could be interpreted as a slight segregation of the free $Mn^{2+}$ in pockets, raising the metal concentration in these pockets. The presence of the enzyme itself in the $Mn^{2+}$+ ADP solution has the same effect on the signal, enlarging the linewidth but reducing its intensity. A similar interpretation is therefore considered: the complexing reduces the amount of free $Mn^{2+}$ and the segregation enhances the metal concentration in certain regions of the aqueous solution. Since the $K_S$ of ADP for ATP phosphoribosyltransferase is 175 μM (A. Ballesteros, unpublished), this means that under the present experimental conditions nearly 60% of the MnADP complex is bound to the enzyme. Our results (cf. lines 2 and 3 in the table) do not show significant direct interactions of either MnADP or $Mn^{2+}$ with the enzyme. This indicates that the metal does not interact with the protein, at least not with high affinity. Hence, in the ternary complex (enzyme, nucleotide, metal), the nucleotide must act as a bridge[17]. When histidine is added to the system, it does not affect the spectrum appreciably, as would be expected for a ligand which binds at a molecule separated from the metal by the nucleotide.

## Karyotypes of shrews of the genera *Cryptotis* and *Blarina* (Mammalia: Soricidae)[1]

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*Summary.* Cryptotis parva has a diploid number of 52 and a fundamental number of 50. Blarina brevicauda in Nebraska and Pennsylvania has a diploid number of 49 or 50 and a fundamental number of 48. Blarina carolinensis in Nebraska and Kansas has a diploid number of 52 and a fundamental number of 62. The X-chromosome in all 3 species is a large metacentric chromosome. The Y-chromosome is a small acrocentric in Blarina, whereas in Cryptotis it is a small subtelocentric.

Information has been published (for example, Baker and Hsu[2]; Fedyk and Ivanitskaya[3]; Meylan[4–9]; Meylan and Hausser[10,11]; Hausser et al.[12] and papers cited therein) on various aspects of the karyology of shrews (family Soricidae), but few data are available for the North American genera Cryptotis and Blarina. The genus Cryptotis is represented in the United States by only one species, C. parva (the least shrew), which occurs throughout much of the eastern half of this country as well as in mesic and montane habitats in Mexico and Central America (distribution and habitats summarized by Whitaker[13]). The relationships of this species to other members of the genus in Latin America recently have been reviewed (Choate[14]), and the taxonomy of the species in the United States probably contains few problems. This is not true, however, for the genus Blarina (short-tailed shrews), the distribution of which includes only the eastern half of the United States and adjacent regions of Canada (Hall and Kelson[15]). Prior to 1972, the genus Blarina generally was assumed to consist of only one species, B. brevicauda; a second species, B. telmalestes, had been described from the Dismal Swamp of coastal Virginia and North Carolina (Paul[16]), but was of doubtful taxonomic status (Choate[17]). Then, in 1972, Genoways and Choate[18] presented data indicating that in Nebraska a large, northern subspecies (B. b. brevicauda) and a smaller, southern subspecies (B. b. carolinensis) were behaving as good biological species. Subsequently, most authors have treated these taxa as a distinct species (B. brevicauda and B. carolinensis, respectively). Later, based on their study of fossils of Blarina, Graham and Semken[19] recognized a third Recent species (B. kirtlandi) in the genus. We continue to recognize only 2 species of Blarina in this paper.

Certainly, much additional systematic work is needed on North American shrews, especially Blarina. To aid in these studies, we present below the karyotypic data on these shrews that we have amassed over the past several years. The only previously published information for these shrews pertained to B. brevicauda talpoides (Meylan[6,8]) and B. b. kirtlandi (Lee and Zimmerman[20]). All karyotypic preparations were made according to methods described by Baker[21].

Cryptotis parva (figure 1). The diploid number for the least shrew is 52 and the fundamental number without the sex-chromosomes is 50. The autosomes, which are all acrocentric, range in size from one large pair to several minute pairs. The X-chromosome is a large metacentric and the Y-chromosome is a small subtelocentric.

Blarina brevicauda (figure 2). Specimens of B. b. brevicauda from Nebraska have a diploid number of either 49 or 50 and a fundamental number of 48. The polymorphism in diploid number is the result of a Robertsonian fission/fusion between a pair of large acrocentric autosomes and a pair of small acrocentric autosomes. Specimens with a diploid number of 48, resulting from fusion of both members of these pairs, were not represented in our material. The X-chromosome is a large metacentric and the Y-chromosome is a small acrocentric.

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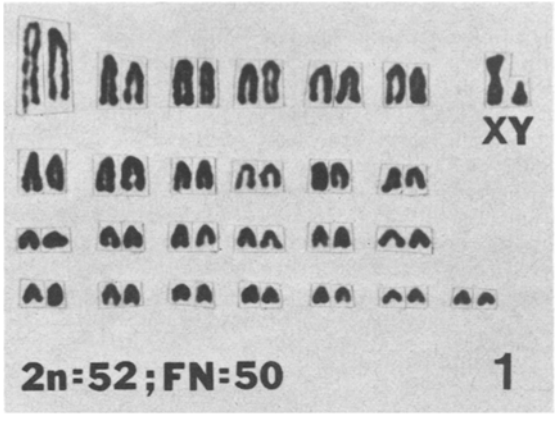
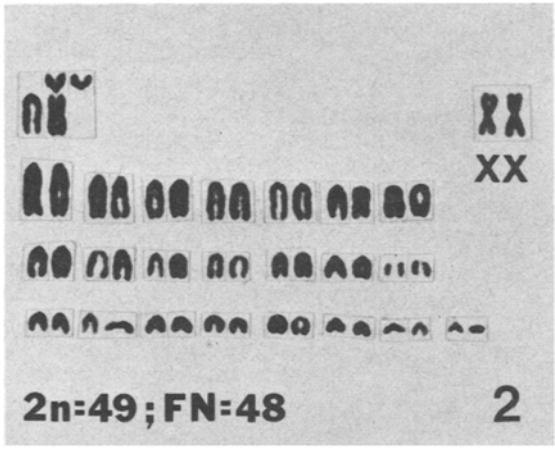
These diploid and fundamental numbers are the same as those reported by Meylan[6,8] for B. b. talpoides from Ontario and by Lee and Zimmerman[20] for B. b. kirtlandi from Illinois. Our 2 specimens of B. b. kirtlandi from Pennsylvania also agree in these numbers. The Robertsonian polymorphism described above also was noted by Meylan and by Lee and Zimmerman; Meylan found 2 N = 50 in 16 and 2 N = 49 in 5 specimens, whereas Lee and Zimmerman found 2 N = 50 in 46 specimens, 2 N = 49 in 6, and 2 N = 48 in 1 specimen. Combined with our specimens in which 6 had 2 N = 50 and 4 had 2 N = 49, this gives a ratio of 68:15:1 for this Robertsonian polymorphic system.



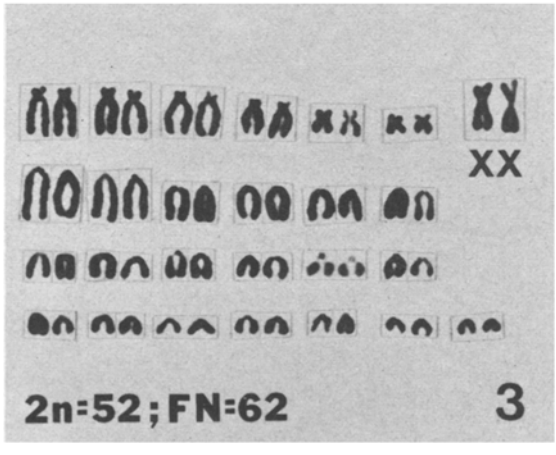




Fig. 1. Male Cryptotis parva from 4 1/2 miles N, 7 miles E Palo Pinto, Palo Pinto Co., Texas. – Fig. 2. Female Blarina brevicauda from 1 mile W Kearney, Buffalo Co., Nebraska. – Fig. 3. Female Blarina carolinensis from 3 miles W Hays, Ellis Co., Kansas.

Meylan[6] described (but did not illustrate) the Y-chromosome of his material as being a very small metacentric chromosome, whereas we found it to be a small acrocentric. Lee and Zimmerman[20] do not describe the Y-chromosome in their specimens.

Blarina carolinensis (figure 3). Specimens of B. carolinensis from Nebraska and Kansas had a diploid number of 52 and a fundamental number of 62. There are 4 pairs of large to medium-sized subtelocentric autosomes and 2 pairs of small submetacentric autosomes; the remaining 19 pairs of autosomes are acrocentric. The X-chromosome is a large metacentric and the Y-chromosome is acrocentric.

The specimen of B. carolinensis from 1 mile west Otoe, Otoe County, Nebraska, was obtained only 15 miles south of the locality of capture of the 3 specimens of B. brevicauda from Cass and Sarpy counties. The existence of these divergent karyotypes within such a short distance lends support to the contention, based on mophological data (Genoways and Choate[18]), that the 2 phena of Blarina in Nebraska represent distinct species. None of our karyological data indicate interbreeding between these taxa, but considerably more data, especially from zones of contact, will be needed before a definitive statement to this effect can be made.

*Discussion.* The karyotypes of these 3 shrews of the Tribe Blarini show some interesting similarities and differences. Cryptotis parva has the same diploid number as Blarina carolinensis; however, the entirely acrocentric complement of chromosomes in C. parva more nearly resembles that of B. brevicauda (although the latter possesses 2 fewer autosomes). The 2 species of Blarina differ in both diploid numbers and morphology of at least 6 pairs of autosomes. The morphology of the X-chromosome apparently is the same in the 3 species, but the Y-chromosome is acrocentric in both species of Blarina and subtelocentric in Cryptotis. The origin of these chromosomal differences and the course of chromosomal evolution in this group are unclear at the present time. It is hoped that planned studies of chromosomal banding patterns will help resolve these problems.

The discovery that the nominal taxa B. brevicauda, kirtlandi and talpoides possess the same chromosomal numbers and Robertsonian polymorphism casts serious doubt, in our minds, that these are distinct from each other at the species level. Consequently, we have not followed the proposal by Graham and Semken[19] that kirtlandi represents a species distinct from brevicauda. If kirtlandi is a distinct species, then specific divergence between kirtlandi and brevicausa must have been much more recent than that between brevicauda and carolinensis; the Robertsonian polymorphism, which is present in brevicauda but not in carolinensis, would need to have developed and become established in populations of brevicauda subsequent to its split with carolinensis and prior to divergence of brevicauda and kirtlandi.

*Specimens examined.* Cryptotis parva: 4 1/2 miles N, 7 miles E Palo Pinto, Palo Pinto Co., Texas, 1.

Blarina brevicauda: 1 mile W Kearney, Buffalo Co., Nebraska, 5; 1/2 mile W Manley, Cass Co., Nebraska, 1; 1 mile N, 2 miles W Weeping Water, Cass Co., Nebraska, 1; 4 miles N Springfield, Sarpy Co., Nebraska, 1; 2 miles S Rector, Westmoreland Co., Pennsylvania, 1; 3 miles S Rector, Westmoreland Co., Pennsylvania, 1.

Blarina carolinensis: 3 miles W Hays, Ellis Co., Kansas, 5; 5 miles N, 2 miles W Parks, Dundy Co., Nebraska, 3; 1 mile W Otoe, Otoe Co., Nebraska, 1.

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