Karyotypes of three gerbil species of the genera *Tatera* and *Gerbilliscus* from Turkey and Senegal

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Abstract. In this study, we examined karyotypes of three gerbil species of the genera *Tatera* and *Gerbilliscus*. The diploid number of 68 chromosomes was confirmed in all specimens of *Tatera indica* examined from southeastern Anatolia in Turkey. The C-band positive regions were distributed in centromeric areas of all the autosomal pairs and the X chromosome. The Y chromosome was stained uniformly and C-positively. The active NORs were localized in three out of eight pairs of biarmed autosomes (NF=86). Conventionally stained karyotypes were studied in two species of *Gerbilliscus* from Senegal, western Africa. The female karyotype of *G. gambianus* contained 52 chromosomes including one large subtelocentric, six submetacentric and 16 acrocentric pairs (NF=66). The female karyotype of *G. guineae* contained 50 chromosomes including a large metacentric, eight submetacentric and 16 acrocentric autosomal pairs (NF=68). Minor differences in chromosome morphology were observed in these studied species in comparison with previously published data.

Keywords: cytogenetics, taxonomy, Gerbillinae, Asia Minor, western Africa.

Introduction

The gerbils (Muridae: Gerbillinae) represent a distinct group defined by a set of derived morphological traits (Musser & Carleton 2005). Pavlinov et al. (1990) recognized two lineages of extant gerbil species designated as Taterillinae and Gerbillinae. The genera *Tatera* and *Gerbilliscus*, previously considered congeneric, were included in the former lineage. Pavlinov et al. (1990) and Pavlinov (2001) regarded true *Tatera* to consist only of single Asian species, and separated the African endemic genus *Gerbilliscus*, with *Taterillus* as its closest relative. The Asian *Tatera* and African *Gerbilliscus* are differentiated by certain morphological traits (Musser & Carleton, 2005), and also karyotypes (Rao et al. 1968, Yosida 1981, Qumsiyeh and Schlitter 1991, Yiğit et al. 2001). Cytogenetic data for gerbils were summarized by Viegas-Péquignot et al. (1986) and Qumsiyeh & Schlitter (1991).

The Indian gerbil, *T. indica* (Hardwicke, 1807) occurs from Mesopotamia across Iran, Afghanistan, and Pakistan to India and Sri Lanka. The species is known from south-eastern Turkey in the area between Akçaahale and Ceylanpınar (in Şanlıurfa), close to the Syrian border (Kryštufek & Vohralík 2009). A number of dispersed karyotypic data has been obtained by Matthey (1953), Rao et al. (1968), Aswanthanarya and Manjunatha (1981), and Yosida (1981). In Turkey, the conventionally stained karyotype of *T. indica* was described by Yiğit et al. (2001) from Ceylanpınar. However, information on differentially stained chromosomes and detailed structure of the karyotype is still lacking in this species.

The genus *Gerbilliscus*, previously included as a part of the *Tatera* genus, consists of about 11 species. The western Africa *Gerbilliscus* species reveal a relatively high level of karyotype variability (Colangelo et al. 2001, Volobouev et al. 2007). The species studied by us belong to well-supported western clade including *G. gambianus*, *G. guineae*, *G. kempfi*, and possibly other not yet described species (Colangelo et al. 2007, Volobouev et al. 2007). The northern savanna gerbil, *G. gambianus* (Wroughton, 1906) was listed as *G. kempfi* by Musser and Carleton (2005) but the species nomenclature was revised and proposed to be changed by Colangelo et al. (2007) and Volobouev et al. (2007). The species is distributed in a vast range throughout Sub-Saharan northern savanna from western to eastern Africa. The karyotype was studied from Senegal, Niger, Chad, and Mali (Matthey 1969, Hubert et al. 1973, Dobigny et al.
The diploid number of 52 chromosomes was uniformly reported. The Guinean gerbil, *Gerbilliscus guineae* (Thomas, 1910), with the partly symmetrical range, was recorded from Guinea, Sierra Leone, and southern Mali to Burkina Faso and Ghana (Musser and Carleton 2005). The karyotype of this species was examined in Burkina Faso and Mali (Matthey & Petter 1970, Benazzou et al. 1984, Volobouev et al. 2007) and the chromosome diploid number of 2n=50 was reported. Colangelo et al. (2001) and Volobouev et al. (2007) performed comparative chromosome banding analyses of the western African gerbils of the genus *Gerbilliscus*.

The aim of this study is to evaluate chromosomal differences between the two genera studied, and to contribute to karyotype faunistic mapping of the three species examined. In this respect, this study is continuation of our survey of cytogenetic characteristics of mammals from Asia Minor and western Africa (Koubínová et al. 2010, Arslan & Zima 2011, Arslan et al. 2011a,b). Chromosomal banding analysis of the karyotype of *T. indica* with the use of C-banding and Ag-NOR staining is aimed to facilitate further comparative cytogenetic studies among gerbils.

Materials and methods

The specimens of *T. indica* (6 males and 4 females) were collected in the Ceylanpinar, Şanlıurfa Province, southeastern Turkey (36° 51´ N, 40° 04´ E). Single female of *G. gambianus* was collected in Diala Koto, south-eastern Senegal (13°18´ N, 13°16´ E). Two females of *G. guineae* originated from Dar Salam, Senegal (13°16´ N, 13°12´ E). All the animals were collected with the permission and under supervision of the Senegal’s National Parks General Management.

Karyotype preparations were obtained from the bone marrow of animals treated with colchicine (Ford and Hamerton 1956). After preparation of chromosome slides, conventional Giemsa-staining was carried out. In *T. indica*, constitutive heterochromatin and nucleolus organizer regions (NORs) were detected in individual autosomal and sex chromosome pairs via C-banding (Sumner 1972) and Ag-NOR staining (Howell and Black 1980), respectively. From each specimen, 4 to 20 slides were prepared, and at least 20 well-spread metaphase plates were analysed.

Standard voucher specimens (skins and skulls) are deposited in collections of the Department of Biology, Faculty of Science, Selçuk University, Konya, Turkey (*T. indica*), and the Institute of Vertebrate Biology ASCR, Brno, Czech Republic (*Gerbilliscus spp.*).

Results

The karyotype of *T. indica* consists of 68 chromosomes including eight bi-armed pairs and 25 acrocentric pairs of autosomes (NFa = 82). The X chromosome is large and metacentric, while the Y chromosome is small acrocentric (NF = 86) (Fig. 1). The C-banded karyotype of this species is illustrated in Fig. 2. Most of the autosomes possess distinct pericentromeric C-bands. The X chromosome has a centromeric C-positive band and the Y chromosome appears to be uniformly and C-positively stained. By using silver-nitrate staining, NORs are localized in the secondary constrictions in the short arms of the three bi-armed pairs (nos. 1, 2, and 4). All the observed NORs are homomorphic and occur in both the homologues (Fig. 3).

The female karyotype of *G. gambianus* (Fig. 4) consists of 52 chromosome that can be differentiated into one large subtelocentric pair, six medium-sized and small submetacentric pairs, and 19 acrocentric pairs (NF=66). The largest subtelocentric pair can be tentatively designated as the X chromosomes (NFA=62), based on the comparison with other published data.

The female karyotype of *G. guineae* (Fig. 5) consists of 50 chromosomes including single large metacentric pair, eight submetacentric pairs, and 16 acrocentric pairs (NF=68). The largest metacentric pair can be tentatively designated as the X chromosomes considering the published data on karyotypes of the species. Consequently, NFA is 64.

Discussion

Aside from the distinct karyotypic differences between the genera *Tatera* and *Gerbilliscus*, which play a role in the generic division, these species share common features which well illustrate their common belonging to a clade based on mt DNA data (Colangelo et al. 2007). Contrary to differences in their number of chromosomal arms (86 in *Tatera* vs. 60-68 in *Gerbilliscus*, cf. Qumsiyeh and Schlitter 1991, Volobouev et al. 2007), there is a similar proportion of bi-armed and uni-armed autosomes, as well as the large X chromosomes which usually represent the largest elements of the complement. Both the studied species of *Gerbilliscus* have similar karyotypes that differ in the centromere position on their largest chromosome (presumably the X chromosome) and in the pro-
portion of the bi-armed and uni-armed chromosomes. An autosomal fusion may be assumed as a mechanism of divergence between the autosomal complements of both the species (Volobouev et al. 2007). The banding analyses showed that the variation in the morphology of the X chromosome may be related to a pericentric inversion (Colangelo et al. 2001).

Certain differences can be found between the results reported in this study and published records in individual species. Matthey (1953) reported diploid number of 72 chromosomes, and fundamental number of 80 chromosomal arms in T. indica. Different findings were reported by Rao...
et al (1968), Yosida (1981), and Aswanthanaryana and Manjunatha (1981) from India who found 2n = 68 in the somatic cells of the species. Aswanthanaryana and Manjunatha (1981) further reported variation in the number of chromosomal arms (NF = 80-86) in the Indian subspecies *T. indica hardwickei*. Yosida (1981) described the karyotype containing eight bi-armed and 25 acrocentric autosomal pairs (NF=86 and NFa=82), a large and metacentric X chromosome, and an acrocentric Y
chromosome as in our case. Rao et al (1968) recorded NF= 84 and NFa= 80 in the subspecies T. indica cuvierii, and the same fundamental numbers were reported in populations examined from Turkey (Yiğit et al. 2001). The differences between published data are therefore caused by variable proportion of the bi-armed and uni-armed autosomes reported in individual papers. However, this variation reveals no clear geographical pattern, and could be influenced by varying interpretation of individual authors.

According to Yosida (1981), almost all autosomes of Indian gerbil had a small centromeric C-band, and the X and Y chromosomes were rather universally stained. The whole body of the Y chromosome was always stained heavily, but the C-staining pattern of the X was somewhat variable. In most cells, both arms of the X were also intensively stained. This pattern of C-banding is congruent with our findings in the autosomal complement but certain differences are indicated in staining of the X chromosome. Similar C-banding pattern with the positive regions in centromeric position in all autosomes was recorded also in the Gerbilliscus species (Colangelo et al. 2001, Volobouev et al. 2007). There are only few data about the distribution of NORs in the karyotype of gerbils. Colangelo et al. (2001) reported the maximum number of four NORs in G. kempi. Similarly as in T. indica, these NORs were located in telomeric position on biarmed autosomes.

Chromosomal studies of G. gambianus from various parts of western Africa (Matthey & Petter 1970, Hubert et al. 1973, Dobigny et al. 2002, Granjon & Dobigny 2003) revealed similar results as those reported in this paper, but a different number of autosomal arms was recorded. The complement described in this study contains seven bi-armed autosomal pairs (NFa=62) compared to eight bi-armed pairs reported in other studies (NFa=64). This difference may be related to autosomal heteromorphism recorded in a bi-armed pair in certain Gerbilliscus species from western Africa (Matthey & Petter 1970, Hubert et al. 1973, Dobigny et al. 2002, Granjon & Dobigny 2003). However, the homologous chromosomes in this heteromorphic pair were usually bi-armed (Volobouev et al. 2007), and the exact mechanism of the observed variation thus remains unknown. Certain differences between the published results can be found also in the centromere position in the X chromosome (e.g., Matthey & Petter 1970), however, these differences may be explained by presumed misidentification of the sex chromosomes (Volobouev et al. 2007).

The data on the karyotype of G. guineae (Matthey & Petter 1970, Benazzou et al. 1984, Volobouev et al. 2007) are similar to the results reported in this paper (2n=50, NF=68, NFa=64). We
can conclude that minor differences in the karyotype structure may be revealed within individual \textit{Tatera} and \textit{Gerbiliscus} species provided that dense geographical sampling is available.

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\textbf{References}


