Chromosomal relationships among three species of jackrabbits (*Lepus*: Leporidae) from Mexico

Consuelo Lorenzo  
*El Colegio de la Frontera Sur, Carretera Panamericana y Periférico Sur, Chiapas, Mexico*

Fernando A. Cervantes  
*Universidad Nacional Autónoma de México, Distrito Federal, México*

Julieta Vargas  
*Universidad Nacional Autónoma de México, Distrito Federal, México*

Follow this and additional works at: https://scholarsarchive.byu.edu/wnan

**Recommended Citation**  
Available at: https://scholarsarchive.byu.edu/wnan/vol63/iss1/2

This Article is brought to you for free and open access by the Western North American Naturalist Publications at BYU ScholarsArchive. It has been accepted for inclusion in Western North American Naturalist by an authorized editor of BYU ScholarsArchive. For more information, please contact scholarsarchive@byu.edu, ellen amatangelo@byu.edu.
Jackrabbits belong to the genus *Lepus* of the family Leporidae. The genus has approximately 29 species, is widespread in both the Old and New World, and is adapted to different habitats (Flux and Angermann 1990). In Mexico there are 15 species of leporids, represented by 10 species of rabbits (*Romero-lagus* and *Sylvilagus*) and 5 species of jackrabbits (*Lepus*). Two species of jackrabbits are endemic: the black jackrabbit, *Lepus insularis*, restricted to the Espíritu Santo Island in the southern portion of the Baja California Peninsula (Thomas and Best 1994), and the Isthmus jackrabbit, *Lepus flavigularis*, occurring solely in the Isthmus of Tehuantepec in the southeastern portion of the State of Oaxaca. The Isthmus jackrabbit is considered the most endangered *Lepus* species at present (Chapman et al. 1990, Flux and Angermann 1990, SEDESOL 1994, Baillie and Groombridge 1996) because of poaching and encroachment of agriculture into its habitat (Flux and Angermann 1990). The white-sided jackrabbit, *Lepus callotis*, is found from central Oaxaca, along the Sierra Madre to Chihuahua, and East Sonora; in the United States it is restricted to 2 valleys in Hidalgo County, New Mexico (Hall 1981, Flux and Angermann 1990). The black-tailed jackrabbit, *Lepus californicus*, has a wide distribution in northern Mexico and Baja California (Hall 1981). The antelope jackrabbit, *Lepus alleni*, has a broad distribution in Mexico and is the largest Mexican jackrabbit. *Lepus flavigularis*, *L. callotis*, and *L. alleni* comprise the *callotis* or white-sided jackrabbit group (Flux and Angermann 1990, Cervantes 1993).

The species of jackrabbits in Mexico are distinguishable by morphological characters (Hall 1981, Flux and Angermann 1990). *Lepus flavigularis* has a black stripe in the nape, extending back from the base of each ear, and the upper parts and flanks are white. *Lepus callotis* has black on the upper part of the tail, and the dorsal parts and flanks are white. *Lepus californicus*, which lacks much white on the sides, has black on the upper surface of the tail and black-tipped ears. *Lepus alleni* is one of the largest North American jackrabbits; it lacks black ear-tips, and white extends from the undersurface well up its sides. There are observable differences in some skull measurements between *L. flavigularis*, *L. callotis*, and subspecies of *L. californicus* from the Mexican Plateau. Particularly, the tympanic bullae of *L. flavigularis* are smaller than in any other *Lepus* species of Mexico, and the lengths of nasals and palatal bridge are larger than those of *L. californicus* and *L. callotis* (Dixon et al. 1983, Cervantes and Lorenzo 1997).

**Key words:** chromosomes, karyotypic evolution, jackrabbits, Lepus, hares, Mexico.
On the basis of morphological and distribu-
tional criteria, species of the callotis group are
more closely related to \textit{L. californicus} than to
any other species of \textit{Lepus}. Probably, a popu-
lation of \textit{L. californicus} became isolated in
Mexico and diverged into \textit{L. callotis}. Later, a
population of this divergent stock became iso-
lated on the western coastal plain, differenti-
fating further into \textit{L. alleni}. In a small area in
southeastern Oaxaca, a 2nd isolated popula-
tion evolved into \textit{L. flavigularis} (Anderson and
Gaunt 1962), which is morphologically distinc-
tive (Cervantes and Lorenzo 1997).

A morphometric study of jackrabbit species
of North America concluded that \textit{L. flavigual-
aris} is more similar to \textit{L. callotis} than to \textit{L.
alleni}. A further cluster analysis showed only
partial separation of \textit{L. californicus} and \textit{L.
callotis}, but nearly complete separation between
the clusters of these 2 species and \textit{L. alleni}.

Species of \textit{Lepus} have the same diploid
chromosome number (2\(n = 48\)); in addition,
their autosomal arms numbers or fundamental
numbers (FN) are very similar, as are their G-
banded patterns. This means that the genus
\textit{Lepus} has been chromosomically conserved
through its karyotypic evolution (Robinson
1981). At present, the karyotype and chromo-
somal classification of the jackrabbit species
examined in this study are known (Lorenzo
1996), but there are no comparisons of their
chromosome bands of euchromatin (G-bands).

The objectives of this paper therefore are:
(1) to compare the non-stained karyotype and
the G-banded pattern in 2 species of the callotis
group (\textit{L. callotis} and \textit{L. flavigularis}) and \textit{L.
californicus} of Mexico; (2) to identify the chro-
omosomal rearrangements that took place in
these species during their karyotypic evolution;
and (3) to determine if the patterns of geographic
variation and distribution of these species co-
incide with the karyotypic changes that led to
the chromosomal evolution of the ancestral
lineage \textit{L. californicus}–\textit{L. callotis}–\textit{L. flavigularis}.

**Materials and Methods**

We studied taxa collected from several locali-
ties in Mexico: \textit{Lepus flavigularis}: Santa Maria
del Mar, Municipio Juchitan, Oaxaca (4 males,
3 females); \textit{Lepus callotis}: Mazamitla, Municipio
Mazamitla, Jalisco (2 males, 1 female); \textit{Lepus
californicus}: 20 km ENE de Apizaco, Municipio
Capula, Tlaxcala (4 males, 3 females). Voucher
specimens were deposited as museum speci-
mens (skin, skeleton, and frozen-tissue samples)
in the mammal collection (Coleccion Nacional
de Mamíferos) of Instituto de Biología, Univer-
sidad Nacional Autónoma de México, in Mex-
ico City.

Slides with mitotic cells were prepared from
bone marrow following conventional colchicine-
hypotonic treatment (Baker et al. 1982). We
determined diploid counts (2\(n\)) by scoring 25
selected metaphase spreads from each speci-
men examined and established fundamental
numbers based on number of autosomal arms
(excluding the sex pair) as defined by Patton
(1967). Computation of the centromeric index
and the nomenclature for centromeric position
on chromosomes follow Levan et al. (1964).

G-bands were produced using trypsin and
Giemsa stain according to the method of De
Grouchy and Turlue (1977). Karyotypes of
the mitotic chromosomes were prepared from
photomicrographs. Individual chromosomal
elements were cut from prints and paired with
their presumed homologue.

**Results**

The chromosomal complements of \textit{Lepus
flavigularis}, \textit{L. callotis}, and \textit{L. californicus}
all share the same 2\(n = 48\) (Table 1). \textit{Lepus
flavigularis} has an FN of 88; its autosomes are 21
pairs of biarmed chromosomes, with 2 pairs of
uniarmed chromosomes. The X and Y chromo-
somes are both median and submetacentric
(Fig. 1). \textit{Lepus callotis} has an FN of 90; its
autosomes are 22 pairs of biarmed chromo-
somes, with 1 pair of uniarmed chromosomes.
The X chromosome is a median submetacen-
tric, the Y chromosome small subtelocentric
(Fig. 2). \textit{Lepus californicus} has an FN of 82; its
autosomes are 18 pairs of biarmed chromo-
somes, with 5 pairs of uniarmed chromosomes. The X and Y chromosomes are both
median and submetacentric (Fig. 3).

Sizes of chromosomes are variable, ranging
from small to large. No secondary constrictions
were observed in any chromosome. Sex chro-
mosomes are biarmed, and compared with their
autosomal counterparts, X chromosomes are
median to large, whereas Y chromosomes are median to small. Sex chromosomes are the typical XX/XY mammalian system.

Comparisons between *L. californicus* and *L. callotis* indicate noticeable differences in autosomal classification that account for the difference in their FNs (Fig. 4). Differences in euchromatin among these taxa are explained by occurrences of 6 pericentric inversions: (1) chromosome pair 6 is metacentric in *L. californicus* but submetacentric (pair 10) in *L. callotis*; (2) chromosome pair 7 is metacentric in *L. californicus*, submetacentric (pair 11) in *L. callotis*; distribution of euchromatin also indicates that an addition of euchromatin took place in chromosome pair 11 of *L. callotis*; (3) pair 19 is telocentric in *L. californicus* but subtelocentric (pair 19) in *L. callotis*; (4) pair 20 is

---

**Table 1.** Diploid chromosome number (2n), fundamental number (FN), and chromosomal classification in 3 species of jackrabbits of Mexico; m = metacentric chromosomes; sm = submetacentric chromosomes; st = subtelocentric chromosomes; t = telocentric chromosomes.

<table>
<thead>
<tr>
<th>Species</th>
<th>2n</th>
<th>FN</th>
<th>Autosomes</th>
<th>Sexual chromosomes</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>L. californicus</em></td>
<td>48</td>
<td>88</td>
<td>-------2-------</td>
<td>2 sm t</td>
<td>Worthington and Sutton 1966</td>
</tr>
<tr>
<td><em>L. californicus</em></td>
<td>48</td>
<td>82</td>
<td>7 4 7 5</td>
<td>sm sm</td>
<td>Present study</td>
</tr>
<tr>
<td><em>L. callotis</em></td>
<td>48</td>
<td>90</td>
<td>5 6 11 1</td>
<td>m t</td>
<td>González and Cervantes 1996</td>
</tr>
<tr>
<td><em>L. callotis</em></td>
<td>48</td>
<td>90</td>
<td>5 6 11 1</td>
<td>sm st</td>
<td>Present study</td>
</tr>
<tr>
<td><em>L. flavicularis</em></td>
<td>48</td>
<td>88</td>
<td>5 4 12 2</td>
<td>sm sm</td>
<td>Uribe-Alcocer et al. 1989</td>
</tr>
<tr>
<td><em>L. flavicularis</em></td>
<td>48</td>
<td>88</td>
<td>5 4 12 2</td>
<td>sm sm</td>
<td>Present study</td>
</tr>
</tbody>
</table>

---

**Fig. 1.** Non-differentially stained karyotypes of *Lepus flavicularis* (m = metacentric chromosomes; sm = submetacentric chromosomes; st = subtelocentric chromosomes; t = telocentric chromosomes; X,Y = sexual chromosomes).
Fig. 2. Non-differentially stained karyotypes of *Lepus callotis* (m = metacentric chromosomes; sm = submetacentric chromosomes; st = subtelocentric chromosomes; t = telocentric chromosomes; X,Y = sexual chromosomes).

Fig. 3. Non-differentially stained karyotypes of *Lepus californicus* (m = metacentric chromosomes; sm = submetacentric chromosomes; st = subtelocentric chromosomes; t = telocentric chromosomes; X,Y = sexual chromosomes).
telocentric in *L. californicus*, but in *L. callotis* it is subtelocentric (pair 20); (5) chromosome pair 21 is telocentric in *L. californicus*, subtelocentric (pair 21) in *L. callotis*; and (6) chromosome pair 22 is telocentric in *L. californicus* but subtelocentric (pair 22) in *L. callotis* (Fig. 5). Moreover, distribution of euchromatin also indicates that additions of euchromatin took place in chromosome pair 9 and 17 of *L. callotis*, and loss of euchromatin took place in chromosome pair 20 of *L. callotis* (Fig. 4).

*Lepus callotis* and *L. flavigularis* have similar FNs. The differences in euchromatin among these taxa are explained by occurrences of 2 pericentric inversions (Fig. 4). Chromosome pair 10 is submetacentric in *L. callotis* but telocentric (pair 23) in *L. flavigularis*. Distribution of euchromatin also indicates that a loss of euchromatin took place in chromosome pair 10 of *L. flavigularis*. Chromosome pair 11 is submetacentric in *L. callotis* but subtelocentric (pair 21) in *L. flavigularis*. Distribution of euchromatin also indicates that a loss of euchromatin took place in chromosome pairs 15 and 17 of *L. flavigularis* (Figs. 4, 6).

Comparisons of *Lepus callotis* and *L. flavigularis* indicate the FN of *L. californicus* is low. Differences in euchromatin between these taxa are explained by the occurrence of 5 pericentric inversions (Fig. 4): chromosome pair 6 is metacentric in *L. californicus* but subtelocentric (pair 20) in *L. flavigularis*; pair 7 is metacentric in *L. californicus*, subtelocentric (pair 21) in *L. callotis*; chromosome pair 19 is telocentric in *L. californicus* but subtelocentric (pair 17) in *L. flavigularis*; likewise, chromosome pair 20 is telocentric in *L. californicus* but subtelocentric (pair 18) in *L. flavigularis*; and pair 21 is telocentric in *L. californicus*, subtelocentric (pair 19) in *L. flavigularis* (Fig. 7).

We constructed a dendrogram on the basis of 2n, FN, G-bands, and chromosomal rearrangements observed in the evolutionary lineage of all taxa studied, where the ancestor of *Lepus* had 2n = 48 (Fig. 8). In summary, 5 pericentric inversions are considered in the basal point of the dendrogram, and they all involved the same chromosome pairs in the lineage that led to *L. callotis* and *L. flavigularis* from the ancestor of *L. californicus*. Just 3 of these pericentric inversions altered the FN.

Another pericentric inversion is considered in the ancestral lineage of *L. callotis*, where the resulting chromosomal pair involved is unique in this lineage; this pericentric inversion
Fig. 5. Differences between G-banded karyotypes of *Lepus californicus* and *L. callotis* are explained by 6 pericentric inversions. *L. californicus* (CL); *L. callotis* (CA). Letters a and b represent points where breaks occurs. The symbol $180^\circ$ represents a $180^\circ$ rotation of a chromosome fragment corresponding to a pericentric inversion.

Fig. 6. Differences between G-banded karyotypes of *Lepus callotis* and *L. flavigularis* are explained by 2 pericentric inversions. *L. callotis* (CA); *L. flavigularis* (FA). Letters a and b represent points where breaks occurs. The symbol $180^\circ$ represents a $180^\circ$ rotation of a chromosome fragment corresponding to a pericentric inversion.
altered the FN. Two pericentric inversions in the ancestral lineage of *L. flavigularis* after diverging from *L. callotis* are unique in *L. flavigularis* (Fig. 8). One of these altered the FN and the other did not. There are 2 more pericentric inversions in the ancestral lineage of *L. flavigularis* that did not alter the FN.

Distribution of euchromatin indicates 3 additions and 1 deletion of euchromatin in chromosomal pairs of *L. callotis* in the ancestral lineage of *L. californicus*–*L. callotis*, and 3 deletions of euchromatin in chromosomal pairs of *L. flavigularis* in the ancestral lineage of *L. callotis–L. flavigularis* (Fig. 8).

**Discussion**

Our findings on the 2n and FN of *L. flavigularis*, *L. callotis*, and *L. californicus* are similar to karyotypes reported in previous studies (except the FN of *L. californicus*).

*Lepus californicus* has the lowest FN (82) compared with *L. flavigularis* (88) and *L. callotis* (90). The most similar FNs were those of *L. callotis* and *L. flavigularis*. This is supported by the difference of only 1 pair of uniarmed chromosomes between them. Morphology of the X chromosome in the species of jackrabbits studied is in accord with the general
patterns of the genus *Lepus* because all species share a median submetacentric X chromosome (with exception of *L. callotis* in González and Cervantes 1996). In contrast, the morphology of the Y chromosome is more variable. Previous reports indicate this chromosome is small telocentric, but our study found it submetacentric to telocentric in the species examined herein. *Lepus flavigularis* and *L. californicus* each present a medium Y chromosome.

Our results on morphology of autosomes and sexual chromosomes differed from previous reports. This turns out to be remarkable in *L. californicus* regarding differences in biarmed and uniarmed chromosomes (Worthington and Sutton 1966) and in morphology of the Y chromosome. *Lepus californicus* has a broad distribution in Mexico and the United States, and within-species comparisons of chromosomal morphology have included different subspecies from distant, isolated localities. There are differences in chromosomal structure of sexual chromosomes in *L. californicus* (González and Cervantes 1996), and the size of the X chromosome is different in *L. flavigularis* (Uribe-Alcocer et al. 1989). These differences could depend on the classification system used by each author and on the inter-individual variation in how chromosomal measurements were made.

In general, the G-banding patterns of the jackrabbit species were clear and consistent. Our results are consistent with previous findings on the karyotypic characteristics of these species and support predictions on the types of chromosomal rearrangements. Similar patterns of chromosomal changes have taken place in other lagomorph lineages. Particularly, paracentric inversions are the mechanisms of change in *Lepus* and additions of heterochromatin in lagomorphs (Stock 1976).

The extant species of jackrabbits, of course, inherited their chromosomal complements from their ancestors. However, this does not mean
that their present complements are the same as those of their ancestors. The chromosomal rearrangements documented in this study illustrate changes fixed through the chromosomal evolution of the genus *Lepus*.

Between *L. californicus* and *L. callotis* exists a difference in 4 pairs of uniarmed chromosomes, due to 4 pericentric inversions that changed uniarmed into biarmed chromosomes in the ancestor of *L. callotis*. *Lepus callotis* also exhibits 2 fewer pairs of metacentric chromosomes due to 2 pericentric inversions.

*Lepus callotis* and *L. flavigularis* differ in only 1 pair of biarmed chromosomes, due to 1 pericentric inversion that changed 1 pair of biarmed into uniarmed chromosomes in the ancestor of *L. flavigularis*. *Lepus flavigularis* also has 1 more pair of subtelocentric chromosomes due to another pericentric inversion.

*Lepus californicus* differs from *L. flavigularis* in having 3 more pairs of uniarmed chromosomes. Three pericentric inversions of uniarmed chromosomes changed them to biarmed in the ancestor of *L. flavigularis*. Two further pericentric inversions resulted in 2 fewer pairs of metacentric chromosomes in the ancestor of *L. flavigularis*.

This is the first study of differentially stained karyotypes that addresses the karyotypic evolution of *Lepus* from Mexico. Our data indicate that the species of jackrabbits studied are closely related, particularly *L. callotis* and *L. flavigularis*. They have a similar FN and a lower number of chromosomal rearrangements. This indicates closer evolutionary development between these 2 species with a common origin derived from 1 ancestral karyotype. Our results confirm the hypothesis on karyotypic changes that led to the chromosomal evolution ancestral of the *Lepus* lineage examined; they also coincide with reported patterns of morphological differentiation and species distribution of the sequence: *L. californicus–L. callotis–L. flavigularis* (Fig. 8).

**Acknowledgments**

We thank P. Delgado, C. Reséndiz, R. Martínez, F.X. Gonzalez, R.M. González, M. Garcia, and M. Uribe-Alcocer for their assistance during fieldwork and laboratory work. This project was supported in part by Dirección General de Asuntos del Personal Académico, Universidad Nacional Autónoma de México (grant IN203793), Comisión Nacional para el Conocimiento y Uso de la Biodiversidad (grant FB312/H054/96), and MacArthur Foundation (grant 282.311.010). Jim Patton and an anonymous reviewer made valuable suggestions on early drafts.

**Literature Cited**


Received 21 December 2000
Accepted 25 March 2002