FINAL REPORT

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Project No. 45

Taxonomic Status of Hog-nosed Skunks (Genus Conepatus) in Texas

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STATE:	Texas	**GRANT NO.:**	E-1-7

GRANT TITLE: Endangered and Threatened Species Conservation

PERIOD COVERED: 1 September 1994 - 31 August 1995

PROJECT NUMBER: 45

PROJECT TITLE: Taxonomic Status of Hog-nosed Skunks (Genus *Conepatus*) in Texas

PROJECT OBJECTIVE: To utilize morphometric and genetic analyses to determine the taxonomic status of the *Conepatus* complex of species in Texas.

ACCOMPLISHMENTS: Final Report. See attachment.

DEVIATIONS: 1. Twenty-four, rather than 30, cranial measurements were made on each specimen for the morphometric analyses.
2. Contractors elected not to continue isolating nuclear DNA microsatellite loci because they felt more attention should be placed on resolving the major taxonomic issues which could be better addressed using mitochondrial DNA.

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ABSTRACT

A combination of morphological and molecular characters were used to evaluate the current taxonomy of hog-nosed skunks, genus *Conepatus*, from primarily the United States and Mexico. Variation in color pattern was examined for the taxa (*Conepatus leuconotus texensis, C. mesoleucus mearnsi*, and *C. m. telmalestes*) from Texas and adjacent states. Although color patterns associated with the dorsal region and head have been used to recognize species and subspecies, both these traits were shown to be variable and overlap among the named taxa. This suggests that color pattern is not an accurate character for the recognition of either subspecies or species. Morphometric analyses were performed using 24 cranial characters and 614 museum specimens. The three species from Central and South America (*C. chinga, C. humboldtii*, and *C semistriatus*) were morphologically distinct, whereas all the subspecies of both *C. leuconotus* and *C. mesoleucus* demonstrated considerable overlap. The only exception may be *C. m. telmalestes*, which was distinct with one morphological analysis. Nucleotide sequence data from the mitochondrial control region (D-loop) were used to examine primarily taxa from the United States and Mexico. These data also revealed considerable overlap among the *C. leuconotus* and *C. mesoleucus* subspecies, with the possible exception of *C. m. figginsi*. As a result of both the morphological and genetic analyses, no more than three significant management units of hog-nosed skunks are recognized. These units include *C. leuconotus leuconotus* (a taxon including the subspecies of both *C. leuconotus* and *C. mesoleucus*), *C. l. telmalestes* (previously recognized as *C. mesoleucus telmalestes*), and *C. l. figginsi* (previously *C. mesoleucus figginsi*).

TAXONOMIC STATUS OF HOG-NOSED SKUNKS (GENUS *CONEPATUS*)

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INTRODUCTION

Many species of mammalian carnivores are provided protection under the Endangered Species Act of 1973, yet the actual number of threatened or endangered carnivores probably is much higher. The primary reason for some species of carnivores not being provided special protection is the absence of biological information pertaining to the systematics, distribution, relative abundance, and ecology of taxa of uncertain status. The unfortunate problem is that many carnivore populations have reached the point of no return prior to the collection of such biological data. For example; in 1920 an estimated 500,000 black-footed ferrets existed, and by the early 1980s the number in the wild declined to approximately 17 (Clark, 1987). Between 1851 and 1981, only one population of black-footed ferret was studied (Clark, 1987). Fortunately, captive breeding programs have increased the current number of black-footed ferrets in the wild.

The real problem faced by those interested in the conservation of carnivores or any form of biodiversity are two-fold. First, how can populations or species at risk be identified prior to their complete extirpation? Second, how can historical and recent data on populations be linked in an effort to devise proper management schemes for the conservation of unique populations and species? The first step toward answering these questions is to identify unique populations through an examination of geographic variation defined by morphology and/or genetics. The uniqueness of particular stocks provides a rational basis for the identification of taxa that need special protection (Moritz, 1994).

In this study we examine both morphologic and genetic variation in hog-nosed skunks of the genus *Conepatus* . Several taxa of hog-nosed skunks currently are considered as candidates for protection. Recent biological information from surveys and research in Texas provide strong evidence of a drastic decline for populations of hog-nosed skunks in the eastern and Gulf Coast regions of Texas (Schmidly, 1983; Rappole and Tipton, 1987; Dragoo et al., 1988). From a taxonomic standpoint these populations are considered as two unique geographic units or species. A detailed systematics study of hog-nosed skunk taxa from Texas and adjacent geographic regions is absolutely imperative if one is to make informed decisions concerning the uniqueness of the declining genetic stocks of hog-nosed skunks in the United States. In an effort to assess the taxonomic status and uniqueness of the currently recognized species and subspecies in the United States, two experimental approaches were employed. First, specimens of hog-nosed skunks from museums throughout the United States were used to evaluate geographic patterns of morphological variation in both color patterns and 24 cranial measurements, including tooth wear and suture lines used to age specimens. Second, the degree of genetic differentiation distinguishing various taxa of hog-nosed skunks in Texas and the continental United States was examined by sequencing selected regions of the mitochondrial control region (D-loop).

Current Systematics of Hog-nosed Skunks

According to Van Gelder (1968), hog-nosed skunks of the genus *Conepatus* have one of the largest geographic distributions of any genus of terrestrial mammal in the Western Hemisphere. These skunks occur from southern Colorado to Argentina. Currently, there are five recognized species of hog-nosed skunks (Wilson and Reeder, 1993). Two of these species, *Conepatus chinga* and *Conepatus humboldtii*, occur in South America, and three species of hog-nosed skunks occur in North and Central America (Hall, 1981). *Conepatus mesoleucus* (with ten subspecies) ranges from the southwestern United States through most of Mexico and into Central America. *C. leuconotus* is represented by two subspecies and has one of the smallest distributions, occurring along the coastal plain of the Gulf of Mexico from Veracruz to the southern tip of Texas. The third species, *C. semistriatus*, consists of three subspecies in Central America and five subspecies in South America.

In the United States the distribution of *C. leuconotus* is restricted to a region of south Texas that includes, but is not limited to, the Gulf Coastal Plains from Aransas County south and southwest to Cameron and Webb counties (Fig. 1). The subspecies in Texas, *C. l. texensis*, continues into Mexico as far south as western San Luis Potosi and northern Veracruz (Hall, 1981). The other subspecies, *C. l. leuconotus*, is restricted to Veracruz, Mexico. *Conepatus leuconotus* is presumed to be allopatric or at most parapatric with the closely-related and widely distributed western hog-nosed skunk (*C. mesoleucus)*. In the continental United States *Conepatus mesoleucus* is subdivided into five subspecies, *C. m. figginsi*, *C. m. fremonti*, *C. m. mearnsi*, *C. m. telmalestes*, and *C. m. venaticus*. The most widespread subspecies is *C. m. mearnsi*, which occurs in the southern portion of New Mexico, south and southwest Texas, and a large portion of northern Mexico. The remaining four subspecies occur on the periphery of the range in Arizona, Colorado, and southeastern Texas. There are five additional subspecies (*C. m. filipensis, C. m. mesoleucus, C. m. nelsoni, C. m. nicaraguae, and C. m. sonoriensis,*) that occur in Mexico and Central America.

Since the designation of *Conepatus leuconotus* and *C. mesoleucus* as distinct species (Lichtenstein, 1832; Audubon and Bachman, 1851), the systematics of named taxa within the genus *Conepatus* has been controversial. Based on the descriptions of the different species, Coues (1877) could find no justification for more than one species in the United States and Mexico. In support of Coues' contention, Hall and Kelson (1952) reported that the only significant difference between *C. leuconotus* and *C. mesoleucus* was size, with color pattern differences between these two taxa being at most an indicator of geographic variation rather than a consistent character for the recognition of distinct species. They further stated that proof of intergradation, or lack of it, could best be sought by obtaining specimens from areas between the distributions of these two taxa. Raun and Wilks (1961) subsequently reported a specimen from Atascosa County that, based on size and color pattern, was intermediate between *C. mesoleucus* and *C. leuconotus*. They stated that "although the majority of the published checklists treat *mesoleucus* and *leuconotus* as separate species, most workers agree that the two should be conspecific."

Part of the current controversy over the number of species and uniqueness of geographic variation within the genus *Conepatus* can be related to the taxonomic characters and the overall methodological approaches used in these early systematic studies. For instance, the taxonomy of hog-nosed skunks is based on cranial morphology, body size, and color patterns, all of which are quantitative traits and may be strongly influenced by environmental factors. In spite of this fact, with the exception of Van Gelder's (1968) study of non-geographic variation of cranial measurements and color patterns within hog-nosed skunks from Uruguay, no detailed analysis of non-geographic variation of the taxonomic characters used to describe hog-nosed skunk taxa has been conducted. This is important, because subspecies in Texas that are either extinct or possibly endangered have been described on the basis of these potentially environmentally influenced characters.

METHODS AND MATERIALS

Morphological Analyses

A total of 614 specimens from the 850 specimens available in museums was examined from 22 museum collections (Appendix 1). Twenty-four cranial characters (Fig. 2) were measured to the nearest 0.1 mm with dial calipers including: condylobasal length (CL, B to B1 on figure), basilar length of hensel (BAS, A to A1), palatilar length (PL, H to A1), postpalatal length (PPL, H to A), length of maxillary tooth row (MTR, K to K1), length of PM3 (PM3, P to P1), length of PM4 (PM4, P1 to Q), length of molar (ML, Q to K1), length of bulla (BL, T to T1), zygomatic breadth (ZB, C to C1), mastoid breadth (MB, D to D1), interorbital breadth (IB, E to E1), postorbital breadth (PB, F to F1), width across incisors (WAI, L to L1), width across canines (WAC, M to M1), diameter of canine (CD, K to O), width across molars (WAM, N to N1), width of molar (MW, S to N), width of bulla (BW, U to U1), width of interpterygoid fossa (FW, V to V1), height of cranium (CH, J to J1), length of lower carnassial (LC, W to W1), height of coronoid (HC, X to X1), length of mandible (LM, Y to Y1). These measurements were used to examine patterns of morphological variation using morphometric analysis. All these analyses were conducted using the Statistical Analysis System 84.2 (SAS Institute Inc., 1982*a*, 1982*b*). Descriptive statistics (mean, range, and *SE*) were obtained for each character in each sample. Data were log transformed and any characters with a *CV* above 5% after transformation were excluded from further analysis.

Two preliminary analyses were performed in an effort to determine if individuals from different age and sex classes could be pooled for between group comparisons. In the first analysis, individuals from all four classes (adult males, subadult males, adult females, and subadult males) were treated as individual taxonomic units and variation among these groups was examined using principal component analysis. Second, Tukey's student range test was used to compare the four classes for significant differences related to size, a characteristic that is expressed in high frequency along the first two principal components. Both principal component analysis and discriminant function analyses were used to evaluate the degree of differentiation among populations of hog-nosed skunks.

In addition to the comparisons of morphometric variation among hog-nosed skunks, variation in color pattern was examined. Color photographs were taken of museum skins, and 85 skins representing the currently recognized taxa from Texas were examined. These samples included 21 *Conepatus leuconotus texensis*, 11 *Conepatus mesoleucus telmalestes*, and 53 *Conepatus mesoleucus mearnsi*. Specimens were grouped into taxonomic categories based on geographic locality and assigned to one of six color pattern categories (Fig. 3). These categories are: 1) Category 1 - the median dorsal stripe terminates leaving no white on the rump, and at least one half of the tail is white to the tip (the width of the stripe near the shoulders varied from narrow to wide); 2) Category 2 - the median dorsal stripe and white on the tail is connected by a narrow stripe of white. The basal third of the tail is black on the sides (the width of the stripe between the shoulders ranged from narrow to wide); 3) Category 3 - the median dorsal stripe is narrow in the length between the shoulders and the hips, with only a slight constriction at the hips; 4) Category 4 - the median dorsal stripe is narrow at the neck and expands in the mid-region of the back; 5) Category 5 - the median dorsal stripe is wide from the neck to the hips; 6) Category 6 - the median dorsal stripe completely covers the back. In addition, these specimens were grouped into categories based on whether the terminal white stripe of the head was wedge-shaped, curved, or truncated (Fig. 4).

<u>Genetic Analyses</u>

DNA from frozen tissue (heart, liver, or kidney) was isolated using either a direct purification of mitochondrial DNA (mtDNA) by cesium chloride/propidium iodide gradient centrifugation (Brown, 1980) or phenol/chloroform extraction of total DNA (Maniatis et al., 1982). Total

DNA from museum specimens was isolated using a modified technique described by Paabo et al. (1988). In this technique an approximately 3 to 4 mm^2 piece of dried skin from the museum specimen was combined with collagenase and incubated at 37°C with slow agitation for 3 hours. This solution was digested at 37°C for 20 hours in a 880 ul solution containing 1% sodium dodecyl sulfate (SDS), 10mg/ml of dithiothreitol, and 0.5 mg/ml proteinase K. After digestion the solution was phenol/chloroform extracted and ethanol precipitated.

D-loop Analysis - The entire mitochondrial control region (D-loop) from three species (*Conepatus leuconotus*, *Conepatus mesoleucus*, and *Conepatus chinga*) was amplified using the polymerase chain reaction (PCR). Double stranded DNA products of the D-loop were amplified with primers L16272 - 5'-TACACTGGTCTTGTAAACC-3' and H1008-5'-AAGGCTAGGACCAAACCT-3'. The names of the oligonucleotides indicates the heavy (H) or light (L) strand and the position of the 3' end of the oligonucleotide according to the numbering of *Phoca vitulina* (Arnason and Johnson, 1992). Double stranded DNA was PCR amplified with *Taq* DNA polymerase using the following parameters: denaturation 95°C for 1 min, annealing at 45°C for 1 min, and extension at 72°C for 1 min 15 sec and 30 cycles. As suggested by Paabo, all PCR reactions had amplification controls, in which water was added to the reaction in the place of DNA extract. Double stranded PCR products were ligated into the pBluescript (Stratagene) plasmid modified to contain thymine overhangs at blunt 3' ends by digestion with *Eco*RV and incubation with dTTP and *Taq* polymerase. Plasmid inserts were sequenced by the technique of Kraft et al. (1988) using several additional PCR primers. As a result of potential error associated with *Taq* (Saiki et al., 1988), at least two clones were sequenced per taxon. In cases in which the two clones did differ, a third clone was sequenced and a consensus sequence was derived.

The Clustal V program (Higgins et al., 1992) and visual inspection were used to align the entire D-loop sequences from the above three species (Fig. 5). These aligned sequences were used to identify regions within the D-loop that might be suitable for the design of primers bracketing regions that were both variable and small in size (250 base pairs or less). These smaller regions of the D-loop were used for more extensive comparisons of variation among the various populations of

Conepatus mesoleucus and *Conepatus leuconotus* in Texas and adjacent areas. In the case of these regions, double stranded DNA amplified using PCR was sequenced directly by cycle sequencing (Gibco BRL). We had to employ this strategy because DNA isolated from museum specimens was degraded, thus reducing our ability to isolate larger fragments of D-loop via PCR amplification. In addition to specimens of *Conepatus*, the smaller regions of the D-loop also were sequenced for several other taxa of skunks including: *Mephitis mephitis* (striped skunk), *Mephitis macroura* (hooded skunk), and *Spilogale putorius* (eastern spotted skunk). The oriental stink badger, *Mydaus marchei*, was used as an outgroup for detailed phylogenetic analyses.

Parsimony analyses of the aligned D-loop sequences were conducted with PAUP 3.1.1 (Swofford, 1993). Variable nucleotide positions were treated as unordered discrete characters, and insertion/deletion characters were coded as newstate. A phylogenetic tree was obtained using 1000 heuristic (tree bisection and reconnection algorithm) searches in which input order of taxa was randomized. This phylogenetic analysis was used to evaluate the uniqueness of any recognized subspecies and species of *Conepatus* relative to other skunk taxa.

DNA Microsatellite Loci - Originally, we had proposed to examine some hypervariable loci from the nuclear genome. These variable loci are known as microsatellites because they consist of sequences containing tandem repeats of a 2-5bp subunit that are inherited as a single locus (Tautz, 1989). Although we did isolate approximately 40 microsattelites from *Conepatus leuconotus* and designed primer pairs for three of those loci, we elected not to continue surveying variation with these nuclear gene markers because we felt that more attention should be placed on resolving the major taxonomic issues related to hog-nosed skunks. These microsatellite loci have considerable potential for detailed population studies of hog-nosed skunks but they are less useful for determining phylogenetic relationships among presumably divergent taxa. Mitochondrial DNA, however, is a better choice for identifying unique populations of hog-nosed skunks, and the results can be compared to the morphological analyses that were conducted. Below is a brief description of the experimental procedures used to isolate the microsatellite loci.

Isolated total genomic DNA was digested with *Sau*3A and electrophoresed on a 0.8% agarose gel. DNA fragments between 500 and 800 bp were removed from the gel, and the DNA was extracted. A plasmid DNA library for the hog-nosed skunk was made by ligating the extracted DNA into a Bluescript cloning vector, and the ligation was used to transform DH5alpha competent *E. coli* cells. The transformation was plated on LB plates with ampicillin, X-gal, and IPTG, and screened for positive colonies. The positive clones were replated on LB plates and lifted off the plates with nylon membranes. The membranes were denatured and neutralized, dried, prewashed in a hybridization solution, and then probed with dinucleotide repeats (CA repeats). This hybridization procedure selected specifically for positive clones containing microsatellites. The positive clones were then sequenced, and specific primers were made to the unique sequences bracketing the microsatellite repeats. The following is a list of primer sets that have been developed: 1) CM2 (2 sets) - 5' TGTAAAACGACGGCCAGT 3', 5' CGGATAACAATTATCACACAGG 3' & 5' TAAGTCCCACATCCACAGAGG 3', 5' ACTCAACCTAAGGCATCGAGT 3'; 2) CM3 (1 set) - 5'AGCGAAATAAGTCAACCCAAC 3', 5' ACTCCACGTTAGGTGCAGAGC 3'; 3) CM5 (1 set) - 5' TTGAGTTCCCTCTCTGGCTGT 3', 5' AATTTCTCCCTTTTCCCCATA 3'. The first set brackets a 12 mer CT repeat, the second an 18 mer CA repeat, and the third a 16 mer A repeat. An additional 15 microsatellites containing CA repeats have been isolated but not sequenced, and 15 to 20 plasmids containing microsatellites with GACA repeats are available.

RESULTS

Variation in Color Pattern

Relative to the six categories of stripe pattern, *Conepatus mesoleucus mearnsi* was represented in five of the categories, with 1.9% of the specimens in category 2, 18.9% in category 3, 13.2% in category 4, 41.5% in category 5, and 24.5% in category 6 (Fig. 6A). The terminal white stripe on the head was wedge-shaped in 26.4%, curved in 54.7%, and truncated in 18.9% (Fig. 6B). *C. m. telmalestes* was represented in four of the six categories (3-6), ranging from 9.1% in category 4 to 45.5% in category 3, and subsets of these specimens grouped in all three categories of stripe pattern on the head region (Figs. 6A and 6B). The Gulf Coast hog-nosed skunk, *Conepatus leuconotus texensis,* also was represented in five of the six color pattern categories (Fig. 6A), with 23.8% in category 1, 47.6% in category 2, 14.3% in category 3, 9.5% in category 4, and 4.8% in category 5. Again, there were representative specimens for all three head patterns (Fig. 6B). As can be seen in figure 6A, there was a trend for *C. l. texensis* specimens to have a stripe pattern more like categories 1 and 2, whereas a higher percentage of *C. m. mearnsi* individuals were like categories 4 and 5. Nevertheless, considerable overlap in color pattern on both the back and head were observed.

Morphological Variation

As can be seen in the descriptive statistics for the subspecies *Conepatus mesoleucus mearnsi*, males are larger than females for the measurements recorded in this study (Table 1). A Tukey's studentized range test and principal component analysis demonstrated a significant difference between males and females for most of these measurements (data not shown). Therefore, all further analyses were conducted on males and females separately. Table 2 shows the descriptive statistics recorded for the measurements used to compare all taxa.

A total of 228 females (43 excluded because of missing values) were used in a canonical discriminant analysis. Males showed a similar pattern to females, and results are not reported for them. A principal component analysis for females was conducted using the remaining 21 cranial characters. Because the first principal component is primarily related to size, it was eliminated, and principal components 2 through 21 were used in a canonical discriminant function analysis (Owen, 1987). Table 3 shows the contribution of each of the 21 prinicipal components to the variation of cranial measurements, and Table 4 provides a breakdown of the percent contribution that each individual character had for each principal component. The first two canonical vectors accounted for 72% of the variation in the 21 cranial characters (3 characters were excluded from the analysis based on the descriptive statistics) used (Table 5). Figure 7 shows a plot of all individuals used in the analysis, and Figure 8 shows a plot of the mean values for each recognized taxon, with ellipses enclosing 95% confidence limits around the centroid means. The small sample sizes for *Conepatus mesoleucus telmalestes*, *Conepatus leuconotus leuconotus*, and *Conepatus humboldtii* precluded the derivation of a 95% confidence limit for these taxa. Three subspecies of *Conepatus mesoleucus* (*C. m. figginsi*, *C. m. fremonti*, and *C. m. filipensis*) could not be examined either because of missing data associated with the specimens, unknown sex, or the existence of only a single specimen. As can be seen from both these figures (7 and 8), four distinct groups can be recognized. Three of these groups represent the three South American and Central American species, *Conepatus chinga*, *Conepatus humboldtii*, and *Conepatus semistriatus*. The fourth group represents a series of overlapping groups depicting subspecies of both *Conepatus mesoleucus* and *Conepatus leuconotus*. Except for some possible differences in size among some individuals within these subspecies, there was not a significant break among taxa represented in this fourth group.

The canonical vectors derived from the discriminant analysis were used to produce taxonomic distances (Manhattan distances). Phenetic variation was evaluated using the distance values and the neighbor-joining procedure (Saitou and Nei, 1987). Figure 9 shows the relationships among the various taxa examined. As seen in the canonical discriminant analysis (Fig. 8), the Central and South American species grouped separately from the representative taxa of *Conepatus leuconotus* and *Conepatus mesoleucus*. Except for possibly *Conepatus mesoleucus telmalestes* and *Conepatus mesoleucus venaticus*, the remaining subspecies of both *Conepatus leuconotus* and *Conepatus mesoleucus* were intermixed. The problem, however, with the two more distinct subspecies of *Conepatus mesoleucus* is that both these taxa were represented by small numbers of individuals.

<u>Genetic Variation in the Mitochondrial D-loop</u>

After comparing D-loop variation among *Conepatus leuconotus*, *C. mesoleucus*, and *Conepatus chinga* (Fig. 5), two regions were selected for detailed comparisons of nucleotide sequence variation within and among several subspecies of hog-nosed skunks in the United States. These two regions included: 1) an approximately 170 base pair (bp) region bracketed by primers L398 and H601; 2) an approximately 230 bp region bracketed by primers L724 and H 282. These two regions were sequenced for 22 taxa including the outgroup taxon *Mydaus*, two striped skunks (*Mephitis mephitis* and *M. macroura*), the eastern spotted skunk (*Spilogale gracilis*), *Conepatus chinga*, four representatives of *Conepatus leuconotus*, eight individuals of *Conepatus mesoleucus mearnsi* from several geographic localities, and the subspecies *Conepatus mearnsi sonoriensis*, *C. mesoleucus figginsi*, and *C. mesoleucus venaticus*, all of which represent more peripherially isolated races (Fig. 10). Many of these sequences were obtained from DNA extracted and amplified from museum specimens.

Figure 11 represents a 50% majority rule consensus tree of 12 equally most parsimonius trees (derived using a heuristic search in PAUP) of length 166, consistency index (CI) of 0.843, and retention index (RI) of 0.832. Out of the 427 characters used in this analysis, 98 were informative. As can be seen from the consensus tree, two of the *Conepatus leuconotus* from Tamaulipas, Mexico, formed a monophyletic group. Both of these specimens were collected at the same locality. With the exception of the two representatives of *Conepatus mesoleucus sonoriensis* forming a monophyletic group with a bootstrap value of less than 50%, the only major separation among the various North American hog-nosed skunks was that involving *Conepatus mesoleucus figginsi,* which grouped separately from the other individuals examined. A South American species, *Conepatus chinga,* was found to be the most divergent hog-nosed skunk taxon, differing from the other species by approximately 6.28%. *C. m. figginsi* differed from the other major clade by 2.5%, and skunks within the clade containing the remaining individuals averaged 0.65%. The two species of *Mephitis* differed by approximately 12%. As can be seen in this figure, the eastern Texas hog-nosed skunk (*C. m. telmalestes*) and *C. m. fremonti* were not examined, because we could not obtain PCR amplification products from the museum tissues.

DISCUSSION

Color Pattern as an Indicator of Taxonomic Distinction

Individual color variation is quite common within the subfamily Mephitinae. Davis (1974) and Hall (1946) found stripe patterns to be highly variable in the striped skunk, *Mephitis mephitis*. Hall (1946) found one litter of skunks in Kansas that contained three of four distinct color patterns recognized by fur traders, and Hall and Villa R (1949) found six hooded skunks (*Mephitis macroura*), collected within a three mile radius, that ranged from a single white spot on the head to a white stripe down the back and tail as well as a stripe down each side. Van Gelder (1968) made a similar observation for a population of *Conepatus* from Uruguay, and Patton (1974) found a specimen of *Conepatus mesoleucus mearnsi* from Terrell County, Texas, that had the "typical" *Conepatus leuconotus* pattern.

When Lichtenstein (1832) originally described *Conepatus leuconotus* and *Conepatus mesoleucus*, he relied heavily on color patterns to distinguish the two species. He felt that characters such as dentition were "arbitrary" and of no use to taxonomists, but that color pattern was more reliable. Merriam (1902) and Bailey (1905) relied on Lichtenstein's (1832) description of the species when they described the subspecies in Texas, and most recent keys of hog-nosed skunks have emphasized color pattern as a major distinguishing characteristic for the identification of taxa (Davis, 1974; Hall, 1981; Schmidly, 1984).

Although color pattern has been used in the past as a taxonomic character to diagnose unique populations and taxa of hog-nosed skunks, a closer examination of color pattern variation suggests that the degree of variation associated with this character is too large for any meaningful use as a diagnostic character. For instance, Goldman (1922) realized that color pattern in hog-nosed skunks is not a valid taxonomic character. Under the remarks section of his description of *Conepatus mesoleucus venaticus* (Arizona hog-nosed skunk) he states, "The extension of white of upper parts is variable as usual in the species." Our study of color pattern supports Goldman's (1922) conclusions. In Lichtenstein's (1832) description the terminal shape of the stripe on the head was used as a diagnostic feature. Nevertheless, in our examination of this characteristic, considerable overlap among recognized taxa was found, with all three categories (sharp, wedge-shaped, and truncated) observed for different species and subspecies. The same can be said for stripe pattern on the back and tail. Although there is a trend for hog-nosed skunks from the northwestern part of their range to have more white on the back, there is still considerable overlap with respect to stripe pattern, making it difficult to identify either species or subspecies on the basis of color pattern. Therefore, if color pattern were used as the sole characteristic for the identification of distinct groups of hog-nosed skunks, one would assign all populations of hog-nosed skunks from the United States to the same taxonomic group.

Morphometric Variation

Although the three Central American and South American species are distinct from those species seen in Mexico and the United States, the evidence for the recognition of the currently named species and subspecies of *Conepatus* is less apparent. There is a trend toward *Conepatus leuconotus* being somewhat larger than *Conepatus mesoleucus* (Table 2), yet the phenetic analyses performed for representative subspecies of these two taxa did not reveal any apparent difference that would merit the recognition of these two forms as distinct species. In addition, morphological distinction among most of the currently recognized subspecies of *Conepatus mesoleucus* also is not apparent. Although the phenetic analysis did reveal *C. m. telmalestes* and *C. m. venaticus* to be somewhat divergent (Fig. 9), the specimens that could be examined for these taxa fall well within the large group identified in the canonical discriminant analyses (Figs. 7 and 8).

Mitochondrial Gene Tree

Mitochondrial DNA has proven useful for examining patterns of phylogeographic variation in many species of vertebrates (Avise et al., 1987), and in many cases patterns of mitochondrial DNA variation have been much more effective than traditional taxonomy in terms of defining units of conservation (Avise, 1989; Avise and Nelson, 1989; Bowen et al., 1991; Avise, 1992; Bowen et al., 1993; Morin et al., 1994). For instance, the Dusky Seaside Sparrow, an endangered species, was originally described on the basis of plumage color, yet based on mtDNA variation, this subspecies was found to be similar to other populations of the Seaside Sparrows distributed along the Atlantic coast (Avise and Nelson, 1989). In terms of uniqueness, the major genetic split between populations of Seaside Sparrows was found to involve Atlantic versus Gulf Coast populations. Therefore, the taxonomy provided an inaccurate picture of the actual geographic demarcations separating distinct populations.

Recently, Moritiz (1994) has provided a discussion regarding the use of genetics and phylogenetics to identify "evolutionary significant units" (ESU) and "management units" in conservation biology. In terms of such units, Moritz (1994) suggested that ESU's represent historically isolated and distinct populations. As pointed out by Moritz, the identification of such units is important to the long-term management of biodiversity. The criterion set for the identification of ESUs is that members of such units should reflect reciprocal monophyly with regard to mtDNA haplotype relationships as well as significant divergence in terms of allelic variation at nuclear loci. In most respects an ESU is equivalent to a phylogenetic species (Cracraft, 1989). No mention was made regarding morphological divergence. With respect to this criterion, an evolutionary significant unit should be unique from other such units in terms of its mtDNA phylogeny. The concept of a management unit was introduced by Moritz for the identification of units essential for short-term management. Although such units do not necessarily have to be monophyletic in a phylogenetic sense, they should reveal changes in allele frequencies.

In terms of the patterns of mtDNA variation in hog-nosed skunks, the phylogenetic relationships derived from the D-loop sequence data are not congruent with traditional taxonomic designations. As said before, many species and subspecies of hog-nosed skunks were named on the basis of limited phenotypic information that reflected either differences in color pattern or size. If one examines the phylogenetic tree in Fig. 11, there is no clear difference between the two species *Conepatus leuconotus* and *Conepatus mesoleucus*, with only *Conepatus chinga* and possibly *Conepatus mesoleucus figginsi* representing unique lineages relative to the larger clade containing the remaining taxa from the United States. Therefore, if one were identifying evolutionary significant units on the basis of the mtDNA data, at the most three major lineages can be recognized in the United States, Mexico, and Central America. These include *Conepatus leuconotus*, *Conepatus mesoleucus figginsi*, and *Conepatus chinga*.. In the case of *Conepatus leuconotus*, this unit would include all subspecies of the remaining subspecies of both *C. leuconotus* and *C. mesoleucus*.

RECOMMENDATIONS AND CONCLUSIONS

Taxonomy of Hog-nosed Skunks

Taxonomy provides a formal representation of how variation is partitioned, and it has influenced conservation biology by defining potentially important units of conservation. In addition, taxonomic designations can influence environmental policy with respect to providing formal protection (O'Brien and Mayr, 1991). Therefore, it is important to have an accurate assessment of variation among populations and species, and sometimes the resultant patterns of variation can be interpreted quite differently by various investigators.

Carnivores provide an excellent example of how taxonomic issues and an overall assessment of variation can influence conservation biology. For instance, there has been considerable debate over the systematic status of swift fox (*Vulpes velox*) and kit fox (*Vulpes macrotis*). One recent study using a combination of morphometrics and allozyme variation suggested that these two taxa were conspecific (Dragoo et al., 1990). This decision was based on a minimal degree of morphological separation among the subspecies and species and a lack of genetic differentiation. A study of mtDNA variation, however, suggested that populations of swift and kit foxes represented two distinct groups (Mercure et al., 1993). Based on these data, the recognition of these two groups as species was recommended. However, in the case of the swift and kit foxes reciprocal monophyly of mitochondrial haplotypes was not found, making the recognition of these two forms as species rather equivocal.

The results from the detailed analysis of both morphological and genetic variation in North American hog-nosed skunks are more consistent than that seen for the swift and kit fox example. From a morphological standpoint, there is no clear separation among the named subspecies and species of *Conepatus* in the United States and Mexico, whereas the South American taxa and *Conepatus chinga* consistently fall out as distinct on the basis of cranial measurements, overall color pattern, and genetics. The patterns of mtDNA variation among the North American populations are congruent with the detailed morphological assessment, except that

Conepatus mesoleucus figginsi does group separately from the other taxa examined. Although the two *Conepatus mesoleucus sonoriensis* samples formed a monophyletic group, they still resided within the major clade that contained all the other samples. In addition, these two specimens were from localities in close geographic proximity, an observation similar to that seen for the two *Conepatus leuconotus* samples from northern Mexico. Although the small samples sizes and quality of existing specimens precluded a detailed analysis of some of a few subspecies from Mexico and Colorado, we suggest that on the basis of the overall patterns seen in the taxa that were examined it is unlikely for these subspecies to be morphologically distinct. However, we do withhold a decision on *Conepatus m. telmalestes* and *Conepatus m. fremonti* until genetic data can be obtained. In all likelihood *Conepatus m. figginsi* and *Conepatus m. fremonti* are genetically similar. There is a possibility of verifying this if one can amplify mtDNA fragments from the one skin that exists for *C. m. fremonti.* Thus far we have been unable to accomplish this goal.

As a result of these findings, we would like to offer several suggestions regarding the taxonomy of hog-nosed skunks. First, on the basis of either morphology, genetics, or both, the three species (*Conepatus chinga*, *Conepatus semistriatus*, and *Conepatus humboldtii*) from Central America and South America should be recognized as species. In North America and Mexico we suggest that only one species be recognized. According to Lichtenstein (1832) *Conepatus leuconotus* has page priority. This conclusion is merited by the results from the combined morphological and genetic analyses. An examination of morphological and genetic variation throughout most of the range of the inclusive species *Conepatus leuconotus* suggests that many of the currently recognized subspecies should be synonymized. In this regard we recommend that only three subspecies be maintained, and these include *Conepatus leuconotus leuconotus* (now includes *Conepatus leuconotus texensis, Conepatus mesoleucus mearnsi, Conepatus mesoleucus mesoleucus, Conepatus mesoleucus nelsoni, Coneapatus mesoleucus venaticus, Conepatus mesoleucus nicaraguae, Conepatus mesoleucus sonoriensis,* and *Conepatus mesoleucus filipensis*), *Conepatus leuconotus figginsi* (including *Conepatus mesoleucus fremonti*), and *Conepatus leuconotus telmalestes.* In the case of *Conepatus leuconotus telmalestes* further genetic research may indicate that this taxon is not valid. Figures 13 and 14 depict the distribution of taxa before and after this recommended taxonomic revision.

Current Status of Hog-nosed Skunks

Hog-nosed skunk populations are declining in number throughout a major portion of their historical range in the United States. The east Texas subspecies, *C. mesoleucus telmalestes,* is presumed extinct throughout its range in the Big Thicket region (Schmidly, 1983). To quote Bailey (1905), "the white-backed skunk [*C. m. telmalestes*] is said to be the commonest species, and under a trapper's shed at a ranch on Tarkington Prairie in November,1904, I saw eight or ten of their skins hanging up to dry with a small number of skins of *Mephitis mesomelas* [striped skunk]." No new specimens of this subspecies have been collected in the Big Thicket area of Texas since Bailey's report in 1905. Although Raun and Wilks (1961) found a road killed *Conepatus* in Waller County, 30 miles southwest of the range of *C. m. telmalestes,* they were unable to identify the specimen to species but suggested it was geographically *C. mesoleucus* (possibly *C. m. telmalestes*). The disappearance of *C. m. telmalestes* is even more apparent when one considers that in the seven years of concentrated research within the range of this subspecies, no direct evidence of the hog-nosed skunk was obtained (Schmidly et al., 1980).

Another subspecies, *C. leuconotus texensis*, is potentially threatened or endangered as well. Rappole and Tipton (1987) presented a report to the U.S. Fish and Wildlife Service, Office of Endangered Species, that briefly summarized information on terrestrial mammals that might be declining, threatened, or endangered in Texas. While not currently assigned to special protective status under federal law, Rappole and Tipton (1987) recommended that *C. l. texensis* be considered as "threatened." In January, 1989 this subspecies (as well as *C. m. telmalestes* and *C. m. figginsi*) was placed in category 2 of the Department of the Interior, Fish and Wildlife Service, Endangered and Threatened Wildlife and Plant, Animal Notice of Review. *Conepatus leuconotus* is classified as a "fur-bearing animal" under Texas law, as provided in Chapter 71, Parks and Wildlife Code. Recent research (Schmidly et al., 1980; Dragoo et al., 1988) agrees with Rappole and Tipton (1987).

In the case of what was *C. leuconotus texensis*, 80% of all museum specimens from Texas were collected before the turn of the century (mid-1800's to 1900), 13% between 1901 and 1950, and only 7% after 1950 (Dragoo et al., 1988). Recent surveys and detailed scent station studies in south Texas also verify the reduction of this subspecies' range and numbers in the lower Rio Grande Valley possibly as a result of habitat loss (Fig. 12; Dragoo et al., 1988). The question as to whether or not this population has experienced a similar reduction of numbers throughout its range in Mexico is more difficult to answer. Nevertheless, only four specimens have been collected in Mexico since 1953 (Dice, 1937; Dalquest, 1953; Schmidly and Hendricks, 1984; Dragoo et al., 1994).

Finally, no new specimens of hog-nosed skunks in Colorado, referred to as *C. mesoleucus figginsi* and *C. m. fremonti,* have been collected since between 1920 and 1933, respectively (Warren, 1921; Miller, 1925; Armstrong, 1972). Armstrong (1972) examined these specimens and suggested that rather than distinct subspecies they may represent sex and age variants of the more widely distributed *C. m. mearnsi.*

What has caused the demise of hog-nosed skunk populations? As reported by Tewes and Schmidly (1987), in the past 60 years, 95% of the native vegetation in the Rio Grande Valley has been transformed from subtropical plant communities to cotton, sorghum, sugar cane, vegetable crops, and citrus orchards. Because hog-nosed skunks are generally associated with rough rocky areas (Patton, 1974) and brushy habitat (Schmidly and Hendricks, 1984), the conversion of native vegetation to row-crop agriculture may be a partial explanation of hog-nosed skunk decline. However, habitat modification may not be the primary cause of the observed decline because specimens of *C. leuconotus leuconotus* have been collected in cultivated areas near Veracruz, Mexico (Hall and Dalquest, 1963). A more direct cause of population decreases may be associated with the use of pesticides in agriculture. Hog-nosed skunks are more strictly insectivorous (Bailey, 1905; Seton, 1926; Davis, 1951; Hall and Dalquest, 1963; Patton, 1974) and the use of pesticides has increased throughout their range in conjunction with row-crop agriculture. One must realize, however, that no data are available to support or refute this hypothesis.

Although this study suggests that the two species and many of the currently recognized subspecies of hog-nosed skunks in the United States and Mexico do not merit formal recognition, these small furbearing mammals are on the decline throughout their range, and with the exception of anecdotal accounts and the unpublished thesis of Patton (1974), practically nothing is known about the ecology and behavior of these animals. Therefore, we wish to make the following suggestions for further research.

First, until further information is obtained, hog-nosed skunks should be considered three management units in the United States. We do acknowledge, however, that two of these units (*Conepatus leuconotus figginsi* and *Conepatus leuconotus telmalestes*) are presumed extinct. In addition, the third unit is declining throughout a large portion of its range in the United States.

Second, we recommend that ecological studies be conducted on populations of *Conepatus leuconotus leuconotus* in central and southwestern Texas. These skunks still are common enough in this region of the state to allow for detailed radio-marking studies of their movement pattern, food habits studies, and genetic studies (employing DNA microsatellite markers) of population structure. In addition, there is a large enough population to allow some detailed toxicological studies on the potential hazards of pesticides. We feel that these studies are needed in order to develop a realistic management plan for the remaining hog-nosed skunks in the United States. Otherwise, their populations may continue to decline until recovery becomes impossible.

Third, we recommend that the Texas Parks and Wildlife issue with all fur taking licenses a questionnaire that requests reports of all hog-nosed skunks taken in different regions of the state. This should provide the most expedient way to assess the health of remaining populations throughout the state on a year to year basis. In addition, such a survey may uncover new records of hog-nosed skunks from regions of the state where populations are on the decline or presumed extinct, and access to specimens will enhance continued monitoring of genetic variation.

Finally, there should be more emphasis on the status of other fur-bearing mammals in the state. Again, part of the information can be obtained from annual surveys as well as census information from designated localities throughout those regions of the state where land use patterns are changing as well as the overall ecological landscape. Such monitoring is necessary if one is to properly manage fur-bearing mammals. One thing that is currently unknown is how well the overall patterns of geographic variation in hog-nosed skunks mirrors patterns seen in other furbearers. Detailed analyses of geographic patterns of genetic variation in other small carnivores may reveal similar patterns in terms of recognized breaks that denote potential management units. We feel that the identification of such management units is essential to any realistic conservation plan for not only small furbearers but other forms of wildlife.

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Appendix 1.--Specimens examined. Museum acronyms listed at end of appendix.

Conepatus leuconotus leuconotus.

MEXICO: TCWC (1),USNM (1);Veracruz AMNH (4),KU (3)

Conepatus leuconotus texensis.

MEXICO: SanLuisPotosi MSUMZ(1); Tamaulipas KU (2), TCWC (2), UMMZ (1), USNM (1), MSUM (1). Texas: Aransas Co. AMNH (2); Brooks Co. TCWC (1); Cameron Co. KU (5), USNM (14); Kleberg Co. AMNH (1), TCWC (3); Webb Co. USNM (3).

Conepatus mesoleucus figginsi

Colorado: Baca Co. DMNH (7). Oklahoma: Cimmarron Co. ECOSU (1); Kenton Co. USNM (1)

Conepatus mesoleucus filipensis

MEXICO: Oaxaca USNM (1).

Conepatus mesoleucus mearnsi.

UMMZ (1). MEXICO: Chihuahua ANSP(1), MVZ (1), KU (4), MSUM (1), MVZ (2), USNM (2); Durango MSUM (2); Guadalajara AMNH (2); Guerrero UMMZ (1); Jalisco KU (3), USNM (1); NuevoLeon KU (2), USNM (1); SanLuisPotosi KU (1), USNM (4); Tamaulipas KU (3); Zacatecas LACM (3), MSUM (1), OUM (1). NewMexico USNM (2); Bernalillo Co. MCZ (1); DonaAna Co. MVZ (1), UTEP (2); Eddy Co. USNM (1), UTEP (1); Lincoln Co. USNM (1); Otero Co. NMSU (1); Sierra Co. USNM (2); Socorro Co.MSB (3). Texas FMNH (2), USNM (9); Atascosa Co. FMNH (1); Bexar Co. TCWC (1); Brewster Co. AMNH (1), FMNH (1), MVZ (2), SRSU (2), TCWC (6), TTU (2), UF (1), USNM (3), UTEP (2); Brown Co. MWSU (1); Coke Co. ASNHC (1), TTU (1); Crockett Co. TCWC (1); Culberson Co. TCWC (8), TTU (1); Dawson Co. TTU (1); Hudspeth Co. UTEP (1); JeffDavis Co. TCWC (2), TTU (3), UMMZ (1), USNM (3); Kerr Co. MCZ (2), TCWC (4); Kimble Co. MWSU (7); Mason Co. TCWC (3), USNM (1); McCulloch Co. MWSU (2); Menard Co. MWSU (1); Pecos Co. CM (1), MSB (1), MWSU (1); Presidio Co. TCWC (6); Reagan Co. ASNHC (1); Runnels Co. TTU (1); Terrell Co. TCWC (1); TomGreen Co. ASNHC (1); Uvalde Co. KU (1); ValVerde Co. TTU (1); Webb Co. USNM (1).

Conepatus mesoleucus mesoleucus

UMMZ (1). MEXICO: UIMNH (2); Chiapas TCWC (1); Guanajuato USNM (1); Mexico USNM (2); Michoacan USNM (1); Morelos TCWC (1); Oaxaca AMNH (9), FMNH (1), TCWC (1), USNM (2).

Conepatus mesoleucus nelsoni

MEXICO: Colima AMNH (1), KU (1), LACM (8), OUM (1), USNM (3); Guerraro MCZ (1), TCWC (3), USNM (2); Jalisco KU (1); Michoacan USNM (2); Oaxaca USNM (1).

Appendix 1.--Continued.

Conepatus mesoleucus nicaraguae

ElSalvador: Chalatenango MVZ (2), UMMZ (2); Morazan MVZ (2); SanMiguel MVZ (2); Usulutan MVZ (4). GUATEMALA FMNH (3); Huchuelenango LACM (2); Jutiapa FMNH (2); SanMarcos FMNH (1); Zacapa TCWC (1). HONDURAS AMNH (14). NICARAGUA AMNH (3); Boaco KU (1); Choutales KU (1); Leon USNM (1); Matagalpa TCWC (1).

Conepatus mesoleucus sonoriensis.

MEXICO: Jalisco AMNH (30), KU (1), USNM (2); Sinaloa AMNH (11), KU (28), LACM (1), MVZ (1), USNM (2); Sonora MVZ (3), USNM (3); Zacatecus USNM (3).

Conepatus mesoleucus telmalestes

Texas: Hardin Co. USNM (5); Liberty Co. USNM (2).

Conepatus mesoleucus venaticus

UMMZ (1). MEXICO USNM (1); Chihuahua KU (1), MVZ (3), USNM (2). Arizona AMNH (6), USNM (7); Cochise Co. AMNH (4), FMNH (1), KU (3), MCZ (4), MVZ (8), TTU (1), OSUMNH (2), UIMNH (7), USNM (1); Graham Co. UIMNH (5), USNM (2); Greenlee Co. USNM (4); Mohave Co. UIMNH (1); Pima Co. KU (1), MWSU (1), OSU (1), UCLA (6), UIMNH (3), UMMZ (7), USNM (2); Pinal Co. AMNH (1), FMNH (1); SantaCruz Co. LACM (1), UIMNH (2). NewMexico ANSP (1), USNM (8); Grant Co. AMNH (3); Hialgo Co. AMNH (1), MSB (3), UIMNH (1).

Conepatus chinga

ARGENTINA: AMNH (2), FMNH (1), OUM (2). BOLIVIA: AMNH (1). BOLIVIA: USNM (1). BRAZIL: AMNH (6). CHILE: AMNH (2), FMNH (1). PARAGUAY: AMNH (4). PERU: AMNH (1), FMNH (15), MSB (1), MVZ (5), USNM (7). URUGUAY: AMNH (50), FMNH (14), USNM (1).

Conepatus humboldtii

ARGENTINA: AMNH (5), FMNH (1), KU (2), MCZ (5), MVZ (4), UCLA (7), USNM (3), FMNH (4).

Conepatus semistriatus

BELIZE FMNH (1). BRAZIL: Piatry MCZ (1). COLOMBIA: AMNH (2), USNM (12); Cartage KU (1); Cordoba FMNH (1); Magdalena CM (2). COSTARICA: AMNH (7), USNM (1); Puntarenas LACM (1). ECUADOR: AMNH (10), FMNH (2), MCZ (2); Carchi TCWC (1); Tunquraqua MCZ (1). GUATEMALA UF (1).
MEXICO: USNM (1); VeraCruz FMNH (1), AMNH (2), KU (3), USNM (4); Yucatan KU (2), USNM (2). NICARAGUA: USNM (1); Managoa KU (1). PANAMA: USNM (3); Boquete MCZ (2); Chiriui ANSP (3). PERU: FMNH (2); Piura MVZ (1). VENEZUELA: AMNH (2), CM (1), FMNH (3), USNM (11); Portuguesa UF (1); Urunaco MCZ (1).

Appendix 1.--Continued.

AMNH American Museum of Natural History, New York
ANSP Academy of Natural Sciences of Philadelphia, Philadelphia, Pennsylvania
ASNHC Angelo State University Natural History Collection, San Angelo, Texas
CM Carnegie Museum of Natural History, Pittsburg, Pennsylvania
DMNH Denver Museum of Natural History, Denver, Colorado
ECOSU East Central Oklahoma State University, Ada
FMNH Feild Museum of Natural History, Chicago, Illinois
KU Museum of Natural History, University of Kansas, Lawrence
LACM Los Angeles County Museum of Natural History, Los Angeles, Califorina
MCZ Museum of Comparative Zoology, Harvard University, Boston, Massachusetts
MSB Museum of Southwestern Biology, University of New Mexico, Albuquerque
MSUM Michigan State University Museum, East Lansing
MSUMZ Memphis State University Museum of Zoology, Memphis, Tennessee
MVZ Museum of Vertebrate Zoology, Berkeley, California
MWSU Midwestern State University, Wichita Falls, Texas
NMSU New Mexico State University, Las Cruces
OSU Oregon State University, Corvallis
OSUMNH Oklahoma State University Museum of Natural History, Stillwater
OUM Oklahoma Museum of Natural History, Norman
SRSU Sul Ross State University, Alpine, Texas
TCWC Texas Cooperative Wildlife Collections, Texas A&M University, College Station
TTU The Museum, Texas Tech University, Lubbock
UCLA University of California, Los Angeles
UF Florida State Museum, University of Florida, Gainesville
UIMNH University of Illinois Museum of Natural History, Urbana-Champaign
UMMZ University of Michigan Museum of Zoology, Ann Arbor
USNM United States National Museum, Washington, D. C.
UTEP University of Texas, El Paso

Table 1.--Descriptive statistics of cranial measurements for each sex and age class of a sample of the hog-nosed skunk, Conepatus mesoleucus mearnsi. Means and Ranges are measured in centimeters. Coefficient of Variation (CV) was determined from log transformed data.

Age	Sex	n	Mean	2SE	Range	CV
Condylobasal Length						
Subadult	Male	17	6.700	0.168	6.210-7.315	1.230
Adult	Male	36	7.073	0.124	6.390-8.225	1.211
Subadult	Female	06	6.531	0.121	6.320-6.675	0.544
Adult	Female	31	6.631	0.143	5.780-7.690	1.406
Basilar Length of Hensel						
Subadult	Male	17	5.938	0.159	5.420-6.550	1.348
Adult	Male	36	6.256	0.116	5.525-7.235	1.329
Subadult	Female	06	5.719	0.115	5.505-5.880	0.611
Adult	Female	31	5.811	0.123	5.080-6.580	1.441
Palatilar Length						
Subadult	Male	18	2.904	0.107	2.575-3.255	2.332
Adult	Male	35	3.025	0.057	2.535-3.510	1.657
Subadult	Female	07	2.786	0.096	2.595-2.945	1.384
Adult	Female	31	2.804	0.067	2.485-3.180	1.993
Postpalatal Length						
Subadult	Male	17	3.178	0.105	2.940-3.615	1.938
Adult	Male	35	3.373	0.079	2.955-4.025	1.935
Subadult	Female	06	3.014	0.129	2.815-3.220	1.536
Adult	Female	31	3.120	0.057	2.745-3.445	1.487
Length of Maxillary Tooth Row						
Subadult	Male	18	2.105	0.051	1.930-2.335	1.670
Adult	Male	37	2.177	0.046	1.940-2.685	2.018
Subadult	Female	07	2.021	0.054	1.930-2.130	1.178
Adult	Female	31	2.054	0.050	1.605-2.300	2.358
Length of PM3						
Subadult	Male	18	0.294	0.013	0.235-0.350	8.748
Adult	Male	37	0.301	0.010	0.250-0.385	8.615
Subadult	Female	07	0.291	0.010	0.275-0.305	4.131
Adult	Female	31	0.299	0.010	0.220-0.355	8.642

Table 1.-- Continued

Age	Sex	n	Mean	2SE	Range	CV
Length of PM4						
Subadult	Male	18	0.631	0.016	0.565-0.720	2.952
Adult	Male	36	0.626	0.017	0.535-0.760	4.312
Subadult	Female	07	0.617	0.034	0.565-0.685	4.002
Adult	Female	31	0.603	0.017	0.525-0.695	4.470
Length of Molar						
Subadult	Male	18	0.699	0.026	0.585-0.845	4.057
Adult	Male	37	0.685	0.020	0.585-0.815	4.519
Subadult	Female	07	0.666	0.030	0.615-0.720	3.167
Adult	Female	31	0.660	0.018	0.560-0.775	4.007
Length of Bulla						
Subadult	Male	17	1.037	0.034	0.905-1.145	2.994
Adult	Male	37	1.137	0.047	0.970-1.665	4.665
Subadult	Female	07	1.071	0.047	1.005-1.170	2.445
Adult	Female	31	1.090	0.049	0.865-1.645	4.772
Zygomatic Breadth						
Subadult	Male	15	4.290	0.114	3.945-4.685	1.356
Adult	Male	35	4.779	0.096	4.225-5.350	1.536
Subadult	Female	06	4.227	0.147	4.035-4.440	1.137
Adult	Female	30	4.412	0.106	3.900-5.130	1.723
Mastoid Breadth						
Subadult	Male	17	3.737	0.126	3.465-4.555	1.813
Adult	Male	37	3.990	0.085	3.250-4.525	1.781
Subadult	Female	07	3.629	0.108	3.400-3.810	1.105
Adult	Female	30	3.792	0.076	3.350-4.215	1.500
Interorbital Breadth						
Subadult	Male	17	2.176	0.057	1.930-2.425	1.749
Adult	Male	37	2.400	0.053	2.135-2.705	2.092
Subadult	Female	07	2.153	0.026	2.105-2.205	0.523
Adult	Female	29	2.250	0.054	1.940-2.565	2.064

Table 1.--Continued

Age	Sex	n	Mean	2SE	Range	CV
Postorbital Breadth						
Subadult	Male	17	1.999	0.051	1.820-2.260	1.754
Adult	Male	36	2.010	0.034	1.785-2.255	1.669
Subadult	Female	07	1.938	0.087	1.790-2.075	2.018
Adult	Female	30	1.982	0.051	1.660-2.455	2.341
Width Across Incisors						
Subadult	Male	18	1.038	0.023	0.960-1.145	2.011
Adult	Male	36	1.057	0.022	0.850-1.200	2.726
Subadult	Female	07	0.989	0.040	0.935-1.055	2.316
Adult	Female	31	1.003	0.024	0.870-1.160	2.912
Width Across Canines						
Subadult	Male	18	1.711	0.049	1.540-1.855	2.137
Adult	Male	36	1.804	0.028	1.630-2.040	1.619
Subadult	Female	07	1.606	0.097	1.440-1.725	2.910
Adult	Female	31	1.604	0.050	1.390-1.930	3.045
Diameter of Canine						
Subadult	Male	18	0.415	0.015	0.355-0.475	5.557
Adult	Male	37	0.434	0.009	0.390-0.505	4.272
Subadult	Female	07	0.390	0.050	0.305-0.470	13.068
Adult	Female	31	0.365	0.014	0.305-0.465	8.335
Width Across Molars						
Subadult	Male	18	2.664	0.089	2.140-3.005	2.238
Adult	Male	36	2.712	0.046	2.454-3.080	1.540
Subadult	Female	07	2.597	0.050	2.510-2.695	0.778
Adult	Female	30	2.611	0.052	2.395-2.940	1.657
Molar Width						
Subadult	Male	18	0.792	0.024	0.705-0.865	3.142
Adult	Male	37	0.798	0.020	0.685-0.940	3.719
Subadult	Female	07	0.781	0.039	0.690-0.835	3.309
Adult	Female	31	0.778	0.017	0.705-0.875	2.917

Table 1.--Continued.

Age	Sex	n	Mean	2SE	Range	CV
Width of Bulla						
Subadult	Male	17	0.580	0.026	0.470-0.690	5.277
Adult	Male	37	0.601	0.021	0.465-0.810	5.918
Subadult	Female	07	0.606	0.047	0.530-0.720	5.562
Adult	Female	31	0.589	0.014	0.505-0.665	3.808
Width of Interpterygoid Fossa						
Subadult	Male	18	0.846	0.041	0.730-1.080	4.631
Adult	Male	33	0.910	0.024	0.745-1.005	3.510
Subadult	Female	07	0.851	0.066	0.750-1.000	4.718
Adult	Female	31	0.865	0.032	0.655-1.105	4.929
Height of Cranium						
Subadult	Male	17	2.752	0.032	2.660-2.945	0.709
Adult	Male	36	2.989	0.062	2.695-3.445	1.804
Subadult	Female	06	2.702	0.140	2.560-2.940	1.886
Adult	Female	30	2.741	0.060	2.455-3.165	1.780
Length of Lower Carnassial						
Subadult	Male	18	0.914	0.028	0.800-1.025	2.970
Adult	Male	37	0.883	0.022	0.755-1.035	3.460
Subadult	Female	07	0.884	0.050	0.780-0.995	3.448
Adult	Female	30	0.859	0.025	0.705-1.025	3.660
Height of Coronoid						
Subadult	Male	18	2.067	0.056	1.900-2.345	1.857
Adult	Male	37	2.216	0.062	1.955-2.740	2.682
Subadult	Female	07	2.069	0.202	1.860-2.650	3.917
Adult	Female	30	2.034	0.064	1.625-2.495	2.838
Length of Mandible						
Subadult	Male	18	4.320	0.118	3.950-4.685	1.549
Adult	Male	37	4.629	0.085	4.215-5.270	1.436
Subadult	Female	07	4.131	0.058	4.045-4.240	0.494
Adult	Female	30	4.255	0.118	3.745-5.265	1.955

Table 2.--Descriptive statistics of cranial measurements for each nominal subspecies of white-backed hog-nosed skunks and nominal species of striped hog-nosed skunks.

Taxon	Sex	n	Mean	2SE	Range
Condylobasal Length					
C. l. texensis	Female	8	7.326	0.184	6.815-7.560
	Male	12	7.966	0.219	7.245 8.460
C. l. leuconotus	Female	3	7.168	0.084	7.085 7.220
	Male	4	7.675	0.454	7.275 8.265
C. m. mearnsi	Female	31	6.631	0.143	5.780 7.690
	Male	36	7.073	0.124	6.390 8.225
C. m. sonoriensis	Female	22	7.065	0.171	6.485 7.710
	Male	31	7.488	0.096	6.965 8.065
C. m. venaticus	Female	21	6.606	0.109	6.220 7.335
	Male	36	7.099	0.093	6.500 7.705
C. m. telmalestes	Female	4	6.663	0.228	6.420 6.965
	Male	2	7.305	0.380	7.115 7.495
C. m. mesoleucus	Female	7	6.994	0.143	6.630 7.170
	Male	7	7.712	0.234	7.130 8.015
C. m. nelsoni	Female	8	6.789	0.128	6.445 6.995
	Male	10	7.307	0.232	6.790 7.775
C. m. nicaraguae	Female	11	6.877	0.204	6.365 7.510
	Male	13	7.205	0.199	6.610 7.690
C. humboltii	Female	4	6.210	0.233	5.945 6.445
	Male	8	6.362	0.224	6.075 6.970
C. chinga	Female	49	6.958	0.130	6.335 8.065
	Male	37	7.381	0.127	6.615 8.275
C. semistriatus	Female	41	7.410	0.129	6.475 8.260
	Male	29	7.863	0.196	7.155 8.905

Table 2.--Continued.

Taxon	Sex	n	Mean	2SE	Range	
Basilar Length of Hensel						
C. l. texensis	Female	8	6.498	0.157	6.115	6.800
	Male	12	7.071	0.218	6.360	7.525
C. l. leuconotus	Female	3	6.323	0.089	6.235	6.375
	Male	4	6.813	0.450	6.390	7.415
C. m. mearnsi	Female	31	5.811	0.123	5.080	6.580
	Male	36	6.256	0.116	5.525	7.235
C. m. sonoriensis	Female	22	6.153	0.140	5.680	6.720
	Male	29	6.601	0.102	5.840	7.210
C. m. venaticus	Female	20	5.758	0.094	5.335	6.250
	Male	36	6.228	0.093	5.605	6.855
C. m. telmalestes	Female	4	5.885	0.204	5.655	6.145
	Male	2	6.425	0.390	6.230	6.620
C. m. mesoleucus	Female	7	6.150	0.144	5.760	6.315
	Male	7	6.836	0.228	6.285	7.170
C. m. nelsoni	Female	8	5.968	0.128	5.760	6.240
	Male	10	6.441	0.219	5.925	6.950
C. m. nicaraguae	Female	11	6.102	0.200	5.550	6.715
	Male	13	6.399	0.189	5.890	6.935
C. humboltii	Female	4	5.474	0.191	5.310	5.685
	Male	7	5.606	0.214	5.360	6.140
C. chinga	Female	49	6.135	0.120	5.525	7.245
	Male	36	6.564	0.131	5.980	7.805
C. semistriatus	Female	39	6.550	0.125	5.510	7.280
	Male	29	6.976	0.175	6.360	7.960
Palatilar Length						
C. l. texensis	Female	8	3.124	0.109	2.860	3.290
	Male	14	3.389	0.111	3.095	3.690
C. l. leuconotus	Female	3	3.095	0.087	3.020	3.170
	Male	4	3.251	0.334	2.805	3.585
C. m. mearnsi	Female	31	2.804	0.067	2.485	3.180
	Male	35	3.025	0.057	2.535	3.510
C. m. sonoriensis	Female	22	2.988	0.059	2.735	3.265
	Male	31	3.233	0.073	2.695	3.540
C. m. venaticus	Female	21	2.815	0.069	2.535	3.185
	Male	36	3.070	0.066	2.630	3.765
C. m. telmalestes	Female	4	2.834	0.159	2.640	3.025
	Male	2	3.028	0.165	2.945	3.110
C. m. mesoleucus	Female	7	2.991	0.077	2.815	3.100
	Male	7	3.245	0.125	3.065	3.520
C. m. nelsoni	Female	8	2.891	0.092	2.705	3.060
	Male	10	3.158	0.093	2.935	3.390
C. m. nicaraguae	Female	11	2.958	0.094	2.740	3.225
	Male	13	3.079	0.102	2.790	3.330
C. humboltii	Female	4	2.635	0.087	2.530	2.720
	Male	8	2.726	0.105	2.460	2.900
C. chinga	Female	49	2.996	0.056	2.600	3.600
	Male	37	3.180	0.057	2.915	3.690
C. semistriatus	Female	41	3.116	0.065	2.595	3.620
	Male	29	3.331	0.089	2.905	3.880

Table 2.--Continued.

Taxon	Sex	n	Mean	2SE	Range	
Postpalatal Length						
C. l. texensis	Female	8	3.486	0.089	3.310	3.705
	Male	12	3.722	0.154	3.255	4.030
C. l. leuconotus	Female	3	3.372	0.038	3.335	3.400
	Male	3	3.663	0.401	3.320	4.015
C. m. mearnsi	Female	31	3.120	0.057	2.745	3.445
	Male	35	3.373	0.079	2.955	4.025
C. m. sonoriensis	Female	22	3.305	0.107	2.935	3.825
	Male	29	3.482	0.058	3.185	3.840
C. m. venaticus	Female	20	3.100	0.064	2.815	3.385
	Male	36	3.324	0.061	3.000	3.785
C. m. telmalestes	Female	4	3.146	0.111	3.050	3.280
	Male	2	3.545	0.240	3.425	3.665
C. m. mesoleucus	Female	7	3.301	0.129	3.080	3.570
	Male	7	3.694	0.188	3.345	4.010
C. m. nelsoni	Female	8	3.216	0.078	3.080	3.390
	Male	10	3.421	0.151	3.130	3.880
C. m. nicaraguae	Female	11	3.245	0.126	2.930	3.650
	Male	13	3.437	0.111	3.140	3.795
C. humboltii	Female	4	3.150	0.516	2.780	3.900
	Male	7	2.974	0.146	2.715	3.295
C. chinga	Female	49	3.204	0.072	2.840	3.770
	Male	36	3.438	0.081	3.095	3.945
C. semistriatus	Female	39	3.525	0.072	2.960	3.950
	Male	29	3.735	0.096	3.400	4.340
Length of Maxillary Tooth Row						
C. l. texensis	Female	9	2.457	0.217	2.240	3.305
	Male	15	2.398	0.087	1.900	2.560
C. l. leuconotus	Female	3	2.305	0.035	2.270	2.325
	Male	5	2.308	0.180	2.155	2.470
C. m. mearnsi	Female	31	2.054	0.050	1.605	2.300
	Male	37	2.177	0.046	1.940	2.685
C. m. sonoriensis	Female	22	2.197	0.031	2.000	2.320
	Male	32	2.258	0.030	2.085	2.415
C. m. venaticus	Female	21	2.054	0.035	1.900	2.190
	Male	36	2.152	0.027	1.995	2.355
C. m. telmalestes	Female	4	2.016	0.045	1.960	2.070
	Male	2	2.143	0.115	2.085	2.200
C. m. mesoleucus	Female	7	2.181	0.064	2.040	2.315
	Male	7	2.276	0.074	2.130	2.410
C. m. nelsoni	Female	9	2.200	0.057	2.085	2.355
	Male	10	2.273	0.079	2.100	2.425
C. m. nicaraguae	Female	11	2.162	0.055	2.030	2.305
	Male	13	2.204	0.062	2.035	2.420
C. humboltii	Female	4	1.905	0.086	1.805	1.995
	Male	8	1.945	0.070	1.765	2.020
C. chinga	Female	48	2.092	0.034	1.745	2.340
	Male	37	2.222	0.056	2.000	3.015
C. semistriatus	Female	40	2.281	0.038	2.050	2.590
	Male	29	2.386	0.044	2.165	2.655

Table 2.--Continued.

Taxon	Sex	n	Mean	2SE	Range	
Length of PM4						
C. l. texensis	Female	9	0.704	0.033	0.635	0.76
	Male	15	0.708	0.020	0.635	0.780
C. l. leuconotus	Female	3	0.702	0.044	0.675	0.745
	Male	5	0.675	0.044	0.610	0.735
C. m. mearnsi	Female	31	0.603	0.017	0.525	0.695
	Male	36	0.626	0.017	0.535	0.760
C. m. sonoriensis	Female	22	0.644	0.020	0.560	0.760
	Male	32	0.664	0.013	0.565	0.725
C. m. venaticus	Female	21	0.622	0.013	0.570	0.690
	Male	36	0.631	0.014	0.530	0.690
C. m. telmalestes	Female	4	0.589	0.028	0.550	0.615
	Male	2	0.538	0.025	0.525	0.550
C. m. mesoleucus	Female	7	0.665	0.038	0.580	0.720
	Male	7	0.634	0.024	0.580	0.675
C. m. nelsoni	Female	9	0.633	0.033	0.575	0.740
	Male	10	0.667	0.025	0.600	0.740
C. m. nicaraguae	Female	11	0.640	0.023	0.565	0.690
	Male	13	0.641	0.028	0.560	0.725
C. humboltii	Female	4	0.651	0.049	0.590	0.710
	Male	8	0.639	0.032	0.575	0.700
C. chinga	Female	48	0.664	0.012	0.595	0.755
	Male	37	0.693	0.015	0.580	0.775
C. semistriatus	Female	41	0.742	0.016	0.655	0.845
	Male	29	0.773	0.020	0.695	0.890
Length of Molar						
C. l. texensis	Female	9	0.768	0.045	0.660	0.870
	Male	15	0.789	0.029	0.715	0.875
C. l. leuconotus	Female	3	0.750	0.010	0.740	0.755
	Male	5	0.728	0.066	0.655	0.850
C. m. mearnsi	Female	31	0.660	0.018	0.560	0.775
	Male	37	0.685	0.020	0.585	0.815
C. m. sonoriensis	Female	22	0.694	0.027	0.575	0.815
	Male	32	0.707	0.021	0.580	0.835
C. m. venaticus	Female	21	0.651	0.020	0.550	0.735
	Male	36	0.657	0.018	0.495	0.765
C. m. telmalestes	Female	4	0.590	0.016	0.575	0.610
	Male	2	0.628	0.005	0.625	0.630
C. m. mesoleucus	Female	7	0.726	0.027	0.680	0.780
	Male	7	0.688	0.035	0.620	0.750
C. m. nelsoni	Female	9	0.724	0.031	0.635	0.800
	Male	10	0.750	0.033	0.690	0.840
C. m. nicaraguae	Female	11	0.694	0.024	0.625	0.780
	Male	13	0.705	0.028	0.600	0.780
C. humboltii	Female	4	0.524	0.069	0.445	0.600
	Male	8	0.527	0.039	0.420	0.605
C. chinga	Female	48	0.597	0.020	0.260	0.720
	Male	37	0.632	0.018	0.460	0.740
C. semistriatus	Female	40	0.701	0.016	0.530	0.800
	Male	29	0.724	0.022	0.625	0.830

Table 2.--Continued.

Taxon	Sex	n	Mean	2SE	Range	
Length of Bulla						
C. l. texensis	Female	9	1.106	0.046	1.010	1.225
	Male	15	1.172	0.045	1.030	1.330
C. l. leuconotus	Female	3	1.127	0.033	1.110	1.160
	Male	4	1.098	0.101	0.950	1.180
C. m. mearnsi	Female	31	1.090	0.049	0.865	1.645
	Male	37	1.137	0.047	0.970	1.665
C. m. sonoriensis	Female	22	1.138	0.055	0.990	1.635
	Male	32	1.196	0.060	0.965	1.690
C. m. venaticus	Female	21	1.097	0.054	0.970	1.580
	Male	36	1.156	0.049	0.995	1.735
C. m. telmalestes	Female	4	1.015	0.041	0.975	1.060
	Male	2	1.048	0.005	1.045	1.050
C. m. mesoleucus	Female	7	1.083	0.038	1.020	1.175
	Male	7	1.201	0.070	1.075	1.325
C. m. nelsoni	Female	8	1.076	0.030	1.005	1.135
	Male	10	1.160	0.054	0.975	1.270
C. m. nicaraguae	Female	11	1.073	0.030	0.995	1.155
	Male	13	1.162	0.040	1.065	1.330
C. humboltii	Female	4	1.194	0.265	1.045	1.590
	Male	8	1.091	0.044	0.975	1.175
C. chinga	Female	49	1.060	0.031	0.840	1.325
	Male	37	1.132	0.042	0.945	1.585
C. semistriatus	Female	41	1.147	0.028	0.980	1.340
	Male	29	1.229	0.048	1.010	1.675
Zygomatic Breadth						
C. l. texensis	Female	8	4.898	0.145	4.705	5.330
	Male	12	5.267	0.204	4.450	5.640
C. l. leuconotus	Female	3	4.652	0.058	4.595	4.690
	Male	4	5.034	0.380	4.675	5.540
C. m. mearnsi	Female	30	4.412	0.106	3.900	5.130
	Male	35	4.779	0.096	4.225	5.350
C. m. sonoriensis	Female	20	4.568	0.110	4.105	4.990
	Male	24	4.988	0.126	4.470	5.460
C. m. venaticus	Female	19	4.354	0.106	4.035	5.045
	Male	36	4.788	0.095	4.300	5.550
C. m. telmalestes	Female	4	4.364	0.148	4.155	4.505
	Male	2	4.723	0.615	4.415	5.030
C. m. mesoleucus	Female	7	4.627	0.159	4.265	4.925
	Male	7	5.359	0.212	4.895	5.650
C. m. nelsoni	Female	7	4.501	0.094	4.335	4.650
	Male	9	4.928	0.267	4.510	5.635
C. m. nicaraguae	Female	11	4.497	0.171	4.105	5.040
	Male	13	4.824	0.162	4.325	5.475
C. humboltii	Female	4	3.968	0.127	3.885	4.155
	Male	8	4.146	0.170	3.795	4.475
C. chinga	Female	46	4.438	0.067	3.980	5.045
	Male	33	4.732	0.102	4.175	5.335
C. semistriatus	Female	38	4.814	0.098	4.320	5.575
	Male	28	5.156	0.190	4.200	6.110

Table 2.--Continued.

Taxon	Sex	n	Mean	2SE	Range	
Mastoid Breadth						
C. l. texensis	Female	8	4.113	0.050	4.030	4.245
	Male	12	4.469	0.135	4.015	4.740
C. l. leuconotus	Female	3	4.198	0.171	4.045	4.340
	Male	4	4.200	0.229	3.990	4.420
C. m. mearnsi	Female	30	3.792	0.076	3.350	4.215
	Male	37	3.990	0.085	3.250	4.525
C. m. sonoriensis	Female	22	3.928	0.090	3.615	4.345
	Male	30	4.162	0.063	3.895	4.530
C. m. venaticus	Female	21	3.773	0.068	3.540	4.220
	Male	36	4.033	0.067	3.770	4.545
C. m. telmalestes	Female	4	3.719	0.141	3.595	3.920
	Male	2	4.220	0.430	4.005	4.435
C. m. mesoleucus	Female	7	3.934	0.059	3.790	4.045
	Male	7	4.344	0.165	3.950	4.570
C. m. nelsoni	Female	8	3.765	0.091	3.540	3.945
	Male	10	4.121	0.134	3.850	4.575
C. m. nicaraguae	Female	11	3.712	0.113	3.485	4.130
	Male	13	3.904	0.090	3.550	4.180
C. humboltii	Female	4	3.458	0.101	3.365	3.555
	Male	8	3.624	0.085	3.470	3.850
C. chinga	Female	49	3.818	0.074	3.375	4.365
	Male	37	3.993	0.081	3.520	4.525
C. semistriatus	Female	41	4.093	0.089	3.325	4.705
	Male	29	4.344	0.123	3.755	5.175
Interorbital Breadth						
C. l. texensis	Female	8	2.545	0.069	2.420	2.720
	Male	12	2.699	0.101	2.395	3.000
C. l. leuconotus	Female	3	2.450	0.051	2.400	2.485
	Male	3	2.637	0.174	2.535	2.810
C. m. mearnsi	Female	29	2.250	0.054	1.940	2.565
	Male	37	2.400	0.053	2.135	2.705
C. m. sonoriensis	Female	22	2.367	0.080	2.060	2.790
	Male	29	2.503	0.048	2.290	2.790
C. m. venaticus	Female	21	2.190	0.049	1.995	2.440
	Male	36	2.345	0.038	2.150	2.705
C. m. telmalestes	Female	4	2.205	0.065	2.135	2.285
	Male	2	2.418	0.345	2.245	2.590
C. m. mesoleucus	Female	7	2.379	0.079	2.220	2.560
	Male	7	2.626	0.153	2.205	2.830
C. m. nelsoni	Female	7	2.277	0.064	2.125	2.375
	Male	10	2.424	0.090	2.240	2.645
C. m. nicaraguae	Female	11	2.299	0.092	2.040	2.600
	Male	12	2.370	0.092	2.145	2.755
C. humboltii	Female	4	2.066	0.114	1.905	2.165
	Male	8	2.031	0.124	1.780	2.230
C. chinga	Female	49	2.294	0.050	2.040	2.750
	Male	37	2.409	0.058	2.115	2.760
C. semistriatus	Female	41	2.394	0.066	2.005	2.795
	Male	29	2.537	0.108	2.120	3.165

Table 2.--Continued.

Taxon	Sex	n	Mean	2SE	Range	
Postorbital Breadth						
C. l. texensis	Female	8	2.212	0.057	2.090	2.330
	Male	13	2.329	0.093	1.995	2.660
C. l. leuconotus	Female	3	2.127	0.130	2.000	2.215
	Male	5	2.237	0.133	2.070	2.420
C. m. mearnsi	Female	30	1.982	0.051	1.660	2.455
	Male	36	2.010	0.034	1.785	2.255
C. m. sonoriensis	Female	22	2.025	0.065	1.730	2.330
	Male	30	2.135	0.053	1.715	2.405
C. m. venaticus	Female	21	1.922	0.060	1.685	2.235
	Male	36	1.985	0.037	1.750	2.200
C. m. telmalestes	Female	4	1.930	0.065	1.855	2.010
	Male	2	2.058	0.235	1.940	2.175
C. m. mesoleucus	Female	7	1.993	0.094	1.820	2.140
	Male	7	2.113	0.081	1.960	2.265
C. m. nelsoni	Female	8	1.999	0.104	1.830	2.165
	Male	9	2.049	0.099	1.755	2.270
C. m. nicaraguae	Female	11	1.925	0.070	1.745	2.105
	Male	13	2.015	0.059	1.785	2.215
C. humboltii	Female	4	1.663	0.068	1.585	1.750
	Male	7	1.662	0.082	1.510	1.815
C. chinga	Female	49	1.807	0.060	1.420	2.185
	Male	37	1.830	0.073	1.400	2.235
C. semistriatus	Female	41	2.045	0.062	1.415	2.410
	Male	29	2.032	0.076	1.510	2.450
Width Across Incisors						
C. l. texensis	Female	9	1.175	0.043	1.045	1.240
	Male	15	1.257	0.046	1.095	1.375
C. l. leuconotus	Female	3	1.137	0.054	1.105	1.190
	Male	5	1.176	0.058	1.095	1.265
C. m. mearnsi	Female	31	1.003	0.024	0.870	1.160
	Male	36	1.057	0.022	0.850	1.200
C. m. sonoriensis	Female	22	1.103	0.027	0.960	1.195
	Male	31	1.136	0.022	0.995	1.235
C. m. venaticus	Female	21	1.021	0.024	0.915	1.190
	Male	36	1.082	0.031	0.945	1.530
C. m. telmalestes	Female	4	0.968	0.051	0.925	1.025
	Male	2	1.023	0.155	0.945	1.100
C. m. mesoleucus	Female	7	1.094	0.038	1.005	1.155
	Male	7	1.159	0.065	1.035	1.290
C. m. nelsoni	Female	8	1.059	0.031	1.010	1.135
	Male	10	1.106	0.045	0.970	1.205
C. m. nicaraguae	Female	11	1.087	0.030	1.025	1.150
	Male	13	1.133	0.028	1.065	1.215
C. humboltii	Female	4	0.921	0.076	0.835	0.985
	Male	8	0.958	0.033	0.910	1.060
C. chinga	Female	49	1.043	0.025	0.845	1.230
	Male	37	1.102	0.029	0.960	1.285
C. semistriatus	Female	41	1.140	0.036	0.925	1.355
	Male	29	1.196	0.047	1.035	1.460

Table 2.--Continued.

Taxon	Sex	n	Mean	2SE	Range	
Width Across Canines						
C. l. texensis	Female	9	1.821	0.049	1.720	1.975
	Male	15	2.053	0.069	1.765	2.365
C. l. leuconotus	Female	3	1.753	0.037	1.735	1.790
	Male	5	1.966	0.104	1.875	2.165
C. m. mearnsi	Female	31	1.604	0.050	1.390	1.930
	Male	36	1.804	0.028	1.630	2.040
C. m. sonoriensis	Female	22	1.671	0.053	1.425	1.925
	Male	31	1.897	0.031	1.720	2.050
C. m. venaticus	Female	21	1.596	0.048	1.445	1.945
	Male	36	1.792	0.027	1.640	1.980
C. m. telmalestes	Female	4	1.566	0.062	1.490	1.640
	Male	2	1.803	0.235	1.685	1.920
C. m. mesoleucus	Female	7	1.674	0.033	1.605	1.735
	Male	7	1.950	0.120	1.625	2.090
C. m. nelsoni	Female	8	1.628	0.035	1.575	1.720
	Male	10	1.887	0.061	1.740	2.030
C. m. nicaraguae	Female	11	1.679	0.044	1.585	1.840
	Male	13	1.871	0.055	1.735	2.060
C. humboltii	Female	4	1.478	0.072	1.380	1.545
	Male	8	1.603	0.059	1.490	1.745
C. chinga	Female	49	1.679	0.030	1.430	1.965
	Male	37	1.874	0.029	1.685	2.065
C. semistriatus	Female	41	1.824	0.038	1.575	2.080
	Male	29	2.046	0.079	1.750	2.800
Width Across Molars						
C. l. texensis	Female	9	3.122	0.165	2.905	3.760
	Male	15	3.160	0.056	2.990	3.315
C. l. leuconotus	Female	3	2.907	0.007	2.900	2.910
	Male	5	3.031	0.190	2.810	3.380
C. m. mearnsi	Female	30	2.611	0.052	2.395	2.940
	Male	36	2.712	0.046	2.454	3.080
C. m. sonoriensis	Female	22	2.731	0.043	2.555	2.920
	Male	30	2.867	0.044	2.620	3.075
C. m. venaticus	Female	21	2.590	0.047	2.445	2.845
	Male	36	2.674	0.041	2.165	2.885
C. m. telmalestes	Female	4	2.596	0.039	2.560	2.650
	Male	2	2.630	0.230	2.515	2.745
C. m. mesoleucus	Female	7	2.789	0.066	2.630	2.895
	Male	7	2.901	0.130	2.635	3.105
C. m. nelsoni	Female	8	2.770	0.053	2.655	2.900
	Male	10	2.898	0.058	2.775	3.045
C. m. nicaraguae	Female	11	2.825	0.045	2.745	2.955
	Male	13	2.923	0.062	2.735	3.060
C. humboltii	Female	4	2.496	0.116	2.365	2.610
	Male	8	2.581	0.069	2.430	2.725
C. chinga	Female	48	2.774	0.045	2.180	3.105
	Male	37	2.893	0.046	2.630	3.225
C. semistriatus	Female	40	3.065	0.057	2.695	3.380
	Male	29	3.201	0.085	2.825	3.620

Table 2.--Continued.

Taxon	Sex	n	Mean	2SE	Range	
Molar Width						
C. l. texensis	Female	9	0.933	0.062	0.785	1.075
	Male	15	0.965	0.023	0.905	1.040
C. l. leuconotus	Female	3	0.900	0.061	0.840	0.940
	Male	5	0.907	0.060	0.810	0.990
C. m. mearnsi	Female	31	0.778	0.017	0.705	0.875
	Male	37	0.798	0.020	0.685	0.940
C. m. sonoriensis	Female	22	0.803	0.024	0.660	0.890
	Male	32	0.840	0.019	0.685	0.930
C. m. venaticus	Female	21	0.809	0.016	0.725	0.905
	Male	36	0.806	0.015	0.710	0.875
C. m. telmalestes	Female	4	0.723	0.027	0.690	0.755
	Male	2	0.758	0.035	0.740	0.775
C. m. mesoleucus	Female	7	0.856	0.030	0.795	0.905
	Male	7	0.864	0.048	0.785	0.955
C. m. nelsoni	Female	9	0.828	0.034	0.750	0.910
	Male	10	0.859	0.022	0.815	0.920
C. m. nicaraguae	Female	11	0.836	0.035	0.730	0.930
	Male	13	0.845	0.033	0.765	0.970
C. humboltii	Female	4	0.798	0.059	0.745	0.875
	Male	8	0.799	0.037	0.715	0.870
C. chinga	Female	46	0.857	0.017	0.745	1.065
	Male	37	0.891	0.015	0.795	0.990
C. semistriatus	Female	40	0.931	0.027	0.775	1.085
	Male	29	0.987	0.040	0.720	1.155
Width of Interpterygoid Fossa						
C. l. texensis	Female	8	0.979	0.042	0.905	1.095
	Male	13	1.039	0.046	0.890	1.160
C. l. leuconotus	Female	3	0.965	0.055	0.935	1.020
	Male	4	1.005	0.102	0.895	1.130
C. m. mearnsi	Female	31	0.865	0.032	0.655	1.105
	Male	33	0.910	0.024	0.745	1.005
C. m. sonoriensis	Female	21	0.910	0.029	0.790	1.025
	Male	29	0.978	0.023	0.865	1.100
C. m. venaticus	Female	21	0.842	0.030	0.730	1.050
	Male	36	0.904	0.018	0.745	0.990
C. m. telmalestes	Female	4	0.838	0.020	0.820	0.865
	Male	2	0.843	0.005	0.840	0.845
C. m. mesoleucus	Female	7	0.900	0.052	0.755	0.960
	Male	7	1.005	0.055	0.905	1.100
C. m. nelsoni	Female	8	0.854	0.037	0.770	0.960
	Male	9	0.943	0.071	0.795	1.155
C. m. nicaraguae	Female	10	0.892	0.051	0.795	1.020
	Male	13	0.892	0.039	0.820	1.035
C. humboltii	Female	4	0.803	0.058	0.725	0.860
	Male	8	0.806	0.035	0.755	0.885
C. chinga	Female	48	0.943	0.018	0.810	1.065
	Male	35	0.956	0.020	0.775	1.045
C. semistriatus	Female	40	0.916	0.023	0.785	1.050
	Male	27	0.956	0.037	0.690	1.200

Table 2.--Continued.

Taxon	Sex	n	Mean	2SE	Range	
Height of Cranium						
C. l. texensis	Female	8	2.890	0.066	2.770	3.065
	Male	12	3.190	0.110	2.795	3.515
C. l. leuconotus	Female	3	2.807	0.123	2.740	2.930
	Male	3	2.957	0.185	2.795	3.115
C. m. mearnsi	Female	30	2.741	0.060	2.455	3.165
	Male	36	2.989	0.062	2.695	3.445
C. m. sonoriensis	Female	22	2.851	0.048	2.645	3.070
	Male	30	2.988	0.062	2.630	3.300
C. m. venaticus	Female	21	2.623	0.055	2.395	2.910
	Male	36	2.899	0.059	2.635	3.410
C. m. telmalestes	Female	4	2.719	0.144	2.535	2.875
	Male	2	2.920	0.280	2.780	3.060
C. m. mesoleucus	Female	7	2.798	0.063	2.695	2.915
	Male	7	3.131	0.138	2.855	3.385
C. m. nelsoni	Female	8	2.729	0.086	2.555	2.910
	Male	10	2.940	0.139	2.670	3.215
C. m. nicaraguae	Female	11	2.706	0.088	2.445	2.970
	Male	13	2.908	0.097	2.605	3.250
C. humboltii	Female	4	2.378	0.015	2.365	2.395
	Male	7	2.531	0.147	2.325	2.900
C. chinga	Female	48	2.646	0.056	2.395	3.135
	Male	36	2.800	0.061	2.320	3.150
C. semistriatus	Female	41	2.847	0.061	2.475	3.410
	Male	29	3.053	0.108	2.615	3.715
Length of Lower Carnassial						
C. l. texensis	Female	9	1.008	0.035	0.940	1.100
	Male	14	1.002	0.047	0.795	1.120
C. l. leuconotus	Female	3	1.005	0.017	0.990	1.020
	Male	5	0.954	0.058	0.875	1.055
C. m. mearnsi	Female	30	0.859	0.025	0.705	1.025
	Male	37	0.883	0.022	0.755	1.035
C. m. sonoriensis	Female	22	0.912	0.027	0.770	1.055
	Male	32	0.933	0.016	0.825	1.015
C. m. venaticus	Female	20	0.869	0.023	0.770	0.950
	Male	36	0.879	0.016	0.770	0.975
C. m. telmalestes	Female	4	0.838	0.024	0.810	0.860
	Male	2	0.810	0.010	0.805	0.815
C. m. mesoleucus	Female	7	0.946	0.037	0.890	1.020
	Male	7	0.891	0.049	0.820	0.985
C. m. nelsoni	Female	9	0.926	0.039	0.810	1.025
	Male	10	0.929	0.032	0.835	1.015
C. m. nicaraguae	Female	11	0.888	0.035	0.805	1.010
	Male	13	0.944	0.026	0.860	1.040
C. humboltii	Female	4	0.791	0.046	0.740	0.845
	Male	8	0.789	0.032	0.725	0.850
C. chinga	Female	48	0.874	0.015	0.770	1.000
	Male	35	0.897	0.022	0.765	1.050
C. semistriatus	Female	41	0.992	0.018	0.880	1.115
	Male	29	1.053	0.045	0.905	1.560

Table 2.--Continued.

Taxon	Sex	n	Mean	2SE	Range	
Height of Coronoid						
C. l. texensis	Female	9	2.276	0.065	2.110	2.405
	Male	14	2.400	0.103	2.020	2.685
C. l. leuconotus	Female	3	2.455	0.231	2.255	2.655
	Male	4	2.343	0.156	2.180	2.535
C. m. mearnsi	Female	30	2.034	0.064	1.625	2.495
	Male	37	2.216	0.062	1.955	2.740
C. m. sonoriensis	Female	22	2.138	0.056	1.900	2.425
	Male	32	2.280	0.053	1.975	2.540
C. m. venaticus	Female	20	2.014	0.051	1.865	2.285
	Male	36	2.115	0.041	1.870	2.390
C. m. telmalestes	Female	4	2.025	0.100	1.935	2.145
	Male	2	2.205	0.040	2.185	2.225
C. m. mesoleucus	Female	7	2.144	0.043	2.050	2.225
	Male	7	2.408	0.142	2.085	2.660
C. m. nelsoni	Female	9	2.069	0.094	1.885	2.255
	Male	10	2.226	0.090	2.010	2.395
C. m. nicaraguae	Female	11	2.129	0.096	1.845	2.395
	Male	13	2.249	0.113	1.950	2.600
C. humboltii	Female	4	1.950	0.108	1.820	2.060
	Male	8	2.053	0.112	1.785	2.280
C. chinga	Female	49	2.222	0.048	1.915	2.705
	Male	34	2.389	0.062	2.015	2.730
C. semistriatus	Female	41	2.374	0.052	2.075	2.770
	Male	29	2.544	0.099	2.100	3.100
Length of Mandible						
C. l. texensis	Female	9	4.745	0.113	4.500	5.000
	Male	13	5.053	0.188	4.395	5.465
C. l. leuconotus	Female	3	4.568	0.032	4.550	4.600
	Male	5	4.855	0.273	4.565	5.310
C. m. mearnsi	Female	30	4.255	0.118	3.745	5.265
	Male	37	4.629	0.085	4.215	5.270
C. m. sonoriensis	Female	22	4.500	0.092	4.150	4.860
	Male	32	4.867	0.054	4.545	5.220
C. m. venaticus	Female	20	4.179	0.082	3.885	4.670
	Male	36	4.550	0.068	4.125	5.060
C. m. telmalestes	Female	4	4.225	0.145	4.100	4.430
	Male	2	4.615	0.370	4.430	4.800
C. m. mesoleucus	Female	6	4.443	0.131	4.245	4.650
	Male	7	5.046	0.167	4.625	5.270
C. m. nelsoni	Female	9	4.409	0.084	4.230	4.630
	Male	10	4.750	0.191	4.210	5.080
C. m. nicaraguae	Female	11	4.437	0.131	4.145	4.870
	Male	13	4.707	0.138	4.355	5.105
C. humboltii	Female	4	4.000	0.179	3.835	4.160
	Male	8	4.073	0.145	3.760	4.415
C. chinga	Female	49	4.448	0.072	4.055	5.215
	Male	34	4.717	0.089	4.230	5.285
C. semistriatus	Female	41	4.740	0.090	4.185	5.300
	Male	29	5.067	0.143	4.560	5.815

Table 3.--Contribution of each of the 21 principal components to the variation of cranial measurements of hog-nosed skunk populations.

	Eigenvalue	Difference	Proportion	Cumulative
PRIN1	0.01538	0.01266	0.574	0.574
PRIN2	0.00272	0.00061	0.101	0.675
PRIN3	0.00211	0.00080	0.079	0.754
PRIN4	0.00131	0.00049	0.049	0.803
PRIN5	0.00082	0.00014	0.031	0.834
PRIN6	0.00068	0.00013	0.025	0.859
PRIN7	0.00055	0.00007	0.021	0.880
PRIN8	0.00048	0.00004	0.018	0.898
PRIN9	0.00045	0.00005	0.017	0.914
PRIN10	0.00040	0.00006	0.015	0.929
PRIN11	0.00034	0.00006	0.013	0.942
PRIN12	0.00029	0.00001	0.011	0.953
PRIN13	0.00028	0.00003	0.010	0.963
PRIN14	0.00025	0.00005	0.009	0.972
PRIN15	0.00020	0.00004	0.008	0.980
PRIN16	0.00016	0.00002	0.006	0.986
PRIN17	0.00014	0.00003	0.005	0.991
PRIN18	0.00011	0.00004	0.004	0.995
PRIN19	0.00007	0.00004	0.003	0.998
PRIN20	0.00004	0.00002	0.001	0.999
PRIN21	0.00002	.	0.001	1.000

Table 4.--Character loading on the 21 principal components for cranial measurements of samples of *Conepatus*. Character abbreviations are as found in text under materials and methods.

	Prin1		Prin2		Prin3		Prin4		Prin5		Prin6		Prin7	
	Vector	%	Vector	%	Vector	%	Vector	%	Vector	%	Vector	%	Vector	%
CL	0.2176	4.79	0.1381	3.69	-0.0082	0.24	-0.0122	0.47	-0.1012	3.14	0.0503	1.71	-0.2164	5.42
BAS	0.2326	5.12	0.1234	3.30	-0.0318	0.94	-0.0278	1.08	-0.1234	3.83	0.0326	1.11	-0.2989	7.48
PL	0.2172	4.78	0.0582	1.55	-0.0592	1.76	-0.0045	0.17	-0.0878	2.73	-0.0225	0.77	-0.4532	11.34
PPL	0.2310	5.09	0.1548	4.13	0.0321	0.95	-0.0743	2.90	-0.1330	4.13	0.1091	3.72	-0.1130	2.83
MTR	0.2115	4.66	-0.0431	1.15	0.0704	2.09	0.0475	1.85	0.0645	2.00	0.1515	5.16	0.0329	0.82
PM4	0.2213	4.87	-0.3023	8.07	-0.3768	11.18	-0.0557	2.17	0.2480	7.70	-0.2991	10.19	0.1089	2.73
ML	0.2060	4.54	-0.6153	16.43	0.3160	9.38	0.0794	3.09	0.0814	2.53	0.4562	15.54	-0.0870	2.18
BL	0.1650	3.63	0.2299	6.14	0.1989	5.90	-0.7916	30.83	0.4475	13.90	0.0708	2.41	0.0753	1.88
ZB	0.2078	4.58	0.1513	4.04	0.0941	2.79	0.1379	5.37	-0.0975	3.03	0.0231	0.79	0.3169	7.93
MB	0.2026	4.46	0.1710	4.57	0.0827	2.46	0.0144	0.56	-0.0773	2.40	0.0291	0.99	0.1146	2.87
IB	0.2124	4.68	0.1515	4.05	0.1435	4.26	0.2006	7.81	-0.0602	1.87	-0.0693	2.36	0.3009	7.53
PB	0.1845	4.06	-0.0933	2.49	0.6092	18.08	0.1302	5.07	0.0991	3.08	-0.7035	23.96	-0.1136	2.84
WAI	0.2661	5.86	-0.0753	2.01	0.0415	1.23	-0.0484	1.88	-0.1958	6.08	0.1309	4.46	0.3230	8.08
WAC	0.2527	5.57	0.0390	1.04	-0.0962	2.85	-0.0327	1.27	-0.1125	3.49	0.0118	0.40	0.1636	4.09
WAM	0.2357	5.19	-0.1189	3.18	-0.1535	4.56	0.0817	3.18	-0.0293	0.91	-0.0425	1.45	0.1639	4.10
MW	0.2469	5.44	-0.2070	5.53	-0.3554	10.55	-0.1784	6.95	-0.0892	2.77	-0.2504	8.53	0.2342	5.86
FW	0.1709	3.77	0.2637	7.04	-0.1827	5.42	0.4751	18.50	0.7245	22.50	0.1143	3.89	-0.0272	0.68
CH	0.1489	3.28	0.1538	4.11	0.2607	7.74	0.0888	3.46	-0.0154	0.48	0.2376	8.09	0.1748	4.37
LC	0.2225	4.90	-0.3495	9.33	-0.0342	1.02	-0.0511	1.99	0.1404	4.36	0.0464	1.58	-0.2471	6.18
HC	0.2606	5.74	0.1956	5.22	-0.1903	5.65	0.0133	0.52	-0.1605	4.98	-0.0551	1.88	-0.2620	6.56
LM	0.2265	4.99	0.1095	2.92	-0.0319	0.95	0.0219	0.85	-0.1313	4.08	0.0292	1.00	-0.1690	4.23

Table 4.--Continued.

	Prin8		Prin9		Prin10		Prin11		Prin12		Prin13		Prin14	
	Vector	%	Vector	%	Vector	%	Vector	%	Vector	%	Vector	%	Vector	%
CL	-0.0710	2.03	0.1695	4.68	-0.0689	1.94	-0.0021	0.05	-0.0794	2.32	0.0438	1.40	-0.0284	0.97
BAS	-0.0821	2.35	0.1515	4.18	-0.0198	0.56	0.0140	0.36	-0.1363	3.98	0.0171	0.55	-0.0267	0.91
PL	-0.2810	8.04	-0.0883	2.44	-0.2721	7.66	0.1990	5.08	0.1186	3.46	0.1064	3.41	0.1007	3.44
PPL	0.1607	4.60	0.4363	12.04	0.2580	7.26	-0.1378	3.52	-0.4255	12.43	-0.2522	8.09	-0.2935	10.01
MTR	-0.1935	5.54	0.3587	9.90	-0.2391	6.73	-0.4500	11.49	0.1536	4.49	-0.0384	1.23	0.5529	18.87
PM4	0.3783	10.82	0.3947	10.90	-0.3395	9.56	0.2723	6.95	0.1541	4.50	-0.1426	4.57	-0.1042	3.56
ML	-0.0330	0.95	-0.0810	2.24	0.1998	5.63	0.2122	5.42	0.0357	1.04	-0.3410	10.93	-0.0130	0.44
BL	-0.0470	1.34	-0.0812	2.24	0.0442	1.24	0.1176	3.00	0.0457	1.33	-0.0410	1.31	0.0869	2.97
ZB	0.1751	5.01	-0.0611	1.69	0.1632	4.59	0.3047	7.78	0.0517	1.51	0.1807	5.80	0.0993	3.39
MB	0.0142	0.41	0.0358	0.99	0.0103	0.29	0.0922	2.36	0.0687	2.01	0.2345	7.52	-0.0824	2.81
IB	-0.3556	10.17	0.2803	7.74	0.2243	6.32	0.3366	8.60	0.3154	9.21	0.0403	1.29	-0.0310	1.06
PB	0.0251	0.72	-0.0965	2.66	-0.0294	0.83	-0.1342	3.43	-0.0989	2.89	-0.0973	3.12	-0.0208	0.71
WAI	-0.2122	6.07	-0.2061	5.69	-0.4724	13.30	-0.2339	5.97	0.1331	3.89	-0.1034	3.32	-0.4207	14.36
WAC	0.0046	0.13	-0.3701	10.22	-0.2345	6.60	0.1070	2.73	-0.4242	12.39	-0.0504	1.62	-0.0172	0.59
WAM	0.0949	2.71	-0.1593	4.40	0.0371	1.04	0.0994	2.54	-0.3705	10.82	0.0379	1.22	0.5618	19.17
MW	-0.2718	7.78	-0.0451	1.24	0.4578	12.89	-0.3608	9.22	0.0013	0.04	0.0161	0.52	-0.0527	1.80
FW	-0.1377	3.94	-0.1463	4.04	0.0483	1.36	-0.1114	2.84	-0.0977	2.85	-0.0783	2.51	-0.1586	5.41
CH	0.5257	15.04	0.0371	1.02	-0.0732	2.06	-0.2894	7.39	0.0848	2.48	0.1999	6.41	0.0087	0.30
LC	0.0989	2.83	-0.0666	1.84	0.1313	3.70	-0.1113	2.84	0.0597	1.74	0.7049	22.60	-0.1770	6.04
HC	0.3295	9.43	-0.3543	9.78	0.2187	6.16	-0.1190	3.04	0.5031	14.69	-0.3533	11.33	0.0875	2.98
LM	-0.0030	0.09	0.0025	0.07	-0.0100	0.28	0.2100	5.36	-0.0657	1.92	0.0391	1.25	-0.0064	0.22

Table 4.--Continued.

	PRIN15		PRIN16		PRIN17		PRIN18		PRIN19		PRIN20		PRIN21	
	Vector	%	Vector	%	Vector	%	Vector	%	Vector	%	Vector	%	Vector	%
CL	0.0606	1.59	0.0922	2.84	0.0295	0.93	0.0751	2.64	0.0903	3.54	-0.5105	19.49	0.7340	35.29
BAS	0.0480	1.26	0.1270	3.92	0.0572	1.81	-0.0370	1.30	-0.2202	8.63	-0.5476	20.91	-0.6340	30.48
PL	0.2833	7.46	0.1703	5.25	0.1578	4.99	0.0567	1.99	-0.3335	13.07	0.4907	18.73	0.0837	4.02
PPL	-0.1788	4.71	-0.1671	5.15	0.0248	0.78	-0.0610	2.14	-0.1742	6.83	0.3777	14.42	0.0637	3.06
MTR	0.0324	0.85	-0.2509	7.73	-0.1753	5.55	-0.2256	7.93	0.1031	4.04	0.0588	2.24	-0.0427	2.05
PM4	0.0805	2.12	0.0172	0.53	-0.0227	0.72	0.0208	0.73	-0.0051	0.20	-0.0212	0.81	-0.0157	0.75
ML	0.1730	4.56	0.0004	0.01	-0.0042	0.13	0.0774	2.72	0.0194	0.76	-0.0605	2.31	0.0059	0.28
BL	-0.0600	1.58	0.0380	1.17	0.0397	1.26	-0.0122	0.43	-0.0040	0.16	-0.0081	0.31	0.0001	0.00
ZB	0.2516	6.62	-0.2574	7.93	0.3244	10.27	-0.5653	19.87	-0.1810	7.09	-0.0667	2.55	0.0698	3.36
MB	0.2710	7.14	-0.5661	17.45	-0.0478	1.51	0.6359	22.35	0.1158	4.54	0.0053	0.20	-0.1103	5.31
IB	-0.3173	8.35	0.2842	8.76	-0.3230	10.22	0.0748	2.63	-0.0868	3.40	0.0492	1.88	-0.0072	0.35
PB	0.0099	0.26	-0.0271	0.83	0.0302	0.96	-0.0132	0.46	0.0303	1.19	-0.0155	0.59	0.0043	0.20
WAI	-0.2851	7.51	-0.0429	1.32	0.3213	10.17	-0.0185	0.65	-0.0344	1.35	-0.0265	1.01	-0.0157	0.75
WAC	0.1462	3.85	0.0046	0.14	-0.6727	21.29	-0.1541	5.42	-0.0156	0.61	0.0180	0.69	0.0133	0.64
WAM	-0.4038	10.63	0.0779	2.40	0.2934	9.29	0.3216	11.30	-0.1057	4.14	0.0067	0.25	0.0250	1.20
MW	0.3785	9.97	0.1929	5.94	0.0884	2.80	0.0328	1.15	0.0610	2.39	0.0261	0.99	0.0042	0.20
FW	0.0310	0.82	-0.0055	0.17	0.0783	2.48	0.0045	0.16	0.0153	0.60	-0.0049	0.19	-0.0085	0.41
CH	0.2195	5.78	0.5393	16.62	-0.0168	0.53	0.1623	5.70	-0.0287	1.12	0.0957	3.65	-0.0351	1.69
LC	-0.3220	8.48	-0.1103	3.40	-0.1590	5.03	-0.1471	5.17	-0.0409	1.60	0.0296	1.13	0.0238	1.15
HC	-0.1975	5.20	-0.1329	4.10	-0.1363	4.31	0.0000	0.00	-0.0409	1.60	-0.0308	1.18	0.0233	1.12
LM	-0.0478	1.26	0.1402	4.32	0.1570	4.97	-0.1494	5.25	0.8458	33.15	0.1694	6.47	-0.1595	7.67

Table 5.--Variable coefficients for canonical vectors I and II with an estimate of the percent influence of each variable on each vector for the populations of hog-nosed skunks.

	Vector I		Vector II	
	Coefficient	%	Coefficient	%
PRIN2	-0.2672	11.44	0.2768	7.38
PRIN3	0.8384	35.88	-0.1690	4.51
PRIN4	0.1820	7.79	0.4332	11.55
PRIN5	0.0789	3.38	0.0608	1.62
PRIN6	0.3823	16.36	0.2437	6.50
PRIN7	0.0333	1.42	-0.2107	5.62
PRIN8	-0.1182	5.06	-0.4255	11.35
PRIN9	-0.0314	1.35	-0.2593	6.91
PRIN10	0.0148	0.64	-0.2216	5.91
PRIN11	0.0017	0.07	0.0981	2.62
PRIN12	0.0208	0.89	0.1203	3.21
PRIN13	0.0478	2.05	-0.1450	3.87
PRIN14	-0.0113	0.48	-0.0726	1.94
PRIN15	0.0825	3.53	-0.0299	0.80
PRIN16	-0.0389	1.67	0.4270	11.39
PRIN17	-0.0198	0.85	0.0549	1.46
PRIN18	-0.0340	1.45	-0.1210	3.23
PRIN19	0.1029	4.40	0.1291	3.44
PRIN20	0.0248	1.06	-0.0896	2.39
PRIN21	-0.0053	0.23	0.1621	4.32

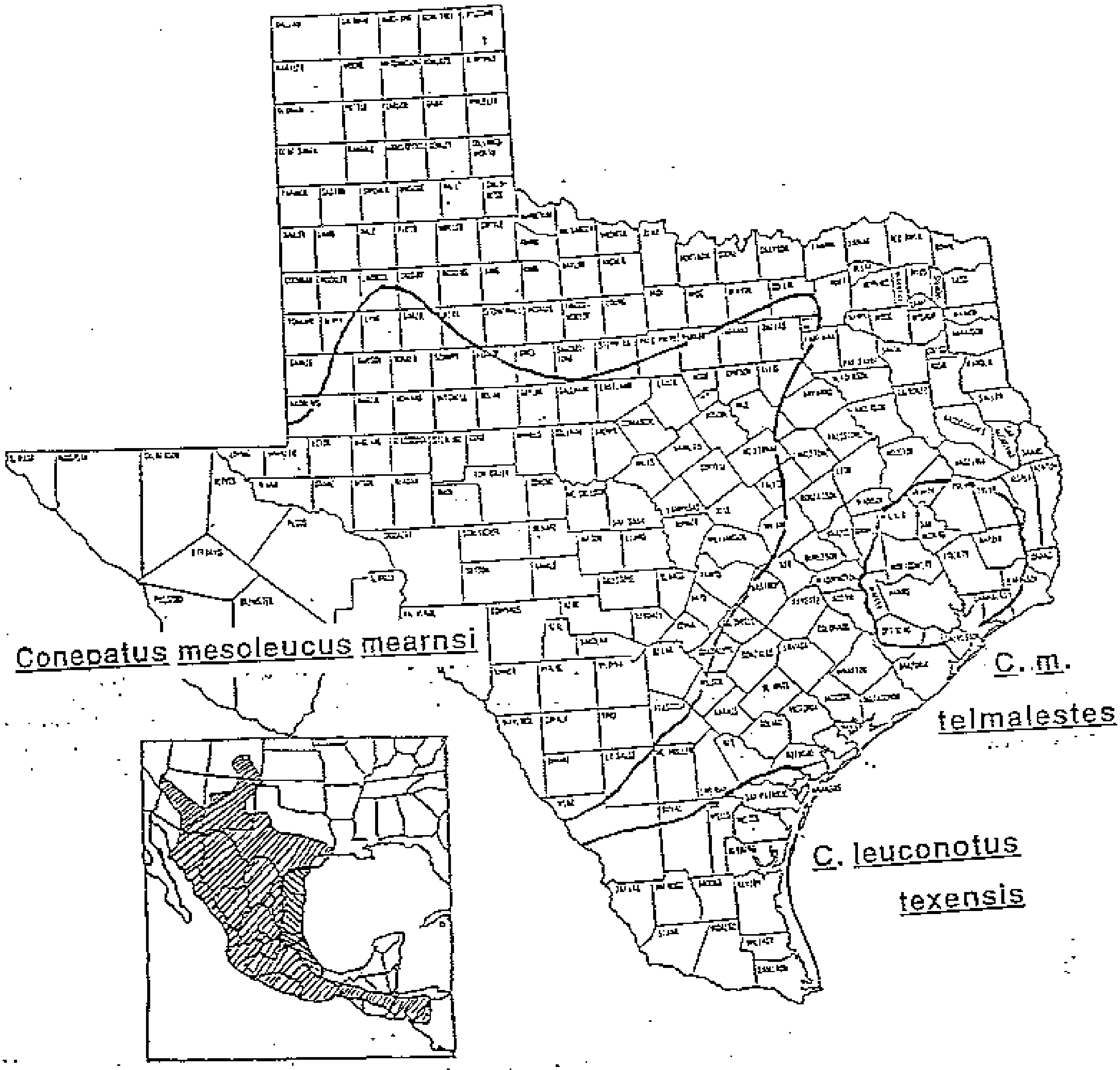

Figure 1 - Distribution of hog-nosed skunks in Texas and historical range of hog-nosed skunks in the United States and Mexico.

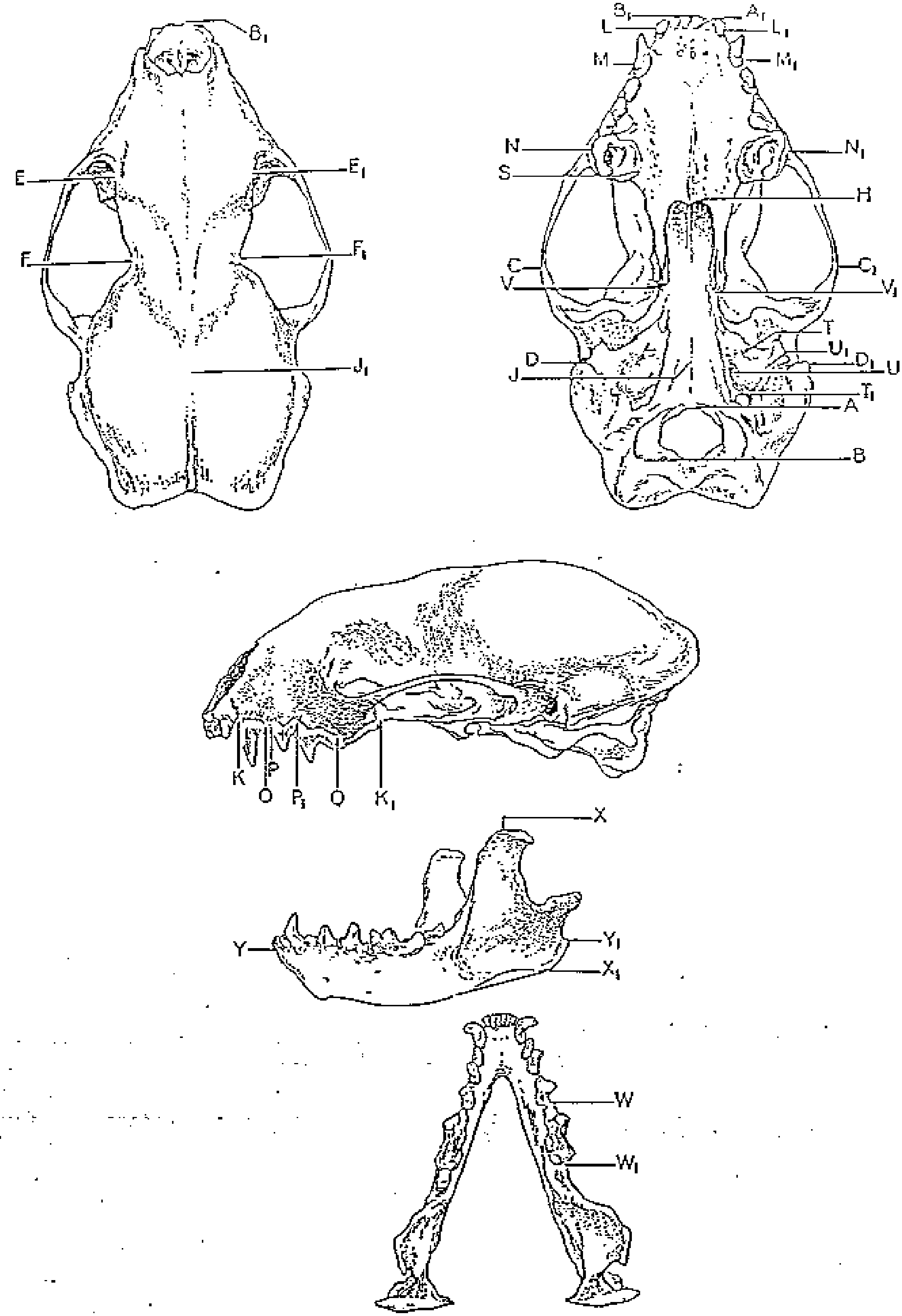

Figure 2 - Skull depicting 24 cranial measurements taken in the morphological study.

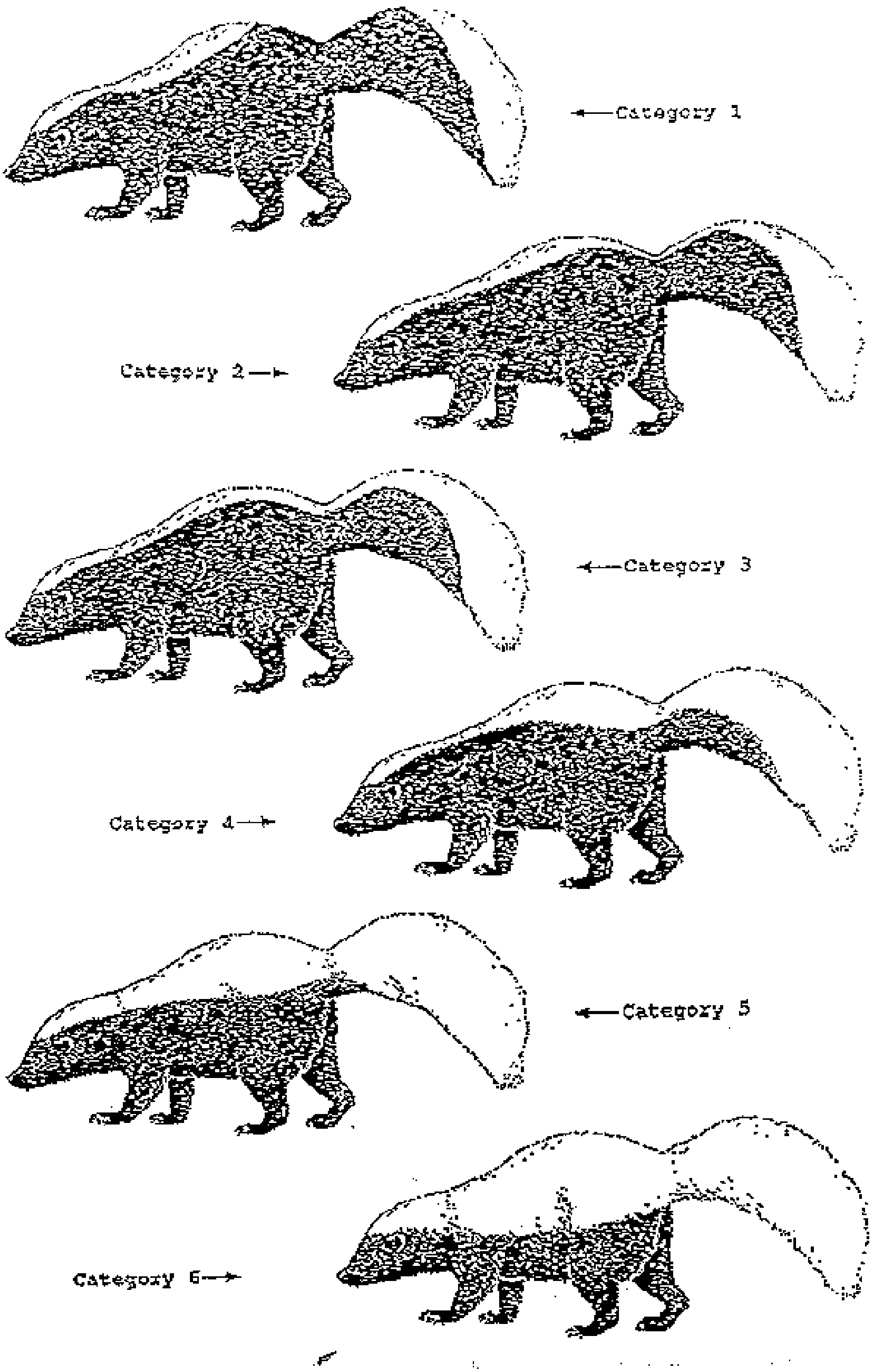

Figure 3 - Six categories of dorsal stripe patterns in hog-nosed skunks.

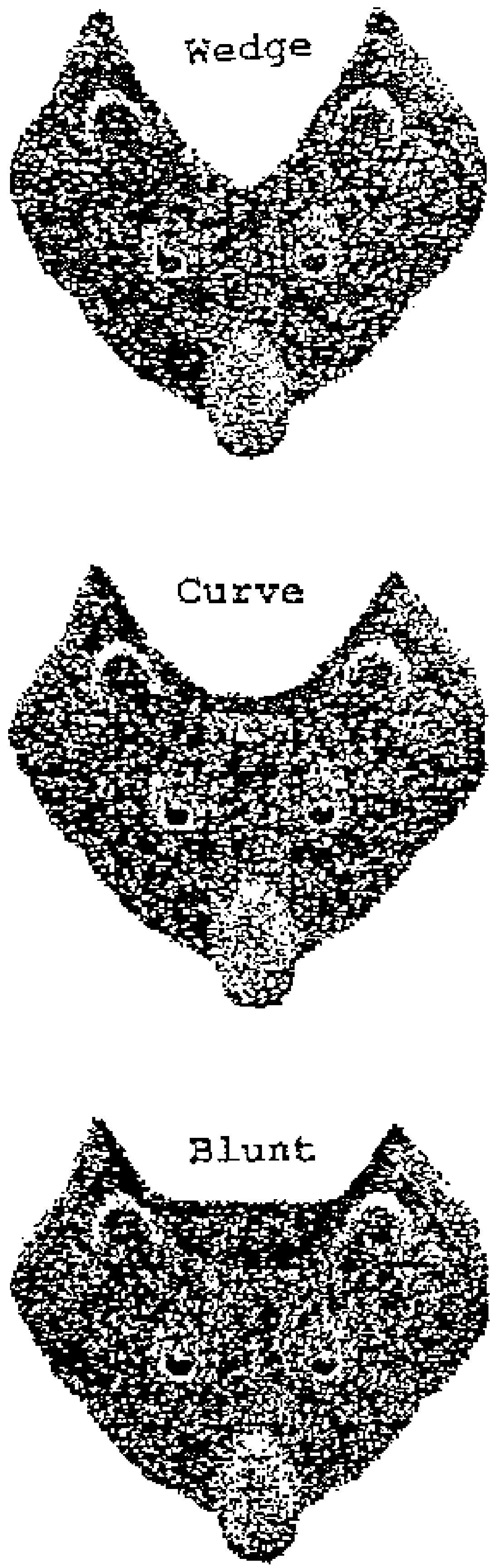

Figure 4 - Three head stripe patterns in hog-nosed skunks.

Figure 5 - Aligned D-loop sequences for three hog-nosed skunks. The primers bracket the regions sequenced in the detailed comparisons of hog-nosed skunk populations.

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                           .         .         .         .         .        60
C.leuconotus      TTTCAAGGAAGAAGCAACAGCCCCACCATCAACACCCAAAGCTGATATTCTAATTAAACT
C.mesoleucus      ............................................................
C.chinga          ....................................................G.......

                           .         .         .         .         .       120
C.leuconotus      ATTCCCTGTTTTCACTCCATAACAACCTAATTCATATATTGCAAAACTTTTACTGTGCTT
C.mesoleucus      ............................................................
C.chinga          ...........C.T.C...C..T.....................................

                           .         .         .         .         .       180
C.leuconotus      CCCCAGTATGTTTTCATTCCCCCCTCCCTATGTACGTCGTGCATTAATGATTTGCCCCAT
C.mesoleucus      .................C.....-....................................
C.chinga          ...........C.C..CCT....GC...................................

                           .         .         .         .         .       240
C.leuconotus      GCATATAAGCATGTACATACAGTGGTTCATCTTACATGATGAATATCACTTACATCACGA
C.mesoleucus      ....................................................G.......
C.chinga          ..............................T.....................G.......

                           .         .         .         .         .       300
C.leuconotus      GCTTAATCACCAAGCCTCGAGAAACCATCAATCCTTGCAAGCAGTATACCTCTTCTCGCT
C.mesoleucus      ............................................................
C.chinga          ............................................................

                           .         .         .         .         .       360
C.leuconotus      CCGGGCCCATGACATGTGGGGGTTTCTACAGTGAAACTATACCTGGCATCTGGTTCTTAC
C.mesoleucus      ............................................................
C.chinga          ...........T.................C..............................

                           .         .         .        [  Primer L398 ->    ]
C.leuconotus      TTCAGGGCCATTTATAGTGTTGTATCCAATCCTACTAACCTCTCAAATGGGACATCTCGA
C.mesoleucus      ...............A............................................
C.chinga          ...........-.........C......................................

                           .         .         .         .         .       480
C.leuconotus      TGGACTAATGACTAATCAGCCCATGATCACACATAACTGTGGTTTCATGCATTTGGTATC
C.mesoleucus      ............................................................
C.chinga          ........................................A.................--

                           .         .         .         .         .       540
C.leuconotus      TTTTTTAATTTTTTAGGGGA-----ACTGGTATCACTCAGCTATGACCGTAAAGGTCTCG
C.mesoleucus      ............................................................
C.chinga          ..............-....GGGGGG.......G............C..............

                           .         .         .        [   <- Primer H601   ]
C.leuconotus      TCGCAGGCAGATATATTGTAGCTGGACTTATTTATTATCATTTACCCGCAT???ACATCC
C.mesoleucus      ...................................................CAT...A..
C.chinga          ............A.C........................T......G....CAT.T.A..
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                           .         .         .    [250-300 bp]    .        660
C.leuconotus   ATA?GGTGCA??TCAGTC?ATGGTC?????????**REPEAT**GCATACGCATATACAC
C.mesoleucus   ...A......AT......A......ACAGGACAT..........................
C.chinga       ...A....T.AT......A......ACAGGACAT..........................

                         .         .         .         .         .       720
C.leuconotus   GTATATATTATACAAATTAACTAAGCCAAACCCCCCTTACCCCCCGTAATTTCAAAGTAT
C.mesoleucus   ............................................................
C.chinga       .........................................................C..

                         .    [ Primer L724 ->]        .         .       780
C.leuconotus   ACAAACATTTATTATTGTTCCGCCAAACCCCAAAAACAGAACTTAAACGAATGCAACTAT
C.mesoleucus   ............................................................
C.chinga       ................A...T.............................G.........

                         .         .         .         .         .       840
C.leuconotus   ATATGAAATTACCTATATGTACCTAACCCATTAATCGACTTATGTTAATCAGAATATCTA
C.mesoleucus   ............................................................
C.chinga       ............T.T...AA........................................

                         .         .         .         .         .       900
C.leuconotus   TAGATACAATTTATTTTGCTCTAATTGCCCCCTATTAAATTTCACTAATTTTAACAAACT
C.mesoleucus   ............................................................
C.chinga       .......................T...................G.C............A.

                         .         .         .         .         .       960
C.leuconotus   AAATCAGTAAAAATAACAGTTAATGTAGCTTAACATACTAAAGCAAGGCACTGAAAATGC
C.mesoleucus   ............................................................
C.chinga       ....T.A.....-....................T.A..C.....................

                        972    [ <- Primer 282  ]
C.leuconotus   TTAGATGAGTTA  /  AGGTTTGGTCCTAGCCTT
C.mesoleucus   C...........
C.chinga       C.??????????

- = insertions / deletions
? = uncertain nucleotide
```

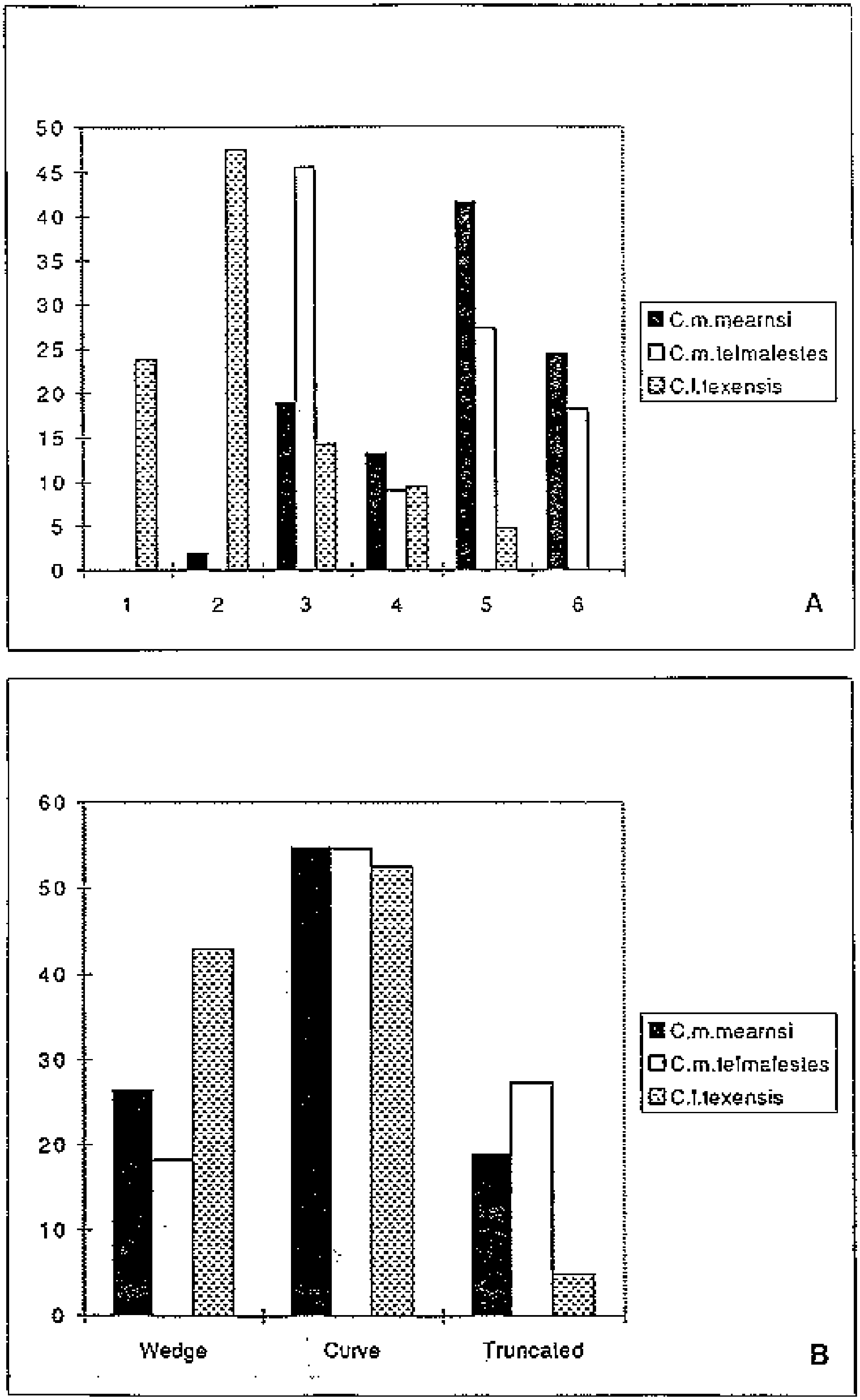

Figure 6 - (A) Bar graph depicting the observed frequency of dorsal stripe patterns observed for the hog-nosed skunks in Texas and adjacent states. (B) Bar graph depicting the observed frequency of head stripe patterns observed for the hog-nosed skunks in Texas and adjacent states.

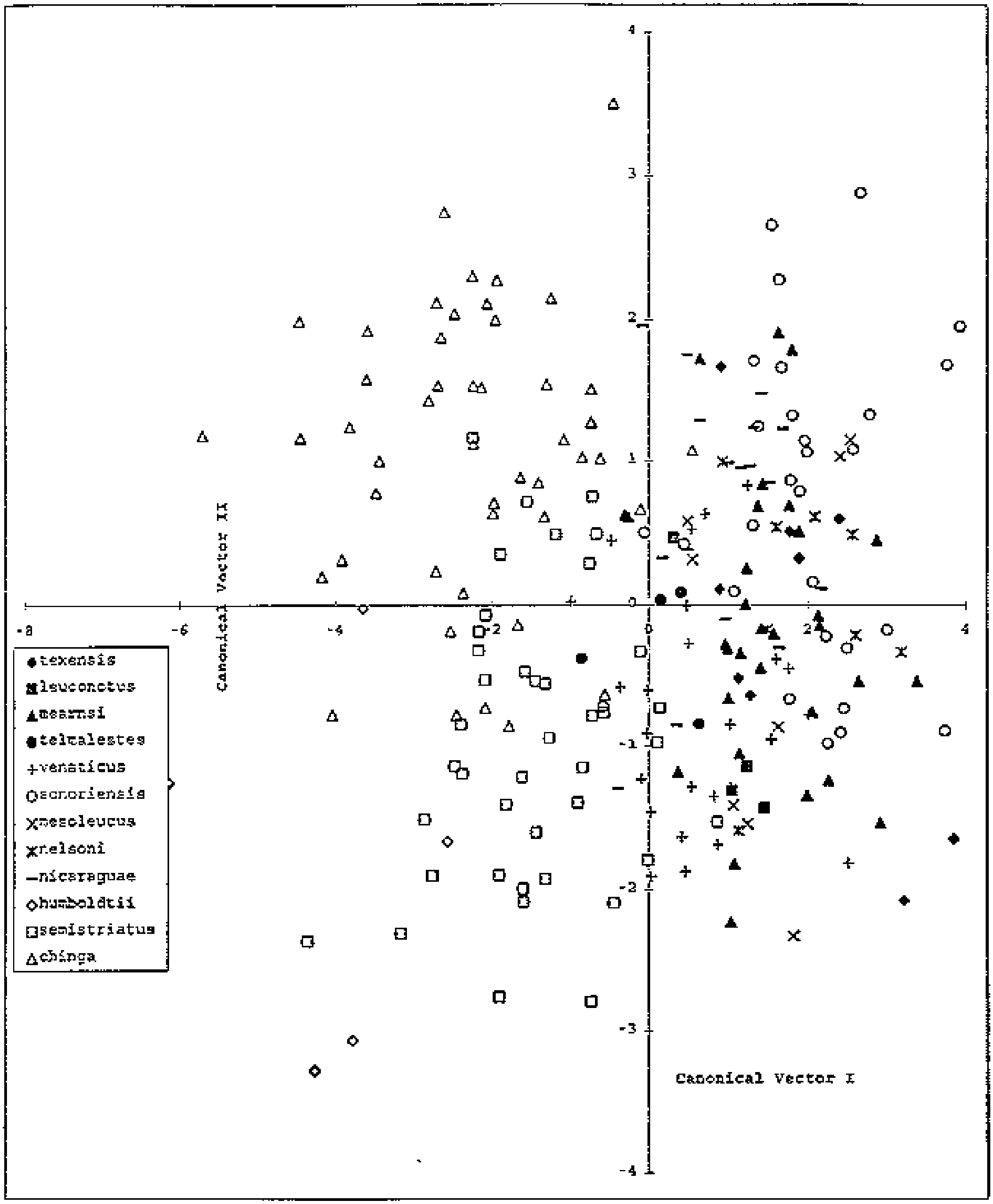

Figure 7 - Plot of the first two canonical vectors for individual samples

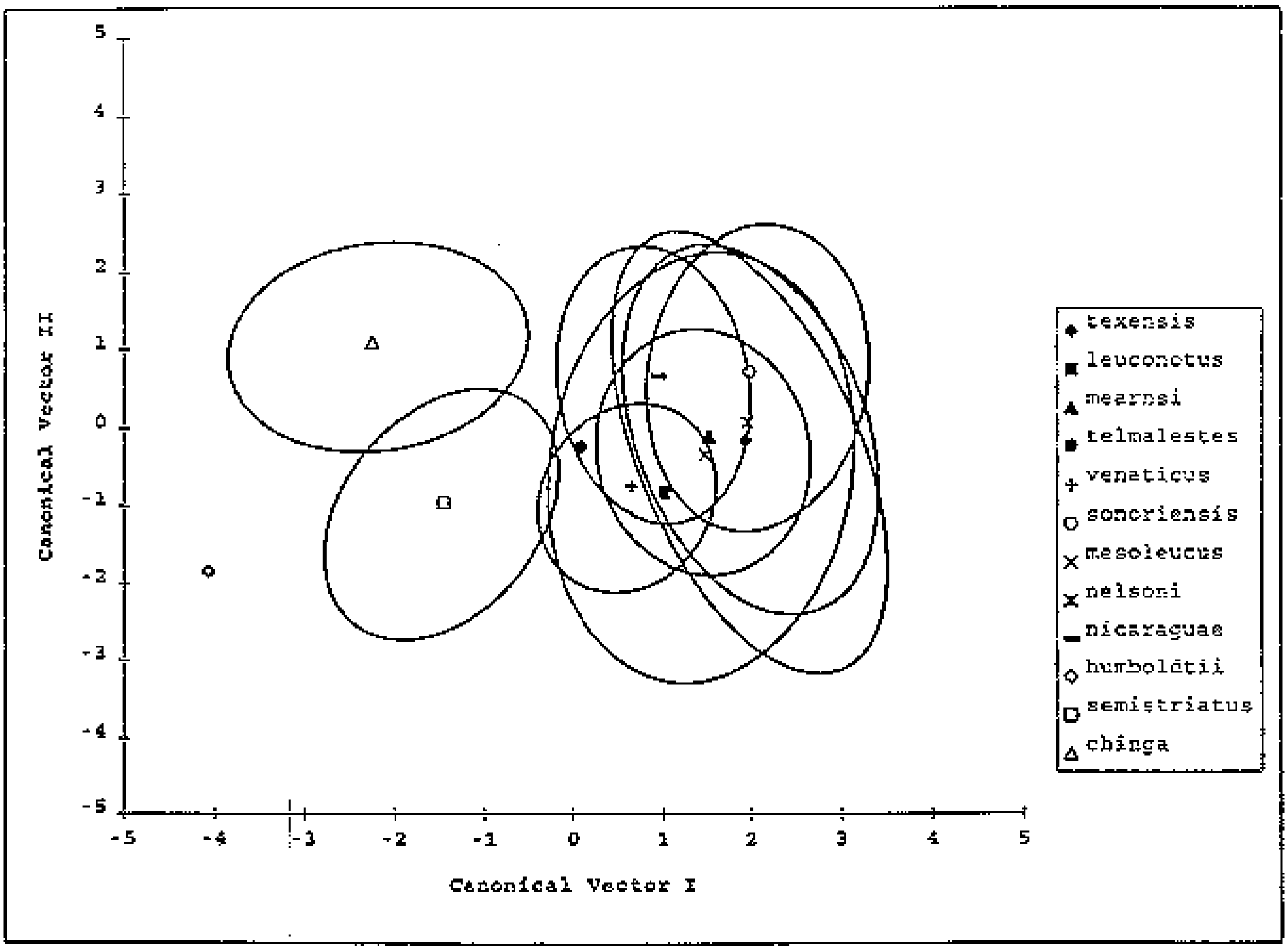

Figure 8 - Plot of the first two canonical vectors showing the mean centroids and 95% confidence ellipses

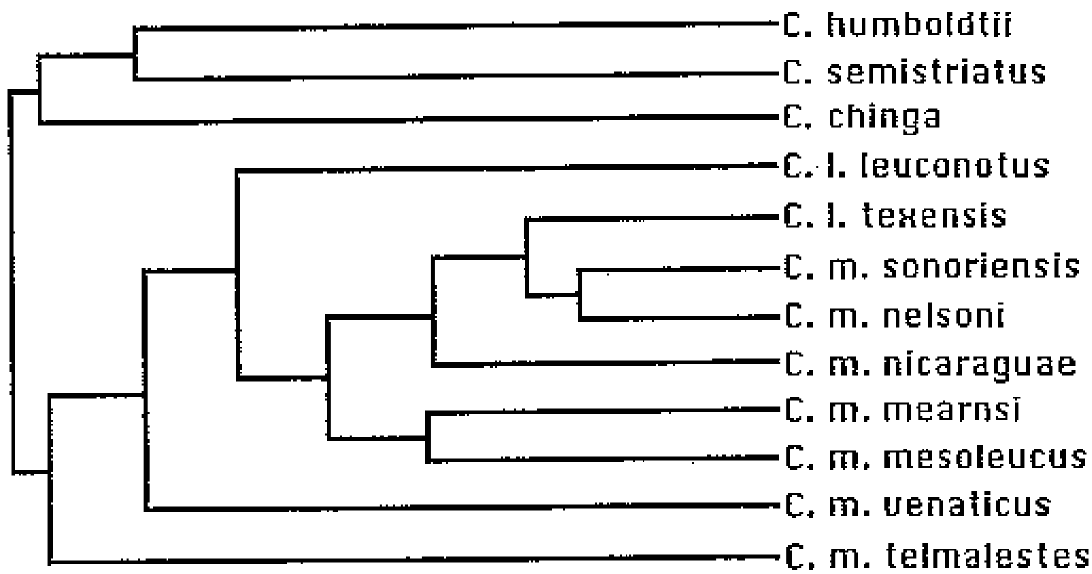

Figure 9 - Phenogram derived using Manhattan Distances (calculated from canonical vectors derived from principal components 2-21) and neighbor-

Figure 10 - Aligned D-loop sequences for the specimens examined in the detailed population studies of hog-nosed skunks. Question marks (?) denote missing or ambiguous data.

```
01 CLE      TCTCAAATGGGACATCTCGATGGACTAATGACTAATCAGCCCATGATCACACATAACTGT
02 CLT      ????????????????????????....................................
03 CLT2     ????????????????????????....................................
04 CLT3     ????????????????????????????????............................
05 CME      ............................................................
06 CMM      ????????????????????????....................................
07 CMM2     ????????????????????????....................................
08 CMM3     ????????????????????????....................................
09 CMM4     ????????????????????????....................................
10 CMM5     ????????????????????????....................................
11 CMM6     ????????????????????????????????............................
12 CMM7     ???????????????????????????????.............................
13 CMV      ............................................................
14 CMV2     ............................................................
15 CMF      ??????????????????????????????????????????????????..........
16 CMS      ............................................................
17 CMS2     ............................................................
18 CCH      ............................................................
19 SGROR    ............................................................
20 MME      CT..........................................................
21 MMA      CT..........................................................
22 mydau    C...........................................................


01 CLE      GGTTTCATGCATTTGGTATCTTTTTTAATTTTTTAGGGGA-----ACTGGTATCACTCAG
02 CLT      ............................................................
03 CLT2     ............................................................
04 CLT3     ............................................................
05 CME      ............................................................
06 CMM      ............................................................
07 CMM2     ............................................................
08 CMM3     ............................................................
09 CMM4     ............................................................
10 CMM5     ............................................................
11 CMM6     ............................................................
12 CMM7     ............................................................
13 CMV      ............................................................
14 CMV2     ............................................................
15 CMF      ............................................................
16 CMS      ............................................................
17 CMS2     ............................................................
18 CCH      .A................--.............-.....GGGGGG.......G.......
19 SGROR    ...G..............--.............-.....GGGGGG...............
20 MME      ...G....A........T--.............-.....GGGGGGG..............
21 MMA      ...G..............--.............-.A...GGGGGGG..............
22 mydau    ...G..............--.C....T....--GG....GGAGGG...............
```

```
                    .         .         .         .         .         .
01 CLE     CTATGACCGTAAAGGTCTCGTCGCAGGCAGATATATTGTAGCTGGACTTATTTATTATCA
02 CLT     ............................................................
03 CLT2    ............................................................
04 CLT3    ............................................................
05 CME     ............................................................
06 CMM     ............................................................
07 CMM2    ............................................................
08 CMM3    ............................................................
09 CMM4    ............................................................
10 CMM5    ............................................................
11 CMM6    ............................................................
12 CMM7    ............................................................
13 CMV     ............................................................
14 CMV2    ............................................................
15 CMF     .........C..................................................
16 CMS     ............................................................
17 CMS2    ............................................................
18 CCH     .....C...........................A.C......................T.
19 SGROR   .................................A..........................
20 MME     .................???????????????????????????????????????????
21 MMA     .................................AT.GTAGCTG.ACT.AT..AT.ATC..
22 mydau   .............-............-...-..A.......-..--.........-....
```

```
                  *           .         .         .         .         .
01 CLE     TTTACCCAAACCCCAAAAACAGAACTTAAACG-AATGCAACTATATATGAAATTACCTAT
02 CLT     ............................................................
03 CLT2    ............................................................
04 CLT3    ............................................................
05 CME     ............................................................
06 CMM     ..................CAGA......................................
07 CMM2    ............................................................
08 CMM3    ............................................................
09 CMM4    ............................................................
10 CMM5    ............................................................
11 CMM6    ............................................................
12 CMM7    ............................................................
13 CMV     ............................................................
14 CMV2    .......?????????????????????????.????????????????????????...
15 CMF     ..A................??????????????????????........????????...
16 CMS     ............................................................
17 CMS2    ............................................................
18 CCH     .....G............................G.....................T.T.
19 SGROR   .........................C-...TAAGTGTAT.A..C..GAA.CTACTTA.CC
20 MME     ???????...................-..G???TGCAG..TAT???..........T.?A
21 MMA     .............A............-..T.A.......TTA...C......C...T.TA
22 mydau   ..........................-..G.AC....T...GT..-......CC..T..A
```

```
01 CL2     ATGTACCTAACCCATTAATCGACTTATGTTAATCAGAA-------TATCTATAGATACAA
02 CLT     ............................................................
03 CLT2    ............................................................
04 CLT3    ............................................................
05 CME     ............................................................
06 CMM     ............................................................
07 CMM2    ............................................................
08 CMM3    ............................................................
09 CMM4    ............................................................
10 CMM5    ............................................................
11 CMM6    ............................................................
12 CMM7    ...................................C........................
13 CMV     ............................................................
14 CMV2    ............................................................
15 CMF     .............?.......??????????????.........................
16 CMS     G.A.........................................................
17 CMS2    ..A.........................................................
18 CCH     ..AA........................................................
19 SGROR   .AT..TA...ATTCCC..CT.......TCCT.ATCA..TTCTTAT.C.A..G.T.CGATT
20 MME     CAAA..GC.TAA.GACCCATATAGCT.A.GTGAATT..AGTC...........T.....T
21 MMA     CCAA..A..TAA.CACCCAATCA.CT.A..TCAATT..?GTC...........T...T.T
22 mydau   .AT..TTATG....AC.TCTA......CCCT..A.ACTTAAAGTC..............T


01 CL2     TTTATTTTGCTCTAATTGCCCCCTA-TTAAATTTCACTAATTTTAA-CAAA-CTAAATCA
02 CLT     ............................................................
03 CLT2    ............................................................
04 CLT3    ............................................................
05 CME     ............................................................
06 CMM     ............................................................
07 CMM2    ........................................................N...
08 CMM3    ............................................................
09 CMM4    ............................................................
10 CMM5    ............................................................
11 CMM6    ............................................................
12 CMM7    ............................................................
13 CMV     .....................................G......................
14 CMV2    ............................................................
15 CMF     ...............C.T..................................A.....T.
16 CMS     ............................................................
17 CMS2    ............................................................
18 CCH     ..............T....................G.C..............A.....T.
19 SGROR   AC.CG..CCTAT.TT..CTTTTT.TCC..CT.AA.G.CT....AC.G....A.C.T.CT.
20 MME     ..?.C.GCA......GAAA......A..G.C.AAT.A.GGACC..C.T.???????????
21 MMA     ...CC.CG?.....-..........?..G.C.AAT..CG?ACC..C??.???????????
22 mydau   CCCC...A....................G....TTACCG..A..T.A.TC.TC.T.AAC
```

```
01 CLE     GTAAAAATAACAGTTAATGTAGCTTAACATACT-AAAGCAAGGCACTGAAAATGCTTAGA
02 CLT     ............................................................
03 CLT2    .......................................................C....
04 CLT3    .......................................................C....
05 CME     .......................................................C....
06 CMM     .......................................................C....
07 CMM2    .......................................................C....
08 CMM3    .......................................................C....
09 CMM4    .......................................................C....
10 CMM5    .......................................................C....
11 CMM6    .......................................................C....
12 CMM7    .......................................................C....
13 CMV     .......................................................C....
14 CMV2    .......................................................C....
15 CMF     A..................................?????????????????????????
16 CMS     .......................................................C....
17 CMS2    .......................................................C....
18 CCH     A.....-....................T.A..C......................C.???
19 SGROR   A.....GC..T................TT....C.....................C...G
20 MME     ????????????????????????????????????????????????????????????
21 MMA     ????????????????????????????????????????????????????????????
22 mydau   -....T-....T...............T.A.T-......G.A..................
```

```
01 CLE     TGAGTTA
02 CLT     .......
03 CLT2    .N.....
04 CLT3    .......
05 CME     .......
06 CMM     .......
07 CMM2    .......
08 CMM3    .......
09 CMM4    .......
10 CMM5    .......
11 CMM6    .......
12 CMM7    .......
13 CMV     .......
14 CMV2    .......
15 CMF     ???????
16 CMS     .......
17 CMS2    .......
18 CCH     ???????
19 SGROR   ???????
20 MME     ???????
21 MMA     ???????
22 mydau   A..A.C.
```

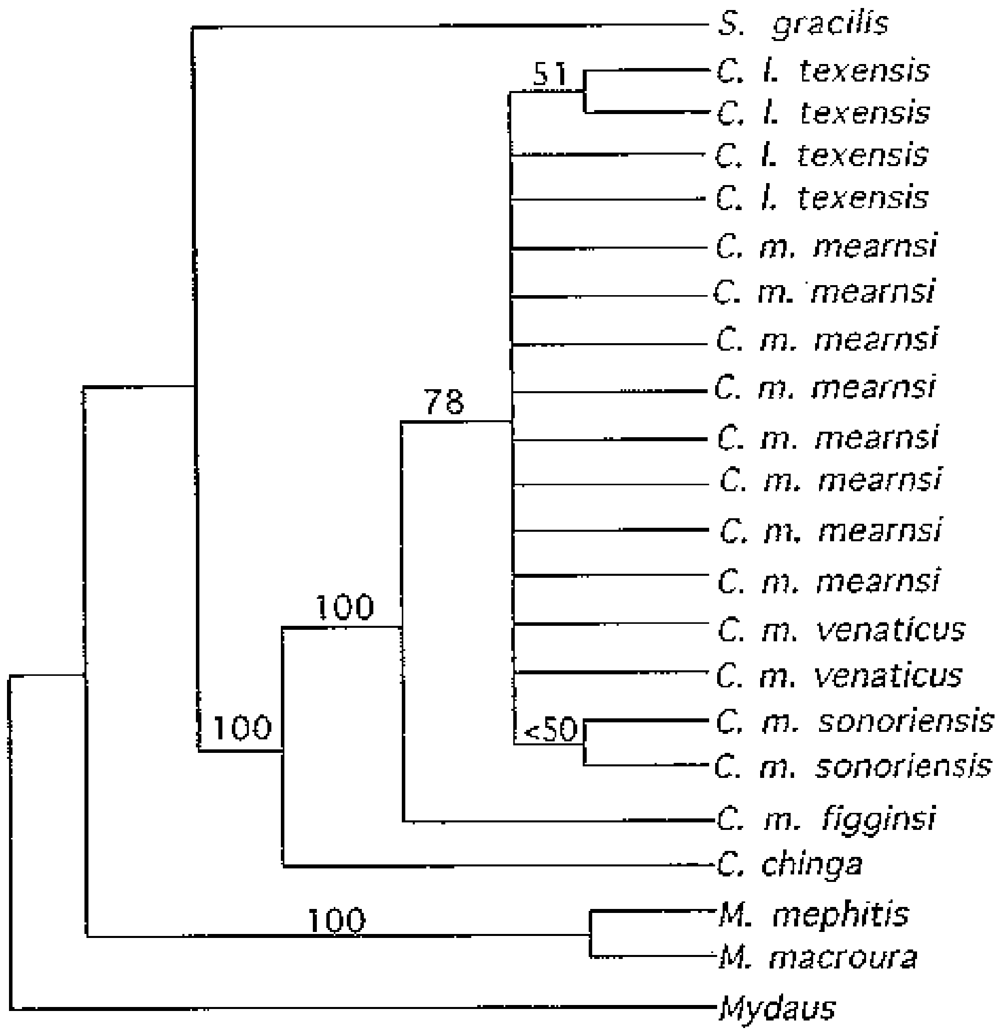

Figure 11 - A 50% majority rule consensus tree, derived using a heuristic search in PAUP. The numbers along branches denote the bootstrap values or support for selected nodes on the tree.

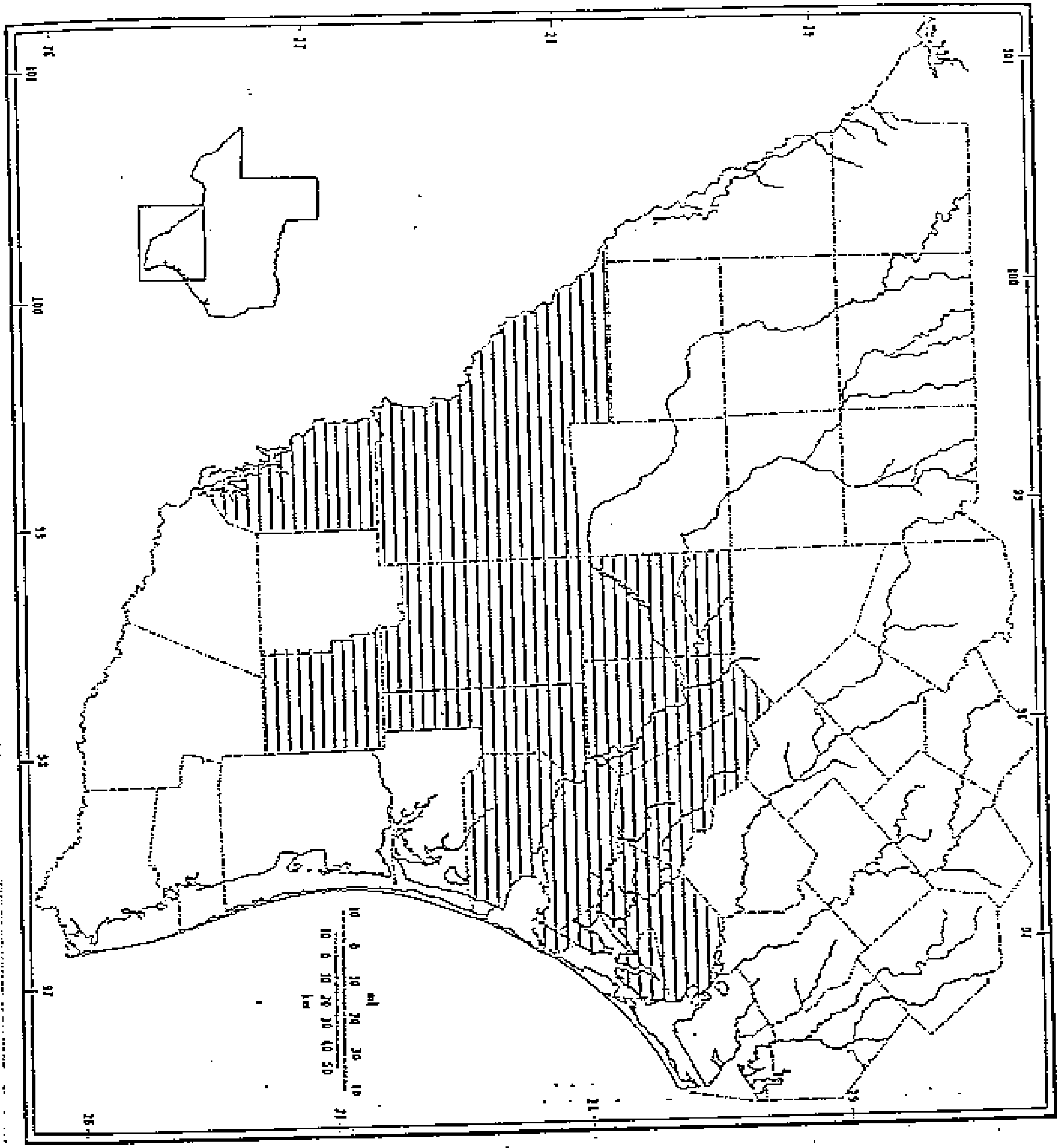

Figure 12 - Counties (shaded) in which hog-nosed skunks were reported by 1987-1988 fur taker licensees.

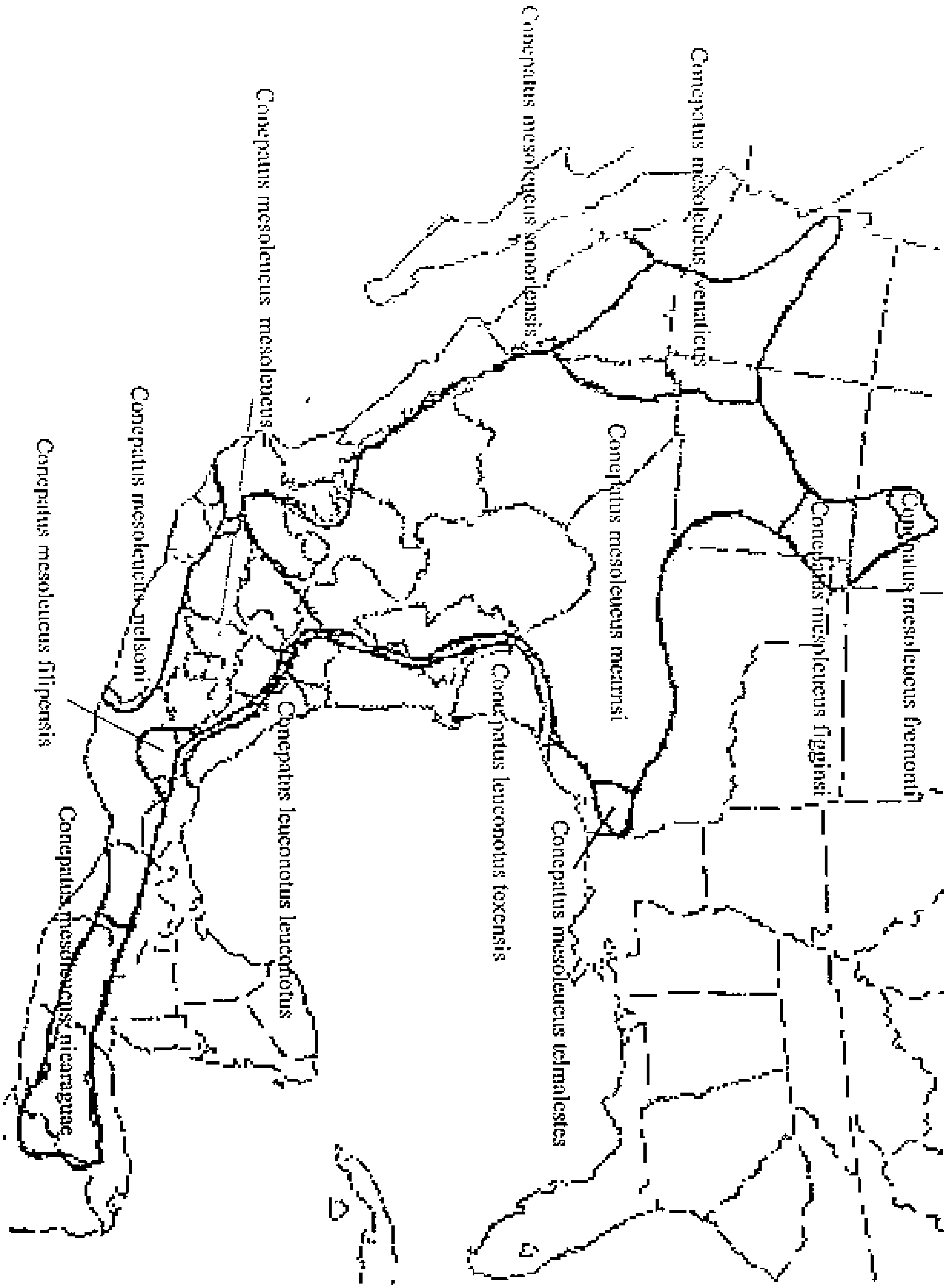

Figure 13 - Range map for hog-nosed skunk taxa from the United States

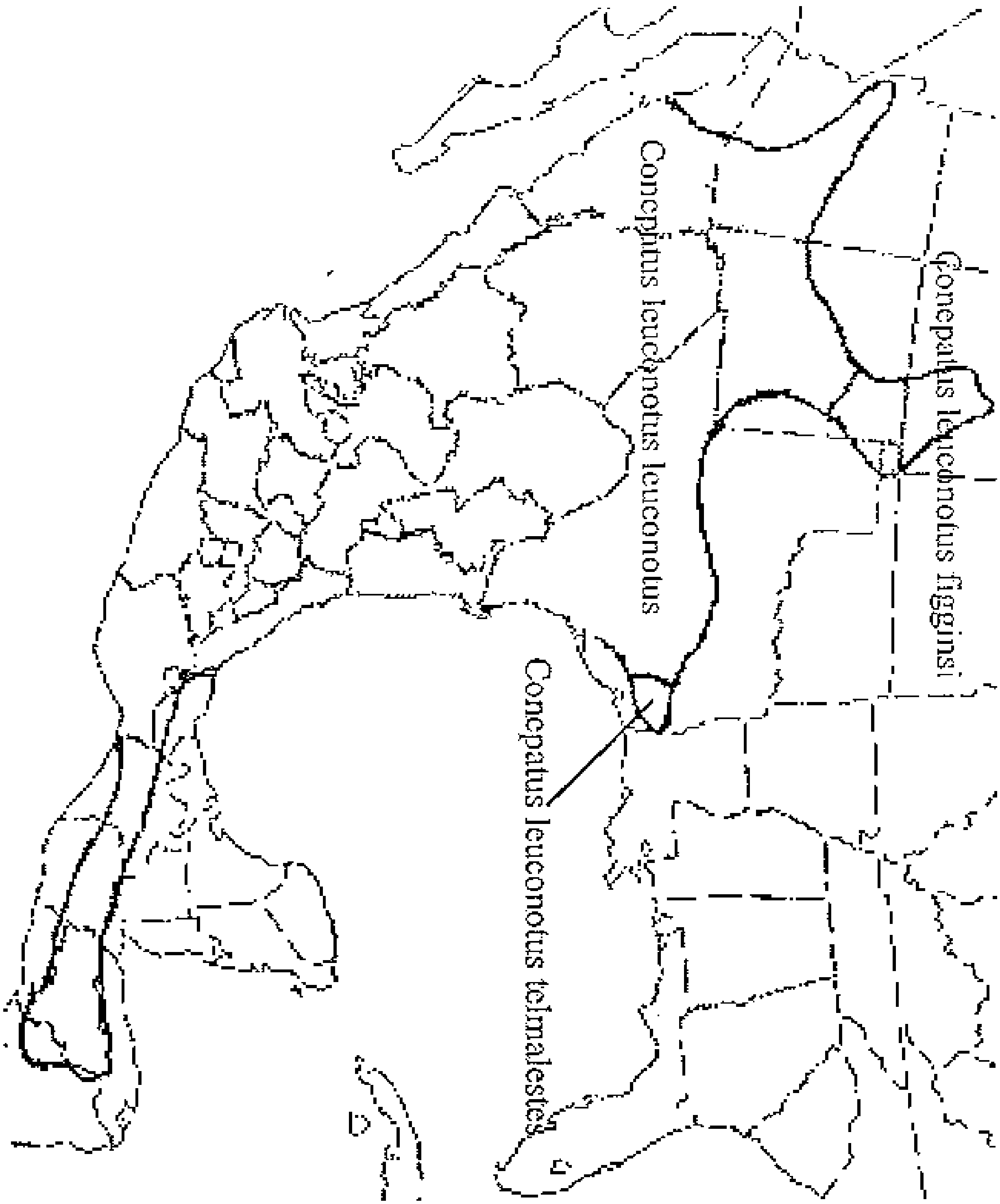

Figure 14 - Modified range map for taxa of hog-nosed skunks subsequent to the taxonomic changes recommended in this report.