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RECENT RESULTS IN CATTLE CYTOGENETICS — A REVIEW

Introduction

When it was recognized that the chromosomes are the vehicles in which genes reside, animal geneticists and practical animal breeders started chromosome observations in agricultural animals. Animal cytogenetics proposes new opportunities for genetic control in animal breeding and selection of breeding animals. It is a valuable tool for finding out genetic disorders which may influence reproduction and so contribute to more economical production of animal products for human consumption. In animal breeding cytogenetics ought to be one part of veterinary practice.

Cytogenetic studies are important not only in applied animal breeding, but they give us theoretical knowledge about chromosome structure, chromosome aberrations, chromosomal polymorphism, karyotype evolution, etc.

Cattle karyotype and cytogenetic methods

About cattle cytogenetics we have been able to speak only during the last ten-fifteen years; still, H. Krallinger got his first results in this field in 1927, when he determined the chromosome number in cattle. In 1957 Y. Melander first investigated the cattle karyotype from tissue culture (Gustavsson, 1977).

The G-banding karyotype. It was not until 1960, however, that techniques became available to enable accurate and detailed observations of mammalian and bird chromosomes. By far the most commonly used method is the Giemsa banding. Actually we cannot speak about a single method but about several techniques that all give the Giemsa banding pattern of chromosomes (Dev, Tantravahi, 1982). Several descriptions of G-banded cattle karyotype have been published during the last fifteen years (Evans et al., 1973; Seth, Kunze, 1974; Исследование . . . , 1976; Lin et al., 1977). The opinions vary considerably and it became desirable, for comparative purposes, that some form of standardization should be formulated. In August 1976 in Reading, England, an international conference was organized with the objective of standardization for the banded karyotypes of domestic animals, including cattle (Ford et al., 1980). Each chromosome pair was described according to its G-banding pattern. The cattle chromosomes were arranged in order of decreasing length and the chromosome pairs were numbered from 1 to 29 and supplied with a description of the X and Y chromosomes. It was stated that all the 29 pairs of autosomes are acrocentric, the X-chromosome submetacentric and the Y-chromosome metacentric according to their morphological types. As all cattle autosomes are acrocentric and the G-banding pattern is variable, it is not easy to identify all the 60 chromosomes. Still, with densitometric and television analysis, it is reported that as many as 25 chromosome pairs

can be identified (Еропова et al., 1985). So, cattle chromosome identification seems to be one of the most complicated points in cattle cytogenetics, but on the other hand, it should be an essential step in carrying out other cytogenetic investigations in cattle. As regards chromosomes, almost no markers are available in cattle yet; however, finding genetic markers is one of the major goals in animal breeding research. I. Krutzler et al. (1986) proposed cattle chromosome identification, using the Giemsa banding combined with centromeric region evaluation. The centromeric heterochromatin pattern permits to characterize each individual and is practicable and reliable for both chromosome identification and detection of size polymorphism in the heterochromatin regions. For example, there are especially large centromeric blocks on chromosomes 1, 2, and 15.

The development of high-resolution banding techniques has a considerable impact on cytogenetics. The using of methotrexate-thymidine synchronization or other agents known to inhibit DNA synthesis (ethidium bromide, acridine orange) enables to increase mitotic yield and obtain elongated chromosomes with increased band number (Yoshida et al., 1983; Maciulis et al., 1984; Romagnano, Richer, 1984; Ikeuchi, 1984; Drouin, Richer, 1985; Morris, Fitzgerald, 1985). Good results are obtained with adding BudR at the mid S-phase of the cell cycle. BUdR substitutes thymin and causes selective despiralization of AT-rich chromatin, which results in elongated metaphase chromosomes with increased band number (Rønne, Thust, 1983; Musilová et al., 1983).

Chromosome studies could be more precise if two or more different techniques are used to obtain a complementary banding pattern; in cattle chromosome research Q- and R-banding is practicable.

The Q-banding karyotype. Staining method involves using the quinacrine mustard or other AT-specific fluorochromes (DAPI, Hoechst 33258) and special Giemsa staining. Several authors describe the Q-banded karyotype of cattle (Hansen, 1971, 1972; Schnedl, 1972; Gustavsson et al., 1976). Brightly fluorescencing Q-bands correspond to positive G-bands in G-banding technique. Both positive G-bands and Q-bands are connected with AT-rich DNA segments (Burkholder, 1981). These regions contain genetically relatively inert heterochromatic regions, the "silent" DNA. There is evidence that in these regions fewer genes are located than in interband (R-band) regions (Родионов, 1985). J. R. Korenberg et al. (1978) have mentioned that trisomy or even monosomy of some bright Q-blocks do not influence phenotype significantly, whereas interband anomalies may be connected with severe phenotypic disorders. In cattle, data concerning phenotypic disorders and Q-bands are not available, only chromosome length variants in the Q-band karyotype are mentioned (Hansen, 1972).

The R-banding karyotype. The R-banding pattern is useful as it stains genetically active GC-rich DNA. These regions are more often altered in individuals with phenotypic abnormalities. R-band method stains darkly the chromosomal tips that are known to be the sites of many anomalies such as translocations and deletions (Romagnano, Richer, 1984; Drouin, Richer, 1985; Родионов, 1985). Several authors have described the R-banded karyotype of cattle (Popescu at al., 1982; Di Berardino, Ianuzzi, 1982). Up to now, there is still only one report of high-resolution RBA-bands in cattle when late BUdR incorporation and synchronization with thymidine or methotrexate was used. In that work the authors report that, when compared with the standard G-banded idiogram of cattle showing 310 bands, the increase in the number of bands achieved by R-banded prometaphase chromosomes is nearly 70% (Di Berardino et al., 1985). The final "standard" R-banded karyotype of cattle has not yet been established.

Constituitive heterochromatin (the C-bands)

The location and the amount of constituitive heterochromation can be visualized with the help of the C-banding method. In cattle it is located mainly pericentromerically (Hansen, 1973). Differently from many other mammalian species the autosomic centric regions in cattle remain faintly stained or unstained with the G-banding technique. Many questions regarding knowledge about the basic biochemical nature of the bovine pericentromeric heterochromatin are yet open (Krutzler et al., 1986). There are data about centromeric region variability in cattle (Hansen, 1973; Moraes et al., 1979), but chromosomal polymorphism has been investigated only in a few chromosome pairs because of chromosome identification being rather complicated. J. C. F. Moraes et al. (1979) studied the constituitive heterochromatin of chromosome pair 1 with densitometric methods, and showed C-band size polymorphism both between homologues and individuals. It is suggested that similar polymorphism is present in other cattle chromosomes as well. As mentioned before, J. Krutzler et al. (1986) showed that C-banding is suitable for the establishing of centromeric markers in cattle. According to those authors, centromeric heteromorphism is striking in chromosomes 4, 8, 17, and 23.

Data concerning other species give information that the amount of pericentromeric heterochromatin could be connected with adaptive mechanisms in extremal environmental conditions. For this reason the investigation of C-bands of cattle from different ecological zones is worthwhile (Яковлев, 1985). Information about C-band polymorphism may provide valuable help in tracing certain chromosomes in controlled crossing programs. An especially important application will be the assignment of gene expression to one or other partner homologue, and heterochromatin polymorphism data will provide a new impetus for the accomplishment of genetic linkage- and trait marker research in cattle breeding (Krutzler et al., 1986).

Y-chromosome variants

The total length of the Y-chromosome and its centromeric index has been investigated in many different cattle breeds (Halnan, Watson, 1982; Eldridge et al., 1983; Смирнов et al., 1985). The total length of the Y-chromosome is different in different breeds. On the whole, in cattle karyotype it is placed between chromosomes 22 and 26. It is found that the biggest Y-chromosome is in Charolais and Simmenthal bulls and the smallest in Romagnola bulls (Halnan, Watson, 1982). The centromeric index of the Y-chromosome is also v ariable. For example, in the Holstein, Brown Swiss and Guernsey breeds the Y-chromosome is typically submetacentric, in the Jersey breed metacentric (Eldridge et al., 1983). So it is supposed that in specific cases the Y-chromosome is sufficiently distinctive to be used as a reference for the determination of disputed paternity by the breed.

Evidently a positive correlation exists between the Y-chromosome length and sperm production, which fact may have important applications in animal breeding (Смирнов et al., 1985).

Nucleolus organizing regions (NOR)

In the cattle karyotype the cistrons coding for 18S and 28S ribosomal RNA are located terminally and do not correspond to secondary con-

strictions (Henderson, Bruère, 1979; Di Berardino et al., 1981). Which concrete chromosomes do appear as the NOR-chromosomes is not absolutely clear as the results differ. So it has been suggested that the NOR-chromosomes are the 2., 3., 4., 5. and 28. chromosome (Henderson, Bruère, 1979), or the 2., 3., 4., 11. and 29. chromosome (Di Berardino et al., 1981) or the 2., 3., 4., 11. and 28. chromosome (Киселева, Амосова, 1985). This discrepancy may be due to some identification error, but, on the other hand, polymorphism may actually exist in the chromosomal location of NORs between different cattle breeds. Scanty information is available, but if such polymorphism really exists, it could be used as a gene marker for distinguishing different breeds (Prakash, Balakrishnan, 1983). It is evident that the maximal number of Ag-positive NORs (the NORs which have been transcriptionally active during the previous interphase (Mikelsaar, Schwarzacher, 1978)) in cattle karyotype is 10. Cattle is reported to have quite high modal number of active NORs — 6—8 per metaphase (Henderson, Bruère, 1979).

There is a different quantitative distribution of NOR activities. This variation is found to be breed dependent (Mayr, Schleger, 1983). In the activity of rRNA genes there appears functional polymorphism not only between different breeds but also between individuals, tissues, cells, and chromosomes. For example, the 28. chromosome is reported to have quite a stable high NOR activity (Киселева, Амосова, 1985). Data about connections of NOR activity and phenotypic traits in cattle are not available.

Cytogenetic research of generative cells

Together with the involvement of superovulation, the *in vitro* fertilization, the cultivation of oocytes *in vitro*, a great number of cytogenetic investigations have been carried out.

Comparing the maturation of oocytes in follicles and in *in vitro* culture, it was concluded that in follicles the maturation takes more time but it involves less chromosome abnormalities than in *in vitro* culture (Ковалев et al., 1985). In *in vitro* cultured oocytes there increases the number of structural rearrangements (breakages, fragments, bridges, fusion) of chromosomes, there appear hyperploid cells, hyperploid cells with chromosome structure disorders, multiple polar bodies (Koenig et al., 1983; Ковалев et al., 1985).

In cytogenetic analysis of bovine zygotes produced after superovulation, the frequency of chromosome abnormalities is usually increased (King et al., 1985).

For cytogenetic analysis of breeding bulls the material is generally obtained from somatic cells. Generative cells could give more information as there are known specific meiotic disorders (conjugation disruption) which also influence fertility. Up to now, for these purposes the castration or biopsy of testes was used. A new perspective method for obtaining chromosome preparations from ejaculation fluid cells has been proposed (Кузнецова et al., 1985). The quality of chromosome preparations enables estimating of structural rearrangements, synaptic disorders and, what is especially important, this method can be used in mass cytogenetic investigations and without hurting the animal.

Cattle gene mapping

Relatively little is known about cattle gene mapping (Heuertz, Hors-Cayla, 1981; Womack et al., 1983; Womack, 1985; Bunch, Maciulis, 1985).

Bovine-hamster somatic cell hybrids show a loss of bovine chromosomes. Therefore it is possible to establish correlations between the different markers and to infer that some markers are syntenic, i. e. localized on the same chromosome. There have been established three syntenic groups (8 enzymes) corresponding to three autosomes and nine other independently segregating enzymes which are probably located on nine other autosomes. One syntenic group (4 enzymes) is found in the X-chromosome (Heuertz, Hors-Cayla, 1981). J. E. Womack (1985) has analyzed cattle chromosomes for 28 enzyme loci, which segregate into 21 independent syntenic groups comprised of one to four gene loci. In these works no exact chromosomal location is mentioned. By fusing bovine B-lymphocytes with a nonsecretor murine hybridoma cell line it was established that cattle chromosome 3 may be responsible for immunoglobulin synthesis (Bunch, Maciulis, 1985).

Today, 21 of the cattle 30 chromosome pairs are identified with biochemical markers, although specific assignments of syntenic groups to chromosomes have not yet been made (Womack, 1985; Womack et al., 1983). This map, though incomplete, represents a potentially valuable tool for the improvement of animal health and productivity.

Cattle chromosome disorders

Generally we may divide chromosome aberrations into two large groups — numerical aberrations and structural aberrations.

Chromosome anomalies giving considerable phenotypic effects become eliminated very quickly from the cattle population due to their pathological effects. The small deviations in phenotypic effects means that there are great risks for extensive distribution of such polymorphic systems. Thus, it is necessary to keep the cytogenetic situation under control by continuous checking of breeding animals (Gustavsson, 1977).

I. Johannson stressed the importance of chromosome aberrations in reproductive performance first in 1960. Since reproductive performance is one of the most important characteristics of domestic animals and is very sensitive to disturbances of the hereditary material, it has become the most decisive factor in relation to chromosome aberrations (Gustavsson, 1980).

NUMERICAL ABERRATIONS

Euploid heteroploidy. Numerical aberrations can occur both in somatic and generative cells during their maturation division. Euploid heteroploidy may appear after endoreduplication, fusion of cells, and in meiosis due to different segregational events (Gustavsson, 1980).

Pure euploid heteroploidy has never been observed in cattle born alive. Pure tetraploidy has been observed in cattle embryos only (Gustavsson, 1980). Otherwise, partial polyploidy is often observed in cattle lymphocytes, but the concentration of polyploids may vary in large ranges.

In normal cattle about 4—10 per cent of blood or bone marrow cells are polyploid. In preleukotic and leukotic animals the number of polyploid cells may be 4—8 times higher. In addition, very high ploidy is detected in leukosis (8n and higher) (Яковлев, 1985; Яковлев, Качура, 1986).

A. Herzog et al. (1977) are convinced that polyploidy represents a symptom of lability of cells in performing the mitotic processes in culture. E. Weinhold, in 1970, first estimated blood cells and tumour cells

polyploidy and aneuploidy as a fundamental characteristic of mitosis disturbances in cases of tumour and leukaemia (Weinhold, 1970; Herzog et al., 1977).

In cattle there are data about negative correlation of higher number of polyploidy and aneuploidy with milk production, fertility and modal insemination index (Жигачев et al., 1985*a*).

Aneuploid heteroploidy and mosaicism. Aneuploid heteroploidy is caused by nondisjunction of single chromosomes at cell division. This may occur in meiosis as well as in mitosis, and the resulting primary products are trisomy ($2n+1$) and monosomy ($2n-1$). On the whole, mosaics survive more easily than pure aneuploids. Compared to autosomal aneuploidy, postnatal occurrence of sex chromosome aneuploidy appears more common (Gustavsson, 1980).

Monosomy is lethal in prenatal stages.

Involving gonosome aneuploidy three concrete cases of X-trisomy karyotype are known in cattle. XXX syndrome was demonstrated in German Simmenthal cattle in 1970, in Norwegian Red cattle in 1976, and in Holstein breed in 1981. Generally the cattle with XXX syndrome may be characterized with retarded development and small ovaries. In the first case also kyphoses of the lumbar region were noted (Herzog et al., 1977; Gustavsson, 1980; Weber, Shoffner, 1981). Some Soviet investigators report that XXX carriers may be phenotypically normal with normal fertility (Яковлев, Качура, 1986).

One XXY case is reported to be connected with testicular hypoplasia (Herzog et al., 1977). According to A. F. Yakovlev (Яковлев, 1985) the XXY carriers would be eliminated in early stages, which may be connected with disturbances in growth and development.

On the other hand, gonosomal trisomy is demonstrated in several mosaic variants. Diploid/triploid mosaicism is formed when a single ovum fertilized by two spermatozoa to form a triploid zygote fuses with a non-extruded polar body fertilized by a third spermatozoa to form a diploid zygote. Another origin of this mosaicism is fertilization of the first polar body which is diploid and the concomitant fusion with a diploid zygote (Gustavsson, 1980).

Genetically different cell populations may be originated in developmental processes due to somatic mutation, somatic recombination or chromosomal non-disjunction (Teinberg, 1983).

Diploidy/triploidy admixture was described in 1970 and in 1973 in a bovine true hermaphrodite. The XXY gonosomal complement of this mosaic caused the masculinization of the gonads and disturbances of differentiation of the sinus urogenitalis (Herzog et al., 1977; Gustavsson, 1980).

Negative effect in XXY/XY, XXY/XX/XY and XXY/XY/XO karyotypes is testicular hypoplasia. A. F. Yakovlev, V. S. Kachura and J. Gustavsson have noted also sterility, developmental and growth disorders (Gustavsson, 1980; Яковлев, Качура, 1986).

XY/XYY mosaicism was first investigated in Bulgarian Brown cattle, but no negative effect has been observed (Popescu, 1977*a*). In 1981 two cases were reported in Japan. Japanese Black bull mosaic XY/XYY had a normal male conformation and no physical abnormalities. Another mosaic carrier in Holstein-Friesian breed had left scrotum in a state of hypoplasia (Hanada, Muramatsu, 1981; Miyake et al., 1981).

One numerical abnormality (60, XY/61, XY+F) was observed in the Norman breed. The C-band analysis indicated the clear heterochromatic nature of the extra fragment. This fact, associated with the presence of a normal lineage, could explain the normal phenotype of the animal (Moraes et al., 1980).

The complement XO has been reported in sterile female cattle (Fechheimer, 1979).

Up to now trisomy 18 and trisomy 23 have been found of cattle autosomal aneuploidies.

Trisomy 18 syndrome is known as the "lethal brachygnathia trisomy syndrome". This aneuploidy has gained a broader distribution, particularly in the German Simmenthal. Trisomy 18 syndrome is associated with several types of congenital malformations. A number of patients are trisomy 18 mosaics 60, XX/61, XX, 18+ (Herzog et al., 1977).

Trisomy 23 is characterized with very small growth (Яковлев, Качура, 1986).

As mentioned before, a higher number of aneuploidy cells occur in preleukosis. In normal Friesian breed 0—5% of white blood cells may be aneuploids (Бакай, Перчихин, 1985).

XX/XY mosaicism and chimerism. One more kind of mosaicism is a XX/XY mosaicism that has been first observed in true hermaphrodites in 1968. Further, the so-called autonomous XX/XY syndrome of cattle was described in 1975. Autonomous XX/XY syndrome was detected both in singleborn animals and in isosexual twins. Partially, XX/XY carriers are absolutely normal, another part of them exhibits more or less severe disturbances of differentiation of sexual organs within wide limits of variation (Herzog et al., 1977; Gustavsson, 1980).

Cytogenetically XX/XY mosaicism is similar to chimerism. While mosaicism is derived from a single zygotic karyotype, chimerism is derived from two or more karyotypes. XX/XY chimerism can originate from the intrauterine fusion of the chorions and the development of vascular anastomoses between heterosexual siblings. Approximately 92% of female calves born as co-twins with male calves, become sterile (Gustavsson, 1980). Such females are unsuitable for breeding and have subnormal weight-gain efficiency compared to males (Stranzinger et al., 1981). X-Y antigen, specified by a gene in the Y-chromosome, is responsible for testicular-like transformation of the freemartin gonad (Dunn et al., 1979).

XX/XY bulls may be normal or deviated in several kinds. Some of them are sterile or with reduced fertility, others have poor semen quality. Some XX/XY bulls are reported to have sired a marked excess of daughters (Popescu, 1977*a*; Dunn et al., 1979; Ford, Evans, 1977; Gustavsson, 1980; Stranzinger et al., 1981).

Chimerism has been described in several breeds.

Structural aberrations. As to structural aberrations in cattle, the translocations are widely spread and have therefore been more thoroughly investigated.

Translocation means the transference of a chromosome segment from its normal position to a position in a different chromosome.

The most common form is the centric fusion or the Robertsonian translocation, which means the association of two one-armed chromosomes to form a bi-armed chromosome (Gustavsson, 1980).

The most frequent type of the Robertsonian translocation in cattle is the 1/29 translocation (1/29t), which occurs in several different breeds throughout the world. The interest towards 1/29t since the 60s was associated with its property of reducing fertility. The first description of 1/29t originated from the Swedish Red and White cattle breed in 1964 and was followed in 1966 with an investigation of the general dairy cattle population of Sweden. It is not known whether the occurrence of the 1/29t in different geographical areas and breeds is due to recurrent mutation or distribution of an ancient mutation (Gustavsson, 1979).

With the help of the C-banding method it has been found that the translocation chromosome has only one block of pericentric chromatin. The same constitution is demonstrated for most breeds of the *Bos taurus*

subspecies. On this basis, many investigators have concluded that this translocation must have originated from common ancestor. It has been proposed that 1/29t originates from Central Europe beef cattle, because in beef breeds the 1/29t is more common than in dairy cattle, and, for example, in American Hereford and Holstein-Friesian breeds there is almost a complete absence of the 1/29t (Gustavsson, 1979; Pinheiro et al., 1981).

On the other hand, one *de novo* 1/29t carrier was detected in the Holstein-Friesian breed cow which was imported form Sweden to the Soviet Union. According to Swedish researchers, exported animals were free from 1/29t. A. I. Zhigatcheff et al. (Жигачев et al., 1985*в*) investigated 70 animals at such a farm and a neighbouring farm but did not find any more 1/29t carriers. Also, her sires' daughters had no centric fusion.

The translocation carrier's chromosome number may be 59 in the heterozygote and 58 in the homozygote condition, but even in homozygous condition there is no apparent damage to carriers (Pinheiro et al., 1979; Pinheiro et al., 1981).

Since the founding of 1/29t influence to fertility and service period, a program was adopted to eliminate all carrier bulls (Pinheiro et al., 1981; Maurer, Vogt, 1985). But sometimes this kind of influence can not be detected either in carrier cattle nor in their offspring (Herzog et al., 1977; Zahner et al., 1979).

In meiosis of heterozygous 1/29t carriers the centric fusion translocation and its homologues may form heterotrivalent. Due to its orientation at anaphase different segregational products may be noted (Logue, 1977; Gustavsson, 1980).

C. P. Popescu (1978) compared sister chromatid exchanges in normal cattle with a 1/29t carrier, but in the latter case exchange frequency was not higher than expected.

On the whole, 1/29t has been described in roughly 30 different breeds, particularly in the European ones. There is a lot of data about the spreading of 1/29t in Europe (Gustavsson, 1979; Яковлев, 1985). According to A. F. Yakovlev (Яковлев, 1985), a very high frequency of 1/29 centric fusion (10% and higher) is observed in Romagnola breed, Aquitane blond, Montbeliard breed, Red and White and Simmenthal breed.

So far little attention has been given to non-European breeds. 1/29t was found in Siamese cattle in Thailand; in Brown Atlas in Morocco; in Kuri cattle in Chad; in Baoulé cattle and in crosses between N'Dama and Zebu in Ivory Coast (Gustavsson, 1979); in Pitangueiras breed (crosses between 5/8 Red Poll and 3/8 Zebu) in Brazil (Pinheiro et al., 1981); in South African cattle in the following indigenous breeds: Nguni, Malawi Zebu and Pedi cattle and in Brahman breed (Nel et al., 1985); in Lebedinski breed and Sitchewski breed in the Soviet Union (Черкасов, 1985; Жигачев et al., 1985*б*; Качура et al., 1985); in Japanese Black breed (Hanada et al., 1981).

According to literature, 24 several centric-fusion types have been found. At that, the autosomes which certainly do not take part in Robertsonian type translocations are chromosomes 10, 17, 19 and 26 (Popescu, 1977*b*; Яковлев, 1985).

Most of the Robertsonian translocations in cattle are monocentric, but also three dicentric translocations have been found. These are the 3/4t in Limousine breed, 5/15 (6/16)t in Dexter cow (Popescu, 1977*b*), and the 7/21t in Japanese Black breed (Hanada et al., 1981).

Two cases of double heterozygotes have been detected — one in Italy in a female of the Podolian type cattle with 1/29t and 14/24t, another in Japan in Japanese Black cattle breed with 1/29t and 7/21t (Di Berardino et al., 1979; Hanada et al., 1981).

The majority of the Robertsonian translocation cases are distributed in normal animals. In a single case 25/27 centric fusion in Alpine Grey bulls was partially connected with bad semen quality and insufficient ejaculation (Popescu, 1977*b*; De Giovanni et al., 1979).

In addition to economic importance, the Robertsonian rearrangements present a certain interest due to their theoretical aspect as a mechanism in *Bovidae* karyotype evolution (Moraes et al., 1980; Качура et al., 1985).

The classical form of translocation is a reciprocal translocation, which means the exchange of terminal segments between nonhomologue chromosomes. One spontaneous translocation in cattle was probably concerned with the X and one autosome, causing a considerable lowering of fertility (Gustavsson, 1980).

In addition to the above-mentioned translocations, tandem fusion and insertion are detected in cattle. Tandem fusion results from a transfer of a whole chromosome arm after one break in the vicinity of the centromere in one chromosome and another break close to the chromosome end in a second chromosome. A tandem fusion was observed in Danish Red cattle breed and this aberration was associated with lowered fertility (Gustavsson, 1980). Insertion results from the transference of an intercalary segment to another position in a different chromosome. Insertion was found in the Charolais cattle presenting familial recurrences (Moraes et al., 1980).

Several breaks and gaps may also take part in cases of deletion and inversion. Deletion is a single-break chromosome aberration resulting in the loss of a chromosome section. One single case of deletion in cattle was observed in 1972; it caused lowered fertility and testicular hypoplasia in bulls (Gustavsson, 1980). Inversion means the 180° reversal of a chromosome segment. One pericentric inversion was found in the Norman breed. It involved chromosome 14 and caused lower fertility of the carrier (Moraes et al., 1980; Gustavsson, 1980).

Typical autosomal defects were found in 1971 in parakeratotic patients in the Holstein-Friesian breed carrying chromatid and isochromatid breaks and different types of autosomal associations (quadri- and triradial figures), gaps, dicentric and acentric chromosomes. Autosomal breaks in three calves with hereditary nanism were observed in 1976 (Herzog et al., 1977).

Conclusions

On the whole, cattle karyotype investigation has a considerable theoretical as well as economic importance. There are still technical problems in identifying individual bovine chromosomes and chromosome segments. Perhaps fragile sites as a new type of chromosomal markers will help to solve this problem (Смирнов, 1985). Investigating homologues chromosome exchange may furnish interesting data on nucleus organization at interphase (Popescu, 1978).

It is supposed that 10% of cattle zygotes are with chromosome anomalies. Causes which bring embryonic mortality are still indistinct (Яковлев, Качура, 1986).

A great number of scientific works in this field gives evidence of marked interest in cytogenetics of domestic animals. In this country the first All-Union conference of cytogenetics of agricultural animals took place in 1985.

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ÜLEVAADE UURIMISTULEMUSTEST VEISE TSÜTOGENEETIKAS

Artiklis on valgustatud koduveise (*Bos taurus*) tsütogeneetika aktuaalseid probleeme ning tehtud kokkuvõte viimase kümne aasta uurimistulemustest. Pikemalt on peatutud veise kromosoomide identifitseerimisega seotud küsimustel ja ära toodud ka uusimad uurimismeetodid karüotüübianalüüsiks. On vaadeldud kromosomaalset polümorfismi peritsentromeerse heterokromatiini koguse, Y-kromosoomi pikkuse ja tuumakeseorganisaatoripiirkondade funktsionaalse aktiivsuse osas ning märgitud senised tulemused veise sugurakkude uurimisel, loote tsütogeneetikas ja geenikaartide koostamisel.

Mahuka osa ülevaatest hõlmab veise karüotüübihäirete kirjeldus, kus eraldi peatükkides käsitletakse seni teadaolevaid kromosoomide arvu- ja struktuurianomaaliaid ning nende seost sigivuse ja produktiivsusega.

Терье РАУДСЕПП, Тийна КУММИК

О РЕЗУЛЬТАТАХ ИССЛЕДОВАНИЙ ПО ЦИТОГЕНЕТИКЕ КРУПНОГО РОГАТОГО СКОТА

Дается обзор актуальных проблем цитогенетики крупного рогатого скота (КРС) и делаются выводы о результатах исследований последних десяти лет. Более подробно затрагиваются вопросы идентификации хромосом КРС. Приводятся новейшие методы анализа кариотипа. Рассматривается хромосомальный полиморфизм перицентромерного гетерохроматина, длины Y-хромосомы и функциональный полиморфизм активности ядрышкообразующих районов. Представлены результаты, полученные до сих пор в области исследования генеративных клеток, цитогенетики эмбриона и составления генных карт КРС. Довольно большой объем обзора отведен описанию аномалии кариотипа КРС, в отдельных главах рассматриваются нарушения числа и структуры хромосом и их связь с размножением и продуктивностью.