

## A karyotypic study of the genus *Gerbillus* (Mammalia: Rodentia: Muridae) from Jordan

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### > Abstract

Karyotypic studies were conducted on six species of the genus *Gerbillus* occurring in Jordan. These gerbils belong to two groups; naked-footed (*G. dasyurus*, *G. henleyi* and *G. nanus*) and hairy footed ones (*G. andersoni*, *G. cheesmani* and *G. gerbillus*). The diploid number ranged between 38–60 and 62–80 respectively. The study confirmed the doubtful presence of *G. andersoni* in Jordan.

### > Kurzfassung

Karyologische Studien wurden an sechs Arten der Gattung *Gerbillus* durchgeführt, die in Jordanien vorkommen. Dabei kann man zwei Gruppen unterscheiden: Arten mit nackten Füßen (*G. dasyurus*, *G. henleyi* und *G. nanus*) und solche mit behaarten Füßen (*G. andersoni*, *G. cheesmani* und *G. gerbillus*). Die diploide Anzahl der Chromosomen schwankt von 38–60 bzw. 62–80. Die Studie stützt das zweifelhafte Vorkommen von *G. andersoni* in Jordanien.

### > Key words

*Gerbillus*, karyotype, taxonomy, Jordan.

## Introduction

The genus *Gerbillus* DESMAREST, 1804 is one of the most diversified groups of rodents inhabiting arid and semi arid habitats in North and East Africa, the Arabian Peninsula and the Indian desert (HARRISON, 1972; LAY, 1983; NOWAK, 1991). Due to the variation in habitat structure, rodents of the genus *Gerbillus* form an important component of the mammalian fauna in these arid zones as they are adapted to tolerate extreme desertic conditions (LAY, 1983; HARRISON & BATES, 1991; QUMSIYEH, 1996; GRANJON *et al.*, 1999).

Karyotypic investigations support taxonomic studies and provide significant clarifications to confirm morphological differences for particular taxa. So far, only one report presented karyotypic data for these animals from Jordan (QUMSIYEH *et al.*, 1986).

Two species of the genus *Gerbillus* were included; *G. dasyurus* (2N=60, FN= 66, 68 and 70) from the Lava rock desert south of Azraq ad Duruz, Shaumari Wildlife Reserve and Al Aqabah and *G. nanus* (2N= 52, FN= 60) from Al Aqabah, Wadi Araba (Wadi El Khanazir) and Azraq (karyotypes not provided).

The genus *Gerbillus* has received particular attention by several workers in different areas throughout its distribution range. Karyotypic and morphometric investigations have been undertaken in Palestine (WAHRMAN & ZAHAVI, 1955), Egypt (WASSIF *et al.*, 1969), Morocco (LAY *et al.*, 1975; COCKRUM *et al.*, 1976) and East of Euphrates (LAY & NADLER, 1975). The genus was also reviewed by LAY *et al.* (1975), and was later revised by LAY (1983), resulting in the first check list for species of the genus *Gerbillus* that included 62 species throughout its range. LAY (1983) employed the plantar surface of the hind feet to divide the genus into 32 naked-footed, 22 hairy-footed,

six were regarded as intermediate and the remaining two species were considered to be unknown. Table (1) summarizes reported karyotypes for species of the genus *Gerbillus* occurring in Jordan.

LAY *et al.* (1975) studied the karyotypes for 20 species of the genus *Gerbillus*. The report included karyotypic results for *G. andersoni* (2N=40 and FN=80 from Egypt), *G. gerbillus* (2N 42 ♀, 43 ♂ and FN 76 ♀ and 78 ♂ from Sinai, Egypt and Morocco), *G. nanus* (2N 52 and FN as 61 ♂ and 62 ♀) and *G. henleyi* (2N =52 and FN 61 ♂ and 62 ♀) from Morocco. This genus was recently reviewed in Jordan based on morphologic and morphometric characters (ABU BAKER & AMR, 2003).

The present study investigates karyotypic features for six species of the genus *Gerbillus* occurring in Jordan and contributes to the taxonomy of this genus.

## Materials and Methods

**Specimens examined:** Mitotic chromosomes were analyzed from 45 specimens representing different populations for all species of the genus *Gerbillus* in Jordan.

***G. andersoni*:** 15.1.2002, ♂, Ra's an Naqb, 30 00 E 35 30 N; 19.1.2002, ♀, Ra's an Naqb. ***G. cheesmani*:** 8.9.2001, ♀, Al Wisad, 31 35 E 37 57 N; 16.9.2001, ♂, Mudawwarah, 29 19 E36 00 N; 16.9.2001, ♂, Mudawwarah; 22.9.2001, ♂, Mudawwarah; 27.9.2001, ♀, Ra's an Naqb, 30 00 E 35 30 N; 27.9.2001, ♀, Disah, 29 34 E 35 35 N; 29.9.2001, ♀, Ra's an Naqb; 12.10.2001, ♂, Mudawwarah; 13.10.2001, ♂, Mudawwarah; 14.10.2001, ♀, Al Jafr, 30 18 E 36 13 N; 14.10.2001, ♂, Al Jafr; 17.10.2001, ♂, Ra's an Naqb; 17.10.2001, ♀, Ra's an Naqb; 22.10.2001, ♀, Ra's an Naqb; 10.11.2001, ♂, Mudawwarah; 10.11.2001, ♀, Ra's an Naqb; 17.11.2001, ♂, Ra's an Naqb; 24.11.2001, ♀, Ra's an Naqb. ***G. gerbillus*:** 19.9.2001, ♂, Quraiqira, 30 40 E 35 26 N; 19.9.2001, ♀, Ar Rishah, 30 12 E 35 13 N; 22.9.2001, ♀, Quraiqira; 22.9.2001, ♀, Quraiqira; 27.9.2001, ♂, Ar Rishah; 12.10.2001, ♀, Rahmeh, 30 01 E 35 03 N; 14.10.2001, ♀, Rahmeh; 29.10.2001, ♂, Quraiqira; 16.11.2001, ♂, Rahmeh; 16.11.2001, ♀, Rahmeh. ***G. dasyurus*:** 11.8.2001, ♂, Azraq ad Duuz, 31 53 E 36 50 N; 23.8.2001, ♂, Burq'u, 32 37 E 37 58 N; 4.9.2001, ♀, Burq'u; 8.9.2001, ♀, Azraq ad Duruz. ***G. henleyi*:** 22.9.2001, ♂, Mudawwarah, 29 19 E 36 00 N; 11.10.2001, ♂, Mudawwarah; 19.10.2001, ♂, Al Jafr, 30 18 E 36 13 N; 29.10.2001, ♀, Al Jafr; 11.11.2001, ♂, Al Jafr. ***G. nanus*:** 23.8.2001, ♀, Azraq ash Shishan, 31 50 E 36 49 N; 28.8.2001, ♀, Shaumari, 31 47 E 36 49 N; 28.8.2001, ♂, Azraq ash Shishan; 4.9.2001, ♂, Shaumari; 24.11.2001, ♂, Ra's an Naqb, 30 00 E 35 30 N; 24.11.2001, ♂, Ra's an Naqb.

**Chromosome Preparation:** Chromosomes were obtained from femoral bone marrow cells and processed as described by TJIO & WHANG (1992) and NADLER & LAY (1968).

Standard karyotypes were constructed from micrographes of well spread chromosomes. Metaphase chromosomes were arranged in homologous pairs according to size and centromere position. The diploid chromosome number was determined from ten photographed spreads for each species. The fundamental number (FN) was counted after constructing the standard karyotypes, only metacentric and submetacentric chromosomes were considered as bi-armed chromosomes (VOLOBOUEV *et al.*, 1995). Sex chromosomes were identified from the difference between male and female karyotypes (the presence of an identical X chromosome in both). Results were used to compare the present data with previously published reports.

## Results

Based on the diploid chromosome number (2N), species of the genus *Gerbillus* in Jordan are classified into two groups: the first consists of three species with diploid numbers ranging from 38–43. This group includes *G. andersoni*, *G. cheesmani* and *G. gerbillus*, with 2N of 40, 38 and 42♀/43♂, respectively (Table 1). All species of this group are hairy-footed gerbils. The second group also contains three species with 2N between 52 and 60. This group includes *G. dasyurus*, *G. henleyi* and *G. nanus* with diploid numbers (2N) of 60, 52 and 52, respectively. These three species are naked-footed gerbils.

### Hairy-footed gerbils:

*G. andersoni* have 2N=40 and FN = 80 (male specimen). There are 14 metacentric and 24 submetacentric autosomes. The X and Y chromosomes are medium and small-sized submetacentric, respectively.

*G. cheesmani* shows a 2N=38 and FN=72 (female specimen). The karyotype includes 16 metacentric, 16 submetacentric and 4 telocentric autosomes. The X is a medium-sized metacentric chromosome (Fig. 1).

*G. gerbillus* have a 2N=42♀/43♂ and FN=70 (female specimen). The autosomal complement of the female includes 18 metacentric, 10 submetacentric, 6 acrocentric and 6 telocentric chromosomes. The X is a large acrocentric chromosome. Due to the lack of clear spreads and probably the small size, the two Y chromosomes could not be identified.

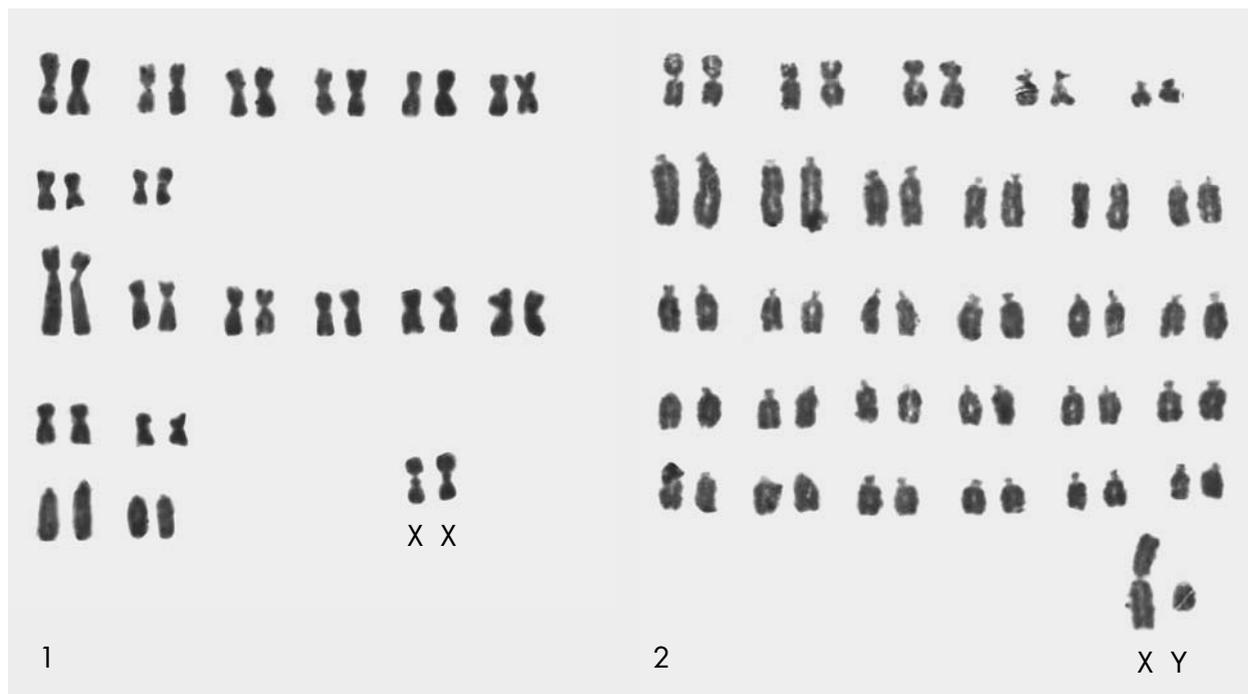


Fig. 1. Standard karyotype of a female *G. cheesmani* from 23 km N. Al Quwayrah (Mag. 6500).

Fig. 2. Standard karyotype of a male *G. dasyurus* from Azraq ad Duruz (Mag. 6500).

### Naked-footed gerbils:

*G. dasyurus* exhibits a  $2N=60$  and  $FN=71$  (male specimen). The karyotype consists of 4 metacentric, 6 submetacentric and 48 acrocentric autosomes. The X and Y are large metacentric and small telocentric chromosomes, respectively (Fig. 2).

*G. henleyi* shows a  $2N=52$  and  $FN=62$ . The karyotype includes 8 submetacentric and 42 acrocentric autosomes. The X and Y are large and medium sized submetacentric chromosomes, respectively.

*G. nanus* possesses a  $2N=52$  and  $FN=62$  (Female specimen). The karyotype consists of 8 submetacentric and 42 acrocentric autosomes. The X is a large submetacentric chromosome.

### Discussion

Table (1) shows the diploid chromosome number for all species of the genus *Gerbillus* investigated in the present study and previously published reports.

Karyotypes for all species of the genus *Gerbillus* known to Jordan were previously reported from other parts of their distribution, while the karyotypic pattern for *G. dasyurus* and *G. nanus*, were studied based on animals collected from Jordan (QUMSIYEH *et al.*, 1986). The present study is considered as the first attempt to study the karyology of the remaining four species of

*Gerbillus* occurring in Jordan (*G. andersoni*, *G. cheesmani*, *G. gerbillus* and *G. henleyi*).

The chromosome number for all species of the genus *Gerbillus* under the present study are in agreement with previous reports, however, some differences appear in their morphology. Hairy-footed species of the genus *Gerbillus*, showed higher number (34 or more) of bi-armed chromosomes, and the highest number of telocentric chromosomes in this group was 4, reported among *G. cheesmani* population. On the other hand, naked-footed species of the genus *Gerbillus* possessed a high number of acrocentric autosomes, reaching up to 48, 42 and 42 chromosomes in *G. dasyurus* and *G. nanus* and *G. henleyi*, respectively. The XY chromosome system was shared in all species, except for *G. gerbillus*, which showed a  $XY_1Y_2$  system.

The chromosome pattern of *G. dasyurus* is clearly different from its closer naked-footed relatives (*G. henleyi* and *G. nanus*). This chromosomal divergence along with other morphologic differences could be easily used to determine the specific level for these species. The diploid numbers for the examined specimens of *G. dasyurus* was 60 and  $FN$  71, with a unique X chromosome, which is a large metacentric one. QUMSIYEH *et al.* (1986) reported fundamental numbers in *G. dasyurus* from Azraq Oasis population as 66 and 68 and 70 from Ghor Nimrin (sex chromosomes are not included). WASSIF *et al.* (1969) reported  $FN$  for Egyptian specimens as 69 and 70. For the same species, LAY & NADLER (1975) reported  $FN$  as 68 from Sinai, while WAHRMAN & ZAHAVI (1955) reported  $FN$  for Wagner's

Tab. 1. Diploid chromosome numbers (2N) and Fundamental numbers (FN) for species of the genus *Gerbillus* according to previous studies.

Species	Surface of hind feet	2N	Autosomes		Sex chromosomes			FN	Country	Citation
			M+SM	A+T	X	Y	Y			
<i>G. andersoni</i>	Hairy	40	38	-	S	M	80	Jordan	<b>Present study</b>	
		40	38	-	-	-	80	Egypt	Wassif et al., 1969	
		40	38	-	S	M	80	Egypt	Lay et al., 1975	
		40	-	-	-	-	-	-	Tunisia	Cockrum et al., 1977
<i>G. cheesmani</i>	Hairy	38	32	4	M	-	72	Jordan	<b>Present study</b>	
		38	34	2	M	S	74	Iran	Lay and Nadler, 1975	
		42♀, 43♂	28	12	S	Y1Y2	70	Jordan	<b>Present study</b>	
<i>G. gerbillus</i>	Hairy	42♀, 43♂	34	6	S	Y1Y2	81-83	Palestine (Negev)	Wahrhan and Zahavi, 1955	
		42♀, 43♂	36-38	-	-	-	79, 81	Egypt	Wassif et al., 1969	
		42♀, 43♂	36	6	S	M	74	Tunisia	Jordan et al., 1975	
		42♀, 43♂	32	8	S	Y1Y2	76, 78	Egypt and Morocco	Lay et al., 1975	
		42♀, 43♂	-	-	-	-	-	76-78	Egypt (Sinai)	Lay and Nadler, 1975
<i>G. dasyurus</i>	Naked	60	10	48	M	T	71,72	Jordan	<b>Present study</b>	
		60	6-8	52-54	-	-	66-68	Palestine and North Africa	Wahrhan and Zahavi, 1955	
		60	9-10	50-51	-	-	69-70	Egypt	Wassif et al., 1969	
		60	8	52	-	-	68	Egypt (Sinai)	Lay and Nadler, 1975	
		60	-	-	-	-	66, 68 and 70	Jordan	Qumsiyeh et al., 1986	
		60	8	52	S	A	69	Turkey	Yigit et al., 1997	
<i>G. henleyi</i>	Naked	52	8	42	S	S	62	Jordan	<b>Present study</b>	
		52	11-13	39-41	-	-	63-65	Egypt	Wassif et al., 1969	
		52	8	42	S	A	62♀, 61♂	Morocco	Lay et al., 1975	
		52	10	40	S	S	59♀, 60♂	Senegal	Granjon et al., 1992	
<i>G. nanus</i>	Naked	52	12	38	S	-	62	Tunisia and Burkina Faso	Volobouev et al., 1995	
		52	8	42	S	-	62	Jordan	<b>Present study</b>	
		52	10-14	36-40	-	-	62-66	Palestine (Negev)	Wahrhan and Zahavi, 1955	
		52	8	42	M	A	58	Tunisia	Jordan et al., 1975	
		52	8	42	S	S	62♀, 61♂	Morocco	Lay et al., 1975	
		52	8	42	S	S	62	Iran	Lay and Nadler, 1975	
		52	-	-	-	-	62	Jordan	Qumsiyeh et al., 1986	
		52	8	42	-	-	58-60	S. A. and Pakistan	Volobouev et al., 1995	

gerbil as 66 and 68 from Sinai.

The present results showed the highest degree of similarities between the two bare-footed gerbils, *G. henleyi* and *G. nanus* both in morphologic (ABU BAKER & AMR, 2003) and cytologic features. In addition to the identical chromosome numbers, chromosome features are very much similar between these two species whereas both showed the same number of submetacentric and acrocentric as well as having similar X chromosome morphology.

Diploid and fundamental numbers of *G. nanus* examined in the present study are in agreement with those reported from Palestine (WAHRMAN & ZAHAVI, 1955), Iran (LAY & NADLER, 1975) and Morocco and Pakistan (LAY *et al.*, 1975).

*G. henleyi* karyotypic pattern is consistent with previous reports from Egypt (WASSIF *et al.*, 1969), Morocco (LAY *et al.*, 1975). Total number of autosomal arms was reported from Senegal as 60 (GRANJON *et al.*, 1992) and 62 from Tunisia and Burkina Faso (VOLOBOUEV *et al.*, 1995).

*G. andersoni* was found as an isolated population south of Ras' en Naqb. Results showed a diploid number of 40 and FN=80. This result is consistent with all previous records for this species (Table 1). Due to chromosomal similarities, COCKRUM *et al.* (1976) considered *G. andersoni*, *G. eatoni* and *G. allenbyi* as conspecific, however, LAY (1983) denied this conclusion.

Chromosome morphology for Jordanian specimens of *G. cheesmani* differs from those described by LAY & NADLER (1975) from Iran. The present result indicates the presence of two pairs of uni-armed chromosomes (considered here as telocentric) rather than only one pair of acrocentric chromosomes (LAY & NADLER, 1975). The karyotype is identical to the superficially similar *G. aquilus* in Iran and Pakistan which was previously described as a race of *G. cheesmani* (LAY & NADLER, 1975). *G. aquilus* does not possess any acrocentric chromosomes in its karyotype. LAY & NADLER (1975) presented evidence to consider *G. aquilus* as a valid species.

Cheesman's gerbil is the largest of the known *Gerbillus* species in Jordan; it is superficially distinguished by its more orangish back color and by the undeveloped tail tuft. Unlike other species of hairy-footed gerbils in Jordan, the skull of *G. cheesmani* has a well-developed tympanic bulla which exceeds the supra occipital bone (ABU BAKER & AMR, 2003).

*G. gerbillus* is readily distinguished by its karyotype of 2N=42 in females and 43 in males. The multiple sex chromosome system was first described by MATTHEY (1954). JORDAN *et al.* (1974) presented the karyotypes of a male and a female *G. gerbillus* from Tunisia. Karyotype for this species was previously reported from several regions (table 1). Unlike other

authors (e. g. LAY *et al.*, 1975; JORDAN *et al.*, 1974), the X chromosome in *G. gerbillus* was considered here as a large acrocentric one. The difference in classification schemes of chromosomes according to morphology causes some differences in the calculated FN. This discrepancy could be over-com by C-banding techniques to identify the specific location of the centromere.

Karyotypic studies proved to be useful in distinguishing species of this genus through the wide range of chromosomal morphology and numbers, especially when carried out in combination with both external and cranial morphology. However, given the normal chromosome pairs seen in the karyotypes, the existence of any chromosomal irregularities can only be resolved by using more advanced techniques.

Future studies employing advanced technique (i.e. chromosome banding techniques, mitochondrial DNA sequencing, etc.) may be considered to assess our understanding to these little known animals. Such approaches could be used in cytotaxonomy, morphology and ecology, which may address evolutionary relationships among similar taxa.

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