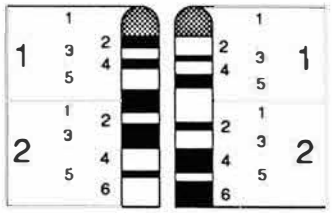
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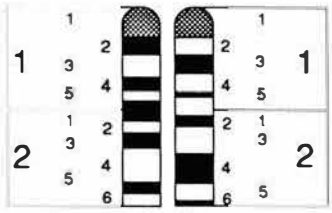
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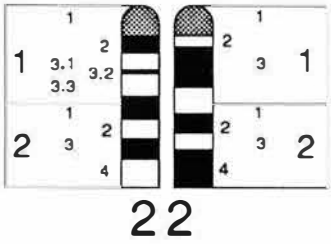
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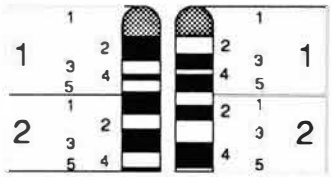
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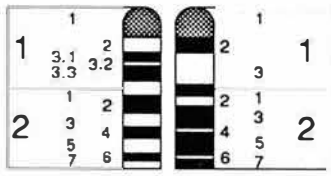
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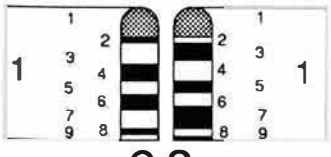
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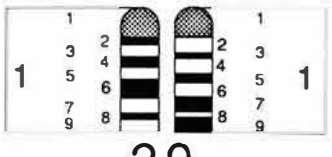
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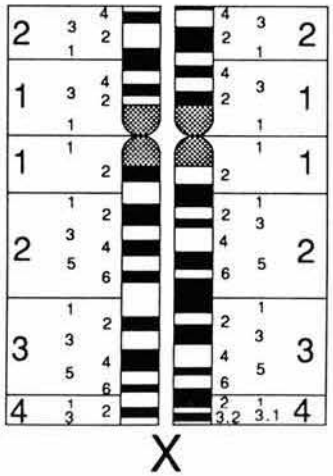
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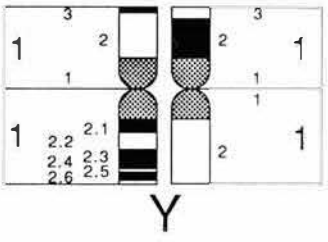
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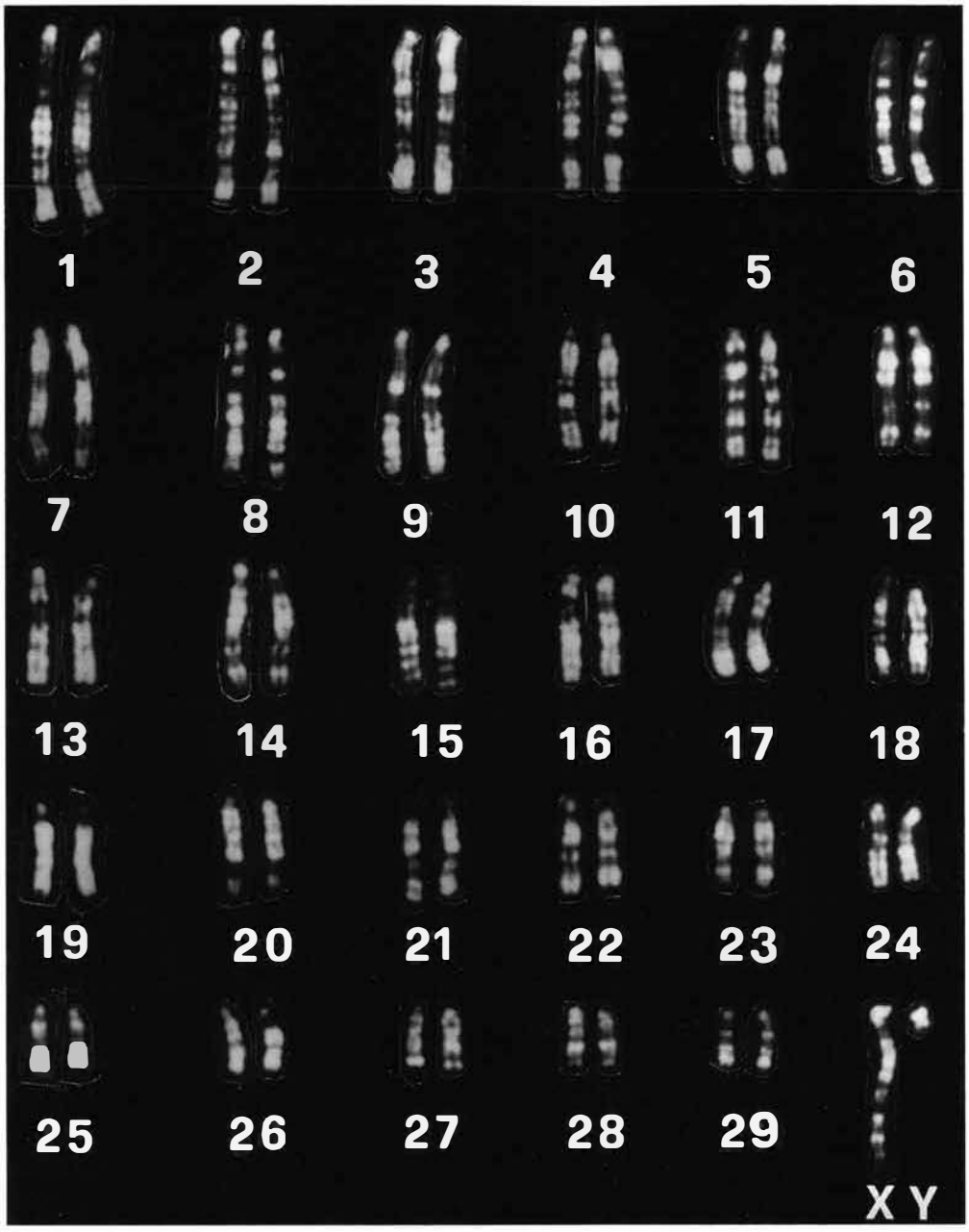

Fig. 6. Standard RBA-banded goat karyotype. (Courtesy of D. Di Berardino and of Journal of Heredity 78:225–230, 1987; copyright 1987 by the American Genetics Association.)

chromosome and two positive bands (17 and 19) of the same size and usually joined in more contracted preparations in the distal half.

Chromosome Xp. Two regions. **8 G-bands**; a central positive band (21) followed by a negative band (22) and a small subtelomeric positive band (23); a negative telomere. **8 R-bands**; a distal positive band (22); a small subtelomeric negative band (23); a positive telomere.

Chromosome Xq. Four regions. **17 G-bands**; a central broad negative band (31); four positive bands (12, 22, 24, and 26) in the proximal half of Xq and four positive bands (32, 34, 36, and 42) in the distal half of Xq; a negative telomere. **18 R-bands**; a cluster of three positive bands (25, 31, and 33) at the center of Xq; a large negative band (24) above this cluster and two negative bands (34 and 36) separated by a small positive band (35) below this cluster; two terminal positive bands (41 and 43.1) often joined; a negative telomere.

Chromosome Yp. One region. **3 G-bands**; entirely negative with a positive telomere. **3 R-bands**; entirely positive with a negative telomere not always visible.

Chromosome Yq. One region. **7 G-bands**; three positive bands (12.1, 12.3, 12.5), with 12.3 being more pronounced. **No R-bands**; R banding reveals an entirely pale Yq.

Goat and Sheep

For these two species less information was available as a basis for establishing the standards than for cattle, particularly for the G-bands, which limited the conclusions.

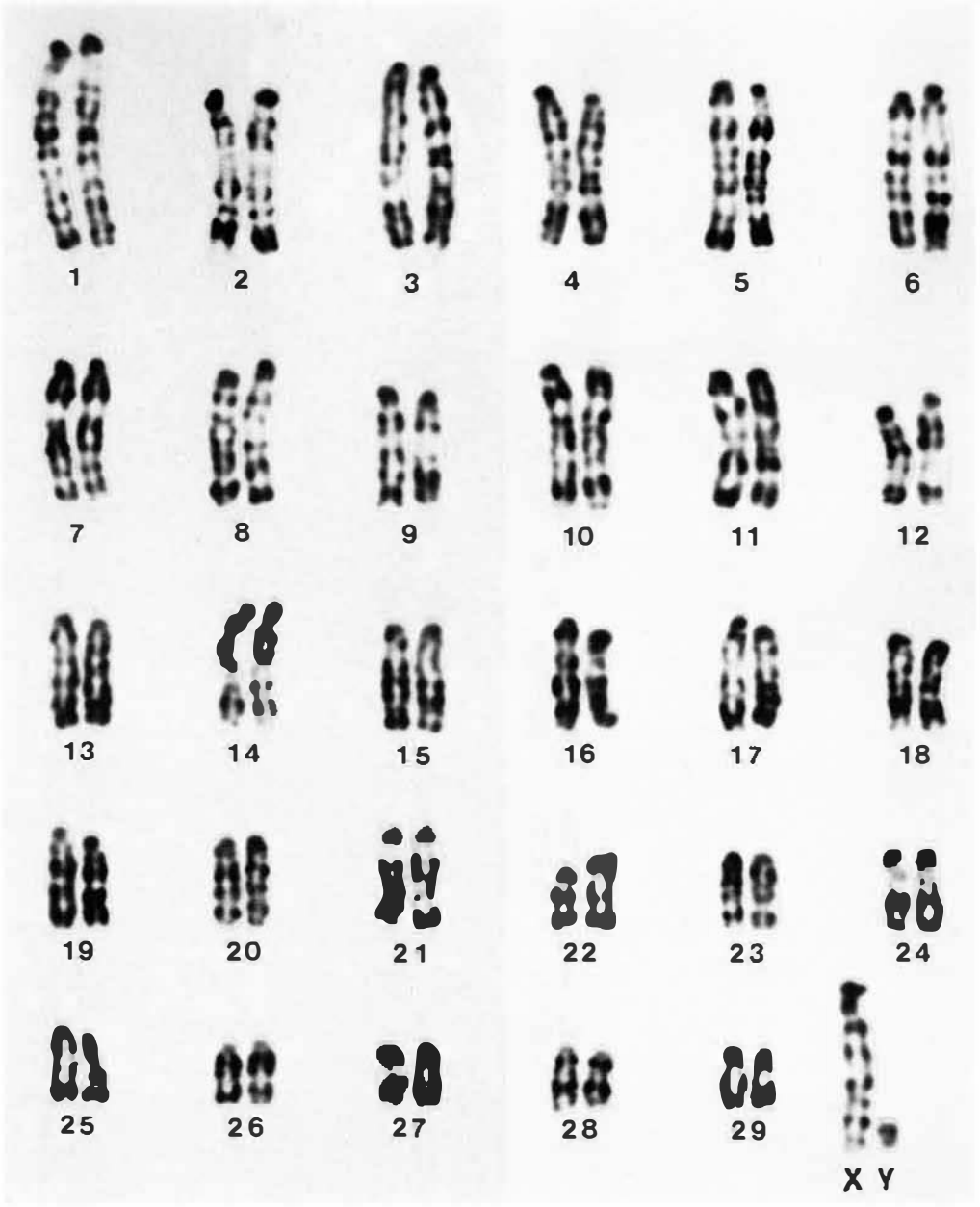

Fig. 7. Standard RBG-banded goat karyotype. (Courtesy of H. Hayes.)

Goat (*Capra hircus*)

Coordinator: H. Hayes

Contributors: H. Hayes, D. Di Berardino; M.B. Lioi, D. Matassino, R. Hediger, H.R. Jung, and G. Stranzinger

Examinations of the G-band patterns of goat and cattle chromosomes led to the same conclusion as that reached at Reading, i.e., that G-banded cattle and goat chromosomes resemble each other closely with the exception of chromosomes 9, the X, and the Y. However, since insufficient information was available for the goat, it was agreed to not present a new GTG-banded karyotype and to not make schematic representations.

Comparison of the R-band patterns (RBA and RBG) of goat and cattle chromosomes confirmed their similarity except for chromosomes 9, the X, and the Y. A precise description of the differences between the band patterns of goat and cattle chromosomes 9 could not be agreed upon.

The extensive similarity between the karyotypes of goat and cattle made it possible to establish a standard karyotype for R-banded goat chromosomes which follows exactly the classification and the numbering of R-banded cattle chromosomes based, as discussed above, on the Reading standard. It was decided to adopt the landmarks established for cattle chromosomes for the R-banded goat chromosomes.

Figures 6 and 7 present standard RBA- and RBG-banded karyotypes, respectively, for the goat.

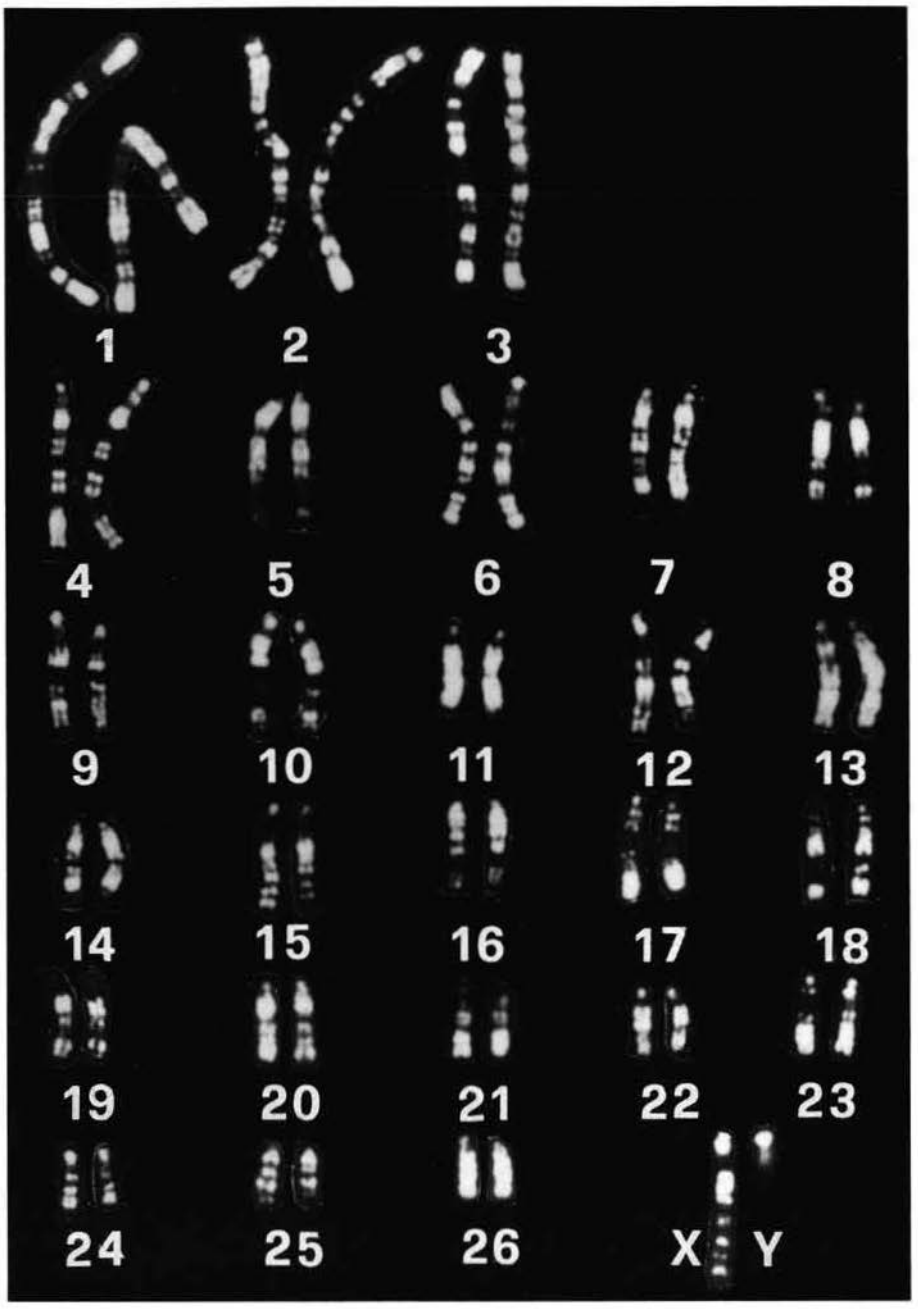

Fig. 8. Standard RBA-banded sheep karyotype. (Courtesy of D. Di Berardino.)

Sheep (*Ovis aries*)

Coordinator: S. Long

Contributors: S. Long, H. Hayes, D. Di Berardino, M.B. Lioi, D. Matassino, R. Hediger, H.R. Jung and G. Stranzinger

As was noted, a karyotype system was recommended for sheep by Long (1985) after the Reading Conference. Since some confusion arose because in the proceedings of the Reading Conference the descriptions of G-banded chromosomes and the corresponding photographs were interchanged in the case of sheep chromosomes 8 and 9, as well as 19 and 20, it was decided to use only the karyotype of Long (1985), as a basis for the one presented here. As was outlined in the Reading Conference proceedings, many similarities exist between the G-band patterns of sheep and cattle chromosomes which were confirmed during the discussions at the Jouy-en-Josas Conference for the chromosomes listed in Table 1.

The relationship is less clear for sheep chromosomes 8, 9, 21, 25, and 26 because of the limited amount of information available for sheep G-banded chromosomes.

Because the amount of information on the karyotype of the sheep is still limited, it was decided to not present a scheme for this species. Instead, it is suggested that the G-band system recommended by Long (1985) be used until further results are obtained. On the other hand, comparison of R-banded karyotypes of sheep and cattle showed that the patterns of these two species are very

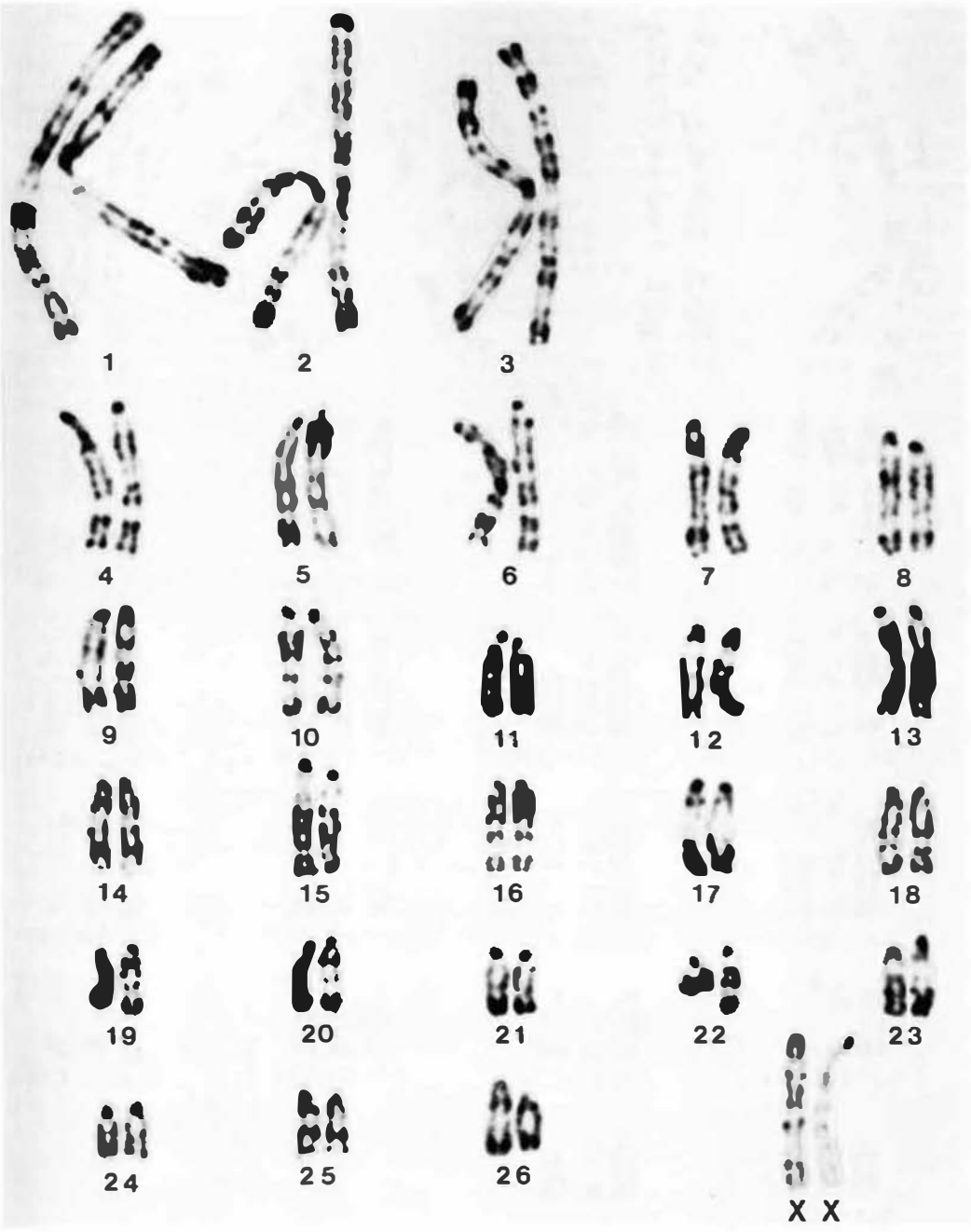

Fig. 9. Standard RBG-banded sheep karyotype. (Courtesy of H. Hayes.)

similar and that each sheep chromosome was similar to one or two cattle chromosomes, depending on whether it is metacentric or not, except for the sex chromosomes.

As for cattle and goat, this relationship has been independently confirmed by two laboratories using two R-banding methods (RBA and RBG).

The same diff observed between cattle and goat chromosomes 9 was found between cattle and sheep chromosomes 9. However, since there is a good correlation between the G-band patterns of cattle and sheep and the R-band patterns of cattle and sheep, it is possible by inference to correlate G- and R-band patterns in sheep and to establish and standard R-banded karyotype for sheep. Figures 8 and 9 represent such RBA- and RBG-banded karyotypes, respectively.

Comparison of R-band patterns of cattle, goat, and sheep

The comparison of the karyotypes of the three main Bovidae species confirmed the extensive similarity of their euchromatin. This is illustrated by the photographic montage combining RBG-banded chromosomes of cattle, goat, and sheep in Fig. 10. As was indicated in the Reading proceedings (1980), this provides further evidence for a close evolutionary relationship between these three species, but may not imply genetic homology.

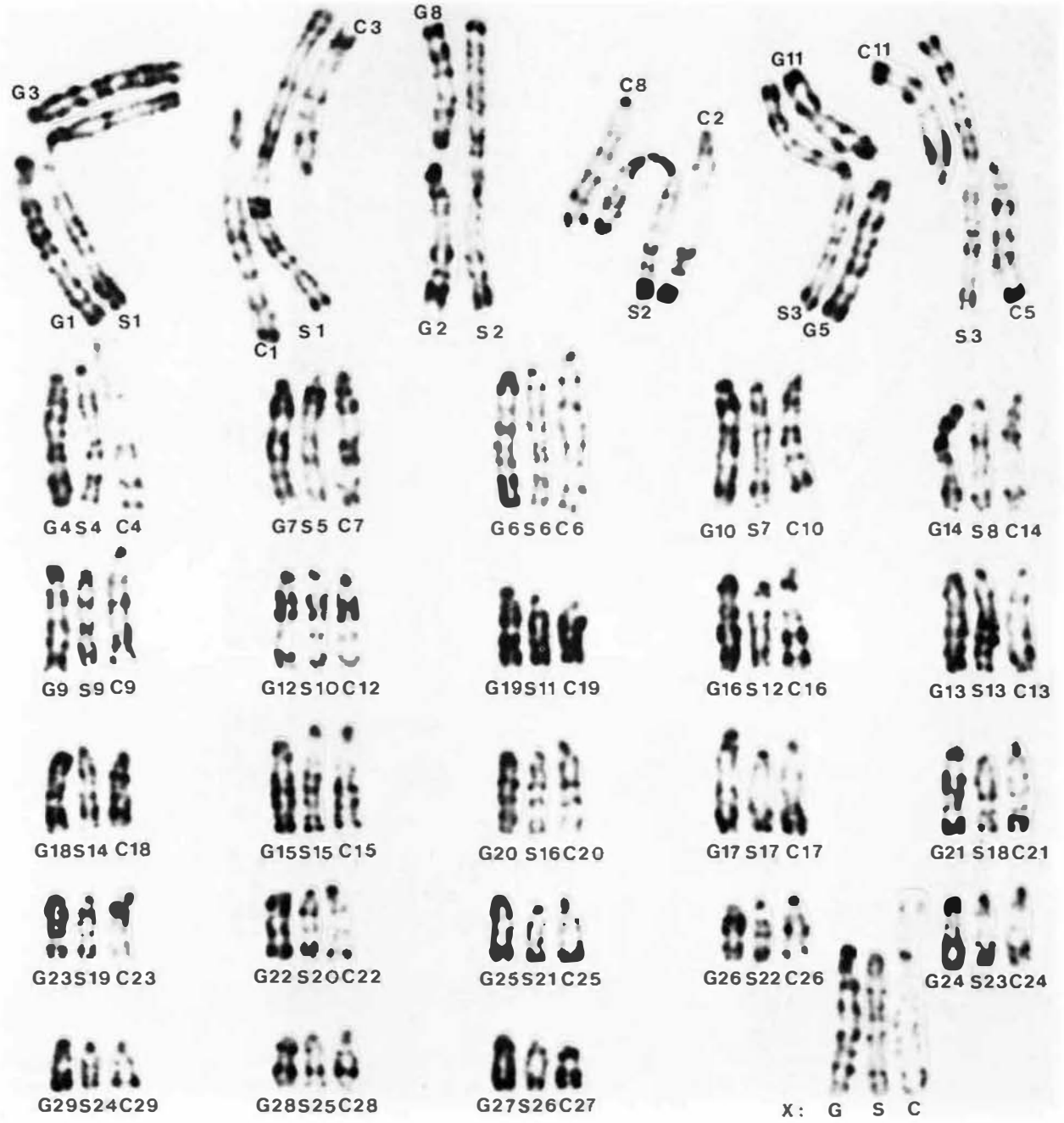

Fig. 10. Combined haploid karyotype of RBG-banded chromosomes of goat (G), sheep (S), and cattle (C) from left to right. (Courtesy of H. Hayes.)

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