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Comparing the Karyotype of the European Domestic Goose and the Asian Goose on the Basis of the Karyotype of their Interspecific Cross-breed, Using the RBG Chromosome Staining Technique

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The aim of the research was to compare the karyotypes of two goose species: the European domestic goose and the Asian goose on the basis of the karyotype of their interspecific cross-breed, using the RBG chromosome staining technique. The karyotype standard for Anseriformes has not been determined yet. The RBG technique is considered as one of the standard methods for analysing chromosomes. It is a dynamic method. The R bands appear during the cell growth cycle in the early S phase. The formation of the characteristic band configuration for each chromosome facilitates chromosome segregation and analysis. The mitotic chromosomes for experiments were obtained from an *in vitro* blood lymphocyte culture and stained according to the RBG technique. The first eight largest autosome pairs and the ZW sex chromosomes were analysed. No differences were found between the band patterns of the analysed chromosomes, except for the fourth autosome pair.

Key words: Goose cross-breed, karyotype, chromosome, RBG staining.

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Among the Vertebrata, birds constitute the most numerous group, though cytogenetically, the least investigated one. Galliformes and Anseriformes are the only surviving orders after the second divergence (GUTTENBACH *et al.* 2003). Birds are a specific group characterised by a small genome (BURT *et al.* 1999; GREGORY *et al.* 2007), heterogameticity of females, a high diploid number, small chromosome size and the division into macro- and microchromosomes (CHRISTIDIS 1989). All three orders show a tendency to reduce the number of small chromosomes and increase the number of large ones as a result of fusion (TAGELSTÖRM & RYTTMAN 1995), as well as repeated fusions and fissions of chromosomes (GRIFFIN *et al.* 2007). These specific characteristics of birds provide for many problems during cytogenetic analysis, discouraging researchers from dealing with bird material. The overriding aim of this cytogenetic investigation is to analyse the accuracy of the chromosome number and structure used in molecular phylogenetics and genetic disorder diagnostics, as well as in genetic counselling with particular emphasis on fertility and reproduction. Conventional staining methods do not always make it possible to distinguish between homologous chromosomes. The problem consists in visually determining the position of the centromere (BITGOOD & SHOFFNER 1990), since the 8 to 10 largest chromosome pairs are constituted by macrochromosomes, the remaining ones being microchromosomes microscopically observed as small points (CHRISTIDIS 1989). In order to identify homologous chromosomes and detect chromosome anomalies, it is necessary to apply various staining differentiation techniques. The characteristic band configuration of each chromosome permits chromosome segregation and analysis.

The RBG technique is considered as one of the standard methods for analysing chromosomes. R bands are present on chromosomes in places where chromatin is less condensed, corresponding to the spaces between chromomeres on meiotic chromosomes (COMINGS 1978). The sites occupied by R bands are the areas of meiotic chromosome recombination (CHANDLEY 1986; ASHLEY 1990). They are characterised by a high incidence of G-C pairs and an elevated degree of transcription (HOLMQUIST 1992; SACCONE *et al.* 1993). R bands are replicated at the earlier S stage of the cell cycle.

They have a large number of Cp-G islets and are rich in genes. The bands contain approximately 200 functional and tissue-specific genes, as well as oncogenes (BERNARDI 1989; BICKMORE & SUMNER 1989; TRENT *et al.* 1989). R bands are characterised by a high frequency of chiasma, cracks and rearrangements (BUCKTON 1976; HOLMQUIST 1992). MANUELIDIS and WARD (1984) as well as KORENBERG and RYKOWSKI (1988) showed that the Alu sequences are exclusively present within R bands. The HMG-I high mobility proteins are not associated with R bands (DISNEY *et al.* 1989).

The karyotype standard for Anseriformes has not been determined yet. Morphological karyotype profiles of various goose species are presented in the following studies: HAMMAR (1966), BHATNAGAR (1968), BEÇAK *et al.* (1975) after CRAWFORD (1990), SHOFFNER *et al.* (1979), BELTERMAN and DE BOER (1984), SILVERSIDES *et al.* (1988), CHRISTIDIS (1989), HIDAS (1993), RABSZTYN *et al.* (1998). The only reports on the replication patterns on goose chromosomes were found in APITZ *et al.* (1995), ANDRASZEK and SMALEC (2007), as well as WÓJCIK and SMALEC (2007, 2008). The closest relatives of Anseriformes are Galiformes. Therefore, SCHMID *et al.* (2000) suggested comparing the analysed bird species with *Gallus domesticus* for which a karyotype standard containing the eight largest autosome pairs and sex chromosomes, out of 39 pairs, had been compiled (LADJALI-MOHAMMEDI *et al.* 1999).

The aim of the research was to compare the karyotypes of two goose species: the European domestic goose and the Asian goose on the basis of the karyotype of their interspecific cross-breed, using the RBG chromosome staining technique.

Material and Methods

The research material consisted of the peripheral blood of 17-week old interspecific F_1 cross-breeds, resulting from bidirectional matings of the European domestic goose *A. anser* and the Asian goose *A. cygnoides.* Material for the study was obtained during slaughter at a company in which every stage of processing was subject to veterinary control and met with the European Union requirements. The blood was collected from twenty birds with wing vein. The chromosome preparations were obtained from an *in vitro* peripheral blood lymphocyte culture prepared by us. The RBG chromosome staining technique by PERRY and WOLFF (1974), well-suited for the bird karyotype specificity, was employed. At the 65th hour of cell culture incubation BrdU and Hoechst 33258 as well as ethidium bromide were added, while colchicine was added at the 69th hour of incubation. The chromosome preparations were incubated in the Hoechst 33258 (basic solution: 1μg /1μl) solution and simultaneously exposed to UV radiation for one hour at room temperature. Next, the culture slides were incubated in 2xSSC at 65°C for one hour and stained with Giemsa. The stained preparations were dried at 40°C for one hour. Ten metaphase slides were analysed for each individual bird. The first eight, largest autosome pairs and the ZW sex chromosomes were investigated. Both chromosomes comprising a homologous pair were studied. The position of the R bands was determined on the selected goose cross-breed chromosomes and the band pattern ideograms of the analysed chromosomes were compiled. The pattern of R bands was determined on the basis of an analysis of 3987 chromosomes obtained from 200 metaphase plates. The R band pattern on the chromosomes was identified using chromosome spectra generated by a computer imaging analysis system (Fig. 1). The results of repeated measurements of the same chromosome from different slides with material from different individual birds served for drawing the band patterns. The R band pattern on the analysed chromosomes was described on the basis of the only available hen karyotype standard (LADJALI-MOHAMMEDI *et al.* 1999).

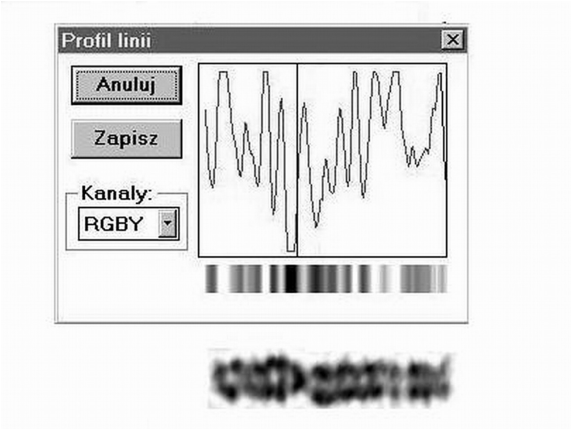

Fig. 1. The spectrum of the first chromosome generated with the imaging analysis software.

Results

In line with the set goal, the karyotypes of two goose species, the European domestic goose and the Asian goose, were compared based on the karyotype of their interspecific cross-breed. The applied RBG staining technique made it possible

to determine the R band pattern on the cross-breed chromosomes. The results are presented as a metaphase slide (Fig. 2), karyogram (Fig. 3) and an ideogram (Fig. 4) of the R band pattern of the nine chromosome pairs. The prepared ideograms were used for comparative analysis. The homologous chromosome pair was marked with letters "a" and "b". The smaller chromosomes in the respective pairs were assigned letter "a" and the bigger chromosomes letter "b". Each analysed chromosome was divided into two arms: the short arm – p and the long arm – q of the chromosome. In order to facilitate the chromosome description, several regions were specified on the chromosome arms and positive (dark) and negative (light) R bands were counted.

Chromosome 1a and b

1-1. Arm p: Two regions. 11 R bands. In the first region three positive bands (11, 13, 15) and three negative bands (12, 14, 16) were observed. In the second region three positive bands (21, 23, 25) alternately divided by light bands (22, 24) were identified.

1-2. Arm q: Three regions. 18 R bands. In the first region, two centrally located dark bands (12, 14) with three alternating light bands (11, 13, 15) were identified. A second region with three dark bands (21, 23, 25) and three light bands (22, 24, 26) occupied the central part of the longer chromosome arm. The third region was characterised by the presence of four dark bands, two of which were in a distal position (31, 37) divided by light bands (32, 36) from two dark and centrally positioned ones (33, 35). A narrow light band (34) located in the central part of the third region separated the dark R bands.

Chromosome 2a and b

2-1. Arm p: Two regions. 12 R bands. A thick, dark and positive R band divided the arm p into two regions. In the first region two positive bands (12, 14) and three negative bands (11, 13, 15) were

Fig. 2. Picture of the metaphase plate.

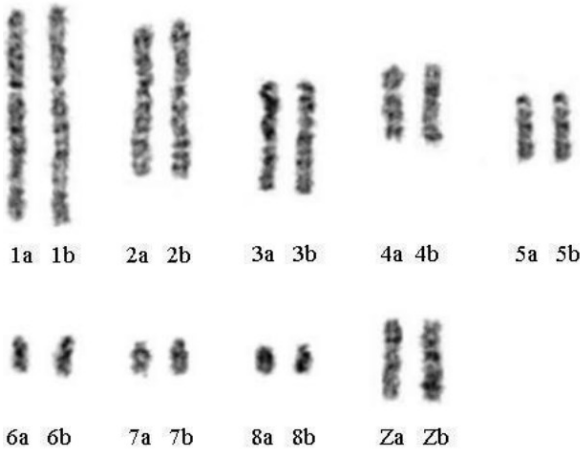

Fig. 3. Karyogram of the chromosomes of the goose cross-breed (chromosomes: a – *Anser anser*; b – *Anser cygnoides*).

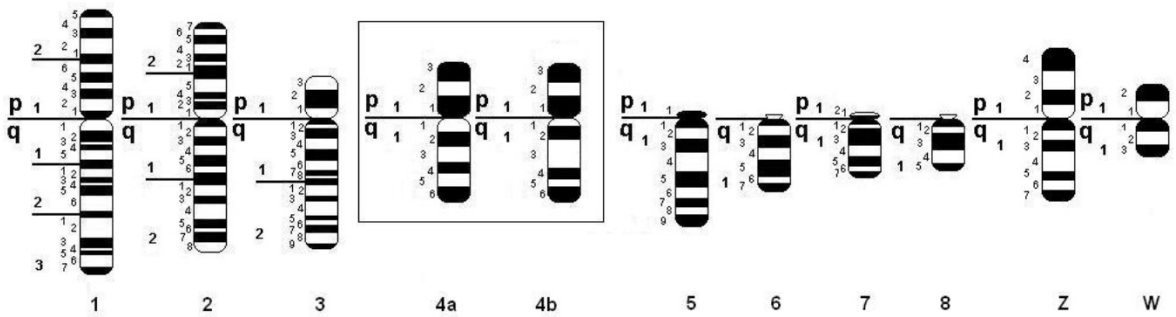

Fig. 4. Ideogram of the chromosomes of the goose cross-breed.

observed. In the second region four positive bands (21, 23, 25, 27) and three negative bands (22, 24, 26) were identified.

2-2. Arm q: Two regions. *14 R bands*. In the first region of arm q three positive bands (11, 13, 15) and three negative bands (12, 14, 16) were observed. In the second region of arm q four positive (21, 23, 25, 27) and three negative bands (22, 24, 26, 28) were identified.

Chromosome 3a and b

3-1. Arm p: One region. 3 R bands. One broad positive interstitially located band (12) surrounded by two negative bands (11, 13).

3-2. Arm q: Two regions. 17 R bands. In the first region four positive (11, 13, 15, 17) and four negative bands (12, 14, 16, 18) were observed. In the second region of chromosome arm q, five narrow positive bands (21, 23, 25, 27, 29) and four negative bands (22, 24, 26, 28) were identified.

Chromosome 4a

4-1. Arm p: One region. 3 R bands. In the first region two broad R-positive bands were observed, the first of them located in the proximal (11) and the second in the distal area (13). They were divided by a broad light band (12).

4-2. Arm q: One region. 6 R bands. Three dark R-positive bands were observed on chromosome arm q. Two of them (12, 14) were interstitially positioned and the third one located in the distal part of arm q (16). The dark R bands alternated with light ones (11, 13, 15).

Chromosome 4b

4-1. Arm p: One region. 3 R bands. On arm p two dark bands, a proximal (11) and a distal one (13) were identified, with a light band (12) between them.

4-2. Arm q: One region. 6 R bands. Three dark bands were noted: a band (12) in the interstitial part of the chromosome and two bands in the distal part (14, 16). These bands were adjacent to three light bands (11, 13, 15).

Chromosome 5a and b

5-1. Arm p: One region. One positive band was identified (11).

5-2. Arm q: One region. 9 R bands. Nine bands were observed: five positive (11, 13, 15, 17, 19) and four negative (12, 14, 16, 18).

Chromosome 6a and b

6-1. Arm q: One region. 7 R bands. Seven bands were observed: four positive (11, 13, 15, 17, 19) and three negative (12, 14, 16, 18).

Chromosome 7a and b

7-1. Arm p: One region. 2 R bands. One positive (11) and one negative band (12) were noted.

7-2. Arm q: One region. 7 R bands. Four positive bands (11, 13, 15, 17) and three negative bands (12, 14, 16) were identified.

Chromosome 8a and b

8-1. Arm q: One region. 5 R bands. Three positive (11, 13, 15) and two negative bands (12, 14, 16) were identified.

Chromosome Za and b

Z-1. Arm p: One region. 4 R bands. Two dark (12, 14) and two light bands (11, 13) were observed.

Z-2. Arm q: One region. 7 R bands. Four positive (11, 13, 15, 17) and three negative bands (12, 14, 16) were identified.

Chromosome Wa and b

W-1. Arm p: One region. 2 R bands. A broad positive band in the distal part of the chromosome (12) and a negative one in the proximal part (11) were observed.

W-2. Arm q: One region. 3 R bands. A positive band in the proximal part of the chromosome (11), a negative one in the interstitial part (12) and a positive one in the distal part (13) were observed.

In total, 131 R bands, 70 R-positive at 61 R-negative, were identified on the analysed chromosomes of the goose *A. anser.* The same number of R bands was observed in the goose *A. cygnoides* (70/61). No differences were found in the band patterns of the chromosomes "a" and "b" in the first, second, third, fifth, sixth, seventh and eighth pair of the autosomes and ZW heterochromosomes. A difference was observed in the band pattern of the fourth chromosome pair (Figs 4, 5). The difference between chromosomes "a" and "b" was connected with the location of the central positive R band on the arm q. The dark band (14) on chromosome "a" was situated in the interstitial part of the chromosome arm q, while on chromosome "b" the positive band (14) was in the distal part.

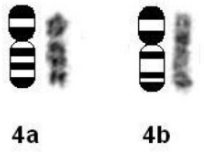

Fig. 5. Ideogram of the fourth chromosome pair of the *Anser anser* and *Anser cygnoides* goose crossbreed. Differences between breeds only (a – *Anser anser;* b – *Anser cygnoides*).

Discussion

No information on RBG staining of goose chromosomes was found in the available sources, apart from our own studies on the goose *A. anser* (WÓJCIK & SMALEC 2007) and the goose *A. cygnoides* (WÓJCIK & SMALEC 2008). The results of the present research correspond with the results published earlier which concerned pure breeds. The advantage of the interspecific cross-breeds F_1 consists of the fact that they have paternal and maternal chromosomes within a homologous pair. Thus, in the homolog chromosome pair the analysed interspecific cross-breed had one chromosome inherited from the goose *A. anser* and another one from *A. cygnoides*. The differences observed in our studies concerning the size of the homologous chromosomes of the cross-breed made it possible to separate the chromosomes in a pair. The cross-breed chromosomes were compared with the chromosomes of the goose *A. anser* and *A. cygnoides*. The smaller chromosomes in a pair, which were assigned letter "a", had the same R band pattern as the chromosomes of the goose *A. anser* (WÓJCIK & SMALEC 2007). The larger chromosomes in the twin pair of chromosomes, marked as "b", had a band pattern that resembled the chromosome band pattern of the goose *A. cygnoides* (WÓJCIK & SMALEC 2008).

Patterns of replication bands, obtained with the GTG technique, on chromosomes of the goose *A. anser* were analysed by APITZ *et al.* (1995) as well as by ANDRASZEK and SMALEC (2007), while on the basis of chromosomes of the goose *A. cygnoides* only by APITZ *et al.* (1995). Our results were compared with APITZ *et al.* (1995) in respect of only the first five pairs of autosomes and ZW chromosomes, and to ANDRASZEK and SMALEC (2007) with regard to the nine largest pairs of chromosomes of the goose *A. anser*. In our experiment on the five successive autosomes and Z and W chromosomes, 58 R-positive and 52 R-negative bands were identified in the goose *A. anser*. The same number of bands (58/52) was observed in the goose *A. cygnoides*. In both *A. anser* and *A. cygnoides,* APITZ *et al.* (1995) identified 32 G-positive and 45 G-negative bands in each case. In turn, on the eight largest autosomes and ZW chromosomes in *Anser anser* ANDRASZEK and SMALEC (2007) observed 48 G-positive and 64 G-negative bands, i.e. 8 more G-positive and 11 more G-negative bands than APITZ *et al.* did (1995) on the additionally analysed chromosomes pairs 6, 7 and 8. On the other hand, in this study we observed 70 R-positive and 61 R-negative bands on the nine analysed chromosome pairs.

The common ancestry of Galiformes and Anseriformes as well as the fact that they retained many highly conservative characteristics of certain chromosomes inherited from their ancestors should, according to SCHMID *et al.* (2000), serve as a point of reference for the current band pattern standard worked out for *Gallus gallus* by LADJALI-MOHAMMEDI *et al.* (1999). On the whole, in our studies 131 R bands were identified, including 70 R-positive bands for *A. anser* and the same number for *A. cygnoides*, the rest being R-negative bands. In *Gallus gallus* LADJALI-MOHAMMEDI *et al.* (1999) detected 70 R-positive and 64 R-negative bands, i.e. three more than we observed, as well as 73 G-positive and 78 G-negative bands.

In the available literature one can come across the assumption that R bands are the reverse of G bands and are in mutual complementary correspondence. In our experiments we noticed the stained R bands on certain chromosomes to be the reverse of the G bands described by APITZ *et al.* (1995) and ANDRASZEK and SMALEC (2007). This mainly refers to the proximal and distal chromosome regions. LEMIEUX *et al.* (1990) observed significant differences in the complementarity of R and G bands on human chromosomes. LADJALI *et al.* (1995, 1999) suggest that GTG bands do not show the reverse of RBG bands which may stem from the fact that the GTG and RBG chromosome staining techniques are two radically different chromosome analysis methods. This not only concerns the visualisation of A/T and G/C pairs on chromosomes. The GTG technique is a morphological method in which already cultured chromosomes are stained on microscopic slides. The RBG chromosome analysis technique is a dynamic method, since the R bands are formed during the cell cycle after adding BrdU to the cultivated culture, 6-7 hours before its termination. The quality of R bands depends on the dose and degree of the BrdU incorporated at the early S phase of the cell cycle.

The advantage of the RBG technique is that it facilitates the recognition of centomeres in chromosomes. As regards the present study, in most cases the centromere region contained dark R-positive bands which showed the primary constriction of the chromosome. The ease of centromere identification on the chromosome facilitated the analysis. LADJALI *et al.* (1995) were of the same opinion. The number of R bands on the chromosomes also depends on the phase at which the chromosome was during BrdU incorporation. Considerably more bands could be observed in longer chromosomes, since they were at an early stage of condensation (prometaphase) than in chromosomes at the metaphase stage during which chromosomes are short and maximally condensed. The computer-generated chromosome profiles used in our analyses made it possible to determine the band pattern of chromosomes both at the early metaphase stage

and later. The configuration of bands on chromosomes is a constant and repeatable characteristic of each species. The employed software for chromosome image analysis made it possible to penetrate deeper into the chromosome structure and obtain a pattern with more R bands.

The experiments conducted on the goose cross-breed chromosomes showed differences in the configuration of R bands on the fourth pair of autosomes. After perfoming differential staining, SILVERSIDES *et al.* (1988) as well as APITZ *et al.* (1995) also identified differences in the configuration of bands on the fourth pair. The fourth chromosome constitutes the greatest enigma in the evolution of birds (CHOWDCHARY & RAUDSEPP 2000). Differences in the morphological structure of the fourth pair of autosomes were also observed by SHOFFNER *et al.* (1979) in the Ross (*A. rossii*) and Emperor goose (*A. canagicus*) (submetacentric and metacentric, respectively) and by SILVERSIDES *et al.* (1988) as well as APITZ *et al.* (1995), RABSZTYN *et al.* (1998) in the goose *A. anser* or *A. cygnoides*. The authors defined these chromosomes as submetacentric in *A. anser* and metacentric in *A. cygnoides*. SILVERSIDES *et al.* (1988) indicated the pericentric inversion of the fourth pair of chromosomes as the reason for the structural differences of this chromosome pair. According to HIDAS (1993), the change which occurred in the karyotype of these two avian species is a fairly recent evolutionary phenomenon and must have taken place already before these two species split, since cross-breeds of geese *A. anser* and *A. cygnoides* are fertile and able to reproduce. APITZ *et al.* (1995) concluded that the loss of heterochromatin present in the proximal and interstitial part of *A. cygnoides* chromosomes may be responsible for the general shortening of the fourth chromosome pair in *A. anser*, as well as for morphological modifications. On the fourth metacentric autosome pair in the Greylag goose (*A. anser*) GUTTENBACH *et al.* (2003) identified a fusion of the acrocentric fourth and tenth chromosomes, the same as in *G. domesticus*, which confirms ancestral consanguinity from before the second divergence period. GRIFFIN *et al.* (2007) advanced 3 hypotheses on the origin of the fourth pair of chromosomes in birds. The first of them proposes 3 independent fusions (in geese, the African collared dove, and a recent turkey/pheasant ancestor) and 1 fission in the turkey/pheasant ancestor which occurred before the second divergence. The next hypothesis assumes a fusion before the 2nd divergence and 8 different fissions. The authors account for the recurrent fusions and fissions with particular sensitivity and susceptibility of the chromosome to cracking. The third hypothesis differs from the first two. It assumes that there was no fusion before the second divergence at all. After the fusion in the Galiform/Anseriform ancestor there occurred 4 independent fissions in the group of turkeys/pheasants, in the group of guinea fowls/quails and in the family Cracidae. However, the above hypotheses were not confirmed by cytogenetic techniques. The authors suggest employing BAC or chromosome marker mapping techniques of the "chromosome walking" type in non-gallinaceous species.

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