VARIATION, SYSTEMATICS, AND INTERSPECIFIC POSITION OF *Heterodon nasicus* (SERPENTES: XENODONTIDAE)

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DEDICATION

This thesis is dedicated to my parents, Mike and Margaret, and my aunt Theresa for supporting me in everything I've ever done, and who encouraged me to follow my dreams. Without them I could not have pursued my love of research.

and

to my grandfather, Melvin Eckerman, for teaching me the values of dedication, hard work and doing what's right no matter what the consequences.

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by

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THESIS

Presented to the Faculty of the Graduate School of
The University of Texas at El Paso
in Partial Fulfillment
of the Requirements
for the Degree of
MASTER OF SCIENCE

Department of Biological Sciences
THE UNIVERSITY OF TEXAS AT EL PASO
DECEMBER, 1996

ACKNOWLEDGMENTS

Over the years I have been here at UTEP, a number of people have contributed to the development of this project and the development of me as a student of biology.

First, I would like to thank all of my committee members.

Dr. Jerry D. Johnson, who served as my recruiter, mentor and friend. I thank him for the opportunity that he has given me here at UTEP and for all those trips to Indio. His teaching was inspirational, his cooking divine and his choice in graduate students exceptional. I hope he continues to turn more minds on to biology.

Dr. Elizabeth J. Walsh, for taking a chance and allowing me to work in her lab on something other than rotifers. She made a large portion of this study possible through her funding, advice and, most importantly, patience. I thank her for this and for introducing me to other areas of biology.

Dr. Carl S. Lieb, who always had a word of encouragement usually follow by a laugh. His wit and his professionalism made him a pleasure to work with whether it was in class, in the lab or in the field. Let's hope that some of this rubbed off.

Dr. Robert G. Webb, who made the library obsolete. If ever I couldn't find some material or had trouble deciding what material to look for, I always started by going straight to Dr. Webb who had his entire catalog of books in his head.

Dr. Jerry Hoffer, who didn't hear from me for a long time but still was patient with me and took the time to review my work.

I would also like to thank Dr. James R. Dixon, Dr. Kathryn Vaughan-Friend, and Martin Whiting who all greatly inspired me as an undergraduate and helped me develop the skills I needed. I am particularly grateful to Martin Whiting who, even though in South Africa, has remained a good friend and a source of inspiration.

A host of fellow graduate students deserve special thanks but I want to especially thank Mark Heimer, Travis LaDuc"k" and Christine Carranza who served as office mates, friends and good listeners. I am forever grateful to them for that.

I must also thank my parents, including my aunt Theresa, for their love and support for all that I have strived for. I could not have made it without them. I would also like to thank Dr. Jack Bristol and Dr. Lillian Mayberry, my surrogate parents, for allowing me to live in their basement. They treated me like a son, which included nagging me to get finished, and for that they will always have a special place in my heart.

Finally, I thank Maria Hartt, soon to be Maria Eckerman, for loving me like she does. She has endured the tough times with me and helped me celebrate the good times. There is no doubt that I would be a wreck without her.

This thesis submitted to committee on April 9, 1996.

ABSTRACT

This study focuses on the species of the genus *Heterodon* (*Heterodon nasicus*, *H. simus*, and *H. platyrhinos*), in particular *Heterodon nasicus*. The purpose of this study was twofold. First, to elucidate the interspecific relationships of *Heterodon* and, second, to examine the taxonomic status of the subspecies within *H. nasicus*. There are only three possible phylogenetic relationships that can be hypothesized for the species of *Heterodon* and yet all three are supported by different authors. An attempt to resolve the phylogeny of this group was done using a molecular marker technique called Randomly Amplified Polymorphic DNAs (RAPDs). Relationships were then identified using the proportion of shared amplified products between species to indicate the degree of similarity. The validity of the three subspecies of *Heterodon nasicus* were then examined using a variety of morphometric and meristic data. The data for each subspecies (*H. n. nasicus*, *H. n. gloydi*, and *H. n. kennerlyi*) were analyzed using analysis of variance statistical tests (ANOVA) and discriminant function analyses. Results indicate that *H. nasicus* and *H. simus* are sister taxa then joined by *H. platyrhinos* and that *H. n. nasicus* and *H. n. kennerlyi* should be the only recognized subspecies of *H. nasicus*.

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INTRODUCTION

The North American hog-nosed snakes of the genus Heterodon , as a result of their striking morphology and their bizarre behavioral characteristics are well known Nearctic organisms. This interest has not been restricted to scientific workers, such that familiarity with the "spread-heads" and death feigning is well known among rural communities throughout the United States. According to Wright (1950) some 61 common names have been applied to the Eastern Hog-nosed snake (Heterodon platyrhinos) alone, indicating that people have general knowledge of this group of snakes. In view of this broad scientific and popular interest in the genus, it is surprising that there have been very few works published on Heterodon. Edgren (1952a, 1952c) first attempted to systematically analyze the genus. This represented the first comprehensive work done on Heterodon and has remained the only comprehensive treatment of systematics for this group in the last 90 years.

The Western Hognose snake, Heterodon nasicus, and its congeners, H. platyrhinos (Eastern Hognose) and H. simus (Southern Hognose), are an ancient group of snakes. The divergence of these three species, according to micro-compliment fixation (MCF) analysis and the fossil record (Fig. 1), appears to have occurred as far back as the Miocene-Pliocene epochs (Platt, 1983; Pinou, 1993; Dowling, 1983). This data

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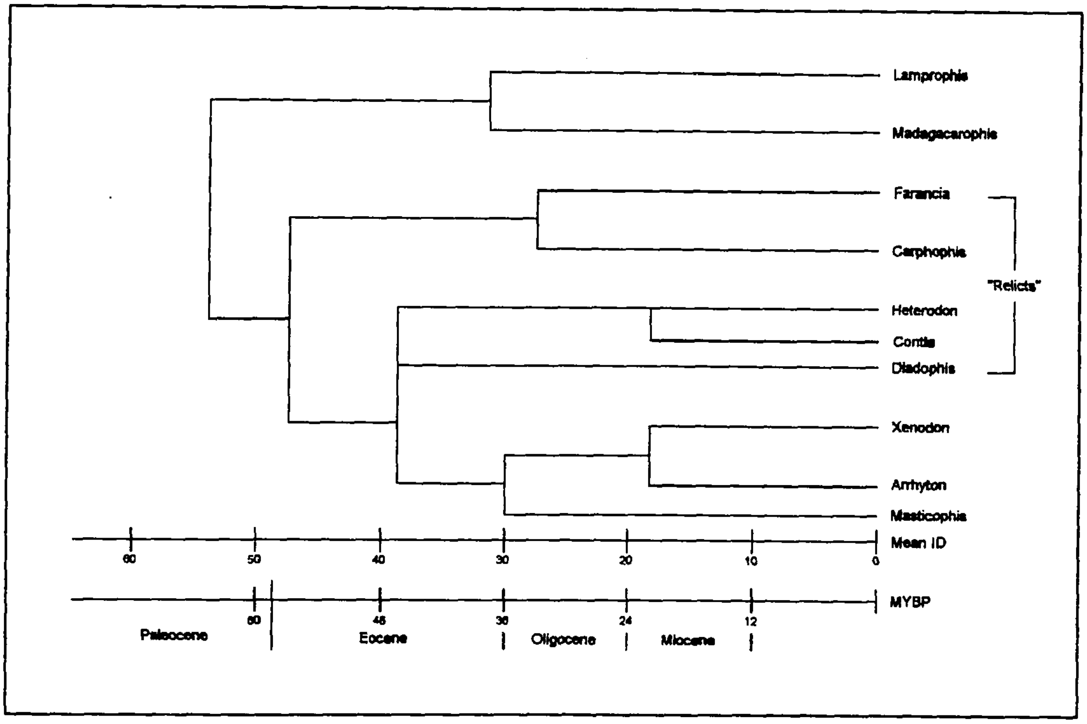


Figure 1: Diagram reconstructed from Pinou (1993) showing Pliocene-Miocene emergence of Heterodon. This is a modified Distance Wagner tree used as a basis for suggesting patterns of chromosomal evolution among the taxa compared.

suggesting that Heterodon is a relict genus has caused many problems in resolving the taxonomy of this group. The relationships of hognose snakes to other members of the family Xenodontidae, as well as to each other, thus remains unclear (Edgren, 1952a; Platt, 1969; Dowling et al., 1983; Weaver, 1965; Pinou, 1993).

Heterodon nasicus is the only member of the genus that contains recognized subspecies. The great amount of variation in coloration and morphology within this species has resulted in the separation of geographic variants into three subspecies (Edgren, 1952c; Kennicott, 1860). However, the validity of the these subspecies, Heterodon nasicus nasicus, H. n. gloydi, and H. n. kennerlyi, remains questionable (Edgren, 1952a; Platt, 1969). The goals of this study are to assess the interspecific relationships of Heterodon and to determine the validity of the subspecies of Heterodon nasicus.

Little has been published about the relationships of the species within the genus Heterodon. There is little doubt that the species of Heterodon are valid in a biological sense due to the lack of recorded hybrids between species over broadly overlapping distributions (Edgren, 1952a). The only species that do not overlap in their range are H. nasicus and H. simus. Edgren (1952a) concluded after examining a suite of morphological characters (Table 1), that it seemed most logical to view H. simus as an off-shoot from the evolutionary line that produced the modern H. platyrhinos. However, Edgren also noted his characters as inconsistent and that the alternate hypothesis of H. simus and H. nasicus as sister taxa was not entirely unlikely. Auffenberg (1963) split the genus into two groups on the basis of vertebral characters, a platyrhinos group and a nasicus-simus group. Using cranial morphology and vertebral characters Weaver (1965)

Table 1: Traits which differ among the species of *Heterodon* used by Edgren (1952a) in determining their relationships.

Traits	*H. platyrhinos*	*H. simus*	*H. nasicus*
Maxilla	Long and Slender	Short and stubby	Short and stubby
Maxillary teeth	9-12+2	9-10+2	8+2
Penes	Long and Slender, few large spines, minute spines common	Short and stubby, many relatively small spines, few minute spines	Short and stubby, intermediate number of small spines, and minute spines
Rostral	Slightly turned up	Sharply turned up	Sharply turned up
Rostral ratio	0.94	0.75	0.69
Size	Longest	Shortest	Intermediate
Head	Longest and narrowest	Intermediate	Shortest and widest
Tail	Longest	Male long as in *H. platyrhinos*, female short as in *H. nasicus*	Shortest
Dorsal Scale Rows	25-25-19	25-25-21	23-23-19
Temporals	3+4	4+4 or 5	4+5
Ventrals: Male	114-141	109-122	129-147
Female	128-154	122-134	139-156
Caudals: Male	42-57	34-47	35-50
Female	34-51	25-37	26-41
Dorsal Blotches:			
Male	12-37	21-29	23-52
Female	17-34	23-30	30-50
Azygous Scalation	1	3-14	2-28

made the same distinctions (Table 2). Yet another hypothesis comes from scale ultrastructure used by Pinou (1993). Her strict consensus cladogram of microdermatoglyphic characters of several "relict" taxa indicated that *H. nasicus* and *H. platyrhinos* are the most closely related, joined then by *H. simus*. A summary of the three hypothesized phylogenetic relationships is provided in Figure 2. Currently the *Heterodon nasicus* species group contains three recognized subspecies differentiated by variable characters which include the number of azygous scales, the number of dorsal blotches, color variation, size and the number of loreal scales. *Heterodon platyrhinos* and *H. simus* have no recognized subspecies. The three subspecies of *Heterodon nasicus* (*H. n. nasicus*, *H. n. gloydi*, and *H. n. kennerlyi*) are separated into three geographical units (Fig. 3). However, the status of these subspecies is suspect. In the description of *H. n. gloydi* Edgren (1952c) noted a broad intergradation zone with *H. n. nasicus*. After studying specimens from Kansas, Oklahoma, and Texas Platt (1969) suggested that these two subspecies represented a cline instead of two separate entities (Fig. 4). However, because his sample sizes were small and collected from a small portion of the entire range, he was unable to test this hypothesis. Edgren (1952c) also remarked that *H. n. kennerlyi* seemed distinct from the other subspecies, but the few specimens from the expected contact zone made it difficult to resolve the taxonomic status of this subspecies.

This study first evaluates the interspecific relationships of *Heterodon* by using a molecular marker technique called Randomly Amplified Polymorphic DNAs (RAPDs). Taxonomic decisions are then evaluated in light of the known distribution and biogeographic history of the species group. These data are then compared to other

Table 2: Myological and osteological traits which are similar among the species of *Heterodon* used by Weaver (1965) in constructing a *nasicus-simus* group and a *platyrhinos* group.

	H. platyrhinos	*H. simus*	*H. nasicus*
Premaxillary		X	X
Maxillary		X	X
Nasal	X	X	
Ectopterygoid		X	X
Pterygoid		X	X
Frontals		X	X
Parietals		X	X
Supraoccipital		X	X
Orbital Foramen	X	X	
Foramen Magnum		X	X
Adductor Extenus Medialis		X	X
Pseudotemporalis		X	X
Retractor Quadrati	X	X	
Cutaneo Quadratus	X	X	
Retractor Quadrati	X		X
Labial glands		X	X

The X's indicate the species that are most similar for the structures listed in the column at the left.

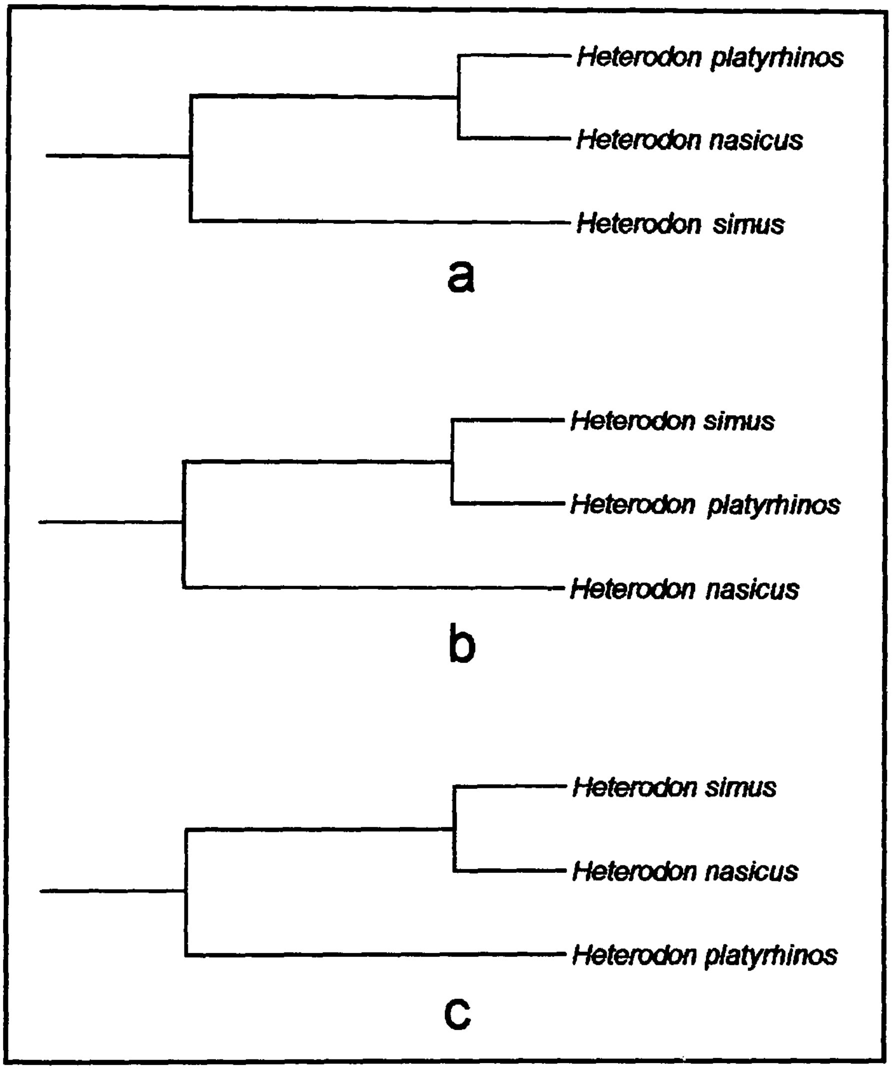


Figure 2: The three hypothesized phylogenetic relationships among the species of Heterodon. (a) Phylogeny proposed by Pinou (1993). (b) Relationships proposed by Edgren (1952a). (c) Relationships proposed by Auffenberg (1963) and Weaver (1965).

Figure 3: Distribution map of Heterodon nasicus. Yellow represents the distribution of H. n. nasicus, blue represents the distribution of H. n. gloydi, red represents the distribution of H. n. kennerlyi, and green represents the proposed intergrade zone between H. n. nasicus and H. n. gloydi.

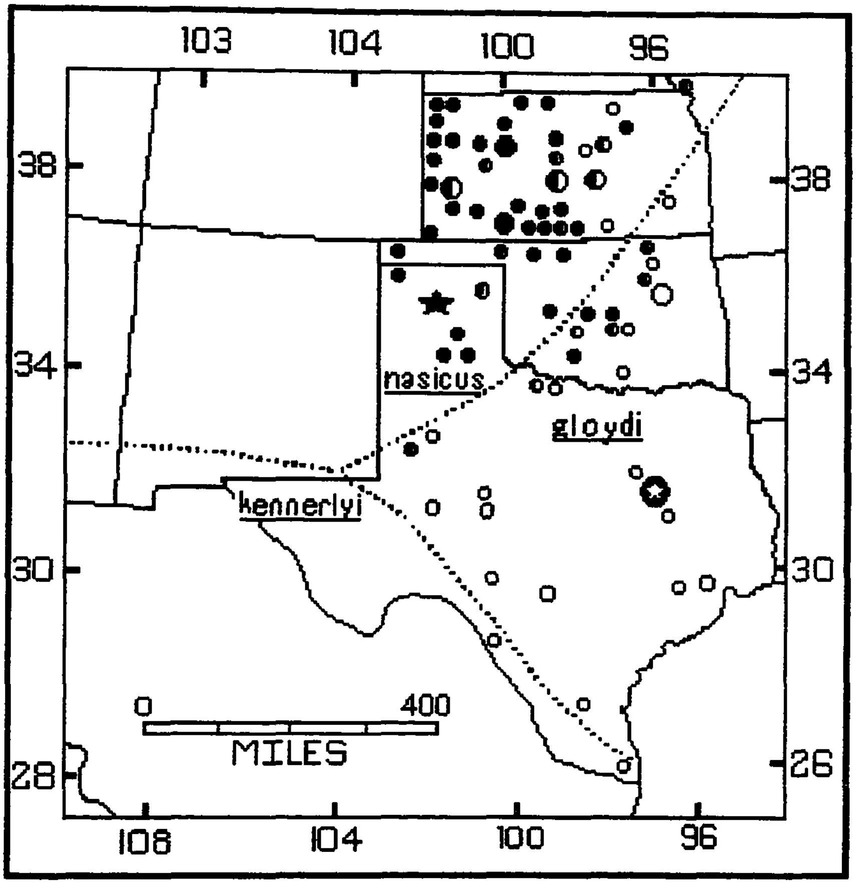


Figure 4: The subspecies of the Western Hognose snake (Heterodon nasicus) in Kansas, Oklahoma, and Texas (Platt, 1969). Dotted lines mark the boundaries of the ranges of the three subspecies as mapped by Edgren (1952a). The symbols represent specimens from various counties that have been examined either by Edgren or Platt. Dots represent counties from which at least 75% of the specimens have numbers of dorsal blotches characteristic of H. n. nasicus, and circles represent counties from which 75% of the specimens are typical of H. n. gloydi. Half circles represent counties with samples of specimens that are intermediate. Small symbols represent counties from which there are samples of only one to four specimens, and large symbols represent counties from which there are five or more specimens. The type locality of H. n. nasicus (Amarillo, Texas) is indicated by a black star and the type locality of H. n. gloydi (Wheelock, Texas) is indicated by a white star.

systematic treatments of this group.

The second goal of this study is to examine the validity of the subspecies of H. nasicus. First, the degree of sexual dimorphism for a variety of meristic and morphometric characters are assessed for the three subspecies of H. nasicus and then compared to each other. Next, the scutellation characters used commonly to identify the subspecies of H. nasicus (azygous scales (AZY), loreal scales (LOR), and dorsal blotches (DB)) are analyzed separately for any possible geographical patterns. Ventral and subcaudal scales will also be analyzed in the same manner due to their strong correlation to the number of dorsal blotches. Finally, character isolation of the three subspecies will be analyzed using a discriminate function analysis. Taxonomic decisions on the status of subspecies of H. nasicus are based upon character analysis, biogeographical information and their known distributions.

MATERIALS AND METHODS

Interspecific relationships of Heterodon.

Liver tissues from Bogertophis subocularis, Farancia abacura, H. nasicus, H. platyrhinos, and H. simus were used for analysis of the infrageneric relationships of Heterodon. The species, the catalog number, and the specific locality of each specimen used in this analysis is recorded in Table 3. A molecular marker technique called Randomly Amplified Polymorphic DNAs (RAPDs) was used to generate genetic distance data. Randomly amplified polymorphic DNA sequences are based on the amplification of unknown DNA sequences using single, short, random oligonucleotide primers. Random primer sequences do not discriminate between coding and noncoding regions, meaning that this technique is able to sample the genome more randomly than conventional methods.

All tissues were obtained from museum specimens initially preserved in 10% formalin, then soaked in water and placed in 70% ethanol for permanent storage. A very small amount of tissue (3-5 µg) was removed from each specimen. Tissue samples were individually placed into 1.5 ml micro centrifuge tubes. Tissues were rinsed in distilled water and then centrifuged (14000 rpm) for 30 seconds. The water was then removed and 300 µl 5% Chelex-100 (BioRad) was added to each tube. Each tube was mixed briefly, followed by boiling for 5 minutes. After mixing, samples were centrifuged for 30 seconds, volume) contained approximately 1.5 µl of genomic DNA and 5 µl of dNTPs (100 µM each of dATP, dCTP, dGTP, and dTTP). Also added to the reaction mixture were 38.5

Table 3: The species, catalog number and specific locality of the specimens used in DNA analysis using the Randomly Amplified Polymorphic DNAs (RAPDs) technique as a molecular marker.

Species	Museum Catalog number	Locality
Heterodon nasicus	UTEP 5558	Kansas: Morton Co.; 8.2 miles north of Elkhart
H. nasicus	UTEP 11365	New Mexico: Hidalgo Co.; Just west of Hatchet Gap, .5 road miles south of post # 29 on state highway 81.
H. simus	CARN 92024	South Carolina: Beaufort Co.; Beaufort
H. simus	CARN 69092	Florida: Alachua Co.; Southwest Gainesville
H. platyrhinos	UTEP 10679	Texas: Refugio Co.; State highway 239, 2.3 road miles west-northwest of the junction with state highway 35 (Tivoli)
H. platyrhinos	UTEP 12202	Texas: Gillespie Co.; 3.6 road miles east of the junction of FM road 1376 and state highway 290 on 290.
Bogertophis subocularis	UTEP 9596	Mexico: Durango; 5 miles south of Rodeo
B. subocularis	UTEP 13659	Mexico: Chihuahua; 13.3 road miles east of Escalón
Farancia abacura	UTEP 12289	Texas: San Jacinto Co.; Sam Houston National Forest, 3.4 road miles northwest of TX highway 59 on Forest road 221
F. abacura	UTEP 12290	Texas: Brazoria Co.; Dauciger, 7.1 road miles west of the junction of FM roads 1728 and 1301 on FM road 1301

and the supernatant was used in amplification reactions. Reaction mixtures (50 µl final µl of water, 3 µl of 25 mM $MgCl_2$, 5 µl of 10X Reaction Buffer, 2 µl of primer (0.2 µM), 1 unit of AmpliTaq polymerase overlaid with 1-2 drops of mineral oil to prevent evaporation. Samples were heated at 80°C for 15 minutes prior to amplification. Amplifications are performed in a Perkin-Elmer Cetus DNA thermal cycler programmed for 45 cycles of 1 minute at 94°C, 1 min at 35°C and 2 min at 72°C.

Each sample was divided into six groups. The DNA of each group was amplified using different oligonucleotide primers. The primers used in each replicate are listed in Table 4.

Fragments generated by amplification were separated by size on 1.8% 3:1 NuSeive (FMC) agarose gels containing ethidium bromide run in 1X TBE buffer (89 mM TrisHCL, 89 mM Boric acid, 5 mM EDTA) and they are shown in Appendix A along with graphical representations of the gels. Molecular weights of resulting DNA bands were approximated by using Gelbase 2.0-pro gel analysis package and a 1kb ladder (Gibco) (Appendix B). Conspecifics were than examined together and unshared bands were eliminated. The amplified products remaining were used for analysis and are graphed in Appendix A.

Genetic distances were obtained for each group and then pooled using Nei's similarity index which uses the relationship between the proportion of fragments shared (Upholt, 1977; Nei, 1972). Let N_x, N_y, and N_{xy} be the number of bands observed in sequences X and Y and shared by X and Y, respectively. The overall proportion of shared

Table 4: List of random oligonucleotide primer sequences used in DNA amplification.

Primer	Sequence
OP-G7	5'-GAACCTGCGG-3'
OP-W8	5'-GACTGCCTCT-3'
OP-W10	5'-TCGCATCCCT-3'
OP-GI3	5'-CTCTCCGCCA-3'
OP-WI7	5'-GTCCTGGGTI'-3'
OP-G10	5'-AGGGCCGTCT-3'
1 kb ladder from GibcoBRL	

fragments is calculated as

$$F = 2N_{xy} / (N_x + N_y)$$

Dendrograms were then generated and compared using the unweighted pair-group method using arithmetic averages (UPGMA) and the neighbor-joining method (NJOIN) with rooting of the tree at Bogertophis subocularis in the NTSYS-pc Numerical Taxonomy and Multivariate Analysis System, Version 1.60 (Rohlf, 1990). The UPGMA clustering method uses the similarity between two groups and is defined as the average similarity of all points of unit involving a member of each group. The NJOIN clustering method does not attempt to obtain the shortest possible tree for a set of data. Rather, it attempts to find a tree that is usually close to the true phylogenetic tree (Rohlf, 1990).

Variation and subspecies in Heterodon nasicus.

Specimens.- Approximately 1000 preserved specimens of Heterodon nasicus, H. platyrhinos, and H. simus from museum collections were examined. The museum of deposit and the locality data for each specimen of Heterodon examined is listed in Appendix C.

Taxonomic characters.- The characters examined in the analysis for each specimen are listed and explained in Appendix D. Eight of the characters (Azygous position, Postnasal - Orbitals, CON M-1, BF&PF, 3-PNB, Rostral Position, Venter Color, by dissection at the base of the tail when necessary. Approximate lengths of body and tail for preserved specimens were measured to the nearest millimeter and checked against pre-preservation measurements when available. Descriptive and quantitative analyses were carried out using SigmaPlot for Windows (Jandel Scientific, 1994) and Statistica (StatSoft, 1995).

Sexual dimorphism.- Sexual dimorphic characters must be quantified and separately characterized otherwise alleged differences between taxa may be erroneous. These differences must also be examined for patterns that might reflect population structure within H. nasicus.

First the morphometric data were analyzed. Due to ontogenetic effects, linear relationships were determined by plotting the total length (TOTL) (mm) of the snake on the snout-to-vent length (SVL) (mm), the total length (TOTL) on the tail length (TL) (mm), the head width (HW) (mm) on the head length (HL) (mm), and the rostral front height (ROSFH) (mm) on the rostral straight height (ROSSH) (mm) for each sex using linear regression techniques. Scatterplots were graphed for both sexes for each subspecies with regression lines indicated for each sex on the graphs. The values for the Y-intercept are usually a positive or negative number, but this does not make much biological sense since a head width of 0 should correspond to a head length of 0. Therefore, separate scatterplot graphs were constructed of the same data but with the regression lines calculated when the Y-intercepts were set equal to 0.

Due to lack of information on age class structure and longevity, the sexes could not be compared using conventional techniques. Instead, a F-test for differences between not be compared using conventional techniques. Instead, a F-test for differences between two regression coefficients (Sokal and Rohlf, 1995) (Appendix E) was utilized to test for differences in the slopes of the regression lines calculated for each sex. Significance levels for both conditions (the different settings of the Y-intercept) for sex differences are then reported for TOTL vs. SVL, TOTL vs. TL, HW vs. HL, and ROSFH vs. ROSSH.

Next, various meristic data were analyzed for sexual dimorphism. Because of the differential placement of the cloacal vent in males and females of H. nasicus, the following meristic characters were considered for the analysis for sexual dimorphism: The number of ventral scales (VENT), the number of subcaudal scales (SC), the number of dorsal blotches (DB), the number of tail dorsal blotches (TDB), the number of lateral blotches (LB), and the number of tail lateral blotches (TLB). Box plots showing the mean ($\bar{x}$), 1 standard deviation (Sd), and 1.96 x 1 standard deviation (~95% confidence limits) were constructed for each variable for each sex of each subspecies. A separate box plot was then constructed using the sum of ventral scales and subcaudal scales (VENT+SC), dorsal blotches and tail dorsal blotches (DB+TDB), and lateral blotches and tail lateral blotches (LB+TLB).

The ANOVA (analysis of variance) statistical method was then used to make intersex comparisons. ANOVA was used in favor over a series of T-tests to reduce the risk of a Type I error. A Tukey Honest Significant Differences test was then used to report pairwise sex significance values (p values).

The ANOVA statistical test was used to analyze the quantitative characters (DB, TDB, LB, TLB, VENT, and SC) for statistical significance of differences between means observed for sexes of each taxa. Box Plots were then constructed as a visual description of these data. The analysis was performed again using DB+TDB, LB+TLB, and VENT+SC to determine if sexual dimorphism still persisted.

Subspecies comparisons.- Data for each regression line constructed earlier for the morphometric variables were used to compare the subspecies and to determine if there were any differences. A test of equality among three regression coefficients (Appendix E) was utilized to make comparisons between the different subspecies (Sokal and Rohlf, 1995). Because of the sex differences in snout-to-vent lengths, tail lengths, and possibly head and rostral dimensions determined earlier, the sexes were analyzed separately. This analysis does not compare actual size differences between the subspecies but determines if the different samples were taken from the same or similar population of data. A significant F-value indicates that one or more of the populations varies from the others in their measurement proportions. The advantage this test has over ANOVA is considerable in light of the affect ontogenetic change has on the variance of the data. The difference between this statistic and finding the level of significant differences between two populations is that when more than two data sets are compared they are compared to a pooled slope (b), or a common slope, to all of the data. Changing the y-intercept and setting it equal to zero does not change b, because of this the differences are exaggerated and tend to indicate differences where there may be none. For this reason the analysis setting the y-intercept equal to zero was not done.

The ANOVA statistical test was employed to determine significance levels of differences between the three subspecies in six meristic characters (DB, TDB, LB, TLB, ANOVA was used separately for each sex. Next, the sexes were combined for the variables DB+TDB, LB+TLB and VENT+SC and were statistically analyzed again for differences in means between the three subspecies. Box plots were constructed to determine the interaction between means of DB+TDB, LB+TLB and VENT+SC for the three subspecies.

The sums (DB+TDB, LB+TLB, and VENT+SC) were then used in a discriminant function analysis. There is some concern that these three variables may be clinal in nature. If this is true then it may be expected that there will be significant differences present between groups depending on how they are defined. The discriminate function analysis provides a method of determining the usefulness and accuracy of these data in separating taxa by examining the uniqueness of *a priori* groups (the subspecies of Heterodon nasicus).

Specific character analysis.- The number of dorsal blotches, the number of ventral scales, the number of loreal scales (LOR) and the number of azygous scales (AZY) have all been used separately and in conjunction with each other as diagnostic tools for separating the three subspecies of H. nasicus. To understand these diagnostic characters, patterns in these variables were looked for across geographic space. Longitude and latitude coordinates obtained from locality data were used as the X- and Y-coordinates respectively. Then each character was treated separately as a Z-coordinate and from this a contour map was constructed. The result is a map of each character over a geographic area. Once the maps were constructed the contour lines were corrected for north-south changes in longitude and mapped onto a map of the current distribution of the three subspecies of H. nasicus. These maps were constructed for DB+TDB (Fig. 5), VENT+SC (Fig. 6), LOR (Fig. 7) and AZY (Fig. 8). The sums, DB+TDB and VENT+SC, were used, instead of each individual component, to account for sex differences. The usefulness of each character as an indicator of geographic and reproductive isolation is discussed as well as any data that suggest clinal patterns.

Discriminant analysis.- Ten meristic characters were used in a discriminate analysis to determine any separation between the three subspecies. The characters used were DB+TDB, VENT+SC, the number of azygous scales (AZY), belly color (BLY), the nature of the first dorsal blotch (1st DB), the location of the loreal scales in relation to the ocular ring (PN-O), the extent of connection of the middle nuchal blotch with the first dorsal blotch (CON-M1), the number of loreal scales (LOR), the nature of the nuchal blotch (3-PNB), and the anal plate color (APC). A forward stepwise discriminate analysis was utilized to determine the characters that contributed significantly to the model. Characters that did not contribute to the model were excluded from analysis.

The entire population was divided into 1° longitude by 1° latitude geographic regions. The values for all the snakes in a given lot were then averaged to represent that area. Each region was then identified as one of the subspecies according to its geographic locality. Individual regions that occurred in the areas between the three subspecies were identified separately as *H.n.n./H.n.g.*, *H.n.n./H.n.k.*, and *H.n.g./H.n.k.* so that the placement of these groups could be analyzed as well. This analysis included 68 H. n. nasicus, 18 H. n. gloydi, 23 H. n. kennerlyi, 22 *H.n.n./H.n.g.*, 3 *H.n.n./H.n.k.*, and 4 *H.n.g./H.n.k.* lots.

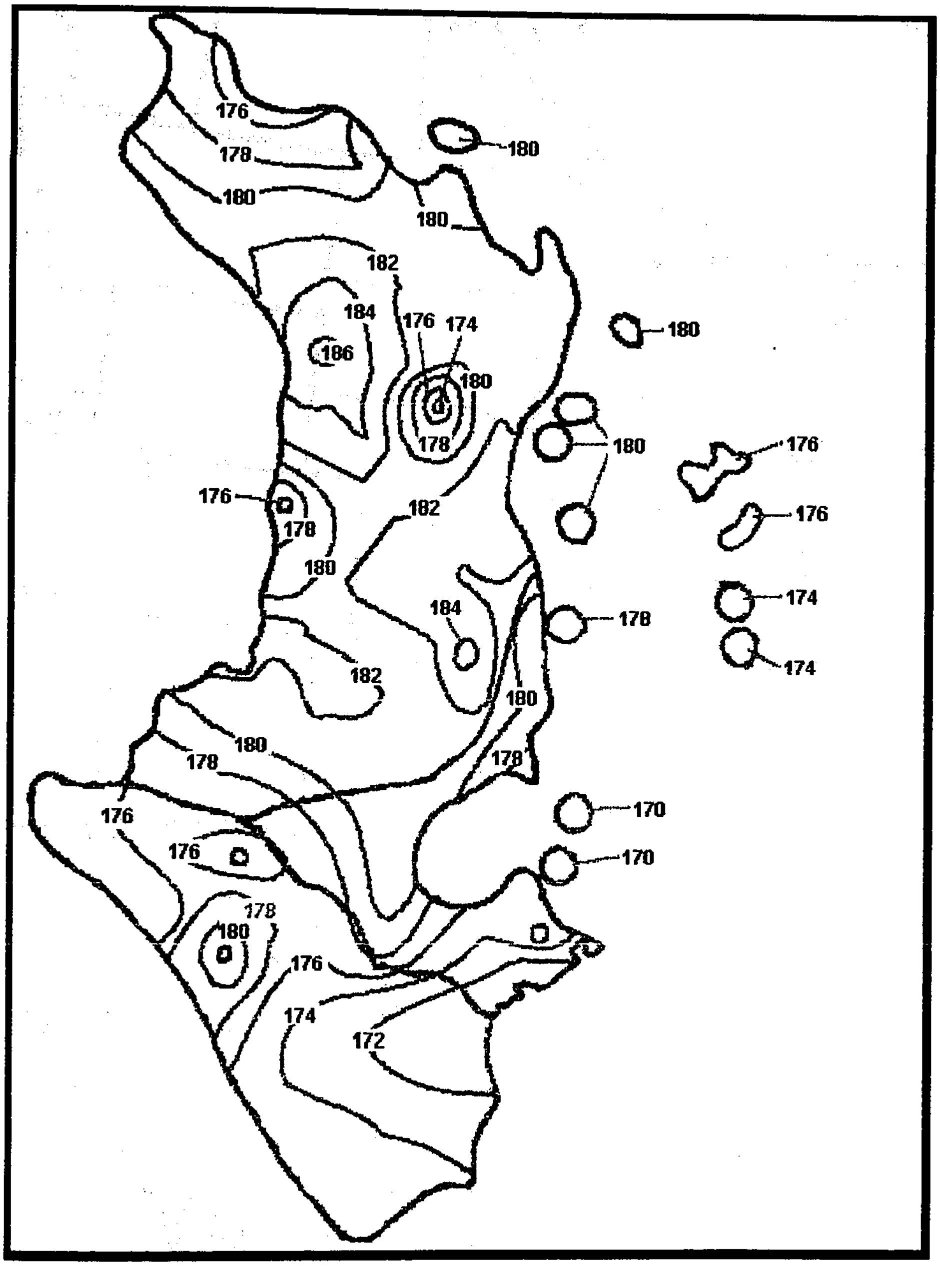


Figure 5: Two dimensional contour map for the number of ventral scales + the number of subcaudal scales constructed and mapped onto the current distribution of H. nasicus. The green lines represent levels of similar values which are labeled in black. The current distribution of H. nasicus is outlined in dark gray.

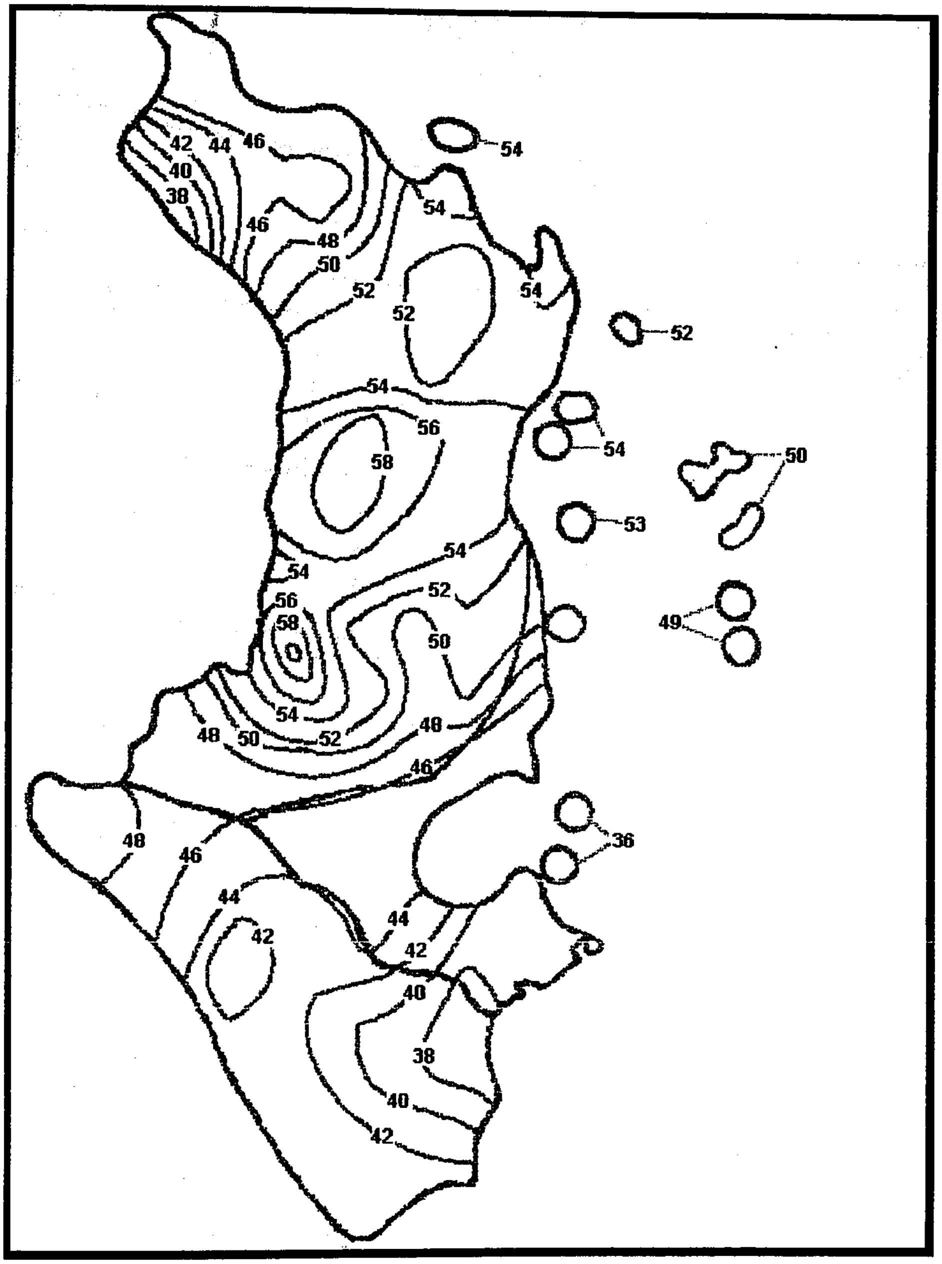


Figure 6: Two dimensional contour map for the number of dorsal blotches + the number of tail dorsal blotches constructed and mapped onto the current distribution of H. nasicus. The green lines represent levels of similar values which are labeled in black. The current distribution of H. nasicus is outlined in dark gray.

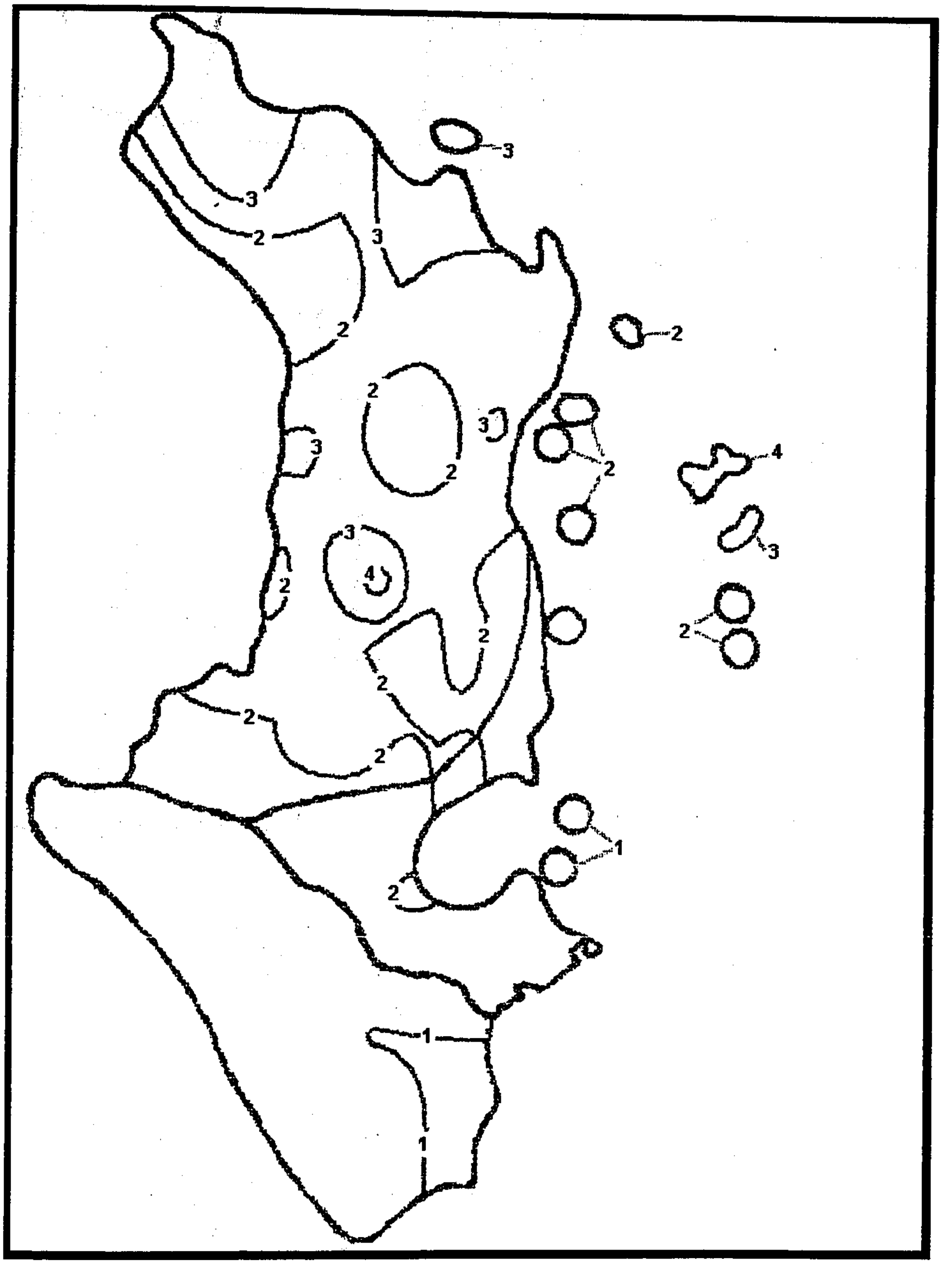


Figure 7: Two dimensional contour map for the number of loreal scales constructed and mapped onto the current distribution of H. nasicus. The green lines represent levels of similar values which are labeled in black. The current distribution of H. nasicus is outlined in dark gray.

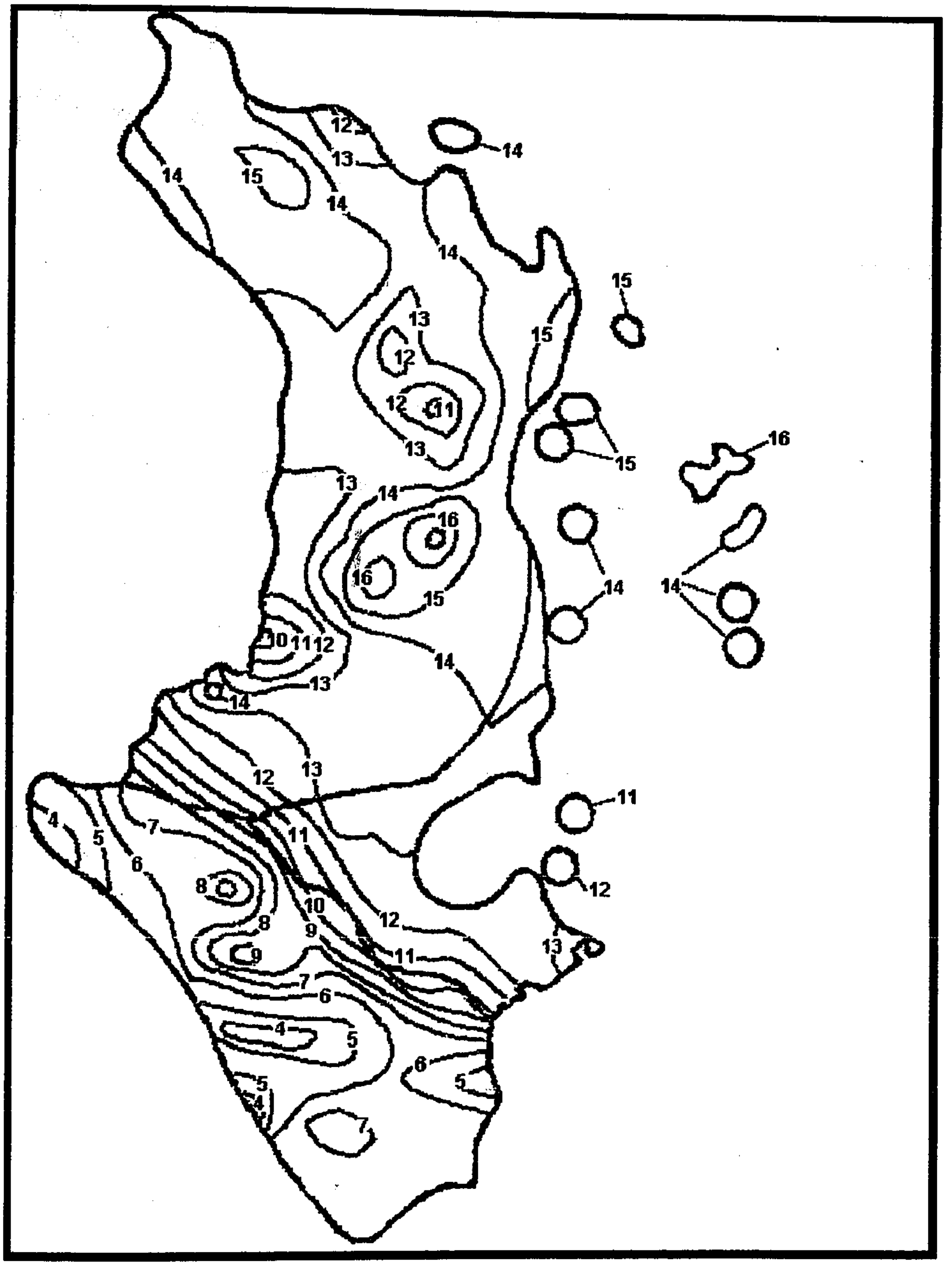


Figure 8: Two dimensional contour map for the number of azygous scales constructed and mapped onto the current distribution of H. nasicus. The green lines represent levels of similar values which are labeled in black. The current distribution of H. nasicus is outlined in dark gray.

The statistical significance of the discriminant functions (eigenvectors) were reported to determine the number of eigenvectors to use in interpretation. Next, the standardized discriminant function coefficients for each variable in each eigenvector are obtained along with the eigenvalues and the cumulative proportion of explained variance accounted for by each function. These data are used in determining the relative value of each variable and its ability to discriminate between groups.

The nature of the discrimination for each eigenvector is determined by using the means of canonical variables as an indication of how far the groups are separated in the vector space. A scatterplot of the discriminate functions is then plotted as a visual summary of the interpretation. A classification function is then obtained from the discriminant analysis for each group along with a classification matrix of the different groups. The classification matrix utilizes the classification functions of each group to determine the percent of each group correctly identified. This analysis provides a numerical method of quantifying the accuracy and usefulness of the model.

RESULTS

Interspecific relationships of Heterodon.

The proportion of shared fragments, calculated from Nei's estimate of similarity equation (Nei, 1972), range from 0.1443 to 0.5347 (Table 5). A dendrogram, generated by UPGMA, displaying hierarchial associations is given in Figure 9. Bogertophis subocularis and Farancia abacura were least similar to the species of Heterodon. Therefore, B. subocularis and F. abacura clustered together while the three Heterodon species grouped together, with H. nasicus and H. simus being the most tightly clustered group.

A separate clustering analysis was run using the neighbor-joining method (NJOIN) defining B. subocularis as the outgroup (Fig. 10). The analysis found a single tree which clustered the 3 Heterodon species with H. nasicus and H. simus again being clustered and joined by H. platyrhinos. The grouping of the three Heterodon species as a separate cluster and the pairing of H. nasicus and H. simus within that cluster is consistent between both clustering algorithms.

Variation and subspecies in Heterodon nasicus

Sexual dimorphism.- In comparing the morphometric data, the F-values and their levels of significance (Table 6) show that males and females are significantly different for SVL and TL relationships to TOTL in both cases where the Y-intercept was calculated and where it was set equal to 0. Scatter plots for both Y-intercept conditions were

Table 5: Similarity matrix of RAPDs data constructed using Nei's similarity index.

	H. s.	H. n.	H. p.	F. a.	B. s.
H. simus (H. s.)	---				
H. nasicus (H. n.)	.5347	---			
H. platyrhinos (H. p.)	.3656	.3810	---		
F. abacura (F. a.)	.2222	.2703	.3725	---	
B. subocularis (B. s.)	.2118	.1443	.3182	.3441	---

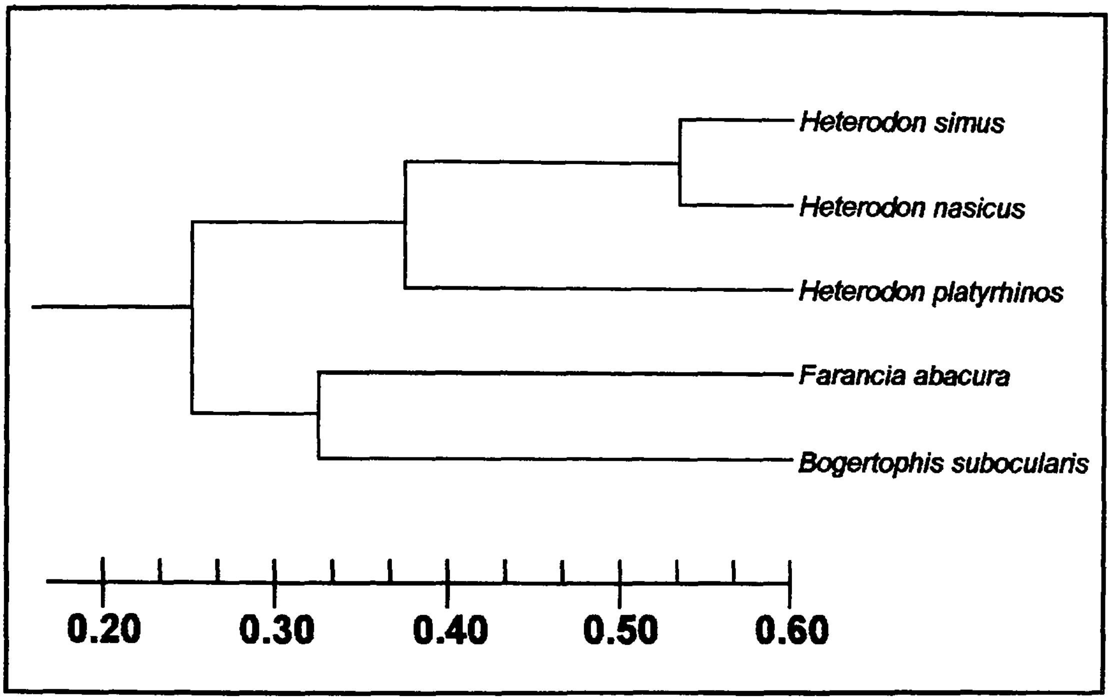


Figure 9: A dendrogram displaying hierarchial associations generated by group average clustering (UPGMA) using genetic distance data calculated from RAPDs data.

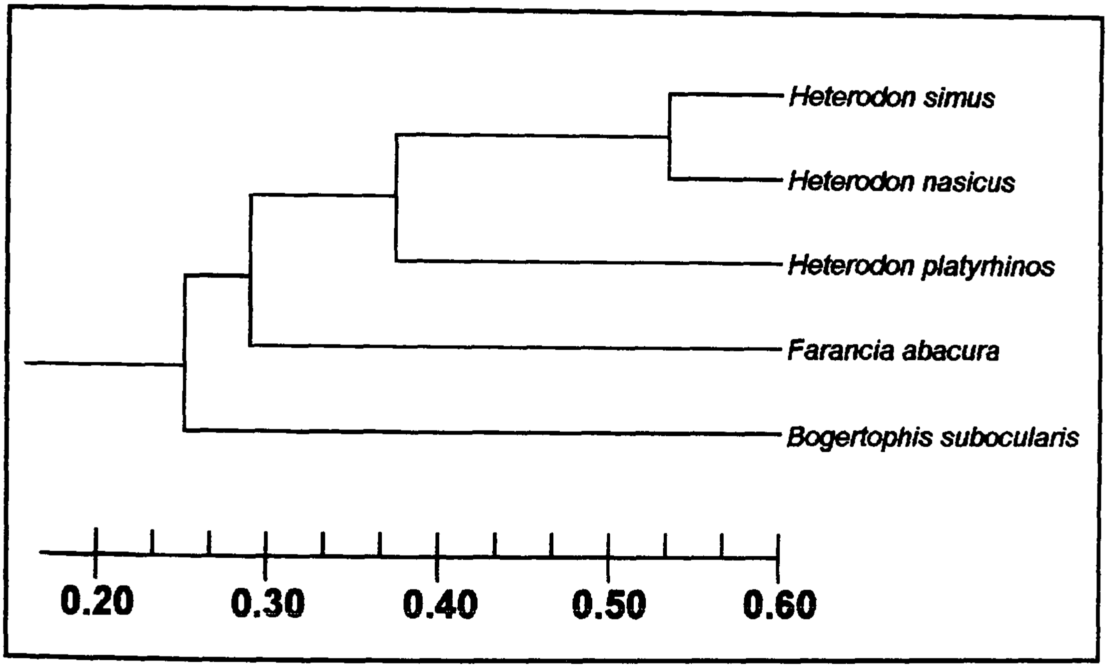


Figure 10: Dendrogram displaying hierarchial associations generated by the neighbor-joining method (NJOIN). The tree was rooted at Bogertophis subocularis as the outgroup. This dendrogram represents the single tree found.

Table 6: Comparison of sexes. F-values and their significance level for morphometric sexually dimorphic characters. The $F_{(a=0)}$-value is the F-value obtained when the Y-intercept was set equal to zero.

	F-value	$F_{(a=0)}$-value
Total length vs. Snout-to-vent length		
H. n. nasicus	152.5223**	58.5401**
H. n. gloydi	12.3806**	6.9612*
H. n. kennerlyi	112.9634**	44.1861**
Total length vs. Tail length		
H. n. nasicus	152.5223**	58.5401**
H. n. gloydi	12.3806**	6.9612*
H. n. kennerlyi	112.9634**	44.1861**
Head length vs. Head width		
H. n. nasicus	0.3611	0.0111
H. n. gloydi	0.1561	0.0816
H. n. kennerlyi	0.0988	0.3745
Rostral front height vs. Rostral straight height		
H. n. nasicus	3.0369*	0.0038
H. n. gloydi	0.0015	0.0228
H. n. kennerlyi	9.6516**	0.5272

constructed for both variables for each subspecies. The Scatter plots for H. n. nasicus are shown in Figures 11-14 and are representative of the other two subspecies (Appendix F). These graphs appear to support the conclusions that males and females are different. The results for the relationships between the sexes regarding HW vs. HL and ROSFH vs. ROSSH are not as conclusive. When the Y-intercept is calculated, both H. n. kennerlyi and H. n. nasicus show significant differences between sexes for the rostral scale dimensions. However, when the y-intercept is set equal to 0 there are no significant differences between sexes of any subspecies for head or rostral dimensions. These results, where the Y-intercept is set to 0, are more consistent and tend to be more conservative. An inspection of the scatterplots of these relationships for H. n. nasicus indicate intuitively that there are no differences. The same conclusions can be make for H. n. gloydi and H. n. kennerlyi (Appendix F). The sample size (n), mean ($\bar{x}$), standard deviation (Sd), equations of the regression lines, and the coefficients of determination (R^2) for each sex in each subspecies are reported in Table 7.

The results of the ANOVA statistical test for comparisons of quantitative meristic data (Table 8) show strong sexual dimorphism in all three subspecies for DB, TDB, LB, VENT, and SC. However, there was not a statistical difference detected for any of the subspecies for TLB. This is most likely due to the fact that the tail lateral blotches terminate close to the vent and do not extend all the way to the end of the tail as do the tail dorsal blotches and subcaudal scales, therefore, making it a poor indicator of relative tail length. When dorsal blotches were added to tail dorsal blotches and ventral scales added to subcaudal scales for each sex and compared again, there were no significant

Figure 11: Scatterplot graph of the total length (TOTL) (mm) on the snout-to-vent length (SVL) (mm) for Heterodon nasicus nasicus. Open circles represent females and open squares represent males. The two graphs are graphed from the same data. Graph (a) uses the calculated Y-intercept to construct the regression line and graph (b) has the regression line constructed with the Y-intercept set equal to 0.

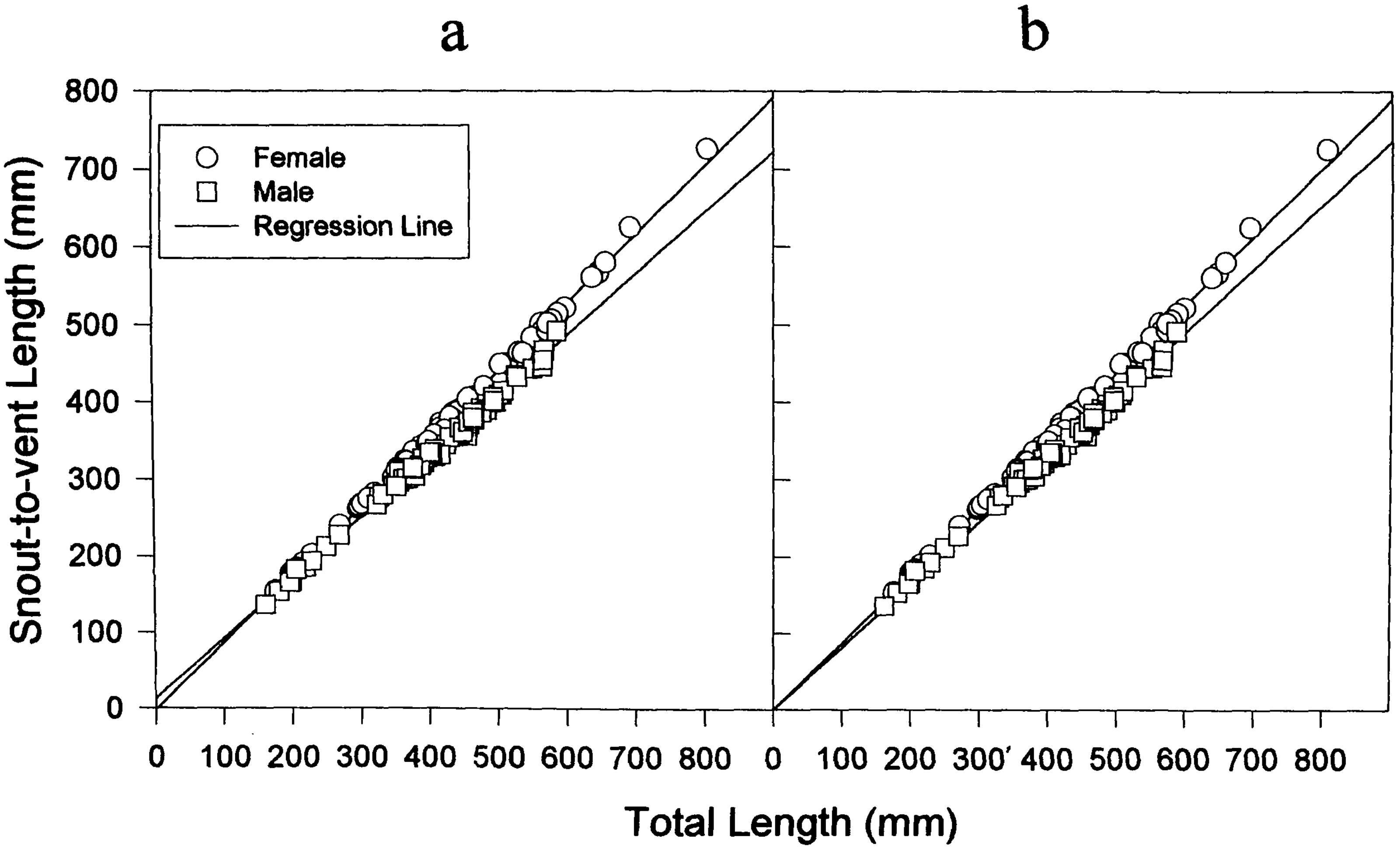

a
b
Female
Male
Regression Line
Snout-to-vent Length (mm)
0
100
200
300
400
500
600
700
800
Total Length (mm)
0
100
200
300
400
500
600
700
800

Figure 12: Scatterplot graph of the total length (TOTL) (mm) on the tail length (TL) (mm) for Heterodon nasicus nasicus. Open circles represent females and open squares represent males. The two graphs are graphed from the same data. Graph (a) uses the calculated Y-intercept to construct the regression line and graph (b) has the regression line constructed with the Y-intercept set equal to 0.

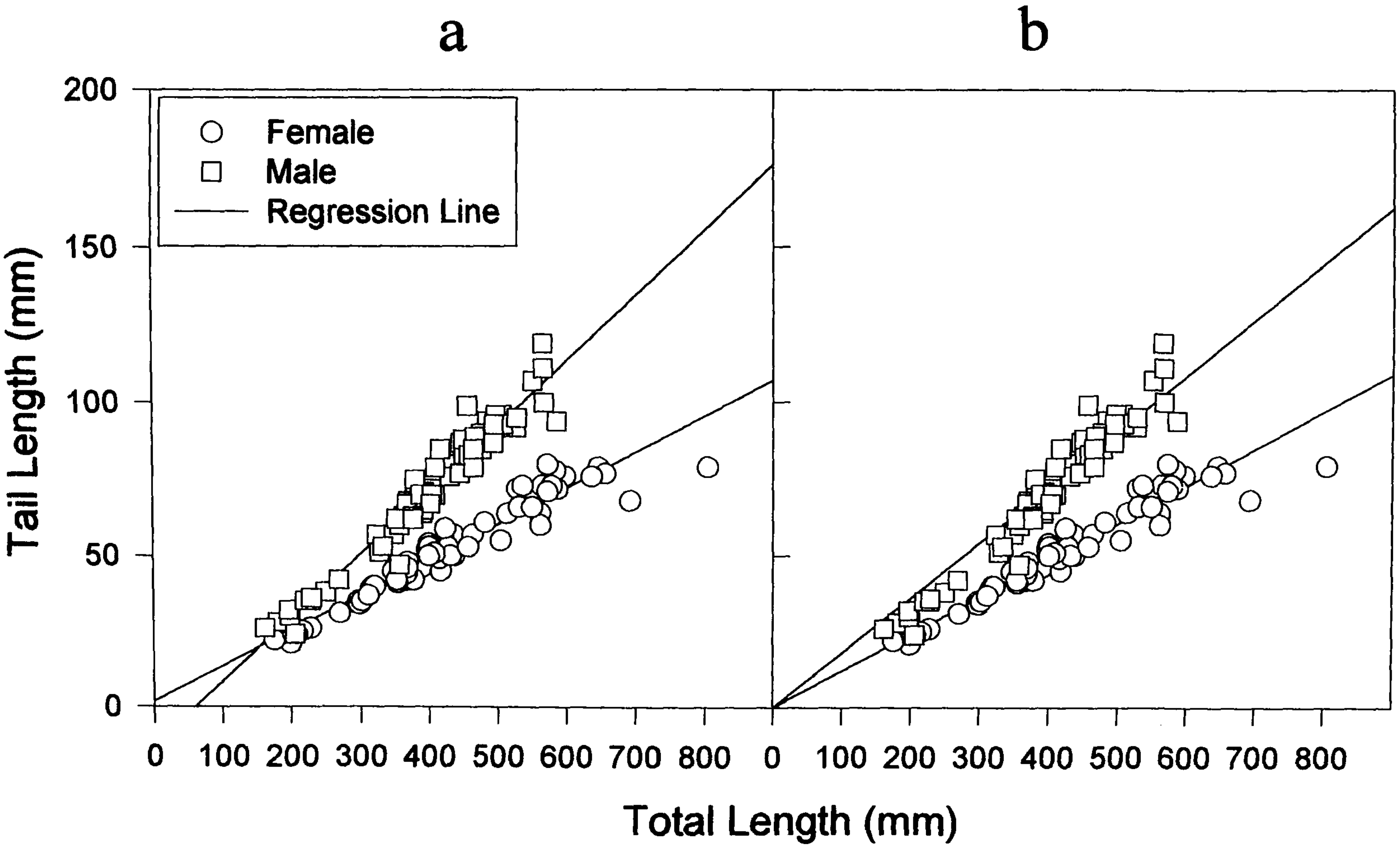

a
b
Female
Male
Regression Line
Tail Length (mm)
200
150
100
50
0
0
100
200
300
400
500
600
700
800
0
100
200
300
400
500
600
700
800
Total Length (mm)

Figure 13: Scatterplot graph of the head width (HW) (mm) on the head length (HL) (mm) for Heterodon nasicus nasicus. Open circles represent females and open squares represent males. The two graphs are graphed from the same data. Graph (a) uses the calculated Y-intercept to construct the regression line and graph (b) has the regression line constructed with the Y-intercept set equal to 0.

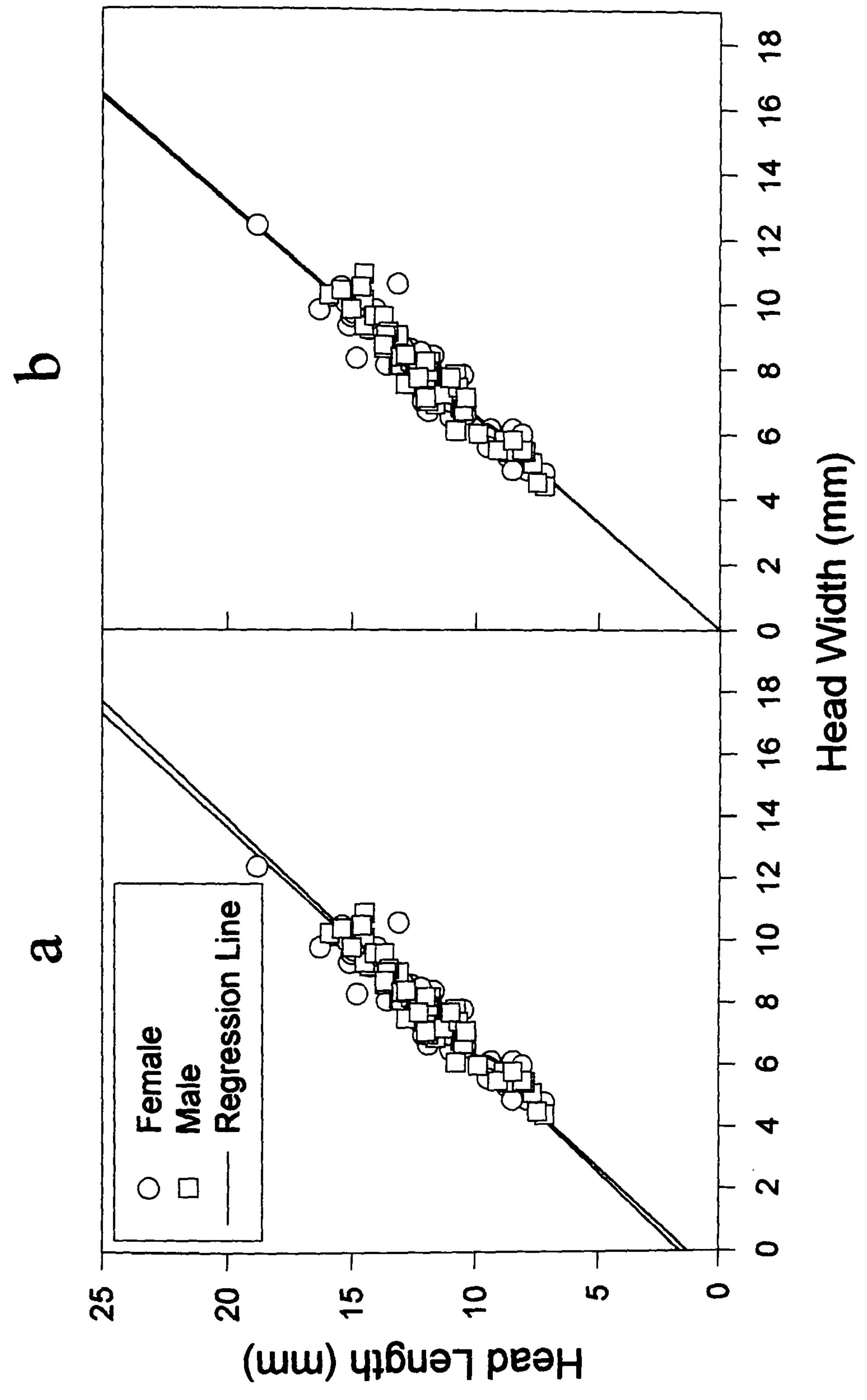

a
b
Female
Male
Regression Line
Head Length (mm)
25
20
15
10
5
0
Head Width (mm)
0
2
4
6
8
10
12
14
16
18

Figure 14: Scatterplot graph of the rostral front height (ROSFH) (mm) on the rostral straight height (ROSSH) (mm) for Heterodon nasicus nasicus. Open circles represent females and open squares represent males. The two graphs are graphed from the same data. Graph (a) uses the calculated Y-intercept to construct the regression line and graph (b) has the regression line constructed with the Y-intercept set equal to 0.

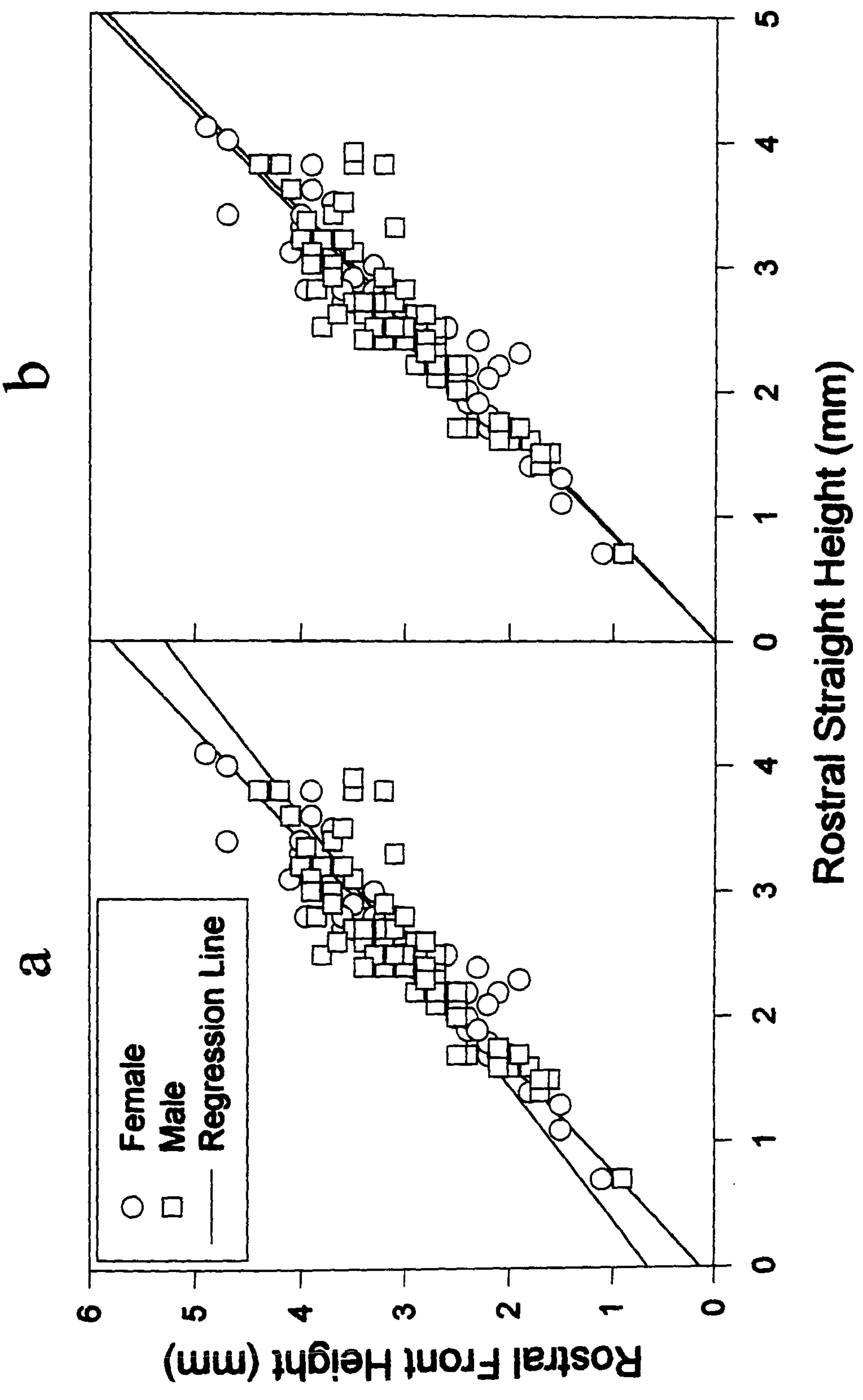

a
b
Female
Male
Regression Line
Rostral Front Height (mm)
0
1
2
3
4
5
6
Rostral Straight Height (mm)
0
1
2
3
4
5

Table 7: The sample size (n), mean ($\bar{x}$) ± standard deviation (Sd), equations of regression lines and regression coefficients (R$^{2)}$ for sexually dimorphic morphometric data. The two regression equations for each sex represents the regression where the Y-intercept is calculated (Y) and where the Y-intercept is set equal to zero ($Y_{(a=0)}$).

	n	Mean (X) ± Sd	Mean (Y) ± Sd	Equation of regression line	R^2
Total length vs. Snout-to-vent length					
H. n. nasicus ♀	65	427.9846 ± 137.7223	376.0000 ± 121.6361	$Y = 0.88(X) - 1.72$ $Y_{(a=0)} = 0.88(X)$	0.998536
H. n. nasicus ♂	67	400.6269 ± 104.5827	329.0000 ± 82.7938	$Y = 0.79(X) + 12.49$ $Y_{(a=0)} = 0.82(X)$	0.995875
H. n. gloydi ♀	28	472.7143 ± 178.9007	418.0714 ± 158.7267	$Y = 0.89(X) - 0.43$ $Y_{(a=0)} = 0.88(X)$	0.99567
H. n. gloydi ♂	35	405.1143 ± 79.22335	335.1714 ± 64.5151	$Y = 0.81(X) + 7.35$ $Y_{(a=0)} = 0.83(X)$	0.987445
H. n. kennerlyi ♀	73	464.7397 ± 154.6431	409.7945 ± 139.2691	$Y = 0.90(X) - 8.19$ $Y_{(a=0)} = 0.88(X)$	0.997351
H. n. kennerlyi ♂	85	359.1647 ± 77.25096	294.5412 ± 61.9974	$Y = 0.80(X) + 6.94$ $Y_{(a=0)} = 0.82(X)$	0.995502
Total length vs. Tail length					
H. n. nasicus ♀	65	427.9846 ± 137.7223	51.9846 ± 16.8314	$Y = 0.12(X) + 1.72$ $Y_{(a=0)} = 0.12(X)$	0.923546
H. n. nasicus ♂	67	400.6269 ± 104.5827	71.6269 ± 22.5945	$Y = 0.21(X) - 12.49$ $Y_{(a=0)} = 0.18(X)$	0.944611
H. n. gloydi ♀	28	472.7143 ± 178.9007	54.6429 ± 23.0237	$Y = 0.11(X) + 0.43$ $Y_{(a=0)} = 0.12(X)$	0.794225
H. n. gloydi ♂	35	405.1143 ± 79.2234	69.9429 ± 16.7542	$Y = 0.19(X) - 7.35$ $Y_{(a=0)} = 0.17(X)$	0.81384
H. n. kennerlyi ♀	73	464.7397 ± 154.6461	54.9452 ± 17.1301	$Y = 0.10(X) + 8.19$ $Y_{(a=0)} = 0.12(X)$	0.824924
H. n. kennerlyi ♂	85	359.6470 ± 77.2510	64.6235 ± 15.9448	$Y = 0.20(X) - 6.94$ $Y_{(a=0)} = 0.18(X)$	0.931997

Table 7 (cont.).

	Sample size	Mean (X) ± Standard deviation	Mean (Y) ± Standard deviation	Equation of regression line	R^2
Head length vs. Head width					
H. n. nasicus ♀	55	7.7536 ± 1.6618	11.9436 ± 2.4163	$Y = 1.37(X) + 1.31$ $Y_{(a=0)} = 1.54(X)$	0.889937
H. n. nasicus ♂	66	7.7939 ± 1.4400	11.9379 ± 1.9906	$Y = 1.32(X) + 1.63$ $Y_{(a=0)} = 1.53(X)$	0.914514
H. n. gloydi ♀	28	8.4768 ± 2.3860	13.1804 ± 3.3526	$Y = 1.33(X) + 1.94$ $Y_{(a=0)} = 1.55(X)$	0.890324
H. n. gloydi ♂	36	8.1861 ± 1.0907	12.3139 ± 1.7700	$Y = 1.40(X) + 0.89$ $Y_{(a=0)} = 1.50(X)$	0.739961
H. n. kennerlyi ♀	65	8.5423 ± 1.7272	13.6108 ± 8.5423	$Y = 1.60(X) + 0.01$ $Y_{(a=0)} = 1.59(X)$	0.916463
H. n. kennerlyi ♂	75	7.2100 ± 1.1034	11.4473 ± 1.5664	$Y = 1.28(X) + 2.23$ $Y_{(a=0)} = 1.59(X)$	0.810936
Rostral front height vs. Rostral straight height					
H. n. nasicus ♀	56	2.4893 ± 0.7029	2.9634 ± 0.8437	$Y = 1.13(X) + 0.14$ $Y_{(a=0)} = 1.19(X)$	0.893681
H. n. nasicus ♂	65	2.5600 ± 0.6730	3.0346 ± 0.7094	$Y = 0.93(X) + 0.65$ $Y_{(a=0)} = 1.19(X)$	0.781124
H. n. gloydi ♀	28	3.2179 ± 1.0712	3.6446 ± 1.1692	$Y = 1.03(X) + 0.33$ $Y_{(a=0)} = 1.13(X)$	0.888455
H. n. gloydi ♂	35	2.9086 ± 0.5543	3.3543 ± 0.6732	$Y = 1.02(X) + 0.38$ $Y_{(a=0)} = 1.15(X)$	0.710450
H. n. kennerlyi ♀	63	3.2397 ± 0.8364	3.6746 ± 0.8792	$Y = 0.94(X) + 0.62$ $Y_{(a=0)} = 1.13(X)$	0.802482
H. n. kennerlyi ♂	72	2.6139 ± 0.5140	3.1257 ± 0.6003	$Y = 0.97(X) + 0.58$ $Y_{(a=0)} = 1.20(X)$	0.694389

Table 8: ANOVA results reported from a Tukey HSD test for comparisons of quantitative character data between Heterodon nasicus nasicus males and females, H. n. gloydi males and females, and H. n. kennerlyi males and females. The values given are the p-values at which the comparisons are significant.

	H. n. nasicus	H. n. gloydi	H. n. kennerlyi
Dorsal Blotches	0.000020*	0.000020*	0.000020*
Tail Dorsal Blotches	0.000020*	0.008967*	0.000020*
Dorsal Blotches + Tail Dorsal Blotches	0.663800	0.100126	0.565812
Lateral Blotches	0.000020*	0.000021*	0.000027*
Tail Lateral Blotches	0.121129	0.998682	1.000000
Lateral Blotches + Tail Lateral Blotches	0.000069*	0.0010086*	0.000141*
Ventral Scales	0.000020*	0.000020*	0.000020*
Subcaudal Scales	0.000020*	0.000020*	0.000020*
Ventral Scales + Subcaudal Scales	0.975376	0.962102	1.000000

* - Indicates significant values.

differences between sexes with the exception of H. n. gloydi in the total number of blotches. Sexual dimorphism was still detected in all of the subspecies for the total amount of lateral blotches (LB+TLB). This again is affected by the fact that the tail lateral blotches do not extend to the end of the tail and therefore remains the only sexually dimorphic character described in H. nasicus when the placement of the cloacal vent is ignored. The sample size (n), mean ($\bar{x}$), and standard deviation (Sd) for the separate sexes of each group for all variables including the sum variables are reported in Appendix G.

Subspecies comparisons.- A comparison of body lengths and rostral and head dimensions are made between the different subspecies of H. nasicus. The F-values calculated for differences in regression coefficients between the different subspecies of the same sex (Table 9) show no differences between the subspecies for either sex. Regression lines are drawn through the data points on the Scatter plots for all three subspecies, both males and females, for each set of variables (Figs. 15-18). Both sexes show similar patterns and are consistent with the calculated significance levels.

When the meristic characters were analyzed separately for the sexes, the ANOVA results (Table 10) revealed several patterns. First, the number of tail lateral blotches do not seem to differ between subspecies except for between male H. n. nasicus and H. n. kennerlyi. Second, H. n. gloydi and H. n. kennerlyi are very similar for many of the characteristics and show few differences. Finally, VENT+SC was the only variable to differ between all taxa. Box plots of these variables (Figs. 19-21) all indicate the same trends with H. n. gloydi and H. n. kennerlyi being similar to each other and H. n. nasicus typically having higher numbers for all of the variables. The results are similar when the

Table 9: F-values obtained from the test for equality among three regression coefficients representing the three subspecies of H. nasicus.

	Total Length vs. Snout-to-vent Length	Total Length vs. Tail Length	Head Width vs. Head Length	Rostral Straight Height vs. Rostral Front Height
Female	2.348406	2.348406	4.500248	2.482955
Male	1.310261	1.310261	0.39873	0.295383

* - Values significant at the $\alpha = 0.05$ level.
** - Values significant at the $\alpha = 0.01$ level.

Figure 15: The linear relationship of total length (TOTL) (mm) vs. snout-to-vent length (SVL) (mm) for each sex of the three subspecies. Regression lines are plotted through each data set. Open circles represent individuals of H. n. nasicus, open squares represent individuals of H. n. gloydi and open triangles represent individuals of H. n. kennerlyi.

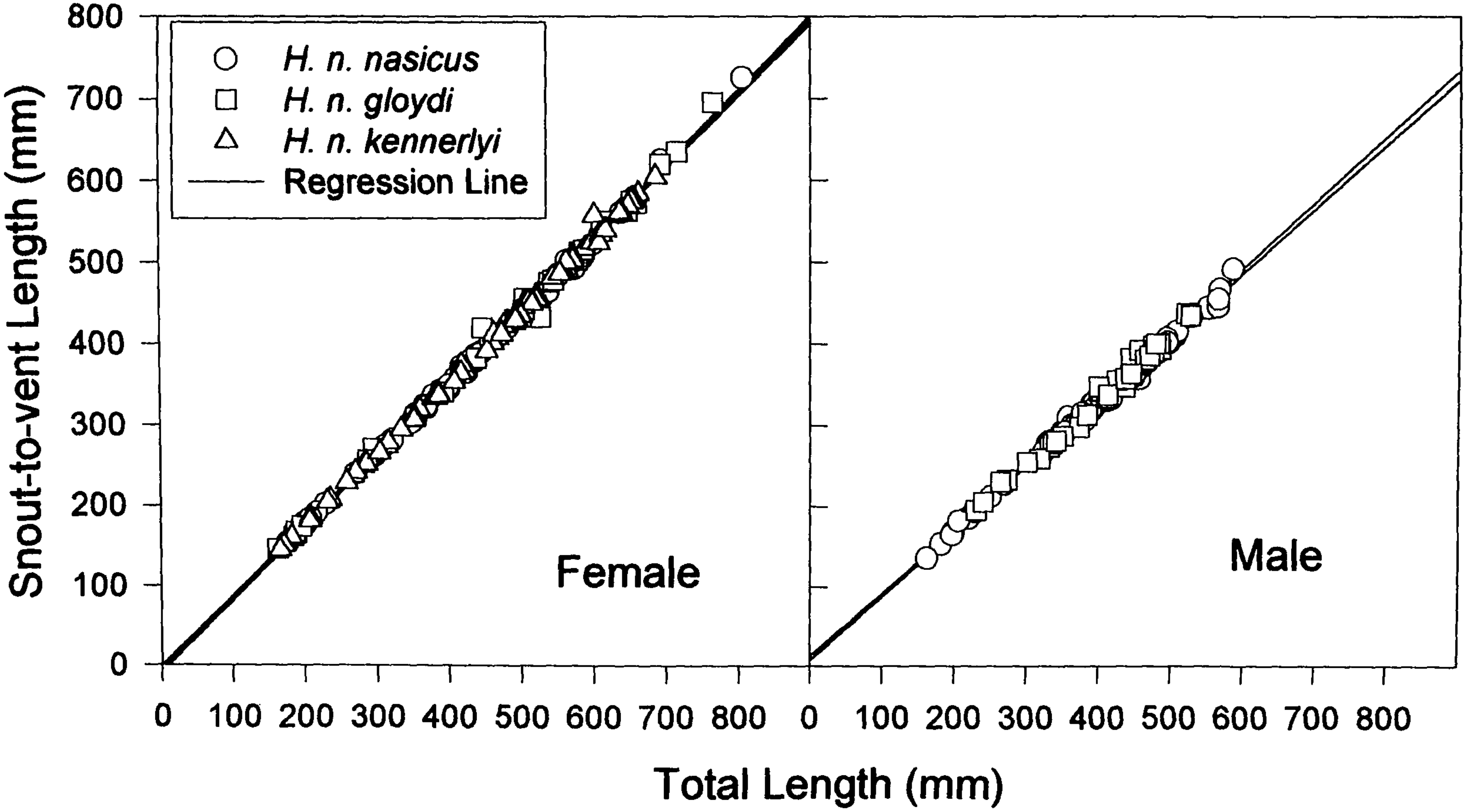

Snout-to-vent Length (mm)
800
700
600
500
400
300
200
100
0
○ H. n. nasicus
□ H. n. gloydi
△ H. n. kennerlyi
Regression Line
Female
Male
0
100
200
300
400
500
600
700
800
Total Length (mm)

Figure 16: The linear relationship of total length (TOTL) (mm) vs. tail length (TL) (mm) for each sex of the three subspecies. Regression lines are plotted through each data set. Open circles represent individuals of H. n. nasicus, open squares represent individuals of H. n. gloydi and open triangles represent individuals of H. n. kennerlyi.

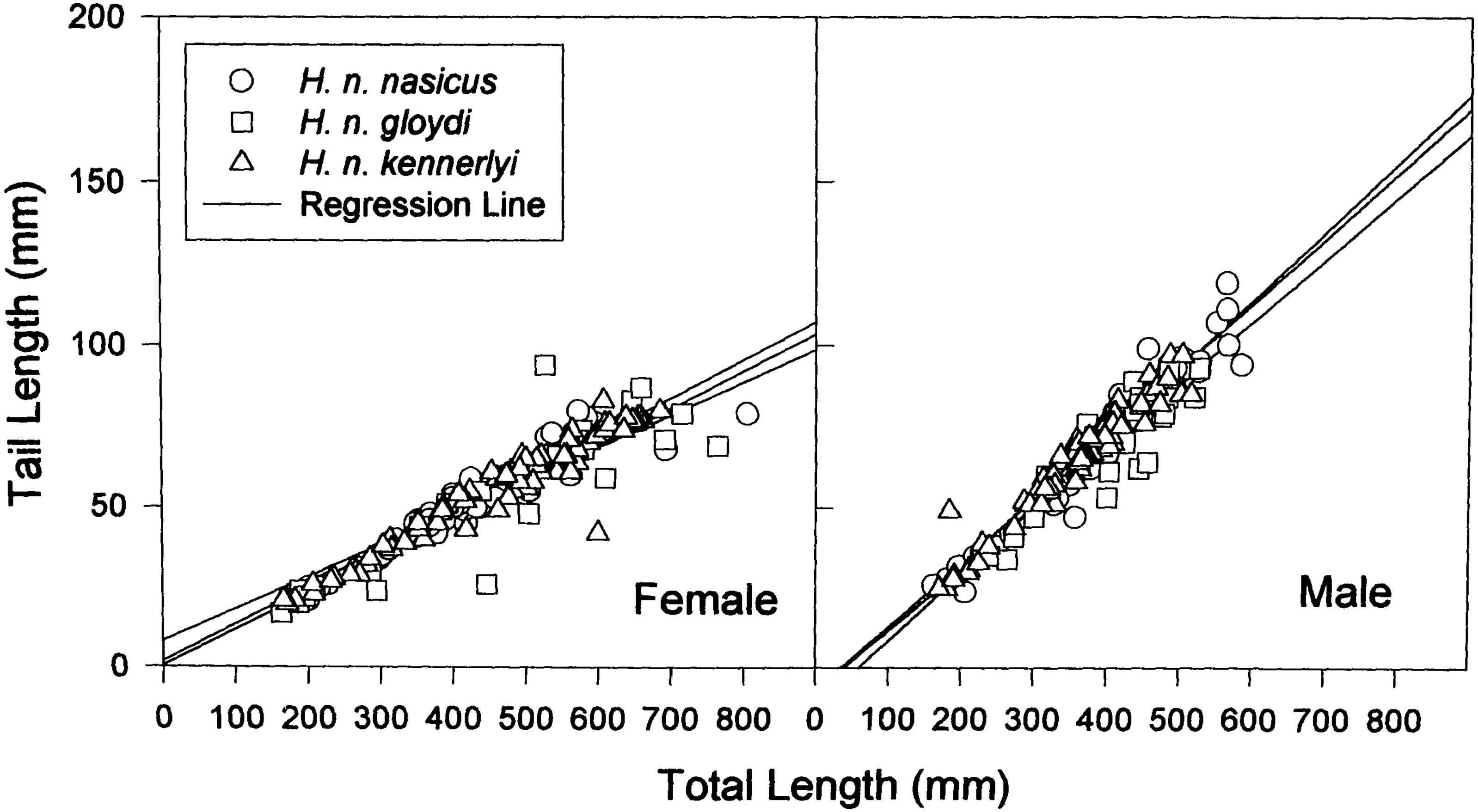
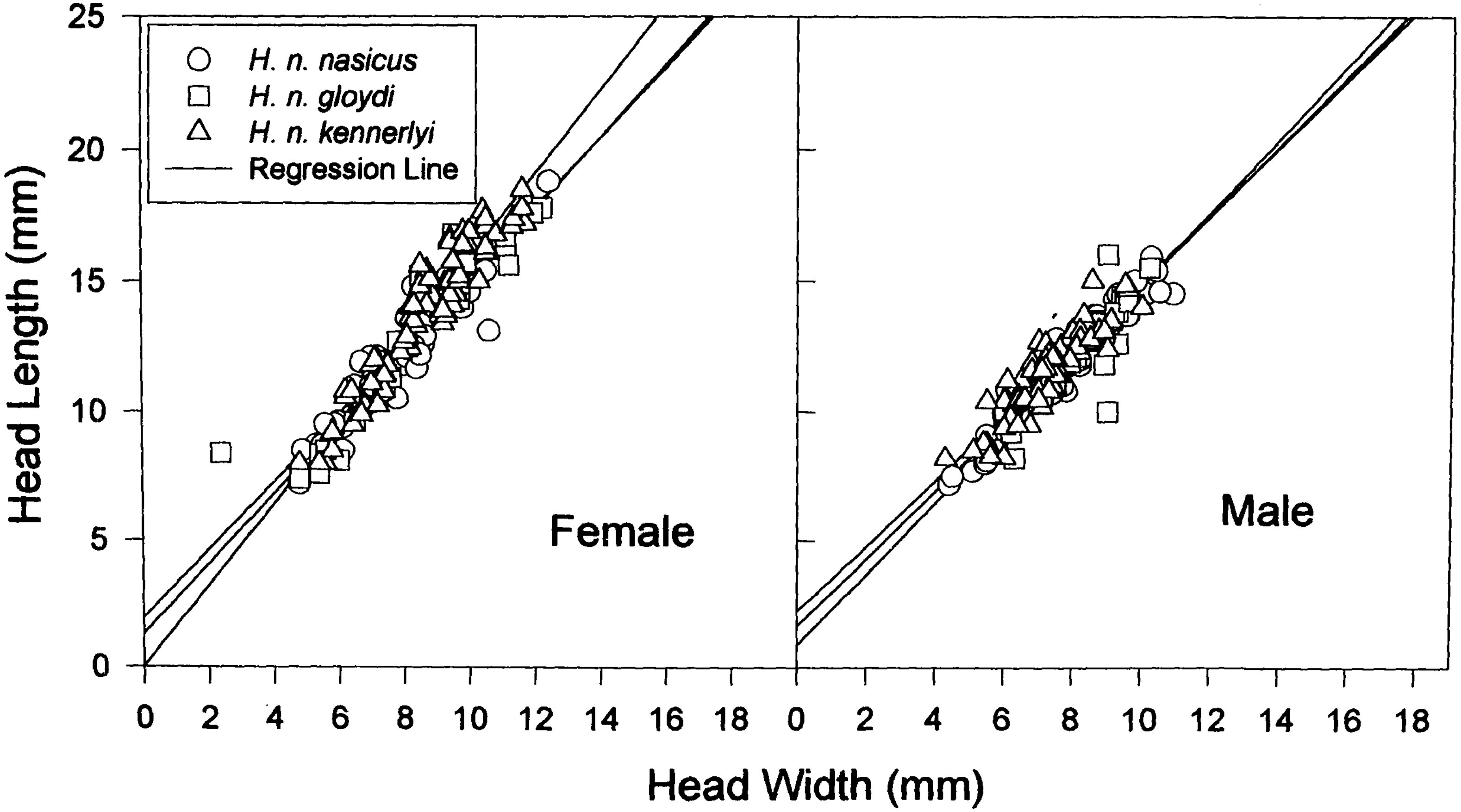

Tail Length (mm)
0
50
100
150
200
H. n. nasicus
H. n. gloydi
H. n. kennerlyi
Regression Line
Female
Male
0
100
200
300
400
500
600
700
800
Total Length (mm)

Figure 17: The linear relationship of head width (HW) (mm) vs. head length (HL) (mm) for each sex of the three subspecies. Regression lines are plotted through each data set. Open circles represent individuals of H. n. nasicus, open squares represent individuals of H. n. gloydi and open triangles represent individuals of H. n. kennerlyi.



H. n. nasicus
H. n. gloydi
H. n. kennerlyi
Regression Line
Female
Male
Head Length (mm)
Head Width (mm)
0
5
10
15
20
25
0
2
4
6
8
10
12
14
16
18

Figure 18: The linear relationship of rostral front height (ROSFH) (mm) vs. rostral straight height (ROSSH) (mm) for each sex of the three subspecies. Regression lines are plotted through each data set. Open circles represent individuals of H. n. nasicus, open squares represent individuals of H. n. gloydi and open triangles represent individuals of H. n. kennerlyi.

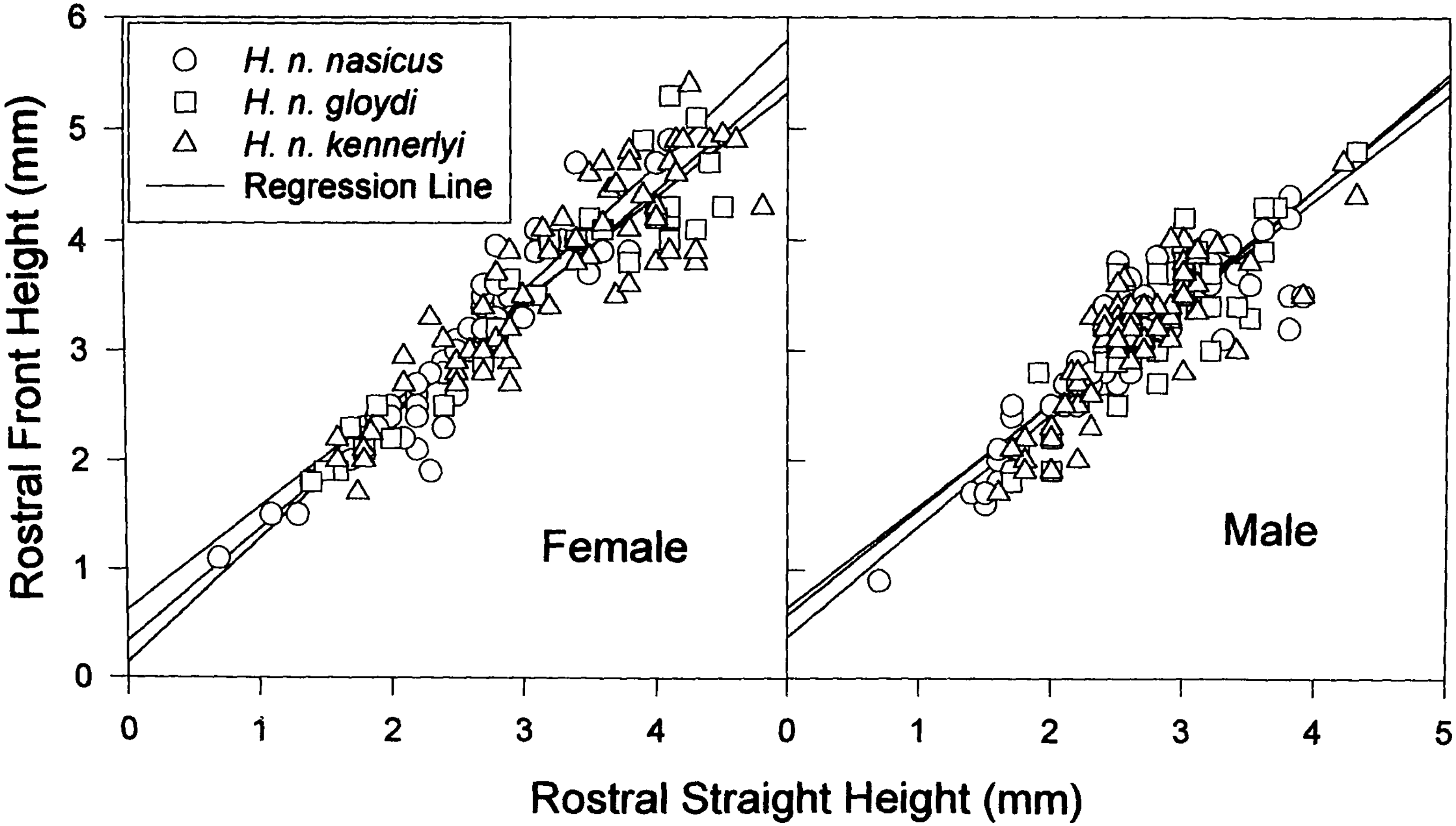

H. n. nasicus
H. n. gloydi
H. n. kennerlyi
Regression Line
Female
Male
Rostral Front Height (mm)
0
1
2
3
4
5
6
Rostral Straight Height (mm)
0
1
2
3
4
0
1
2
3
4
5

Table 10: Significance values from the ANOVA statistical analysis of meristic characteristics.

	H. n. nasicus vs. *H. n. gloydi*		*H. n. nasicus* vs. *H. n. kennerlyi*		*H. n. gloydi* vs. *H. n. kennerlyi*	
	Female	Male	Female	Male	Female	Male
Dorsal Blotches	0.00002*	0.00002*	0.00002*	0.00002*	0.88915	0.05160
Tail Dorsal Blotches	0.00064*	0.00002*	0.00002*	0.00002*	0.78579	0.99658
Dorsal Blotches + Tail Dorsal Blotches	0.00002*	0.00002*	0.00002*	0.00002*	0.99990	0.47806
Lateral Blotches	0.00002*	0.00002*	0.00002*	0.00002*	0.77379	0.00105*
Tail Lateral Blotches	.99969	0.33764	0.43843	0.00006*	0.87148	0.46775
Lateral Blotches + Tail Lateral Blotches	0.00002*	0.00002*	0.00002*	0.00002*	1.00000	0.67716
Ventral Scales	0.02405*	0.00002*	0.00002*	0.00002*	0.05757	0.11066
Subcaudal Scales	0.00021*	0.00002*	0.00002*	0.00002*	0.00525*	0.07726
Ventral Scales + Subcaudal Scales	0.00051*	0.00002*	0.00002*	0.00002*	0.00183*	0.01010*

* - Indicates significant values.

Figure 19: Box plots of the number of dorsal blotches (DB), tail dorsal blotches (TDB) and dorsal blotches + tail dorsal blotches (DB+TDB) for females and males of each subspecies of Heterodon nasicus. The box represents the 25th and 75th percentile, the end bars represent the 10th and 90th percentile, the solid line in the box represents the 50th percentile and the dashed line is the mean. The points on either end of each plot represents the 5th and 95th percentile.

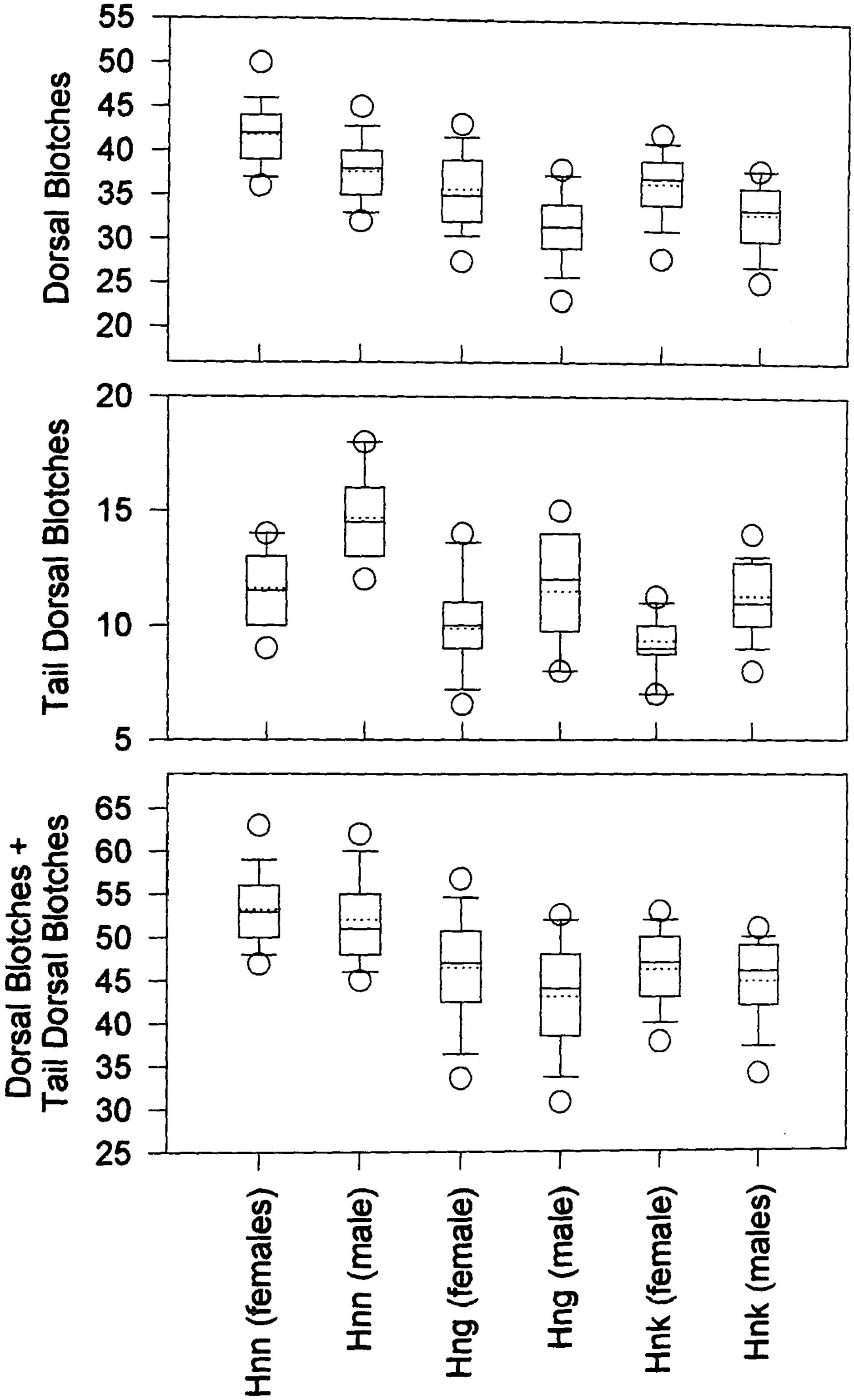

Dorsal Blotches
55
50
45
40
35
30
25
20
Tail Dorsal Blotches
20
15
10
5
Dorsal Blotches +
Tail Dorsal Blotches
65
60
55
50
45
40
35
30
25
Hnn (females)
Hnn (male)
Hng (female)
Hng (male)
Hnk (female)
Hnk (males)

Figure 20: Box plots of the number of lateral blotches (LB), tail lateral blotches (TLB) and lateral blotches + tail lateral blotches (LB+TLB) for females and males of each subspecies of Heterodon nasicus. The box represents the 25th and 75th percentile, the end bars represent the 10th and 90th percentile, the solid line in the box represents the 50th percentile and the dashed line is the mean. The points on either end of each plot represents the 5th and 95th percentile.

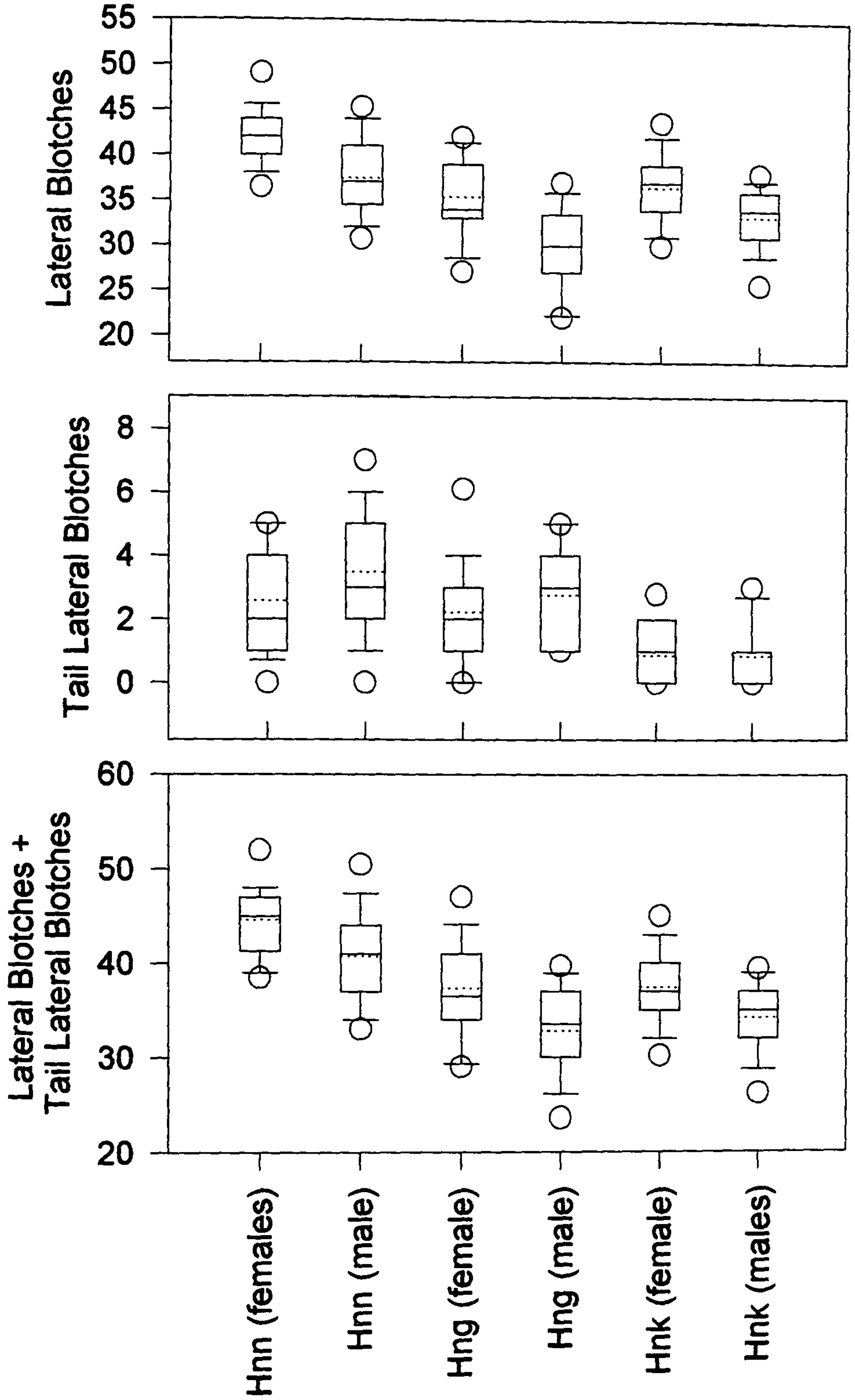
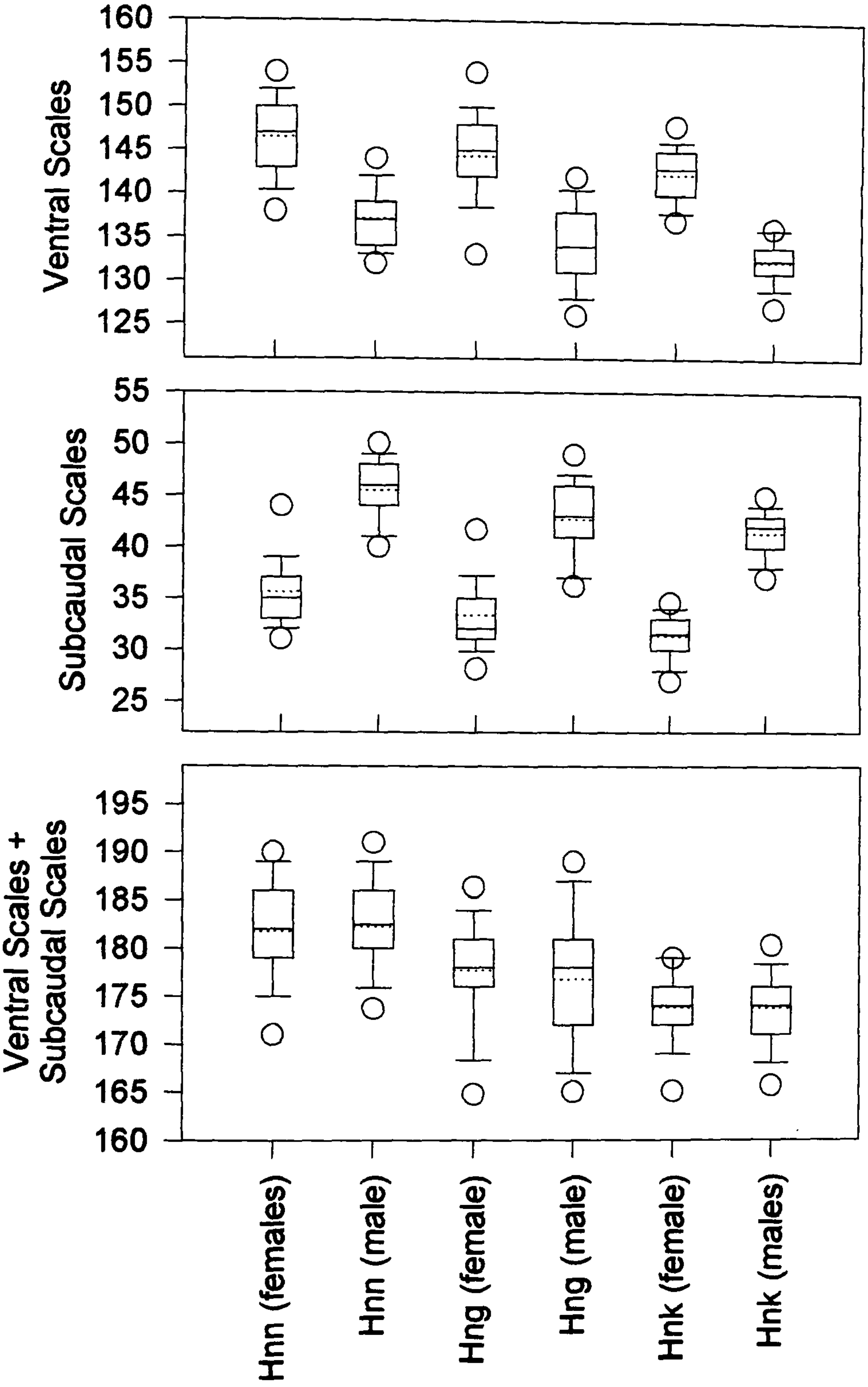

Lateral Blotches
55
50
45
40
35
30
25
20
Tail Lateral Blotches
8
6
4
2
0
Lateral Blotches +
Tail Lateral Blotches
60
50
40
30
20
Hnn (females)
Hnn (male)
Hng (female)
Hng (male)
Hnk (female)
Hnk (males)

Figure 21: Box plots of the number of ventral scales (VENT), subcaudal scales (SC) and ventral scales + subcaudal scales (VENT+SC) for females and males of each subspecies of Heterodon nasicus. The box represents the 25th and 75th percentile, the end bars represent the 10th and 90th percentile, the solid line in the box represents the 50th percentile and the dashed line is the mean. The points on either end of each plot represents the 5th and 95th percentile.


Ventral Scales
160
155
150
145
140
135
130
125
Subcaudal Scales
55
50
45
40
35
30
25
Ventral Scales + Subcaudal Scales
195
190
185
180
175
170
165
160
Hnn (females)
Hnn (male)
Hng (female)
Hng (male)
Hnk (female)
Hnk (males)

sexes are combined and the characters DB+TDB, LB+TLB, and VENT+SC are compared between subspecies (Table 11). Heterodon n. nasicus is significantly different from H. n. gloydi and H. n. kennerlyi for all three variables. Heterodon n. kennerlyi and H. n. gloydi are only different for the number of VENT+SC. The sample size (n), mean ($\bar{x}$), and standard deviation (Sd) for DB+TDB, LB+TLB and VENT+SC when the sexes are combined is listed in Appendix G.

Three variables (DB+TDB, LB+TLB and VENT+SC) were analyzed in a discriminate function analysis for their usefulness in discriminating between the subspecies of Heterodon nasicus. The analysis included 115 H. n. nasicus, 56 H. n. gloydi and 148 H. n. kennerlyi. When all the variables were included in the model, the immediate results (Table 12) indicated that this was not a very good model because the Wilk's lambda score was 0.55980. In general, Wilk's lambda is the standard statistic that is used to denote the statistical significance of the discriminatory power of the current model. Its value will range from 1.0 (no discriminatory power) to 0.0 (perfect discriminatory power). So it is evident that a value of 0.55980 means that the model has little discriminatory power. The examination of the unique contribution of each variable to the discrimination between subspecies indicated that each variable contributes very little to the model with all of their Partial Wilk's lambda (Wilk's lambda score which is adjusted for each individual variable) scores ≥0.9 (Table 12). The Partial Wilk's lambda score also showed that the variable VENT + SC contributed most, the variable DB + TDB second most and the variable LB+TLB the least to the overall discrimination.

Next, the actual discriminate functions were computed to see how the three

Table 11: ANOVA statistical difference levels of combined sexes for all three subspecies of H. nasicus.

	H. n. gloydi vs. H. n. nasicus	H. n. kennerlyi vs. H. n. nasicus	H. n. kennerlyi vs. H. n. gloydi
Dorsal Blotches + Tail Dorsal Blotches	0.000022*	0.000022*	0.292931
Lateral Blotches + Tail Lateral Blotches	0.000022*	0.000022*	0.429641
Ventral Scales + Subcaudal Scales	0.000022*	0.000022*	0.000023*

Table 12: Discriminant function analysis results.

Number of variables in the model: 3
Wilk's Lambda: 0.5597967 F (6, 628) = 35.22544 $p<0.000000$

N = 319	Partial Wilk's Lambda	Tolerance	R^2
Dorsal blotches + tail dorsal blotches	0.923005	0.245230	0.754770
Lateral blotches + tail lateral blotches	0.965952	0.267368	0.732632
Ventral scales + subcaudal scales	0.905470	0.820302	0.179698

Tolerance = the proportion of variance that is unique to the respective variable. It is computed as $1 - R^2$.

variables discriminate between the different subspecies. The discriminate function coefficients (eigenvectors) were calculated and standardized and are listed in Table 13. Eigenvector 1 explains approximately 87 percent of the variance and therefore is considered the most "important" one. The first eigenvector is also weighted most heavily by DB+TDB and the second eigenvector is marked mostly by the same variable. However, it should be noted that the eigenvalues are very low (<1) indicating that the data are very weakly correlated and the variance is large. This would explain how this model which has poor discriminatory power can still account for most of the variability.

It is now known how the variables participate in the discrimination between the subspecies. The next step is to determine the nature of the discrimination of each eigenvector. To do this the means of the canonical variables were calculated (Table 14). The first eigenvector discriminates mostly between H. n. nasicus and the other two subspecies because the canonical mean for H. n. nasicus is somewhat different than the others. The second eigenvector seems to distinguish mostly between H. n. gloydi and the other subspecies. However, based on the review of the eigenvalues earlier, the magnitude of the discrimination of both eigenvectors is very small. To summarize these data the plot of all snakes on the two eigenvectors is shown in Figure 22. The plot confirms the interpretation so far. The means of each group appear to be different, however, the large amount of variance cause the groups to overlap considerably making this a poor model for discriminating between the subspecies of H. nasicus.

Specific character analysis.- The number of dorsal blotches (DB) has been used as an identification tool to separate H. n. gloydi from H. n. nasicus. Because of the sex

Table 13: Discriminant function coefficients.

	Eigenvector 1	Eigenvector 2
Dorsal blotches + tail dorsal blotches	-0.519542	-1.55842
Lateral blotches + tail lateral blotches	-0.335633	0.98530
Ventral scales + subcaudal scales	-0.328597	0.92271
Eigenvalue	0.632337	0.09436
Cummulative proportion of variance explained	87.0153%	100%

Table 14: Means of canonical variables.

Species	Eigenvector 1	Eigenvector 2
H. n. kennerlyi	0.54515	-0.252291
H. n. nasicus	-1.05093	0.031630
H. n. gloydi	0.71742	0.601814

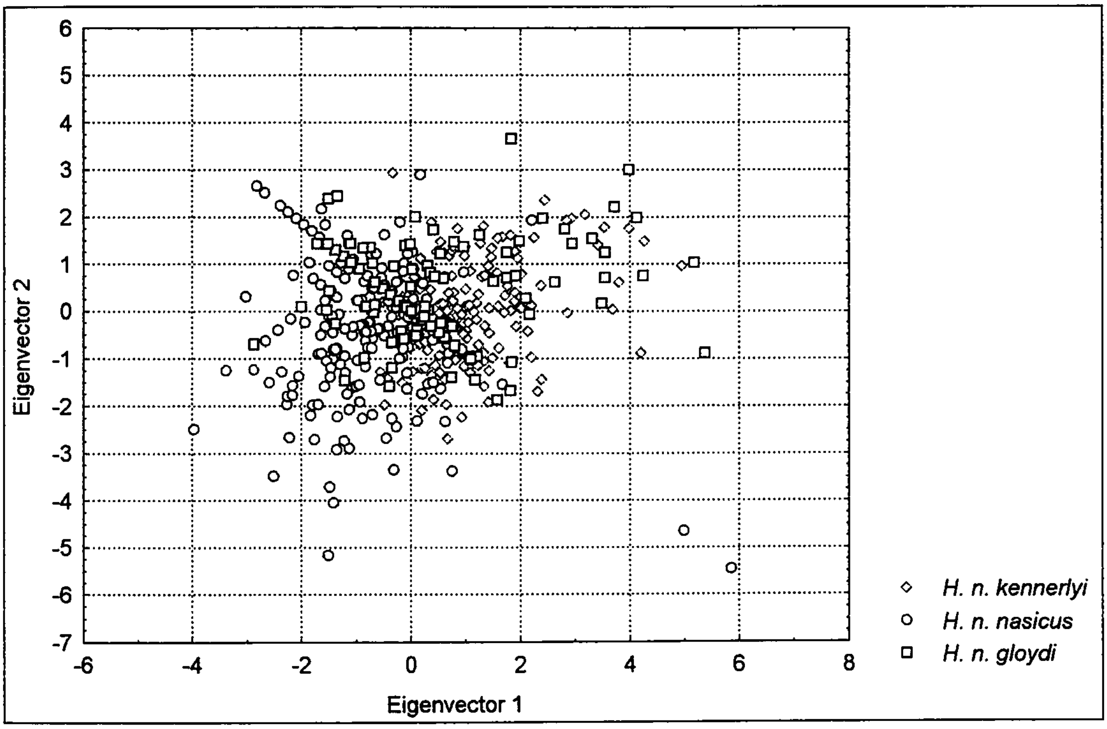


Figure 22: Discriminant function scatterplot of the three subspecies of H. nasicus using sexual dimorphic data. The green diamonds are individuals of H. n. kennerlyi, the blue circles are individuals of H. n. nasicus, and the red squares are individuals of H. n. gloydi. The subspecies identifications are based on their geographic location.

differences in the number of dorsal blotches, there are separate definitions for males and females. According to the identification key H. n. gloydi females have less than 37 dorsal blotches and the males have less than 32 while H. n. nasicus females have greater than 40 dorsal blotches and males have greater than 35. When these numbers are corrected for sex differences, by adding tail dorsal blotches (TDB) to get the total number of dorsal blotches (DB+TDB), there is no need to have separate definitions for males and females. Both males and females of H. n. gloydi have less than or equal to 46 total dorsal blotches while males and females of H. n. nasicus have greater or equal to 47 total dorsal blotches. This definition fits the contour map of DB+TDB (Fig. 6) well. The isophene for the number 46 follows very closely along the boundary that separates H. n. nasicus from H. n. gloydi, however, this character shows a southeast to northwest cline. The total number of dorsal blotches, starting at south Texas and Mexico, increases into northeastern New Mexico and northeastern Colorado and then decrease northward into southern Canada. This map indicates a gradual change in the total number of dorsal blotches and therefore seems to indicate that indeed this character is clinal in nature. Furthermore, this character should not be used because using this definition would identify the majority of H. nasicus in Montana as H. n. gloydi.

The contour map for VENT+SC (Fig. 5) shows some differences from the map of the total number of dorsal blotches, however, the general trends are the same. The number of ventral scales has not been used in identifying the different subspecies (Edgren, 1952a) but its analysis confirms the results found for the total number of dorsal blotches.

The number of loreal scales (LOR) has also been used in identifying H. n. kennerlyi from the other two subspecies (Edgren, 1952c). Heterodon n. kennerlyi is defined as having less than two loreal scales while the other subspecies have two or more loreal scales (Edgren, 1952a). According to the contour map (Fig. 7) H. n. kennerlyi has less than two loreal scales, however, so do almost all of H. n. gloydi populations and some of the H. n. nasicus populations. This suggests that the number of loreal scales also is not very useful in characterizing any of the subspecies taxa.

One of the structures unique to the genus Heterodon is the azygous mass (AZY). In H. nasicus the azygous scales vary in number. This has been used as an identification tool. Heterodon n. kennerlyi is defined as having 7 or less azygous scales while the other two subspecies have more than 9 azygous scales. The contour map for this character (Fig. 8) shows quite a bit of variation in pattern for the northern populations, however, there is a definite pattern of an apparent step cline along the boundary of H. n. kennerlyi and the other two subspecies. Therefore, the number of azygous scales appears to be useful in separating H. n. kennerlyi from the other subspecies.

Discriminant analysis.- The discriminant function analysis determined that three of the variables (LOR, 3-PNB, and APC) contributed very little to the discriminatory power of the model and thus were excluded from the working model. When the other seven variables are included in the model, the immediate results (Table 15) indicate that this is a good model for discriminating between at least two groups because the Wilk's lambda score is 0.06386. The examination of the unique contribution of each variable to the discrimination between subspecies (Wilk's Partial Lambda) indicates that the number of azygous scales contributes the most to discriminate function with the total number of

Table 15: Discriminant function analysis results.

Number of variables in the model: 7
Wilk's Lambda: 0.0638618 F (35, 532) = 14.044 p<0.000000

N = 138	Partial Wilk's Lambda	Tolerance	R^2
Azygous scales	0.440055	0.893134	0.106866
Dorsal blotches + tail dorsal blotches	0.741455	0..956878	0.043122
Connection of middle nuchal blotch to first dorsal blotch	0.770275	0.844413	0.155587
Belly color	0.838730	0.935257	0.064743
Ventral scales + subcaudal scales	0.882245	0.962011	0.037989
Nature of the first dorsal blotch	0.946356	0.860150	0.139850
Connection of loreal scales to ocular ring	0.961140	0.914047	0.085953

Tolerance = the proportion of variance that is unique to the respective variable. It is computed as $1 - R^2$.

dorsal blotches and CON-M1 contributing as well. The characters BLY, VENT+SC, 1st DB and PN-O appear to contribute very little to the overall discriminatory power of this model.

Next, the actual discriminate functions were computed to see how the seven variables discriminate between the different subspecies. The discriminate function coefficients (eigenvectors) were calculated and standardized and are shown in Table 16. Eigenvector 1 explains approximately 88 percent of the variance and therefore is the most "important" one. The second eigenvector explains approximately 10% of the variance and is considered useful as well. The combined contribution of eigenvectors 3, 4 and 5 is less than 1.5%. The first eigenvector is also weighted most heavily by AZY along with CON-M1 and the second eigenvector is marked mostly by DB+TDB, BLY, and VENT+SC. The eigenvalue for the first eigenvector is fairly high (6.74) which means that the variance is relatively low. However, it should be noted that the eigenvalues are very low (<1) for eigenvector 2 indicating that the data are very weakly correlated and the variance is large. The eigenvectors 3, 4 and 5 also have very low eigenvalues (<0.07) meaning that they will not be very useful in discriminating between groups.

It is now known how the variables participate in the discrimination between the subspecies. The next step is to determine the nature of the discrimination of each eigenvector. To do this the means of the canonical variables were calculated (Table 17). After reviewing the means, the first eigenvector appears to discriminate between H. n. kennerlyi and the other two subspecies because the canonical mean for H. n. kennerlyi is quite a bit different than the others. The second eigenvector seems to distinguish

Table 16: Discriminant function coefficients.

	Eigen-vector 1	Eigen-vector 2	Eigen-vector 3	Eigen-vector 4	Eigen-vector 5
Azygous scales	0.840647	-0.150011	-0.141594	-0.010608	-0.094936
Dorsal blotches + tail dorsal blotches	0.015752	0.754671	0.327167	-0.363312	-0.440372
Connection of middle nuchal blotch to first dorsal blotch	-0.496124	0.228971	-.645302	-0.538575	-0.168901
Belly color	-0.280943	0.462731	-0.110642	0.091493	0.768810
Ventral scales + subcaudal scales	0.064727	0.451568	-0.499659	0.630805	-0.119067
Nature of the first dorsal blotch	0.187450	-0.055572	-0.593742	-0.556029	0.110987
Connection of loreal scales to ocular ring	0.125360	0.217575	0.313194	-0.150690	0.268138
Eigenvalue	6.743164	0.827398	0.066029	0.027973	0.009849
Cumulative proportion of variance explained	87.866%	98.647%	99.507%	99.872%	100.000%

Table 17: Means of canonical variables.

Species	Eigenvector 1	Eigenvector 2	Eigenvector 3	Eigenvector 4	Eigenvector 5
H. n. nasicus	1.25116	0.57230	0.151419	0.013688	-0.005180
H. n. gloydi	1.28149	-2.17588	0.145727	-0.049945	-0.001890
H. n. kennerlyi	-5.60868	0.01558	0.035288	-0.038305	-0.021270
H.n.n./H.n.g.	1.12193	0.06683	-0.524725	-0.084969	-0.064575
H.n.n./H.n.k.	-0.15994	0.26504	-0.281288	-0.285809	0.618474
H.n.g./H.n.k.	-0.83718	-0.59365	-0.335815	0.894027	0.110167

H. n. gloydi from the other subspecies. However, based on the review of the eigenvalues earlier, the magnitude of the discrimination of eigenvector 2 is very small. The means for eigenvectors 3, 4 and 5 show very little difference and coupled with the low eigenvalues again indicated that they have little discriminatory power. To summarize these data the plot of all snakes on the two eigenvectors is shown in Figure 23. The plot confirms the interpretation so far. Heterodon n. kennerlyi (green diamonds) clusters separately from the other groups on eigenvector 1 with a canonical mean difference of approximately 4.3. H. n. gloydi (red squares) and H. n. nasicus (blue circles) do not form separate clusters and overlap broadly. Regions that were designated as *H.n.n./H.n.k.* (black closed circles) and *H.n.g./H.n.k.* (gray squares) either clustered with the H. n. gloydi / H. n. nasicus cluster or between the H. n. gloydi / H. n. nasicus cluster and the H. n. kennerlyi grouping. The regions designated as *H.n.n./H.n.g.* all clustered within the H. n. gloydi / H. n. nasicus cluster and broadly overlaps with that group. Eigenvector 2 primarily discriminates on the basis of DB+TDB and VENT+SC. The separation of groups on eigenvector 2 agrees with previous analysis, using the sexually dimorphic data, that determined that these characters have low discriminatory power. However, eigenvector 1 discriminates primarily on AZY. This means that the primary separation of the H. n. kennerlyi group from the H. n. gloydi / H. n. nasicus group is based on the number of azygous scales.

Using the discriminate function analysis, classification functions are computed for each group (Table 18) and can be used directly to classify individual cases. Each new Heterodon can be classified into a group for which it has the highest classification score. The classification function was then used to classify each case in the model and the

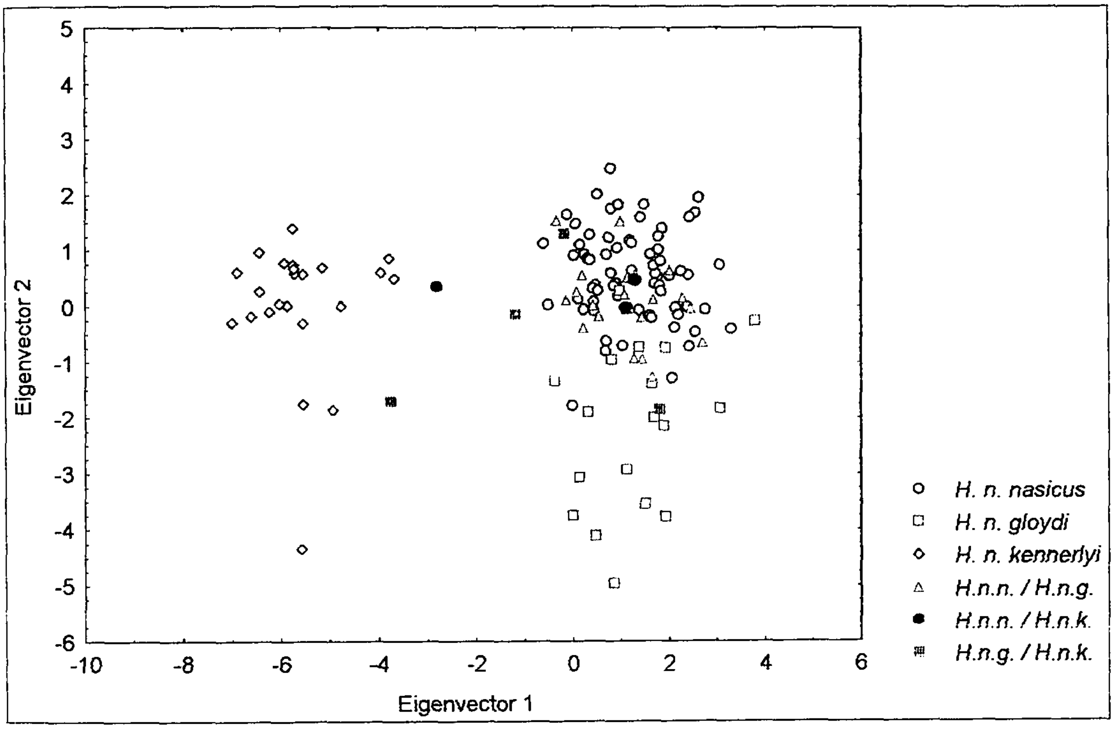


Figure 23: Discriminant function scatterplot of the three subspecies of H. nasicus and the contact zones between the different subspecies using seven meristic characters. The six groups represent the three subspecies and their contact zones. Each point represents a 1° latitude x 1° longitude area. Each area was labeled as one of the six groups based on their geographic location. The blue circles are areas of H. n. nasicus, the red squares are areas of H. n. gloydi, the green diamonds are areas of H. n. kennerlyi, the purple triangles are areas in the contact zone between H. n. nasicus and H. n. gloydi, the black closed circles are areas in the contact zone between H. n. nasicus and H. n. kennerlyi, and the gray closed squares are areas in the contact zone between H. n. gloydi and H. n. kennerlyi.

Table 18: Classification Functions.

Variable	*H. n. nasicus*	*H. n. gloydi*	*H. n. kennerlyi*	*Hnn/Hng*	*Hnn/Hnk*	*Hng/Hnk*
AZY	0.612	0.850	-2.459	0.650	-0.003	-0.218
DB+TDB	1.469	1.074	1.365	1.364	1.361	1.192
CON-M1	13.345	11.903	21.381	14.410	15.638	14.747
BLY	8.861	6.542	11.872	8.540	10.225	9.350
VENT+SC	6.466	6.226	6.340	6.474	6.413	6.489
1st DB	7.173	7.560	4.902	8.062	7.653	6.165
PNO	15.932	13.963	12.522	14.792	15.371	13.343
Constant	-653.568	-590.936	-611.463	-651.888	-639.087	-636.208

resulting classification matrix (Table 19) indicates the percent of cases that are correctly classified in each group. The classification matrix demonstrates the uniqueness of H. n. kennerlyi because 100% of the lots marked as H. n. kennerlyi were correctly identified. 94% of H. n. nasicus were correctly identified, however, only 61% of H. n. gloydi were identified with 28% of them being identified as H. n. nasicus. It is clear from these results that H. n. gloydi cannot be distinguished from H. n. nasicus.

Table 19: Classification Matrix.

Group	Percent Correct	*H. n. nasicus*	*H. n. gloydi*	*H. n. kennerlyi*	*Hnn/ Hng*	*Hnn/ Hnk*	*Hng/ Hnk*
H. n. nasicus	94.1176	64	1	0	2	0	1
H. n. gloydi	61.1111	5	11	0	1	0	1
H. n. kennerlyi	100.0000	0	0	23	0	0	0
Hnn/Hng	4.5455	21	0	0	1	0	0
Hnn/Hnk	0.0000	2	0	1	0	0	0
Hng/Hnk	0.0000	2	1	1	0	0	0
Total	71.7391	94	13	25	4	0	2

DISCUSSION

Familial affiliation of Heterodon

All workers, except Dowling and Jenner (1988), place more than 75% of the known living snake species into the single family, Colubridae. This placement is based on morphological characters which provide few phylogenetic inferences above the generic level (Marx and Rabb, 1972, 1973). Molecular studies have indicated that the family Colubridae is an unnatural taxonomic assemblage containing lineages that appear to be distantly related to one another (Dowling et al., 1983; Cadle, 1984a, 1984b, 1984c). Dowling and Jenner (1988) proposed a comprehensive snake classification that combined information from molecular characters with previously little-utilized morphological characters (Table 20). Based on their classification, snake relationships were further resolved resulting in the recognition of six distinct families within the "Colubridae". These are Colubridae, Natricidae, Lamprophiidae, Psammophiidae, Xenodontidae, and Dipsadidae.

Cope (1893) was the first to create the subfamily Xenodontinae. Later, Underwood (1967) placed this group into the family Dipsadidae, only for it to be reassigned to the large family Colubridae by Dowling and Duellman (1978). However, Cadle suggested that not only was Colubridae a polyphyletic group, but that the subfamily Xenodontinae was as well (Cadle, 1984a, 1984b, 1984c). This implied that the Neotropical xenodontines represented a relict form from an earlier "Xenodon" radiation along with other genera of xenodontines. Dowling and Jenner (1988), in their

TABLE 20: A Current Classification for Caenophidian Snakes (Dowling et al., 1988).

INFRAORDER CAENOPHIDIA -- Advanced Snakes.
- Super family ACROCHORDOIDEA -- Ancient Water snakes.
  - *Family Nigerophiidae -- Early Water snakes.
  - Family Xenodermatidae -- Pebbled Swamp snakes.
  - Family Homolopsiidae -- Rear-fanged Water snakes.
  - Family Acrochordidae -- Asian Water snakes.
- Superfamily DIPSADOIDEA -- Generalized Snakes.
  - *Family Anomalophiidae -- Eocene Water snakes.
  - *Family Russellophiidae -- Eocene Water snakes.
  - Family Lamprophiidae -- House snakes and Allies.
  - Family Psammophiidae -- Sand snakes.
  - Family Xenodontidae -- Neotropical Snakes.
  - Family Dipsadidae -- Middle American Snakes.
- Superfamily VIPEROIDEA -- Vipers and Allies.
  - Family Viperidae -- Vipers.
  - Family Crotalidae -- Pitvipers.
- Superfamily ELAPOIDEA -- Front-fanged Snakes.
  - Family Elapidae -- Cobras and Allies.
  - Family Hydrophiidae -- Sea snakes.
- Superfamily COLUBROIDEA -- Harmless Snakes.
  - Family Colubridae -- Racers and Allies.
  - Family Natricidae -- Modern Water snakes.

* = Extinct taxon.

classification scheme of snakes (Table 20), recognize the family Xenodontidae placed in the superfamily Dipsadoidea. Dowling and Jenner's (1988) classification reflected Cadle's (1984a, 1984b, 1984c) findings by separating Neotropical and middle American xenodontines into the families Xenodontidae and Dipsadidae, respectively.

Five genera of "Xenodontines" in North America, Carphophis, Contia, Diadophis, Farancia and Heterodon have hemipenial morphology similar to that of the South American members of the subfamily. However, preliminary immunological data have suggested that genetically they are only distantly related to South American xenodontids (Dowling et al., 1983; Cadle, 1984a, 1984b, 1984c). Their phylogenetic relationships, however, remain unresolved. These five North American genera contain only eight species, Carphophis amoena, Contia tenuis, Diadophis punctatus, Farancia abacura, F. erytrogramma, Heterodon platyrhinos, H. nasicus, and H. simus. These genera have strictly Nearctic distributions, some have overlapping ranges, and all have very divergent morphologies.

A comparative study combining the analysis of derived characters (e.g. vertebral morphology, tooth arrangement, and hemipenial morphology) led Dowling and Duellman (1978) to suggest that these five North American colubrid genera could be placed within the subfamily Xenodontinae, although this subfamily was thought to be a South American assemblage of taxa. This hypothesized relationship between North and South American "Xenodontines" is not new. Dunn (1928) included these North American genera in a tropical American taxon (subfamily Ophiinae). This taxon includes those American genera whose hemipenes have a forked sulcus.

In a later study of the embryological development of the hemipenes, Clark (1944) suggested that North American xenodontines were relicts of an Old World "Xenodontine" lineage that reached the New World by way of the Bering Land Bridge (or some Afro-American bridge) and developed a wide distribution in the Nearctic region. Extinctions presumably left only the five extant genera. Clark's (1944) hypothesis helps explain the substantial genetic divergence between the North and South American "Xenodontines" as supported by immunological studies (Dowling et al., 1983; Cadle, 1984a, 1984b, 1984c). This divergence simultaneously raises many questions regarding the origins and phylogenetic relationships of these five North American genera. No shared derived morphological feature has been discovered to support the monophyly of this group, nor is there any derived feature that suggests a sister taxon to these relict snakes among any colubrids. The hemipenial features shared with xenodontines (bifurcated sulcus, distal calyces and proximal spines) may thus represent plesiomorphic characters that may erroneously suggest close relations among what are in fact distantly related taxa. Therefore, the phylogenetic relationships of these five caenophidian genera, still tentatively termed "Relict North American Xenodontines", remains unclear.

Heterodon.- The xenodontine genus Heterodon contains three extant species of medium-sized stout bodied snakes with short tails (adult total length, 360-850 mm; maximum, 1155 mm; tail length 12-18% of total length, data from Platt, 1983) as well as two recognized fossil species. The earliest fossil records for Heterodon are from the Pliocene of Florida and Kansas (Auffenberg, 1963; Peters, 1953). The geographic range of the genus is completely within North America east of the Rocky Mountain chain

(Edgren, 1952a, 1952c). Pleistocene records are all within the ranges of the three extant species. The three extant species include Heterodon platyrhinos, H. simus and H. nasicus. The Pliocene forms, H. brevis (Auffenberg, 1963) and H. plionasicus (Peters, 1953) are considered ancestral to H. platyrhinos and H. nasicus, respectively.

Members of the genus Heterodon differ from the typical colubrid head scutellation in several ways including: a prominent rostral scale; one to two azygous scales and 0-27 accessory azygous scales between the pair of internasals, some of which may occur between the prefrontal scales; complete ring of oculars; temporals 3-4 + 4-5; and post genial scales reduced and separated by other small scales. The dorsal body scales are keeled, usually in 23-25 rows at midbody and 19-21 rows anterior to the vent. Ventrals number 109-156 and paired subcaudals 25-57, with significant sexual dimorphism in both characters. The anal scale is divided. Dorsal color pattern is usually blotched with little ontogenetic change.

Heterodon platyrhinos.- Heterodon platyrhinos, the Eastern Hognose Snake, is the largest member of the genus (142-1115 mm). This species is characterized by a straight rostral scale that is only slightly upturned, one median azygous scale with no accessory scales, scale rows 23-25, and about 2 rows of gulars between chin shields and ventrals. There are usually 20-31 pale crossbars (varying in color among individuals) on the body alternating with lateral rows of dark spots. This species is the only Heterodon that exhibits various degrees of melanism (Blem, 1981).

Heterodon platyrhinos occurs throughout the eastern half of North America from Massachusetts and the southern portions of New York, Pennsylvania, Ohio, Indiana, Illinois, and Missouri south to the Gulf Coast (Fig. 24).

Platt (1969) concluded that the variants designated as subspecies in H. platyrhinos were not sufficiently distinct morphologically or geographically to warrant their recognition. No subspecies have been proposed since then (Platt 1969, 1983).

Heterodon simus.- Heterodon simus, the Southern Hognose Snake, was described by Linnaeus (1766) but it is likely that his description was based on a H. platyrhinos specimen. The type specimen has since been lost and this issue is unresolved (Meylan, 1985). Originally Linnaeus described it as Coluber simus but Holbrook (1842) changed it to Heterodon simus.

Heterodon simus is the smallest species of the Heterodon group (116-565 mm). It is characterized by 25-25-21 scale rows and three or more azygous scales posterior to the rostral. Males have 122 or fewer ventrals and 44 or fewer subcaudals, females have 134 or fewer ventrals and 35 or fewer subcaudals. The background color is light brown with three rows of dark brown dorsal blotches (usually 22 to 32). The venter is cream to pale brown with subcaudals similar in color to ventrals. Juveniles are colored as adults. The characters used to separate H. simus from H. nasicus are the venter color (Edgren, 1952c; Platt, 1983), scale row numbers (25-25-21 in H. simus and 23-23-19 in H. nasicus), and the narrow rostral scale in H. simus (Platt, 1983).

Heterodon simus is distributed throughout the southeastern United States from the vicinities of Morehead City and Raleigh, North Carolina south to Lake Okeechobee and Tampa, Florida; west to the Pearl River separating Louisiana and Mississippi; and north to Calhoun County, Alabama (Fig. 25). Populations in the Ridge and Valley Physiographic

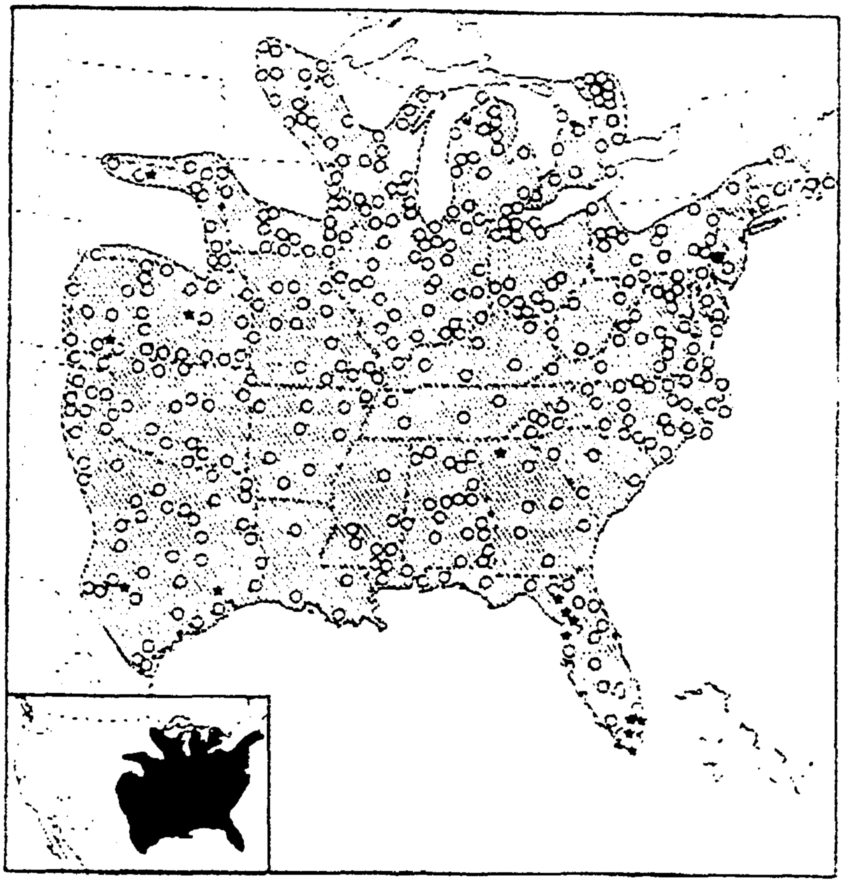


Figure 24: Distribution of Heterodon platyrhinos. Solid circle indicates the type-locality; open circles indicate locality records. Stars mark Pliocene and Pleistocene fossil sites.

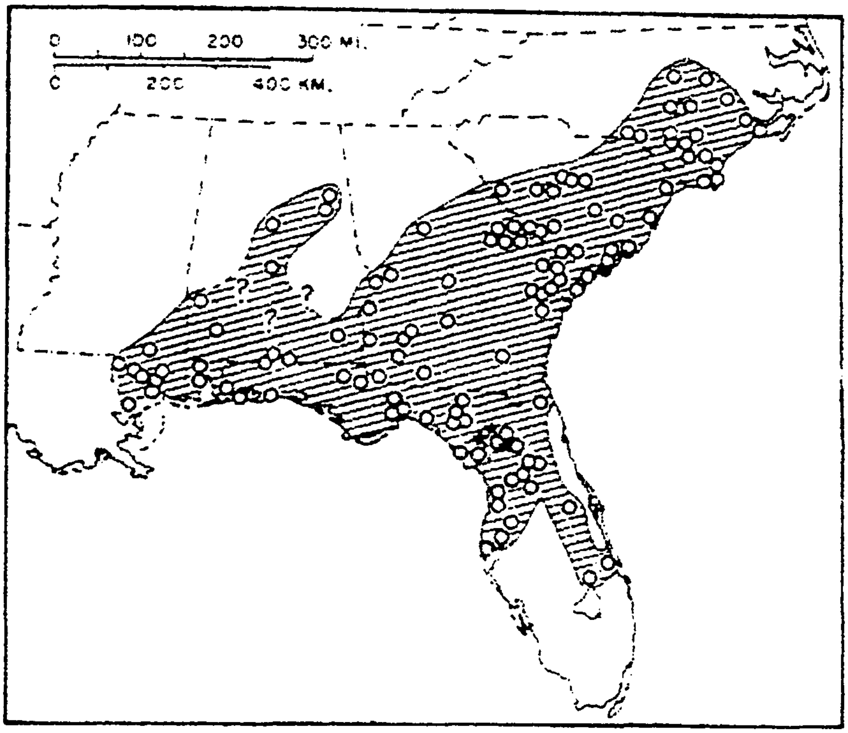


Figure 25: Distribution of Heterodon simus. Solid circle indicates type-locality; open circles indicate locality records. Stars indicate Pleistocene fossil localities. Question marks indicate a possible range hiatus in Alabama.

Province of Alabama may be disjunct from those on the Coastal Plain (Mount, 1975).

The southern hog-nosed snake, *H. simus*, has no recognized subspecies. However, it is very similar morphologically to *H. nasicus* other than differences in the number of scale rows and the venter color. Also, cranial anatomy suggests that *H. nasicus* and *H. simus* are very similar with a few exceptions (Weaver, 1965).

Heterodon nasicus.- *Heterodon nasicus*, the Western Hognose Snake described by Baird and Girard (1852), is intermediate in size between *H. simus* and *H. platyrhinos* (149-790 mm). The dorsal scale rows are generally 23-23-19 and there are 2-28 azygous scales. The number of loreals range from being absent to multiple. The rostral scale is very sharply turned up at the tip. Ventral scales number from 128-145 in males and 138-156 in females. There are 23-52 dorsal blotches anterior to the vent in males and 30-50 dorsal blotches in females. Edgren (1952a) found that the average total length of adults was 500-700 mm for females and 350-500 mm for males. He also observed a cline of increasing maximum length from south to north. Since then three subspecies have been recognized: *Heterodon nasicus nasicus* Baird and Girard, *H. n. kennerlyi* Kennicott, and *H. n. gloydi* Edgren.

Interspecific relationships of Heterodon

Previous studies of the relationships between the three species of *Heterodon* have used a variety of morphological (Edgren, 1952a; Auffenberg, 1963; Weaver, 1965) and molecular (Pinou, 1993) approaches. There are only three possible hierarchial arrangements of these three species, and each one of them has been supported by different authors (Fig. 2). The phylogenetic tree constructed using RAPD molecular markers supported the interspecific relationships hypothesized by Auffenberg (1963) and Weaver (1965) of which identify H. nasicus and H. simus as being sister species.

These results, therefore indicate that H. simus and H. nasicus share a common ancestor. However, these data alone do not completely explain how other authors reached different conclusions concerning phylogenetic relationships within Heterodon. So in addition to the molecular data provided by RAPD markers, the fossil record, the current distribution of the species of Heterodon, and known Pleistocene events were examine patterns that might reinforce the proposed phylogeny.

Fossil record. - An examination of the fossil record shows that a H. plionasicus group (ancestral to H. nasicus) and a H. brevis group (ancestral to H. platyrhinos) already existed in the Pliocene. Records also show that all three species, H. nasicus, H. platyrhinos, and H. simus, existed by the end of the Pleistocene (Dowling, 1958; Holman, 1962, 1972, 1981). These data support the hypotheses proposed by Edgren (1952a), Auffenberg (1963), and Weaver (1965) for an early divergence of H. nasicus and H. platyrhinos and a much later emergence of H. simus (Figs. 2b, 2c). The hypothesis proposed by Pinou (1993) alternatively suggested an early divergence of a H. simus group and a proto-H. nasicus/H. platyrhinos group (Fig. 2a). This indicates that H. simus probably diverged prior to the evolution of the H. nasicus/H. platyrhinos ancestor, however, the available fossil record does not support this. This phylogeny is also based on several microdermatoglyphic characters which have been reported to have a high incidence of homoplasy (Pinou, 1993). Therefore, the early divergence of H. simus from a

H. nasicus/H. platyrhinos clade seems the weakest of the three phylogenetic hypotheses.

Current distribution. - The current distribution of Heterodon species provides some further indication of the relationships of H. simus to the other species. Edgren (1952a) proposed that H. simus and H. platyrhinos had a common ancestor (Fig. 2b). Because H. platyrhinos and H. simus are presently entirely sympatric, a sympatric speciation model, rather than unknown and unlikely dispersal and/or vicariant events, would be the simplest historical mechanism for explaining the current distributions. The lack of hybrids or intergrades between H. simus and H. platyrhinos signifies that the H. simus populations are reproductively isolated. Nevertheless, there is no evidence of habitat partitioning or any other isolating mechanism that would reproductively isolate two species, as would be expected in a case of sympatric speciation (Auffenberg, 1963).

In contrast, the phylogenetic relationship of Heterodon proposed by Weaver (1965) and Auffenberg (1963) which concluded that H. simus and H. nasicus are the most closely related (Fig. 2c), is supported by the current distribution of the three species. Heterodon simus and H. nasicus are completely allopatric species and thus are reproductively isolated. If H. nasicus and H. platyrhinos diverged as long ago as the Pliocene, this would explain the lack of hybridization in areas where their ranges overlap. If H. simus came from a H. nasicus stock, this would explain why H. simus and H. platyrhinos do not form hybrids since H. simus would also be sufficiently divergent from H. platyrhinos as to not hybridize. Moreover, allopatric speciation models tend to be more plausible than sympatric speciation models in explaining species divergence events (Mayr and Ashlock, 1991). In addition, the effects that Pleistocene glacial periods had on dispersal and vicariant events further explain how *H. simus* and *H. nasicus* became isolated from one another (see below).

Pleistocene biogeography. - Auffenberg and Milstead (1965) have proposed that during the Pleistocene the major ecological fluctuations affecting reptilian distributions were: (1) expansion and contraction of temperature zones, (2) expansion and contraction of both xeric and mesic climates, including opening and closing of xeric and mesic dispersal routes, and (3) changes in sea level. These changes were due to the marked glacial and interglacial periods. With each glacial age the level of the sea was lowered while with each interglacial it rose. These fluctuations had considerable influence on geographic ranges of species living in coastal areas. The main effect of high sea-level stages was in providing a physical mechanism for isolation and subsequent speciation. Low sea levels opened certain types of dispersal routes unavailable during high levels. However, the major effects of sea-level changes were probably limited to those reptiles inhabiting the lands bordering the Gulf of Mexico and the Gulf of California (Auffenberg et al., 1965).

The Auffenberg and Milstead model suggests that there were three important dispersal routes for reptiles during various parts of the Pleistocene (Fig. 26): the Circumferential Gulf Coast Corridor (from Mexico to Florida), the Southern Rocky Mountains Corridor (an area of relatively low elevation across the Continental Divide in southern New Mexico and Arizona), and the Southern Great Plains Corridor (Kansas, eastern Colorado, Oklahoma, Texas, eastern New Mexico). The most important of these was probably the Circumferential Gulf Coast Corridor; it was likely the only one in

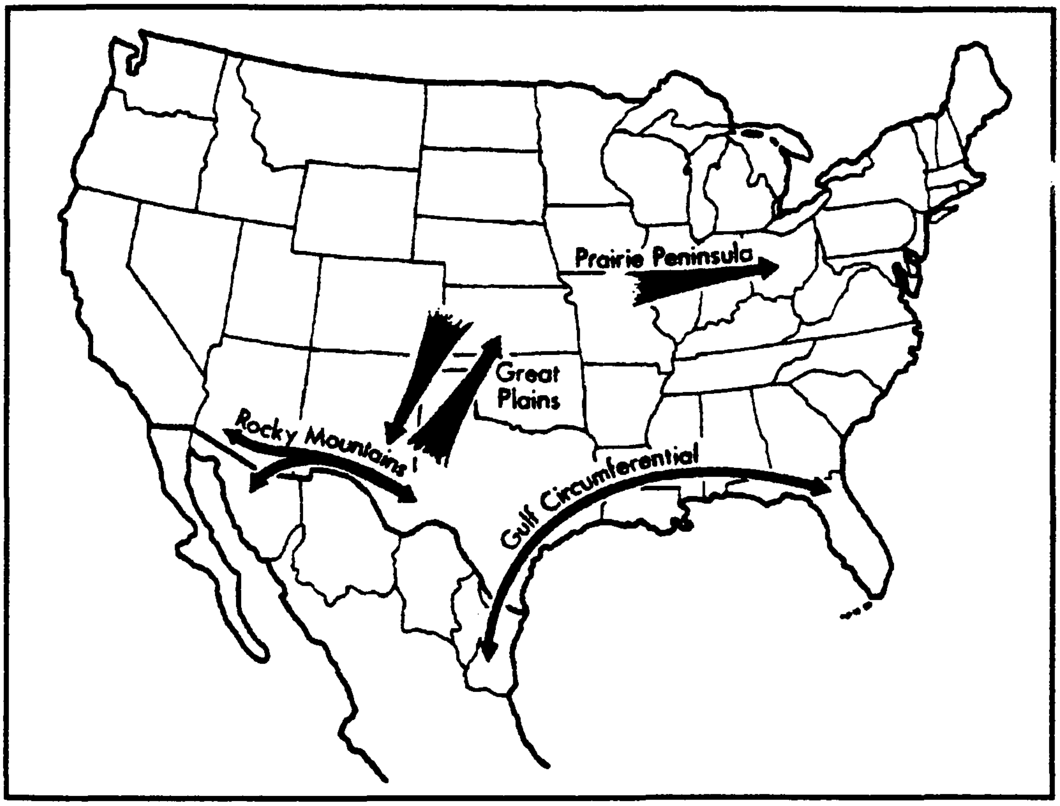


Figure 26: Generalized map of dispersal routes used by reptiles during the Quaternary. The Circumferential Gulf Coast Corridor shown here with a single arrow may have included two actual corridors: an inland forested corridor during pluvial and/or high-sea-level periods, and a more coastal grassland corridor during arid and/or low-sea-level periods.

existence throughout the entire Pleistocene and the most easily established for either xeric or mesic species under conditions of aridity or humidity, respectively. A shift toward more xeric conditions would have allowed grassland types from western United States to move eastward. Conversely, more humid conditions would extend the forest westward, allowing for an expansion of mesic forest dwelling reptiles in that direction.

Auffenberg and Milstead (1965) looked at several species that show a west to east dispersal. These include: Pseudemys concinna, P. scripta, Gopherus polyphemus, Sceloporus undulatus, Cnemidophorus sexlineatus, Masticophis flagellum, Pituophis melanoleucus, Micrurus fulvius, Sistrurus miliaris, Crotalus atrox and Crotalus adamanteus. Examination of these species' distributions indicates a central or western species as well as a southeastern form of that species (subspecies or closely related species). The remarkably similar distribution of H. simus and H. nasicus (Figs. 3 &25) suggests a corresponding history for these species. These dispersal and vicariant events would imply that a H. nasicus-simus common ancestor dispersed eastward along the Circumferential Gulf Coast Corridor during xeric conditions. A subsequent rise in sea level isolated the southeastern populations, which differentiated as H. simus.

This biogeographic scenario, along with the phylogenetic tree construction using RAPDs data, strongly suggests that H. simus and H. nasicus are sister taxa. This explanation thus agrees with the interspecific relationships of Heterodon proposed by Auffenberg (1963) and Weaver (1965), and depicted in figure 2c.

Variation and subspecies in Heterodon nasicus

Sexual dimorphism.- Edgren (1952a) reported sexual dimorphism in body size in populations of H. nasicus. However, his method included taking the average of the smallest and largest individuals of a population. This method does not take into consideration the variability within the population and it also assumes that the mean body size lies exactly halfway between the smallest and largest individuals. Therefore, a more robust approach was undertaken for this study.

The number of dorsal blotches previously used to separate H. n. gloydi from H. n. nasicus as well as other characters, were quantified to determine the extent of dimorphism. This approach allowed for the use of these characteristics in subsequent analysis without having to separate male and female populations. As predicted, all three nominal subspecies proved to be sexually dimorphic in a variety of characters including tail length, snout-to-vent length, the number of dorsal blotches, the number of tail dorsal blotches, the number of lateral blotches, the number of ventral scales and the number of subcaudal scales. It was then determined that the number of ventral scales and dorsal blotches, when added to subcaudals and tail dorsal blotches, respectively, corrects for sex differences in these characters. There is no doubt that these differences stem from the sexually dimorphic placement of the cloacal vent. The shorter bodies and longer tails in males is most likely due to the presence of hemipenes. The male hemipenes are contained in their tail, and the extra length involved may provide for storage.

Geographic distribution of H. nasicus.- Edgren (1952a) believed H. nasicus to be closely correlated with the grassland areas of the west-central portion of the United States.

Platt (1969) indicated that H. nasicus was further restricted to mixed grass prairie and in the south at the eastern edge of savanna communities. However, an examination of a hydrogeologic map of North America (Heath, 1989) indicates that the range of H. nasicus appears to be limited by soil type and structure (Figure 27). The populations of H. nasicus seem to be highly correlated with coarse alluvial and marine deposits. In instances where the snakes occur outside of these broad deposits they are still associated with alluvial deposits. However this presumed dependency on soil type, or on perhaps instead a food preference, still remains to be tested.

Heterodon nasicus extends from southern Canada south into central Mexico and from southeastern Arizona to eastern Texas (Fig. 3). The southern limit of the western hognose range is poorly known because it is rarely collected in Mexico. It extends at least as far as southern San Luis Potosí in the east and Durango and Zacatecas in the west The Rocky Mountains appear to be a barrier limiting the westward distribution of the Western Hognose Snake (Platt, 1969). The northern limit of the Western Hognose Snake may be the temperature gradient as well as soil types. The eastern barrier could be due to soil types or competitive exclusion with H. platyrhinos, however, the ranges of H. nasicus and H. platyrhinos broadly overlap to such an extent that competitive exclusion may not be a factor.

Description of subspecies.- Kennicott (1860) described the first subspecies as H. n. kennerlyi based on the number of loreal scales (generally single), the overall shape of the head, and primarily on the number of azygous scales (generally H. n. kennerlyi has fewer than 7 azygous scales; H. n. nasicus and H. n. gloydi have more than 9 azygous

Figure 27: Hydrogeologic map of North America. The blue-green areas are alluvial and glacial deposits. The yellow areas are marine deposits. Only the alluvial, glacial and marine deposits that are within the H. nasicus range (indicated by the black lines) are indicated.

scales). The type locality for this subspecies is given as "Rio Grand; Sonora"; no type specimen was indicated.

Heterodon n. gloydi was described by Edgren (1952c). He described H. n. gloydi as having more azygous scales than H. n. kennerlyi and having fewer dorsal blotches than H. n. nasicus. There are generally more than 35 dorsal blotches anterior to the vent in H. n. nasicus males, more than 40 in H. n. nasicus females; generally less than 32 dorsal blotches occur in H. n. gloydi males, and less than 37 occur in H. n. gloydi females).

Geographic distribution of subspecies of H. nasicus. - The range of H. n. nasicus (Fig. 3; yellow) includes the Texas panhandle and adjacent New Mexico north thro western Oklahoma and Kansas to southwestern Manitoba and southeastern Saskatchewan in Canada; prairie portions of Minnesota, and prairie relicts in Illinois (Edgren, 1952c).

The range of H. n. gloydi (Fig. 3; blue) includes southeastern Kansas and southeastern Missouri, eastern Oklahoma, all of Texas except for the panhandle, the Trans-Pecos region, and the extreme southern Rio Grande Valley (Edgren, 1952c).

The range of H. n. kennerlyi (Fig. 3; red) includes Mexico from Tamaulipas and central San Luis Potosí north and west along the Cordillera Occidental, invading the United States in extreme southern Rio Grande Valley, trans-Pecos Texas, southwestern New Mexico and southeastern Arizona (Edgren, 1952c).

Evaluation of subspecies.- An analysis of the number of dorsal blotches used by Edgren (1952a) to define H. n. gloydi reveals that H. n. gloydi is significantly different from H. n. nasicus in mean numbers of dorsal blotches. It was also established that H. n. kennerlyi and H. n. gloydi do not differ in this character. Initially, this information supports the use of the number of dorsal blotches as a diagnostic character, a conclusion reached by Edgren, one that led him to describe H. n. gloydi. However, in this study significant differences found in the mean number of dorsal blotches were not biologically meaningful. Inspection of the two dimensional contour map constructed for the total number of dorsal blotches (Fig. 6) indicated a clinal pattern for this character. The nature of a cline is such that populations on either side of an isophene would have different character values and might be interpreted as being different populations. A discriminan function analysis including the total number of dorsal blotches (DB+TDB) also showed that while the mean number of blotches tended to be separate in the different subspecies, its usefulness in identifying individuals of the different subspecies is very poor. The characters LB+TLB and VENT+SC were also included to provide a two-dimensional separation of groups, and because these characters are highly correlated with DB+TDB. Heterodon n. gloydi is thus not sufficiently distinct from H. n. nasicus to warrant its recognition as a valid taxon. Heterodon n. gloydi should therefore be considered a junior synonym of H. n. nasicus.

The number of azygous scales strongly separates H. n. kennerlyi from other H. nasicus populations. Inspection of the two dimensional contour map constructed for the number of azygous scales (Fig. 8) supports the sharp change in character states from a low number of azygous scales (2-7 for H. n. kennerlyi) to a high number (9-28 for H. n. nasicus). Based upon the discriminant function analysis, H. n. kennerlyi is a distinct entity primarily diagnosed by its number of azygous scales. However, the contour map and the results of the discriminant analysis both indicate possible intergrades between H. n.

kennerlyi populations and *H. n. nasicus* populations. Under these circumstances it seems best from the standpoint of practical taxonomy to retain *H. n. kennerlyi* as a subspecies. The occasional intermediates in the areas where this complex abuts the other populations of *H. nasicus* strengthens this idea, but occasional hybridization between population complexes that are ecologically isolated from one another and only partially genetically isolated, could produce the same results. On the basis of the available evidence it is not possible to state with certainty that *H. n. kennerlyi* is a subspecies (as treated here) or a full species that occasionally hybridizes introgressively. This problem may be corrected by further collections near contact zones, or through the use of additional molecular techniques, or both.

Summary species account for Heterodon nasicus

Given these taxonomic conclusions, as well as the data on variation and geographic distribution for *Heterodon nasicus*, the following species account is offered as an overview of the findings of this work.

***Heterodon nasicus* Baird and Girard**

Heterodon nasicus Baird and Girard, in Stansbury' s Exploration and Survey of the Valley of the Great Salt Lake of Utah, 1852:352. Type-locality, "Texas," collected by General Churchill. Type locality restricted to "Amarillo, Potter County, Texas by R.A. Edgren (1952c). See comments.

Content. Two subspecies are herein recognized: *nasicus* and *kennerlyi*.

Definition. Heterodon nasicus is a medium to small, stout and heavy-bodied species (males 663 mm total length, females to 1540 mm) with a light brown, brownish-gray, or tan ground color with a series of 23-50 grayish-brown or deep cinnamon or chocolate brown dorsal blotches down the back and rows of smaller similarly colored spots alternating on the sides, interspaced with background color. Head pattern consists of a dark band across the posterior azygous scales, anterior edge of supraoculars and frontals, and a broad dark band from eye to angle of mouth. The latter band extends along the posterior edge of the eye and across posterior supraoculars to frontal. Two lateral and one middorsal elongate nuchal blotches extend forward to parietal scales. The venter usually black although it may be checkered with irregular white, or yellow, blotches, although sometime it appears pale with large black blotches. Two to 28 small irregular azygous scales separate prefrontals from frontal and internasals from rostral, and rostral sharply upturned. Rostral projection concave dorsally. Small ocular scales 9-13 Anterior temporals two to five, and three to seven posterior temporals. Infralabials 9 to 13 (10-11 normal), and a large anterior (chin shield, while posterior chin shields reduced or absent. Anal plate and subcaudals divided. Ventrals range from 129 to 147 in males and 139 to 156 females; subcaudals 35 to 50 males, and 26-41 females. Dorsal body scales keeled, with 21-26 anterior, 19-26 mid-body and 16-23 anterior to anus. Maxilla short and deep with the mesial process curving posteriorly toward the posterior process. Ten teeth on maxilla, four on palatine, nine on pterygoid and fourteen on dentary.

Diagnosis. Heterodon nasicus can be distinguished from its congeners by the number of azygous scales, the position of the prefrontals, the shape of the rostral scale and the scale row counts.

H. platyrhinos has a single (0-2) azygous plate, the prefrontals are in contact, the rostral is only slightly upturned, and there is usually 25 scale rows at midbody. H. simus has a ventral surface that is paler than that of H. nasicus, is more uniformly dark under the tail, usually has 23 scale rows at midbody, and has a sharply upturned rostrum. H. nasicus also has a sharply upturned rostrum but its ventral surface can be pale, clouded or punctate. H. nasicus also usually has 25 scale rows at midbody.

Range. H. nasicus ranges from southern Canada to San Luis Potosí; southeastern Arizona to central Illinois. From near sea level to around 8000 ft. (2440 m).

Comments. The United States National Museum leger has an entry (made in 1858) indicating that a specimen assigned the number USNM 1272 is the type of Heterodon nasicus. Other data agree with Baird and Girard's statement (1852:353) concerning the collector ("Genl. Churchill") and locality ("Texas") . "Rio Grande" is written in pencil above the original locality, which agrees with a statement made later by Baird and Girard (1853:63). However, both Yarrow (1882:141) and Cope (1900:777), without explanation, state that a different specimen (USNM 4863) from Santa Fe, New Mexico is the type of H. nasicus. See comments under H. n. nasicus.

Fossil Record. Auffenberg (1963) and Holman (1963, 1965) give vertebral characters for separating nasicus from simus. Brattstrom (1967) & Holman (1963, 1965, 1981) reported H. nasicus from Blancan of Kansas, and Brattstrom (1967) from Rancholabrean of Oklahoma and Berends fauna (Brattstrom, 1967; Holman, 1986; VanDevender & Worthington, 1977) from Rancholabrean of New Mexico, while Holman

(1977) records a vertebra from Java, north central South Dakota similar to *H. nasicus* in having its hemal keel less constricted in the middle, and states the species is found within the area today. Holman (1981) summarized known fossil records.

Etymology. *Heterodon* is derived from the Greek words "*heteros*" (meaning different or other) and "odous" (meaning a tooth), probably a reference to the enlarged posterior maxillary teeth. The gender is masculine. The specific epithet *nasicus* is derived from the Latin "nasus" (meaning nose) , referring to the snout.

1. *Heterodon nasicus nasicus* (Baird and Girard)

Plains Hognose Snake

Heterodon nasicus, Baird and Girard, 1852, Rep. Stansbury's Exp., pp. 352-3.

Heterodon catesbyi, part., Günther, 1858, Cat. Colub. Snakes Coll. British Mus., p. 85.

Heterodon simus nasicus, Cope, 1875, Bull. U. S. Nat. Mus., 1, p. 43. First use of trinomial.

Heterodon nasicus nasicus, Cope, 1892, Proc. U. S. Nat. Mus., xiv, pp. 644-5. First use of combination.

Heterodon nasicus gloydi Edgren, 1952, Natur. Hist. Misc., (112): p. 3.

Diagnosis. Intermediate in size between *H. simus* and *H. platyrhinos*. Dorsal scale formula generally 23-23-19; a series of 9-28 scales in the azygous mass. Rostral turned up very sharply at the tip.

Range. Trans-Pecos Texas along the Rio Grande valley of Texas and New

Mexico north through Oklahoma and Kansas to southwestern Manitoba and southeastern Saskatchewan in Canada (Fig. 3; yellow). Eastward extension along the prairie peninsula in Missouri is to be expected, and it is known from Illinois prairie relicts. Present in the prairie portion of Minnesota.

Comments. The type, according to Baird and Girard (1852:353), was collected by General Churchill in Texas; it is now apparently lost. According to their description it was fairly typical of this subspecies on the basis of dorsal blotch counts, and thus probably came from some area in northwest Texas. Edgren (1952a:202) restricted the type locality to the vicinity of Amarillo, Potter County, Texas, "both on the basis of what was known of the type and the possibility that the city was visited by General Churchill"; Platt (1969:284, legend Fig. 10), following Edgren, also noted the type locality as Amarillo, Texas. Edgren (1952a:202) further noted that "Two specimens of this form have been examined from Amarillo; they are USNM 32746, a female collected by Bailey, and SM 3792, a male collected by Nelson. The former may be designated as the neotype and the latter as a neoparatype." Although the alleged type (USNM 1272) is not extant, Edgren's action of designating "neotypes" seems premature in view of the "type" status of USNM 4863 (see comments in account of species). Determination of the type and type locality requires further study.

2. *Heterodon nasicus kennerlyi* Kennicott

Mexican Hognose Snake

Heterodon kennerlyi, Kennicott, 1860, Proc. Acad. Nat. Sci., Philadelphia, p. 336.

Heterodon simus kennerlyi, Coues and Yarrow 1878:271 and

Garman, 1882, Mem. Mus. Comp. Zoöl., 8(3), p. 77. First use of combination.

Heterodon var. kennerlyi, Dumeril, Bocourt and Mocquard (1870). First use of combination.

Heterodon nasicus kennerlyi, Cope, 1892, Proc. U. S. Nat. Mus., xiv, p. 644. First use of trinomial.

Heterodon nasicus, part., Boulenger, 1894, Cat. Snakes British Mus., ii, pp. 156-7.

Diagnosis. Similar to H. n. nasicus but with reduced numbers of azygous scales (2-7).

Range. Heterodon n. kennerlyi ranges in Mexico from Tamaulipas and central San Luis Potosí north and west along the Coahuila Folded Belt, entering the United States in the extreme southern Rio Grande valley, trans-Pecos Texas, southwestern New Mexico and southeastern Arizona (Fig. 3; red).

Comments. The most recent discussions of the types and type locality of H. n. kennerlyi has been presented by Smith and Taylor (1945, 1950). In the former paper they designate the types as USNM 1282 (two cotypes), and in the latter they restrict the type locality to Brownsville, Cameron County, Texas. Edgren (1952a) noted that these two cotypes may have been in the type series utilized by Kennicott, but it was obvious to him that from the description a larger series was examined by Kennicott. For instance, both specimens of USNM 1282 have one loreal on each side, whereas Kennicott stated that H. n. kennerlyi sometimes lacks a loreal completely. Therefore, Edgren concluded that although these specimens may have been in the type series, they neither represented it in its entirety, nor was he sure that they were actually used by Kennicott. Edgren (1952:208) then designated "these two specimens as neotypes of *H*. *n*. *kennerlyi*. The male on [sic = of] USNM 1282 may be considered the neotype and the female the neoparatype." Both of these specimens were collected by Lt. Darius Nash Couch in the vicinity of Matamoras, Tamaulipas, Mexico. Aside from the inappropriateness of designating "neotypes" (instead of lectotype and paralectotype) from existing syntypes Kennicott's original description probably was based on three specimens (Cochran, 1961:185), which could account for the discrepancy in the number of loreals noted above. This third syntype is USNM 7290. Lower Rio Grande, Texas, A. Schott.

KEY TO THE SPECIES AND SUBSPECIES OF *HETERODON*

1a. Single (0-2) azygous scale, prefrontals in contact; rostral only slightly upturned; usually 25 scale rows at midbody.......... *Heterodon platyrhinos*

1b. Accessory scales present around the azygous plate (3-28) usually separating the two prefrontals; rostral sharply upturned; usually 23-25 scale rows at midbody...2

2a. Ventral surface pale, clouded or punctate, similar under tail; usually 25 scale rows at midbody... *Heterodon simus*

2b. Ventral surface mostly black with yellow patches, more uniform under tail; usually 23 scale rows at midbody...3

3a. A series of 9-28 scales in azygous area.............................. *Heterodon nasicus nasicus*

3b. Similar to *H*. *n*. *nasicus* but only 2-6 azygous scales......... *Heterodon nasicus kennerlyi*

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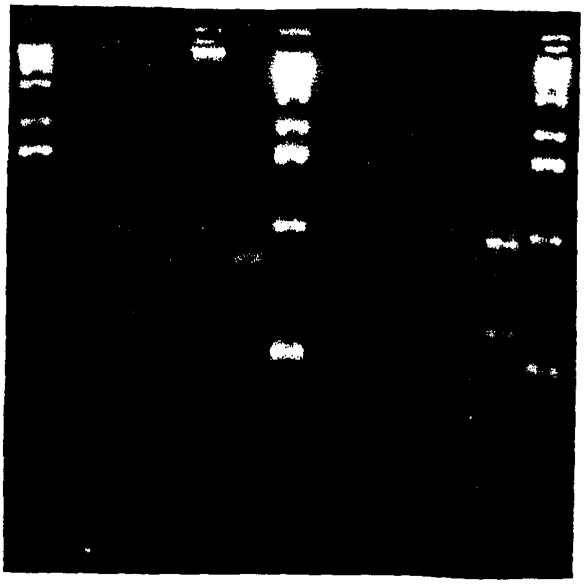
APPENDIX A

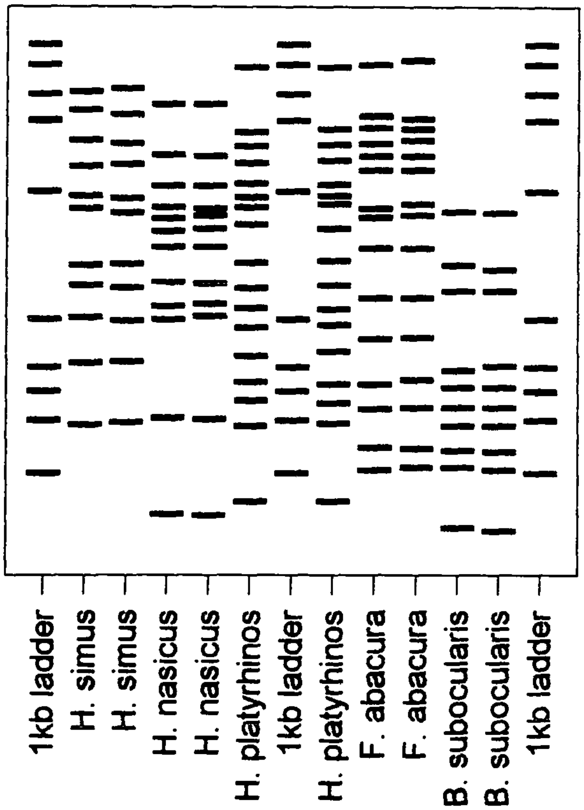
The amplified products generated using random oligonucleotide sequences.

Amplified products generated using the OP-G7 oligonucleotide primer. (a) The gel run on a 1.8% agarose gel and (b) a graphical representation of the shared amplified products used in analysis. Unshared products between individuals of the same species are not shown in the graph. Lanes 1, 6, and 12 are a 1kb ladder (GibCo BRL) used to estimate molecular weights of amplified products.

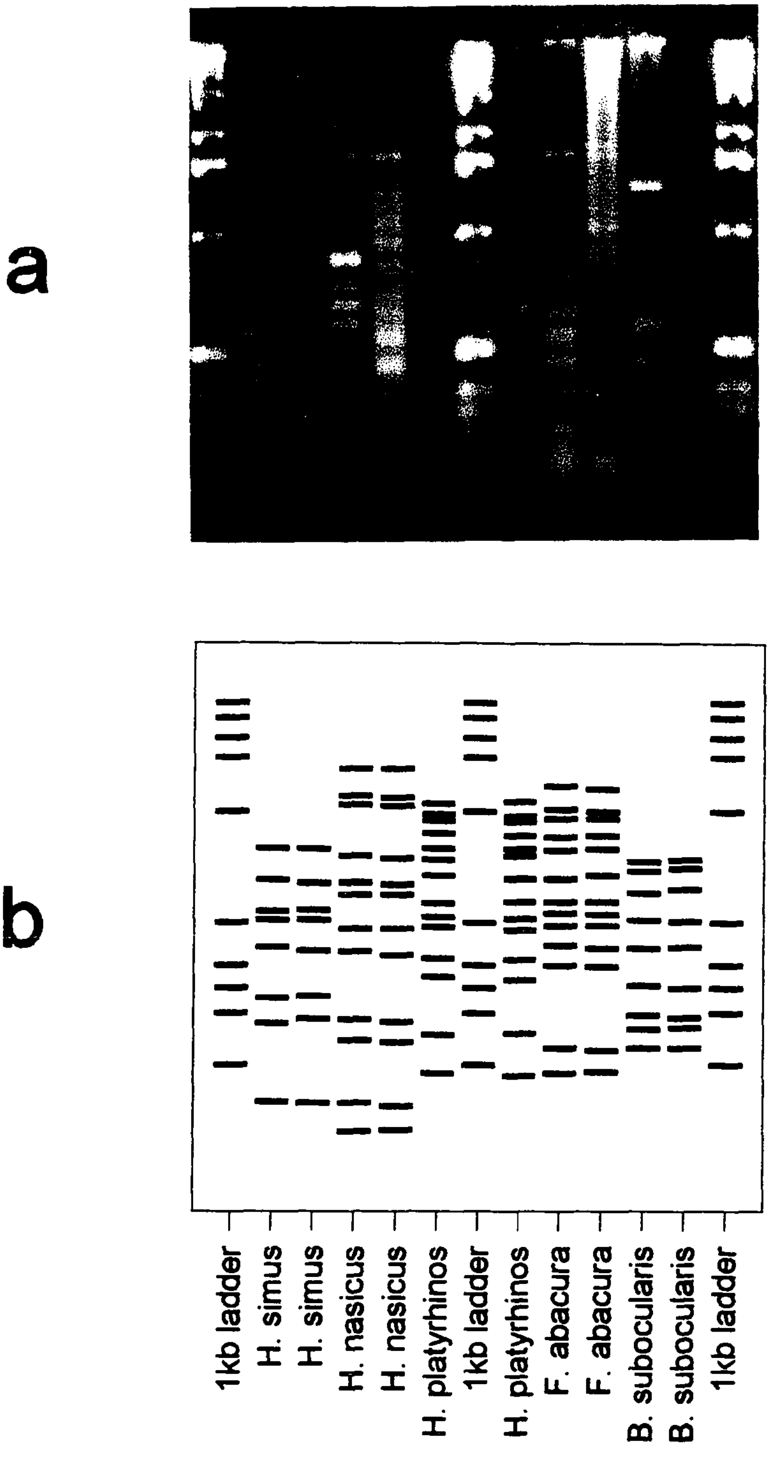
a



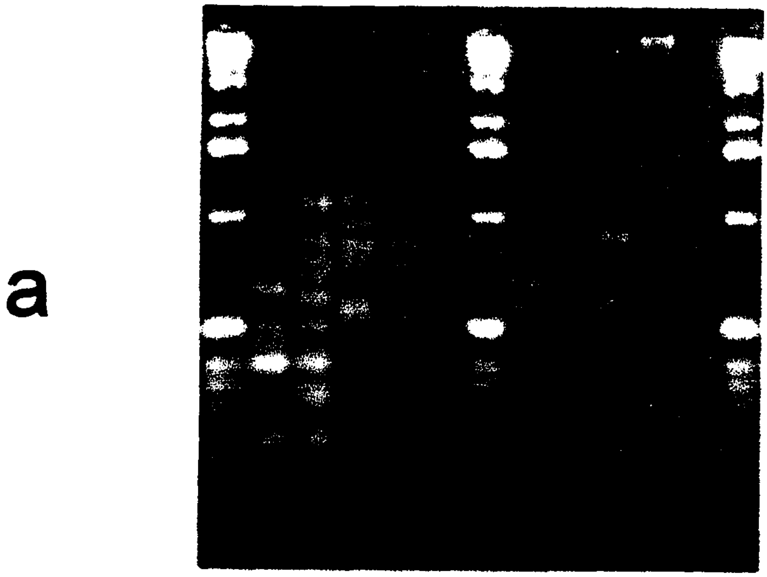
b

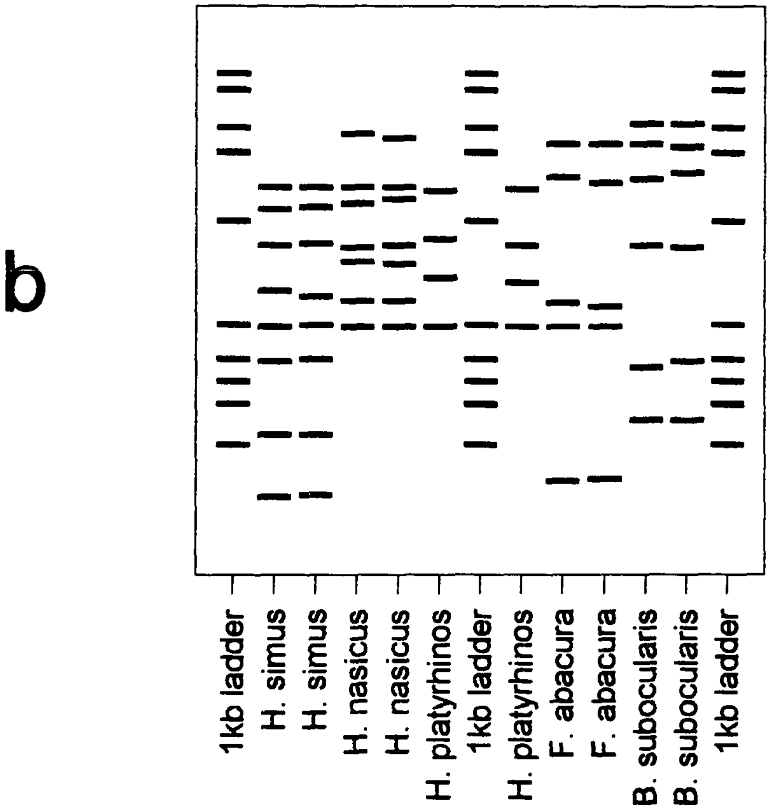

1kb ladder
H. simus
H. simus
H. nasicus
H. nasicus
H. platyrhinos
1kb ladder
H. platyrhinos
F. abacura
F. abacura
B. subocularis
B. subocularis
1kb ladder

Amplified products generated using the OP-W8 oligonucleotide primer. (a) The gel run on a 1.8% agarose gel and (b) a graphical representation of the shared amplified products used in analysis. Unshared products between individuals of the same species are not shown in the graph. Lanes 1, 6, and 12 are a 1kb ladder (GibCo BRL) used to estimate molecular weights of amplified products.

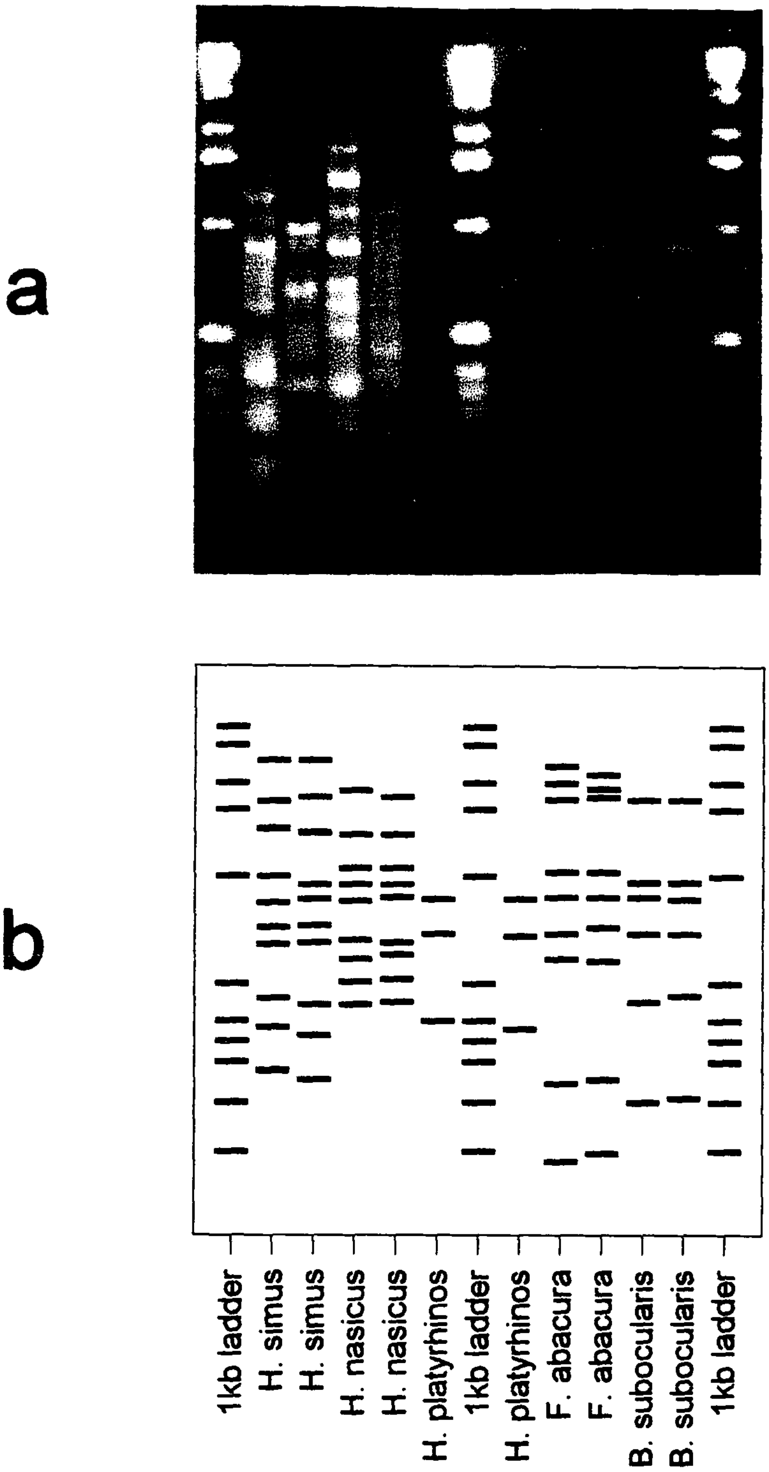

a
b
1kb ladder
H. simus
H. simus
H. nasicus
H. nasicus
H. platyrhinos
1kb ladder
H. platyrhinos
F. abacura
F. abacura
B. subocularis
B. subocularis
1kb ladder

Amplified products generated using the OP-W10 oligonucleotide primer. (a) The gel run on a 1.8% agarose gel and (b) a graphical representation of the shared amplified proc used in analysis. Unshared products between individuals of the same species are not shown in the graph. Lanes 1, 6, and 12 are a 1kb ladder (GibCo BRL) used to estimate molecular weights of amplified products.


a

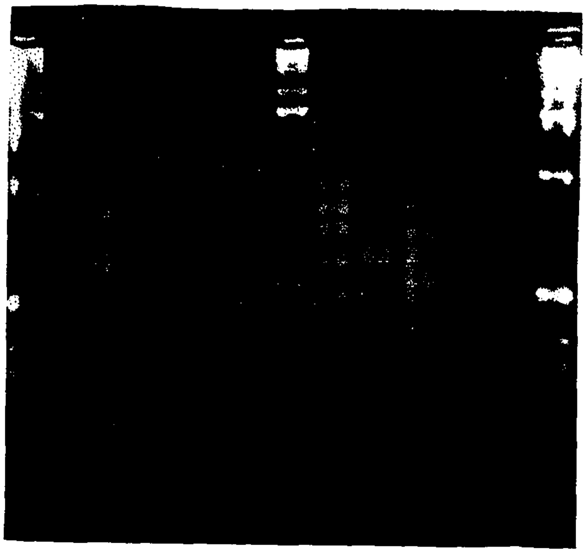

b
1kb ladder
H. simus
H. simus
H. nasicus
H. nasicus
H. platyrhinos
1kb ladder
H. platyrhinos
F. abacura
F. abacura
B. subocularis
B. subocularis
1kb ladder

Amplified products generated using the OP-G13 oligonucleotide primer. (a) The gel run on a 1.8% agarose gel and (b) a graphical representation of the shared amplified products used in analysis. Unshared products between individuals of the same species are not shown in the graph. Lanes 1, 6, and 12 are a 1kb ladder (GibCo BRL) used to estimate molecular weights of amplified products.

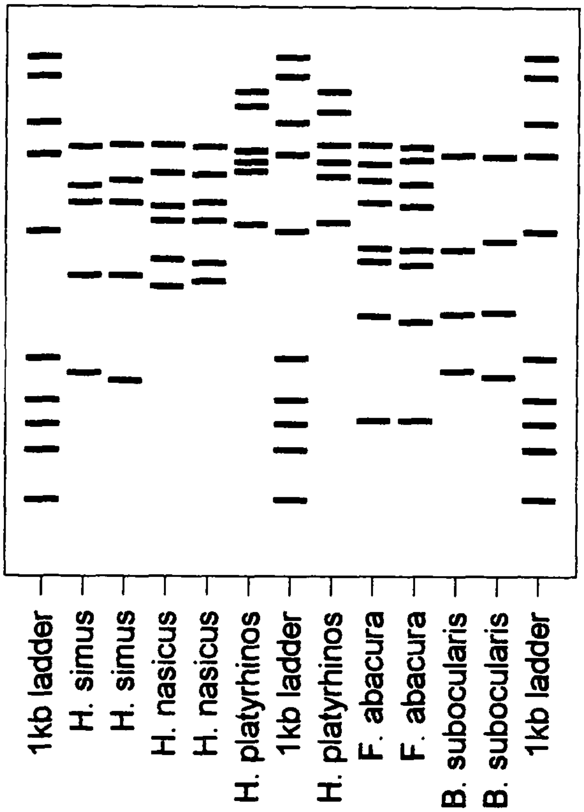

a
b
1kb ladder
H. simus
H. simus
H. nasicus
H. nasicus
H. platyrhinos
1kb ladder
H. platyrhinos
F. abacura
F. abacura
B. subocularis
B. subocularis
1kb ladder

Amplified products generated using the OP-W17 oligonucleotide primer. (a) The gel run on a 1.8% agarose gel and (b) a graphical representation of the shared amplified products used in analysis. Unshared products between individuals of the same species are not shown in the graph. Lanes 1, 6, and 12 are a 1kb ladder (GibCo BRL) used to estimate molecular weights of amplified products.

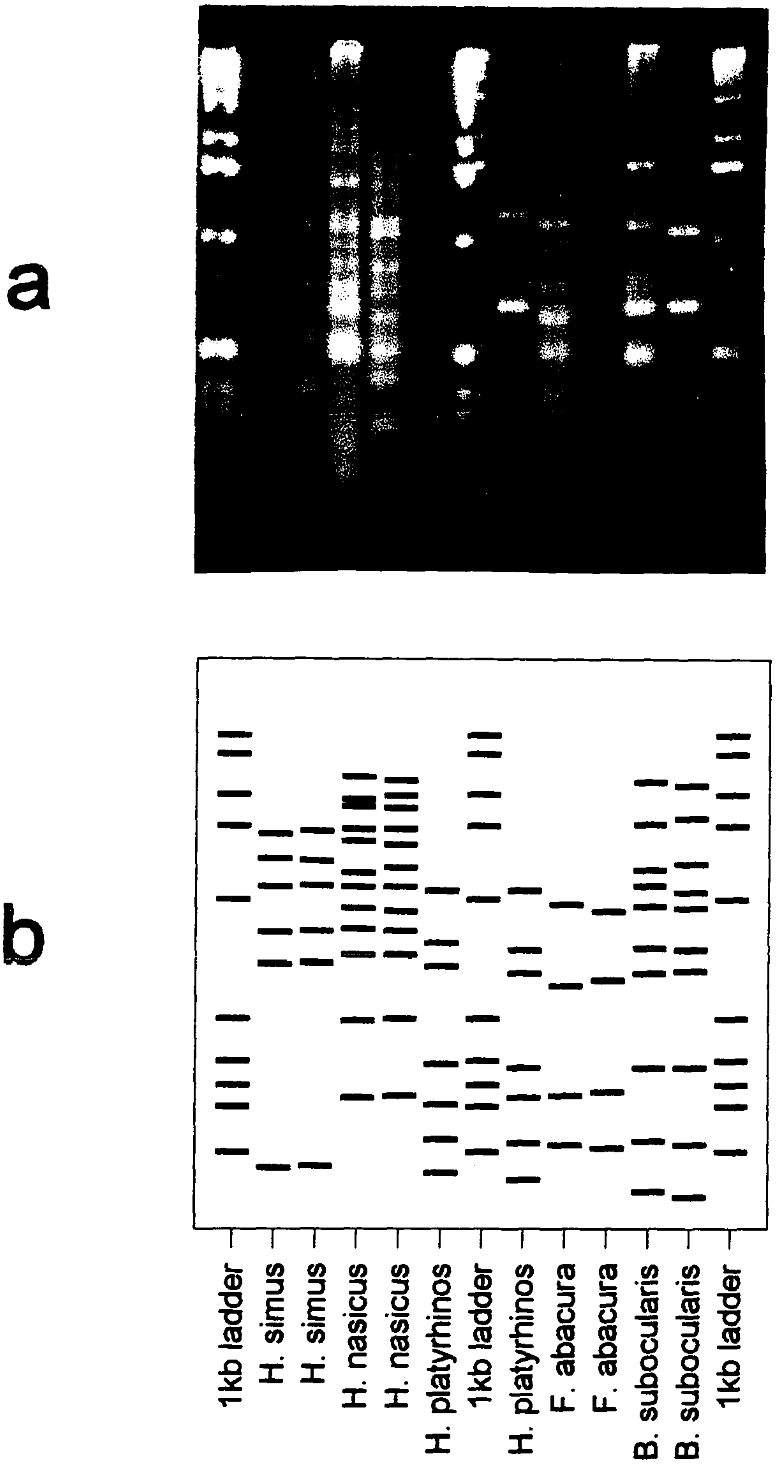
a



b


1kb ladder
H. simus
H. simus
H. nasicus
H. nasicus
H. platyrhinos
1kb ladder
H. platyrhinos
F. abacura
F. abacura
B. subocularis
B. subocularis
1kb ladder

Amplified products generated using the OP-G10 oligonucleotide primer. (a) The gel run on a 1.8% agarose gel and (b) a graphical representation of the shared amplified products used in analysis. Unshared products between individuals of the same species are not shown in the graph. Lanes 1, 6, and 12 are a 1kb ladder (GibCo BRL) used to estimate molecular weights of amplified products.


a
b
1kb ladder
H. simus
H. simus
H. nasicus
H. nasicus
H. platyrhinos
1kb ladder
H. platyrhinos
F. abacura
F. abacura
B. subocularis
B. subocularis
1kb ladder

APPENDIX B

The molecular weights of the amplified products estimated by the Gel-pro gel analysis package.

Molecular weights of amplified products using the OP-G7 oligonucleotide primer estimated using the Gelpro gel analysis package. The columns correspond to the order of the lanes from left to right on the agarose gels in Appendix I.

1 kb ladder	*Heterodon simus*	*Heterodon simus*	*Heterdon nasicus*	*Heterodon nasicus*	*Heterodon platyrhinos*	1 kb ladder	*Heterodon platyrhinos*	*Farancia abacura*	*Farancia abacura*	*Bogertophis subocularis*	*Bogertophis subocularis*	1 kb ladder
4072	2192	2274	2617	2116	2938	4072	3429	3054	3236	2346	2816	4072
3054	1825	1760	1870	1870	1847	3054	2938	2331	2827	1655	2164	3054
2036	1605	1545	1574	1636	1760	2036	1939	1697	2668	1361	1857	2036
1636	1460	1433	1297	1457	1514	1636	1544	1559	2518	1121	1544	1636
1018	1366	1242	1155	1284	1374	1018	1388	1401	1693	1028	1415	1018
517	1231	1130	1048	1100	1224	517	1248	1284	1781	940	1224	517
396	1088	996	930	1048	1068	396	1166	1166	1656	830	1068	396
344	1010	924	876	923	980	344	1058	1068	1544	772	996	344
298	945	858	818	889	930	298	988	988	1429	712	933	298
220	890	734	753	831	850	220	944	923	1284	648	855	220
	808	707	688	753	800		831	882	1166	625	733	
	756	623	624	715	693		759	748	1111	568	697	
	702	525	549	619	629		699	653	944	521	625	
	632	451	513	557	606		658	610	889	471	544	
	533	416	456	521	545		615	574	812	409	505	
	485	378	396	434	488		541	525	748	372	486	
	412	316	331	409	413		496	476	693	334	456	
	347	302	296	344	358		460	456	638	304	418	
	298	244	254	293	324		423	403	574	268	372	
	217	207	220	235	282		372	372	541	248	334	
		204	217	203	236		352	352	460	245	304	
			208	200	208		319	309	434	212	266	
			203		200		286	289	361	177	241	
							254	250	312		183	
							229	220	262		174	
							212	214	248			
							208	213	224			
							197	207				
							190	200				

Molecular weights of amplified products using the OP-W8 oligonucleotide primer estimated using the Gelpro gel analysis package. The columns correspond to the order of the lanes from left to right on the agarose gels in Appendix I.

1kb ladder	*Heterodon simus*	*Heterodon simus*	*Heterdon nasicus*	*Heterodon nasicus*	*Heterodon platyrhinos*	1 kb ladder	*Heterodon platyrhinos*	*Farancia abacura*	*Farancia abacura*	*Bogertophis subocularis*	*Bogertophis subocularis*	1 kb ladder
4072	1037	2010	2010	2010	3524	4072	1620	1959	1604	4164	1291	4072
3054	854	1767	1813	1636	2776	3054	1439	1813	1439	2406	1135	3054
2036	809	1636	1512	1482	2010	2036	1265	1657	1316	2010	1004	2036
1636	711	1439	1397	1383	1790	1636	1204	1343	1241	1679	903	1636
1018	673	1216	1169	1265	1542	1018	1070	1241	1070	1573	853	1018
517	600	1113	962	1070	1411	517	969	1158	969	1453	818	517
396	572	969	929	1004	1291	396	929	1059	872	1356	752	396
344	521	859	878	916	1216	344	859	962	824	1216	695	344
298	448	784	790	835	1091	298	806	897	700	1070	617	298
220	421	710	731	779	976	220	725	806	648	955	571	220
	366	667	662	731	909		700	757	604	897	524	
	359	626	591	639	824		630	700	563	847	470	
	327	571	513	591	757		587	653	524	801	410	
	300	517	338	503	695		559	634	470	741	340	
	267	433	302	457	639		513	604	442	671	321	
	261	393	266	413	600		489	536	401	626	287	
	246	340	213	382	536		433	473	325	600	268	
	232	254	182	333	493		368	454	285	559	242	
	220	213		317	442		313	382	253	524	219	
	204	175		298	352		273	344	220	486	182	
	180			258	338		269	317	183	418	149	
	170			230	311		248	289	166	376	137	
	144			209	251		229	251		347		
	134			183			193	209		321		
	126			163			175			289		
	121						159			251		
	112						140			205		
										191		

Molecular weights of amplified products using the OP-W10 oligonucleotide primer estimated using the Gelpro gel analysis package. The columns correspond to the order of the lanes from left to right on the agarose gels in Appendix I.

1 kb ladder	*Heterodon simus*	*Heterodon simus*	*Heterdon nasicus*	*Heterodon nasicus*	*Heterodon platyrhinos*	1 kb ladder	*Heterodon platyrhinos*	*Farancia abacura*	*Farancia abacura*	*Bogertophis subocularis*	*Bogertophis subocularis*	1 kb ladder
4072	2217	1291	1936	2265	1253	4072	2265	2990	1780	2125	3862	4072
3054	1497	1113	1750	1872	896	3054	2125	2865	1329	1780	2865	3054
2036	1291	873	1475	1565	703	2036	1969	2745	1146	1565	2467	2036
1636	1096	768	1291	1291	565	1636	1721	2125	919	1369	2125	1636
1018	1005	712	1146	1181	517	1018	1390	2036	740	862	1750	1018
517	967	626	967	862	236	517	1349	1780	588	740	1432	517
396	862	524	851	768	162	396	1272	1390	517	643	1163	396
344	740	408	778	694	105	344	862	862	361	524	980	344
298	651	320	610	610		298	685	603	172	384	851	298
220	517	236	517	517		220	595	517		311	703	220
	402	153	355	408			517	170		277	588	
	378			307			459			262	402	
	339						361				262	
	236						273				175	
	193											
	151											

Molecular weights of amplified products using the OP-G13 oligonucleotide primer estimated using the Gelpro gel analysis package. The columns correspond to the order of the lanes from left to right on the agarose gels in Appendix I.

1 kb ladder	*Heterodon simus*	*Heterodon simus*	*Heterdon nasicus*	*Heterodon nasicus*	*Heterodon platyrhinos*	1 kb ladder	*Heterodon platyrhinos*	*Farancia abacura*	*Farancia abacura*	*Bogertophis subocularis*	*Bogertophis subocularis*	1 kb ladder
4072	2729	3402	2986	2130	1129	4072	2130	2438	2854	1903	2494	4072
3054	1810	2729	2384	1840	896	3054	1840	2036	2228	1780	2279	3054
2036	1475	2279	1936	1497	721	2036	1519	1780	1936	1390	1780	2036
1636	1234	1872	1750	1390	544	1636	1253	1329	1872	1198	1565	1636
1018	1049	1588	1390	1272	517	1018	1005	1198	1810	980	1272	1018
517	884	1432	1096	1096	408	517	896	1049	1588	896	980	517
396	759	1129	980	980	181	396	840	896	1049	712	884	396
344	685	992	884	907	132	344	712	712	896	651	712	344
298	626	907	694	740		298	595	610	740	603	558	298
220	487	768	618	685		220	473	487	603	459	480	220
	396	694	537	634			384	420	530	357	402	
	290	530	459	544			232	322	368	282	232	
	206	466	362	466			147	258	265	226	181	
	170	373	278	396				226	206		132	
		273	239					181	156			
			153					147				

Molecular weights of amplified products using the OP-W17 oligonucleotide primer estimated using the Gelpro gel analysis package. The columns correspond to the order of the lanes from left to right on the agarose gels in Appendix I.

1kb ladder	*Heterodon simus*	*Heterodon simus*	*Heterdon nasicus*	*Heterodon nasicus*	*Heterodon platyrhinos*	1 kb ladder	*Heterodon platyrhinos*	*Farancia abacura*	*Farancia abacura*	*Bogertophis subocularis*	*Bogertophis subocularis*	1 kb ladder
4072	2473	1767	2281	2434	2682	4072	3710	2434	3005	2103	2395	4072
3054	1745	1581	1745	2010	2356	3054	2682	2103	1813	1618	1934	3054
2036	1366	1546	1461	1722	1885	2036	2244	1722	1700	1366	1745	2036
1636	1234	1413	1192	1564	1679	1636	1984	1529	1564	1248	1599	1636
1018	1089	1262	1089	1445	1564	1018	1745	1381	1350	1065	959	1018
517	903	1234	877	1305	1529	517	1564	1305	1179	1008	650	517
396	810	1140	755	1220	1478	396	1429	1206	1041	912	452	396
344	718	969	677	1153	1335	344	1192	1102	912	747	378	344
298	577	810	606	1089	1065	298	1077	921	842	644	171	298
220	473	755	340	969	755	220	959	859	690	594		220
	378	625		859	631		842	770	619	543		
	322	452		778	292		663	637	538	468		
	259	344		704			511	560	428	405		
	202	243		644			365	473	378	344		
				566			270	344	344	282		
				473				305	245	230		
				382				256	183			
				301				200				
				251								

Molecular weights of amplified products using the OP-G10 oligonucleotide primer estimated using the Gelpro gel analysis package. The columns correspond to the order of the lanes from left to right on the agarose gels in Appendix I.

1 kb ladder	Heterodon simus	Heterodon simus	Heterodon nasicus	Heterodon nasicus	Heterodon platyrhinos	1kb ladder	Heterodon platyrhinos	Farancia abacura	Farancia abacura	Bogertophis subocularis	Bogertophis subocularis	1kb ladder
4072	1959	1745	3155	2318	1053	4072	1166	1837	2395	2434	2138	4072
3054	1657	1564	3054	2010	894	3054	1053	1495	931	2208	2010	3054
2036	1529	1291	2639	1837	778	2036	834	1291	631	1813	1959	2036
1636	1305	1102	2395	1700	683	1636	747	1089	400	1599	1657	1636
1018	1089	988	2208	1581	625	1018	657	969	315	1335	1234	1018
517	834	903	1959	1429	538	517	571	810	273	1192	1030	517
396	697	842	1861	1291	378	396	447	747	222	1077	940	396
344	631	763	1581	1234	292	344	369	612	195	949	740	344
298	577	704	1461	1089	235	298	305	506		801	657	298
220	365	554	1192	1041	191	220	230	373		747	517	220
	315	500	1089	940			183	308		650	463	
	220	400	959	842			171	227		577	365	
	200	340	851	794				164		489	292	
		292	733	733						365	225	
		237	663	619						308	162	
		202	543	566						230		
		154	506	511						168		
			400	423								
			365	311								
			308									
			270									
			232									

APPENDIX C

Specimens examined

The following specimens were examined and either used in analysis, used as reference material, or both.

Heterodon platyrhinos

SPECIMEN	**STATE**	**COUNTY**	**LOCATION**
LSUMZ 2717	?	?	?
LSUMZ 2718	?	?	?
TCWC 10771	FL	ALACHUA CO.	Gainesville
UTEP 14210	FL	NASSAU CO.	3.2 rd mi SSE jct w/St Hwy 108, 1.4 rd mi N jct w/Musselwhite-Griffin rds) (T3N,R25E,Sec 27)
UTEP 8461	IN	MONROE CO.	Bloomington
UTEP 5565	KS	ELLIS CO.	1.5 mi SW Catherine
UTEP 5566	KS	ELLIS CO.	?
LSUMZ 2719	LA	?	EBR Pav., 5 mi S University
LSUMZ 2720	LA	?	E Baton Rouge Parish
USNM 156799	NC	ROBESON CO.	Maxton - Laurinberg Air Base, Robeson - Scotland Line
UTEP 6367	NC	TRANSYLVANIA CO.	2.5 mi E Cedar Mtn.
UTEP 6366	NC	TRANSYLVANIA CO.	2.5 mi E Cedar Mtn.
UTEP 14158	TX	ATASCOSA CO.	Washburn
UTEP 12202	TX	GILLESPIE CO.	?
UTEP 9432	TX	GOLIAD CO.	3.6 rd mi on Hwy 290, E jct w/FM 1376 at Blumenthough along the Perdenales River
UTEP 9929	TX	GUADALUPE CO.	2 mi W Boydston
UTEP 13894	TX	HARRIS CO.	2 mi W of Brazos River Hwy 90
UTEP 9930	TX	JACKSON CO.	Mertzon, W of, along US Rte 67

UTEP 9055	TX	KENDALL CO.	12 air km ENE Boeme, at jct of Oberly crossing rd w/camp Alzafar rd
UTEP 12222	TX	KENDALL CO.	4 air km SSE Boeme, 1.1 rd mi SSE jct w/Herf rd
UTEP 9985	TX	KENDALL CO.	FM 474, 5 km (air) NNE Boeme, ~.5 air mi NNE summit Malakoff Hill
UTEP 10679	TX	REFUGIO CO.	9 mi ? Miami

Heterodon simus

SPECIMEN	**STATE**	**COUNTY**	**LOCATION**
CM 31941	MS	LEE CO.	10 mi S of Oxford
CM 31946	MS	LEE CO.	10.5 mi S of Oxford
USNM 091023	SC	LEXINGTON CO.	3 mi SE of Leesville
FMNH 60562	SC	LEXINGTON CO.	LEESVILLE
CM 9531	SC	LEXINGTON CO.	LEESVILLE, 5 MI SE OF
CM 9549	SC	LEXINGTON CO.	10 mi SE of Leesville
USNM 048349	SC	CHARLESTON CO.	MT. PLEASANT, CHRIST CHURCH PARISH
USNM 091402	SC	LEXINGTON CO.	5 mi SE of Leesville
CM 9854	SC	LEXINGTON CO.	13 mi SE Leesville
UCM 15238	MI	HARRISON CO.	1 mi E Handsboro
LACM 59039	?	?	?
LACM 2352	?	?	?
LACM 2351	?	?	?
USNM 131732	?	?	?
USNM 307561	??	AUTAUGA CO.	?
USNM 255245	VI	CLARKE CO.	?
USNM 011488	?	?	?
CM 92024	SC	BEAUFORT CO.	Beaufort
CM 21783	SC	BERKELEY CO.	Wando
CM 21782	SC	BERKELEY CO.	16 mi N of Monck's Comers, Santee Canal
USNM 006399	SC	BEAUFORT CO.	Beaufort

FMNH 21538	MS	JACKSON CO.	Vestry
USNM 001197	SC	ABBEVILLE CO.	Abbeville
USNM 267086	SC	AIKEN CO.	Savannah River Plant, Tyler Bridge Rd.
CM 21784	SC	BERKELEY CO.	16 mi N of Monck's Corners, Santee Canal
USNM 048348	SC	CHARLESTON CO.	Mt. Pleasant, Christ Church Parish
USNM 048351	SC	CHARLESTON CO.	Johnson R., James Isl.
LSUMZ 40462	SC	CHARLESTON CO.	Mt. Pleasant, Crhist Church Parish
USNM 048350	SC	CHARLESTON CO.	Mount Pleasant
USNM 033882	SC	BERKELEY CO.	16 mi N of Monck's Corners, Santee Canal
CM 21781	SC	BERKELEY CO.	16 mi N of Monck's Corners, Santee Canal
FMNH 4765	SC	CHARLESTON CO.	Mt. Pleasant, Christ Church Parish
CM 5568	GA	BAKER CO.	?
USNM 246891	FL	WAKULLA CO.	Bethel, NE of, 2.6 MI S of Leon - Wakulla Co. Line, on FL. RTE. 61
LSUMZ 56507	FL	SANTA ROSA CO.	9 mi E on rd to Riley's corner from Hwy 191, Approx. 6 mi S of Munson
FMNH 35451	GA	THOMAS CO.	Thomasville
BYU 21472	GA	DOUGHERTY CO.	Boat Docks, Turner AFB, Albany
BYU 22186	GA	BAKER CO.	Georgia Hwy 91, 4 mi N of Newton
CM 52426	FL	MARION CO.	Silver Springs
CAS 54730	FL	MARION CO.	Silver Springs
FMNH 48260	FL	MARION CO.	Silver Springs
LSUMZ 39949	FL	PINELLAS CO.	Boca Raton
CM 69093	FL	PASCO CO.	Dade City
CAS 10474	FL	ORANGE CO.	Orlando
FMNH 29480	GA	THOMAS CO.	Chakri", Thomasville
USNM 004834	IN	FRANKLIN CO.	Brookville
USNM 308023	IN	FRANKLIN CO.	BROOKVILLE
USNM 330145	NC	NEW HANOVER CO.	Wilmington
USNM 065152	NC	WAYNE CO.	Goldsboro
USNM 065153	NC	WAYNE CO.	Goldsboro
USNM 056353	NC	WAKE CO.	Raleigh
USNM 006422	NC	CRAVEN CO.	Newberne
FMNH 35568	GA	THOMAS CO.	Chakri", Thomasville

FMNH 35567	GA	THOMAS CO.	Chakri", Thomasville
CM 92160	NC	NEW HANOVER CO.	Wilmington
USNM 009117	NC	NEW HANOVER CO.	CAROLINA BEACH, 1.25 MI SW OF
USNM 297336	NC	NEW HANOVER CO.	CAROLINA BEACH, 1.25 MI SW OF
USNM 307562	FL	MARION CO.	Near Ocala
CAS 179089	FL	CITRUS CO.	Floral city, Suburban Acres
CM 69092	FL	ALACHUA CO.	Gainesville
TCWC 10772	FL	ALACHUA CO.	gainesville, SW 3rd place at 38th street
CAS 169501	FL	CITRUS CO.	Lecanto, Hwy 450
CAS 169502	FL	CITRUS CO.	Floral city, Suburban Acres
CAS 195958	FL	CITRUS CO.	Floral city, Suburban Acres
USNM 010447	FL	ALACHUA CO.	Gainesville
UCM 24668	FL	ALACHUA CO.	Archer
USNM 022648	FL	?	?
LSUMZ 28838	FL	ALACHUA CO.	Gainesville
USNM 010691	FL	ALACHUA CO.	Gainesville
USNM 010534	FL	ALACHUA CO.	Gainesville
USNM 085319	FL	DADE CO.	Miami
FMNH 48261	FL	MARION CO.	?
FMNH 25963	FL	MARION CO.	?
FMNH 25964	FL	MARION CO.	Zoo
FMNH 25962	FL	MARION CO.	Silver Springs
LSUMZ 43813	FL	MARION CO.	?
FMNH 48262	FL	MARION CO.	?
LSUMZ 6504	FL	HOLMES CO.	Bonifay
LSUMZ 5901	FL	HOLMES CO.	Bonifay
BYU 9175	FL	ESCAMBIA CO.	Tarkiln Point, 12 mi SW Pensacola
USNM 086896	FL	MARION CO.	4 mi S Ocala
CM 19848	FL	LAKE CO.	Leesburg
LSUMZ 5903	FL	HOLMES CO.	Bonifay.

Heterodon nasicus kennerlyi

SPECIMEN	STATE	COUNTY	LOCATION
UAZ 46322	AZ	COCHISE CO.	4 mi SE of Huachuca mtns.
UAZ 24939	AZ	COCHISE CO.	US Hwy 80 on Portal rd., 2 mi W.
UAZ 32441	AZ	COCHISE CO.	6.3 mi E of US 666 on 181
UAZ 41149	AZ	COCHISE CO.	Douglas
UAZ 43892	AZ	COCHISE CO.	3 mi W on ???? Canyon Rd off I-25
AMNH 109431	AZ	COCHISE CO.	willcox, 6 mi SE of, offf AZ Rte.186
LACM 115794	AZ	COCHISE CO.	11.5 mi N jct rtes 80 and 666.
UAZ 32448	AZ	COCHISE CO.	Rucker Canyon Rd. on US Hwy 80, .1 mi (rd) S.
AMNH 84965	AZ	COCHISE CO.	Douglas
AMNH 91617	AZ	COCHISE CO.	Willcox, 12 mi NW of
UAZ 39617	AZ	COCHISE CO.	Willcox, 25 mi (by rd) SE of, S of jct of AZ Rts 186 + 181
AMNH 84966	AZ	COCHISE CO.	Wilcox, 7.2 mi SE.
CM 63630	AZ	COCHISE CO.	1.1 mi W & 1.4 mi S Rodeo
AMNH 114451	AZ	COCHISE CO.	Cochise, SE of, 12.1 mi SSE of US 10, on US Rte 666
UAZ 37758	AZ	COCHISE CO.	5.4 mi ESE Portal
UAZ 43997	AZ	COCHISE CO.	25 mi W Bisbee
UAZ 46833	AZ	COCHISE CO.	4 mi NE Apache
UAZ 50250	AZ	COCHISE CO.	11.3 mi (by rd) SE Dos Cabezas, on Hwy 186
UAZ 50018	AZ	COCHISE CO.	T21S,R30E, Sec.26
UAZ 24941	AZ	COCHISE CO.	0.9 mi W jct Hwy 90 & hwy 82, E side Whetstone Mtns.
NMSU 3053	AZ	COCHISE CO.	Huachuca mtns.
ASU 13439	AZ	COCHISE CO.	12 N. (by US 666) Pearce + 1 mi W. of Hwy.
CM 64297	AZ	COCHISE CO.	Dos Cabezas, 4 mi. SW
UAZ 39614	AZ	COCHISE CO.	5 mi NE Douglas
UAZ 42458	AZ	COCHISE CO.	1.5 mi (By AZ 186) S Willcox
AMNH 75115	AZ	COCHISE CO.	4 mi N Apache
LSUMZ 34727	AZ	COCHISE CO.	3 mi S jct of AZ 186 & AZ 181
CM 69084	AZ	COCHISE CO.	Apache
FMNH 102686	AZ	COCHISE CO.	0.2 mi E jct AZ 92 & Hereford rd, on AZ 92

UAZ 41150	AZ	COCHISE CO.	1.1 mi N & .4 mi E Portal
UAZ 47323	AZ	COCHISE CO.	Sulphur Springs Valley; 8.4 mi S by Kansas Settlemont Rd. from Kansas townsight.
AMNH 88240	AZ	COCHISE CO.	3.9 mi N. rt. 80 on Rt. 666.
CM 19819	AZ	COCHISE CO.	.6 mi S Apache
AMNH 115940	AZ	COCHISE CO.	5.5 mi SE Portal
AMNH 94850	AZ	COCHISE CO.	San Simon
AMNH 75155	AZ	COCHISE CO.	San Simon
UAZ 46640	AZ	COCHISE CO.	Sulphur Springs Valley; 5.3 mi N. by rd from double Adobe on Central Hwy.
INHS 7810	AZ	COCHISE CO.	1.5 km W of AZ-NM border on Portal Rd.
UAZ 43894	AZ	COCHISE CO.	25 mi W Bisbee
CHAS 72176	AZ	COCHISE CO.	0.5 mi SW by Kansas Settlement rd of Rt 186
UMMZ 71162	AZ	COCHISE CO.	2.5 mi W Hwy 181 on Hwy 186
UAZ 46323	AZ	COCHISE CO.	12 S Bowie
CM 63631	AZ	COCHISE CO.	W. jct. of US Hwy 80, Pedragusa mtns., .8 mi by Tex Canyon/Rucker Canyon rd.
CHAS 12177	AZ	COCHISE CO.	8 mi SSE Apache
UAZ 9365	AZ	COCHISE CO.	Apache
UAZ 39610	AZ	COCHISE CO.	Portal on Portal rd., 1.5 mi E.
AMNH 84967	AZ	COCHISE CO.	Jct. SR 186 and 181, 7.4 mi (rd) N.
CM 69826	AZ	COCHISE CO.	7 mi S & 6 mi E Apache
AMNH 63502	AZ	COCHISE CO.	White River Canyon
UAZ 43570	AZ	COCHISE CO.	Cochise, 1 mi NW of, 3 mi SE of US 10, on US Rte 666
UAZ 41146	AZ	COCHISE CO.	Willcox, SE of. 100 rds NW of jct of AZ Rte. 87 + KS Settlement Rd
UAZ 48011	AZ	COCHISE CO.	1.5 km W of AZ-NM border on Portal Rd.
UAZ 32593	AZ	COCHISE CO.	9.3 mi NE Apache
UAZ 41148	AZ	COCHISE CO.	San Simon
INHS 7567	AZ	COCHISE CO.	5 mi SE of Willcox on State 186, Kansas Settlement
CHAS 7810	AZ	COCHISE CO.	Southwest Research Station, Chiricahua Mtns.
UAZ 39611	AZ	COCHISE CO.	4.8 mi (by Ft. Grant Rd) N Willcox
AMNH 80810	AZ	COCHISE CO.	Dos Cabezas, 6 mi E.
UAZ 24934	AZ	COCHISE CO.	1 mi W Palominas; st. rd. 92
UAZ 35159	AZ	COCHISE CO.	Fry

UAZ 50017	AZ	COCHISE CO.	McNeal on Hwy 666 (181), 1.74 mi S.
UAZ 40146	AZ	COCHISE CO.	San Simon
USNM 246456	AZ	COCHISE CO.	5 mi SW (on Hwy 80) Rodeo
UAZ 32592	AZ	COCHISE CO.	Vicinity of Portal and Apache
UAZ 39618	AZ	COCHISE CO.	Jct. SR 186 and 181, 3.4 mi (rd) N.
USNM 044465	AZ	COCHISE CO.	Jct. SR 186 and 181, 6.3 mi (rd) N.
UAZ 44779	AZ	COCHISE CO.	1.4 km W of AZ-NM border on Portal Rd.
UAZ 46321	AZ	COCHISE CO.	7 mi SE Dos Cabezas
AMNH 75327	AZ	COCHISE CO.	On Fort Grant Rd, 4.7 Rd MI S Bonita
UAZ 24942	AZ	COCHISE CO.	Between Apache and Rodeo
UAZ 39615	AZ	COCHISE CO.	8.05 mi SE Fletcher's - (Carr Canyon entrance)
USNM 246457	AZ	COCHISE CO.	Hwy 80, 0.7 mi (by rd) SW state line jct.
USNM 246458	AZ	COCHISE CO.	Paved rd to Chiricahua National Monument, just E Hwy 186
CAS 48070	AZ	COCHISE CO.	Sulphur Springs Valley, Rt 666 (=191), 3.36 mi (rd) S of Davis Rd, near McNeal
AMNH 115591	AZ	COCHISE CO.	3.5 mi W State Line on Portal Rd.
AMNH 75558	AZ	COCHISE CO.	McNeal
CM 64298	AZ	COCHISE CO.	US Hwy 80, 17 mi S Rodeo at jct. of Rucker Canyon Rd.
AMNH 94851	AZ	COCHISE CO.	On Ramsey Canyon Rd, 1.3 mi W AZ 92.
UAZ 41152	AZ	COCHISE CO.	8.9 mi E of Hwy 92
UAZ 24937	AZ	COCHISE CO.	SE Huachucha mtns.; near jct. of Hwy 92 and coronado memorial rd.
UNM 22345	AZ	COCHISE CO.	5.5 mi W Don Luis
UAZ 39613	AZ	COCHISE CO.	8.3 mi SE Fletcher's (Carr Canyon Entrance)
UAZ 39612	AZ	COCHISE CO.	Sierra Bonita Ranch
UNM 52178	AZ	COCHISE CO.	4 mi SSW Dos Cabezas
UAZ 41151	AZ	COCHISE CO.	1 mi W of NM on Portal Rd.
USNM 246459	AZ	COCHISE CO.	3 mi SW Portal
UMMZ 71161	AZ	COCHISE CO.	Huachuca mtns., flat opposite Ramsey Canyon
AMNH 87290	AZ	COCHISE CO.	El Frida on Rt. 666, 10 mi. N.
UAZ 24935	AZ	COCHISE CO.	Sulphur Springs Valley; .82 mi (rd) w of Rt. 666 (191) on Glenn Rd.
USNM 246455	AZ	COCHISE CO.	?
UAZ 24940	AZ	COCHISE CO.	Sulphur Springs Valley; Rt 666 (=191), 1.31 mi (rd) S. of Davis Rd. jct.; near McNeal

UAZ 24938	AZ	COCHISE CO.	E. Flank Huachuca mtns., at 1.1 mi (rd.) S. AZ 92, on Coronado memorial rd.
UAZ 41147	AZ	COCHISE CO.	Bisbee
UAZ 50041	AZ	COCHISE CO.	10 mi S Apache
UAZ 50016	AZ	COCHISE CO.	Douglas
UAZ 39616	AZ	COCHISE CO.	San Simon
AMNH 103122	AZ	COCHISE CO.	Apache
USNM 044466	AZ	COCHISE CO.	Willcox, 12 mi NW of
USNM 010202	AZ	COCHISE CO.	22 mi W Bisbee
UTEP 9947	AZ	GRAHAM CO.	Tucson Region
ASU 22461	AZ	GRAHAM CO.	Sulphur Spring Valley
ASU 7029	AZ	GRAHAM CO.	Hwy 266, 1.8 mi E of Bonita
UAZ 24936	AZ	PIMA CO.	NW. of Elgin on North Rd. b/w Elgin and Hwy 83.
UAZ 40777	AZ	PIMA CO.	Elgin, 3 mi W.
USNM 156806	AZ	SANTA CRUZ CO.	Patagonia
UAZ 24933	AZ	SANTA CRUZ CO.	Sonoita, 6 mi S of, on Canello Parker Canyon Lake Road
UAZ 43799	AZ	SANTA CRUZ CO.	2 mi E Sonoita
UAZ 50066	AZ	SANTA CRUZ CO.	9.4 mi SE. of Sonoita on AZ Hwy 83.
UAZ 40778	AZ	SANTA CRUZ CO.	Wilcox
UAZ 24944	AZ	SANTA CRUZ CO.	Jct. SR 82 on SR 83, 6.2 mi (rd) mi S.
UAZ 43756	AZ	SANTA CRUZ CO.	Wilcox
UAZ 24946	MEX	?	El Rancho Los Alamos, 6 mi E Cananea
UNM 34387	MEX	CHIHUAHUA	?
UNM 34385	MEX	CHIHUAHUA	Vicinity of Ojos Azules, S. Sierra del Nido.
UAZ 39199	MEX	CHIHUAHUA	Corralitos
USNM 017531	MEX	CHIHUAHUA	Chihuahua, 6.6 mi E Aldama on rte. 16
USNM 056132	MEX	CHIHUAHUA	Chihuahua, Encinillas
USNM 104665	MEX	CHIHUAHUA	MXHY 45, 54 MI S CD JUAREZ
UNM 34386	MEX	CHIHUAHUA	Chihuahua, 13.9 mi E Aldama on rte. 16
TNHC 29855	MEX	CHIHUAHUA	Chihuahua, 6 mi S Gallego
CM 59940	MEX	CHIHUAHUA	17 mi SE of Camargo
AMNH 74428	MEX	CHIHUAHUA	Carrillo, Est Escalon-Cuatro Cienegas Rd.
BYU 15315	MEX	CHIHUAHUA	Chihuahua, 77 km E Chihuahua City on rte 16
UAZ 39198	MEX	CHIHUAHUA	Vicinity of Ojos Azules, S. Sierra del Nido.

CAS 139670	MEX	CHIHUAHUA	Aldama
USNM 105290	MEX	CHIHUAHUA	17 mi W Carmen
UMMZ 117764	MEX	CHIHUAHUA	Tinaja valley, 1 mi S of Hwy
BYU 17104	MEX	CHIHUAHUA	3-5 mi S of North CAS as Grandes on Hwy
UTEP 4696	MEX	CHIHUAHUA	Rio Santa Maria, near Progreso
USNM 105296	MEX	COAHUILA	Coahuila, Piedras Negras
UAZ 37783	MEX	COAHUILA	7 mi N. Cuatro Cienegas on rd. to Ocampo.
UAZ 40396	MEX	COAHUILA	SAN PEDRO, 13 MI W OF
UAZ 42424	MEX	COAHUILA	SAN PEDRO, 13 MI W OF
CM 42771	MEX	COAHUILA	30.5 MI SSE MONCLOVA
STRECK 9732	MEX	COAHUILA	SAN PEDRO, 13 MI W OF
UMMZ 121818	MEX	COAHUILA	Cuatro Cienegas on Rd. to Ocampo, 18.3 mi NNW.
STRECK 10063	MEX	COAHUILA	Cuatro Cienegas on rd. to Ocampo, 5 mi N.
FMNH 47086	MEX	COAHUILA	SAN PEDRO, 13 MI W OF
USNM 105298	MEX	COAHUILA	Cuatro Cienegas on rd. to Ocampo, 15.3 mi N.
USNM 105299	MEX	COAHUILA	Coahuila, 3 mi NW Saltillo
FMNH 102684	MEX	COAHUILA	.7 mi W Sacramento
UAZ 36774	MEX	COAHUILA	San Pedro
ASC 9832	MEX	COAHUILA	Coahuila
USNM 105297	MEX	COAHUILA	Coahuila, 3 mi N Morelos
UAZ 40958	MEX	DURANGO	Vicinity of Durango.
UAZ 40957	MEX	DURANGO	Tlahualilo
UTEP 4052	MEX	DURANGO	Yerbaniz, 12 MI SE, HDA. De Atotonilco
USNM 060923	MEX	DURANGO	Gomez Palacio
USNM 060044	MEX	DURANGO	Durango
CHAS 145	MEX	MATAMOROS	Matamoros (Topotype of H. n. kennerlyi)
TCWC 17185	MEX	NUEVO LEON	Nuevo Leon, Hidalgo, 3.5 mi N, 4 mi E Salinas
UMMZ 77244	MEX	SAN LUIS POTOSI	35 km N San Luis Potosi
FMNH 102687	MEX	SAN LUIS POTOSI	San Louis Potosi, Between CharCAS and Venado
LSUMZ 2420	MEX	SAN LUIS POTOSI	2 km E Illesco
AMNH 67261	MEX	SONORA	North Sonora
AMNH 3665	MEX	SONORA	?
USNM 061954	MEX	SONORA	Sonora, vic. A&P Taleporos?
AMNH 67260	MEX	SONORA	Sonora, Covanea?

TCWC 7002	MEX	TAMAULIPAS	Tamaulipas, 6 mi W Padilla
USNM 001282a	MEX	TAMAULIPAS	*MATAMOROS (COTYPE)
TCWC 7001	MEX	TAMAULIPAS	Tamaulipas, 6 mi W Padilla
USNM 001282b	MEX	TAMAULIPAS	*MATAMOROS (COTYPE)
ASC 9831	MEX	VAL VERDE	26.4 MI. NNW COMSTOCK ON 1024
UTEP 4054	MEX	ZACATECAS	RIO GRANDE, 15 MI (BY MXHY 49) NW
UTEP 4053	MEX	ZACATECAS	VILLA DE COS, 30 MI (BY MXHY 54) NE
UNM 9317	NM	DON ANA CO.	8.4 mi W Hatch, rt 26
UTEP 15468	NM	DONA ANA CO.	7.1 rd mi N jct with I-10 on Corralitas Ranch Rd. (R2W,T22S,NE1/4 of Sec36)
UTEP 16127	NM	DONA ANA CO.	St Hwy 26, 6.2 rd mi SW jct w/St Hwy 185 in Hatch (T19S,R4W,NW1/4,Sec 27)
UTEP 16119	NM	DONA ANA CO.	8.4 rd mi N jct with I-10 on Corralitas Ranch Rd. (R1W,T22S,SW1/4 of Sec19)
UTEP 15810	NM	DONA ANA CO.	Las Cruces, Experimental Station
UTEP 15467	NM	DONA ANA CO.	Jornada Exper. Range
TNHC 16272	NM	EDDY CO.	STHY 81, 9.7 RD MI S JCT WITH IHY 10
UNM 50738	NM	EDDY CO.	El Paso Gap, Carlsbad rd., 20.3 mi off US 285.
UNM 54206	NM	EDDY CO.	Dark Canyon Rd., 0.4 mi W of jct w/US 180
UNM 55769	NM	EDDY CO.	Dark Canyon Rd., ~5 mi E jct US 285
UTEP 9991	NM	GRANT CO.	Hwy 464, 1 mi N of Hwy 70
USNM 001262	NM	GRANT CO.	Silver City Airport
AMNH 80075	NM	GRANT CO.	3 mi S Huxley
NMSU 3684	NM	GRANT CO.	Vaughn
UNM 48112	NM	GRANT CO.	Cobre mines, Fort Webster, Santa Rita Del Cobre – SYNTYPE
UNM 48113	NM	GRANT CO.	NM Hwy 9, 6 mi W Hachita
UNM 395	NM	GRANT CO.	6.4 km S Hurley on Us Hwy 180 (T14S, R12W, Sec14)
UNM 55981	NM	GRANT CO.	Hwy 9, 2.5 mi W Hachita
UTEP 2919	NM	GRANT CO.	Hachita
UTEP 2451	NM	GRANT CO.	Hurley
NMSU 3696	NM	GRANT CO.	Milepost 57.5, Hwy 81 (T25S,R14W,S31,SW1/4)
UNM 42755	NM	GRANT CO.	NM Hwy 146, 10 mi N Hachita
UMMZ 102431	NM	GRANT CO.	Near Faywood Warm Springs (T205, R10W, S20)
AMNH 81872	NM	GRANT CO.	5 mi S Hachita

NMSU 6067	NM	GRANT CO.	NM 146, 3rd mi N Hachita
UNM 52842	NM	GRANT CO.	HACHITA, 15.2 MI. N (ON STHY 81)
UNM 49740	NM	GRANT CO.	6 mi E Hachita
AMNH 75114	NM	GRANT CO.	HACHITA, 2.3 MI (ON STHY 9) W
UTEP 11365	NM	HIDALGO CO.	2.6 mi N Rodeo
CM 51456	NM	HIDALGO CO.	Guadalupe mtns. (T345, R21W, S1)
UTEP 11347	NM	HIDALGO CO.	Cloverdale
UNM 33798	NM	HIDALGO CO.	9 mi N Cotton City on St rd 338
UTEP 11254	NM	HIDALGO CO.	2 mi W Hachita; Two-mile windmill
UTEP 10608	NM	HIDALGO CO.	2 mi N Lordsburg
UNM 41929	NM	HIDALGO CO.	1 mi S Cottendale
UNM 23244	NM	HIDALGO CO.	NM Hwy 533, 0.1 mi W jct US Hwy 80
UNM 41917	NM	HIDALGO CO.	Hwy 80, 5 mi N jct NM Hwy 9
UNM 41916	NM	HIDALGO CO.	1.5 mi W Red Mill
UNM 33815	NM	HIDALGO CO.	Alamo Hueco Ranch
AMNH 112942	NM	HIDALGO CO.	US Hwy 80 at jct NM Hwy 9
AMNH 81870	NM	HIDALGO CO.	Gray Ranch S of Animas, Sacahuiste Well
UNM 48997	NM	HIDALGO CO.	1-3 mi N Animas
UNM 49710	NM	HIDALGO CO.	STHY 9, 4.9 RD MI E ANIMAS
AMNH 109432	NM	HIDALGO CO.	Peloncillo Mtns., Antelope Pass - along NM Hwy 9; 8-9 mi W Animas (jct NM Hwy 9 and NM Hwy 338
UTEP 11253	NM	HIDALGO CO.	Playas Valley, Just W of Hatchet Gap, on STHY 81, 0.5 RD MI S of mile post 29
TCWC 56326	NM	HIDALGO CO.	10 mi S Animas
UTEP 11252	NM	HIDALGO CO.	18 mi S Animas
UTEP 11086	NM	HIDALGO CO.	Antelope Pass (T27S,R21W,S31,SW1/4,SE1/4)
NMSU 3698	NM	HIDALGO CO.	9 mi N Animas
UNM 48996	NM	HIDALGO CO.	Animas Valley, STHY 9, 1.8 RD MI W Animas
UNM 52179	NM	HIDALGO CO.	Playas VAlley, Just W of Hatchet Gap, on STHY 81, 0.5 Rd MI S of mile post 29
AMNH 79925	NM	HIDALGO CO.	1 MI. W ANIMAS
AMNH 77038	NM	HIDALGO CO.	La Jornada Experimental Range
UNM 51465	NM	HIDALGO CO.	US 70, 2 mi NW of jct w/St. rd 90
UNM 49711	NM	HIDALGO CO.	2 mi N Apache

UNM 51458	NM	HIDALGO CO.	Animas Valley, STHY 338, 6.7 Rd MI N Animas, 4.5 RD MI S Cotton City
NMSU 6017	NM	HIDALGO CO.	Hachita Gap, SHTY 81, 1/2 MI W Mile post 31 (T30S, R16W)
ASC 11620	NM	HIDALGO CO.	Gray Ranch S of Animas, Sacahuiste Well
UNM 36935	NM	HIDALGO CO.	Near Rodeo
UNM 4742	NM	HIDALGO CO.	1.5 mi S Animas
NMSU 2745	NM	HIDALGO CO.	IHY10, 3.3 Rd MI E center of Lordsburg, 1.0 Rd MI E E-Side exit to Lordsburg
UNM 6423	NM	HIDALGO CO.	Lordsburg
NMSU 3697	NM	HIDALGO CO.	Hachita Valley AOR STHY 81, 3.3 Rd MI S Grant county line
AMNH 77179	NM	HIDALGO CO.	Gray Ranch S of Animas, Animas valley, Garcia Tank
TCWC 56328	NM	HIDALGO CO.	Rodeo
UTEP 2823	NM	HIDALGO CO.	2 mi W Hachita
AMNH 87289	NM	HIDALGO CO.	NM Hwy 338, 13 mi S Animas
UNM 51674	NM	HIDALGO CO.	Hwy 70, .7 mi S x 464
UTEP 11364	NM	HIDALGO CO.	19.7 mi N Animas
AMNH 117881	NM	HIDALGO CO.	Peloncillo Mtns., Antelope Pass - along NM Hwy 9; 8-9 mi W Animas (jct NM Hwy 9 and NM Hwy 338
UNM 389	NM	HIDALGO CO.	NM Hwy 9, 0.9 mi E US Hwy 80
UTEP 9408	NM	LUNA CO.	2.5 mi SW Nutt on NM Hwy 26
UNM 50081	NM	LUNA CO.	NM Hwy 11, 9 mi S of Deming
UNM 48010	NM	LUNA CO.	Milepost 148, Hwy 180 (T21S,R11W,S23,NW1/4)
UTEP 11311	NM	LUNA CO.	NM Hwy 26, 1.2 mi SW Nutt (jct. NM Hwy 27)
UTEP 10451	NM	LUNA CO.	on Rd to Rock Hound State Park (along W Side of Little Florida mts), 1.0 RD MI S
UTEP 13854	NM	LUNA CO.	STHY 549, 8.5 Rd MI E Deming, 2.4 Rd Mi W JCT With Lewis Flats Rd.
UMMZ 71348	NM	LUNA CO.	4 mi NW Florida (ATSF RR siding between Rincon and Deming)
UTEP 14145	NM	LUNA CO.	STHY 549, 14.2 Rd MI W Dona Ana County line, 12.6 RD MI E Deming
NMSU 6076	NM	LUNA CO.	11 mi N Wagon Mound
UTEP 10450	NM	LUNA CO.	STHY 549, 11.4 Rd MI E Deming (courthouse), 0.8 RD Mi W JCT with Lewis Flats Rd
UNM 388	NM	LUNA CO.	Milepost 25, Hwy 26, 2.3 mi S Nutt (T20S,R6W,S20,SE1/4)

UAZ 41153	NM	LUNA CO.	SE Deming (T24S,R8W, NW 1/4, Sec. 30)
NMSU 6075	NM	LUNA CO.	5 mi (air) SE Deming (T24S,R8N,W edge,Sec.30)
UTEP 11348	NM	LUNA CO.	STHY 26, 26 Rd MI NE Deming, 1.2 MI SW JCT WITH STHY 27
UNM 49548	NM	LUNA CO.	20 mi N Deming
NMSU 6234	NM	OTERO CO.	4.5 mi NE Tucumcair
NMSU 6323	NM	OTERO CO.	White Sands Nat'l Monument HQ, 0.6 MI. W OF
UTEP 13742	NM	SIERRA CO.	Bosque Del Apache NWR, NM 1 ca. 2 mi N refuge HQ
NMSU 2712	NM	DONA ANA CO.	11 mi N Antelope Wells
NMSU 2010	NM	HIDALGO CO.	Long Pine
USNM 007290	TX	?	?
USNM 001272	TX	?	Pecos River
UNM 33114	TX	BREWSTER CO.	Alpine, Sul Ross Exp. Farm
KU 176740	TX	BREWSTER CO.	Bryan
TNHC 29260	TX	BREWSTER CO.	4 mi E Bryan
KU 176741	TX	BREWSTER CO.	11 mi E of Alpine, on Hwy 90.
FMNH 26612	TX	BREWSTER CO.	3 mi N Alpine on St rd 118
FMNH 26613	TX	BREWSTER CO.	Alpine, Sul Ross Exp. Farm
KU 8405	TX	BROOKS CO.	Near Falfurias
TXAI 4111	TX	BROOKS CO.	17.9 mi N jct US 281 & TX 186 on US 281
USNM 032747	TX	CAMERON CO.	El Jaboncilla
TCWC 40056	TX	CULBERSON CO.	12.1 mi NE Van Buren
UAZ 35134	TX	CULBERSON CO.	Farm rd 652, 39 mi E Orla
UTEP 13808	TX	CULBERSON CO.	STHY 54, 7.2 rd mi N jct with USHY 80 in Van Horne
UNM 50224	TX	CULBERSON CO.	29.8 mi by IH-10 (US 80) E Van Horne
LSUMZ 44383	TX	DUVAL CO.	Hwy 16, 10 mi N junction of Hwy 229
CHAS 6529	TX	HIDALGO CO.	Faysville
AMNH 79101	TX	HIDALGO CO.	Edinburg
USNM 082278	TX	HIDALGO CO.	Near Hebbronville
STRECK 2043	TX	HIDALGO CO.	Vicinity of Delhart
UTEP 10494	TX	JEFF DAVIS CO.	38 mi S Kenton Road to Valentine
UMMZ 52800	TX	JEFF DAVIS CO.	Valentine, 15 mi E on Ft. Davis rd.
CAS 27241	TX	JEFF DAVIS CO.	15.6 mi S Tex 118 on Tex 66
TNHC 7331	TX	JEFF DAVIS CO.	USHY 90, 2.7 Rd MI SE Valentine
UTA 2018	TX	JEFF DAVIS CO.	11 mi E Edna on St Hwy 111

MWSU 2866	TX	JEFF DAVIS CO.	?
UTEP 10493	TX	JEFF DAVIS CO.	USHY 90, 13.6 Rd MI NW Valentine
LSUMZ 39561	TX	JIM HOGG CO.	3 mi SW Randado
TXAI 2449	TX	JIM HOGG CO.	5 mi S Randado
TXAI 1066	TX	JIM HOGG CO.	2 mi S Jct 3093/649 on 649
TCWC 48652	TX	JIM HOGG CO.	1 mi N Guerra
TXAI 2425	TX	JIM HOGG CO.	4 mi NW Mabank
ASC 10392	TX	PRESIDIO CO.	3 mi E of Elliot Springs
TNHC 1387	TX	PRESIDIO CO.	2 MI. W Presidio - HWY 120(170?)
TNHC 11622	TX	PRESIDIO CO.	Valentine, 11 mi W on Lazy Eleven Ranch.
BYU 44140	TX	PRESIDIO CO.	14 miles SE Amarrillo
LSUMZ 23176	TX	PRESIDIO CO.	11 mi. W Valentine on C.E. Miller Ranch.
CM 49018	TX	REEVES CO.	4 mi NW Pecos on US Hwy 285
TCWC 33653	TX	REEVES CO.	Pecos
CM 49017	TX	REEVES CO.	Toyahvale
TCWC 33655	TX	STARR CO.	Falcon Lake State Park
LSUMZ 28677	TX	STARR CO.	5 mi W San Isidra at La Gloria
TCWC 33654	TX	STARR CO.	3 mi E of Aspermont on US Hwy 380
TXAI 4364	TX	STARR CO.	La Gloria
TNHC 24716	TX	TERRELL CO.	Sanderson, 21.7 mi E of, on US Route 90
USNM 167728	TX	TERRELL CO.	SAN ANGELO CITY FARM
LSUMZ 24800	TX	VAL VERDE CO.	8 mi N Comstock on TX SH 163
LSUMZ 24799	TX	VAL VERDE CO.	2 mi N Bruni, FR2050
UNM 54849	TX	VAL VERDE CO.	25 mi N Del Rio
TXAI 3710	TX	WEBB CO.	Jct. of 44 & US 83
FMNH 38071	TX	WEBB CO.	JCT of USHY 83 and STHY 44, 2.7 RD MI SSE
UTEP 11561	TX	WEBB CO.	Holiday
TXAI 4525	TX	WEBB CO.	8.2 mi NW jct I-35 on FM 1472
LSUMZ 27720	TX	WEBB CO.	?
TXAI 4380	TX	ZAPATA CO.	Edinburg

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SPECIMEN	STATE	COUNTY	LOCATION
INHS 3185	IL	CARROLL CO.	Thomson
INHS 3231	IL	HENDERSON CO.	Oquawka
INHS 7353	IL	LEE CO.	Amboy
INHS 7355	IL	MASON CO.	2 mi E Havana
INHS 6153	IL	MASON CO.	Havana
INHS 8530	IL	MASON CO.	Havana
INHS 1646	IL	MASON CO.	Havana
INHS 9162	IL	MASON CO.	4 mi S Bath
INHS 1599	IL	MASON CO.	5 mi S Havana
INHS 1566	IL	MASON CO.	S end of L. Chantauquo ?
INHS 1600	IL	MASON CO.	Havana
INHS 3153	IL	MERCER CO.	Keithsburg
INHS 3154	IL	MERCER CO.	Keithsburg
INHS 7354	IL	MORGAN CO.	Menedosia
INHS 6024	IL	MORGAN CO.	Menedosia
CHAS 16563	IL	ROCK ISLAND CO.	2 mi E Cordova
INHS 1117	IL	ROCK ISLAND CO.	2 mi E Cordova
INHS 7262	IL	ROCK ISLAND CO.	Cordova
INHS 5661	IL	TAZEWELL CO.	Extreme SW Corner
INHS 5345	IL	WHITESIDE CO.	2 mi S Thompson
KU 159830	KS	CHAUTA UQUA CO.	Hoisington
CHAS 12174	KS	COWLEY CO.	9 mi E Coldwater
FMNH 25297	KS	COWLEY CO.	Winfield
INHS 12174	KS	COWLEY CO.	Winfield
CHAS 8141	MO	MISSISSIPPI CO.	2 mi W Craig
INHS 8141	MO	SCOTT CO.	2 mi N Diehlstadt
CHAS 8142	MO	SCOTT CO.	2 mi SE Diehlstadt
INHS 8142	MO	SCOTT CO.	1 (3) mi S Diehlstadt
KU 82091	MO	SCOTT CO.	?
UO 20160	OK	CLEVELAND CO.	5 mi N Little Axe

AMNH 60497	OK	CLEVELAND CO.	Norman
UO 25069	OK	CLEVELAND CO.	Norman
UO 27015	OK	CLEVELAND CO.	Wichita mt. Refuge
UO 20234	OK	CLEVELAND CO.	6 mi NW Norman
UO 29764	OK	CLEVELAND CO.	2 mi SW Norman
UO 26024	OK	CLEVELAND CO.	2 mi S of Norman
UO 26849	OK	CLEVELAND CO.	?
UO 28390	OK	CLEVELAND CO.	3 mi E Noble
UO 19690	OK	CLEVELAND CO.	3 mi W Norman
UO 26508	OK	CLEVELAND CO.	Norman
UO 26898	OK	COMANCHE CO.	Wichita mt. Refuge
UO 6514	OK	COMANCHE CO.	Camp Boulder
UO 26896	OK	COMANCHE CO.	Wichita mt. Refuge
UO 26897	OK	COMANCHE CO.	Wichita mt. Refuge
UO 13161	OK	COMANCHE CO.	Wichita Wildlife Refuge
UO 26895	OK	COMANCHE CO	?
MWSU 2874	OK	COTTON CO.	Weatherford
FMNH 15743	OK	CREEK CO.	Weatherford
UO 34934	OK	JEFFERSON CO.	?
UO 19018	OK	MCCLAIN CO.	?
UO 8771	OK	OKMULGEE CO.	Okmulgee
UO 12413	OK	OKMULGEE CO.	?
UO 22970	OK	OSAGE CO.	NW edge Tulsa
UO 26055	OK	OSAGE CO.	6.5 mi E Pawhuska
UO 26056	OK	OSAGE CO.	5 mi W Tulsa
UO 25326	OK	OSAGE CO.	6.5 mi E Pawhuska
CHAS 13302	OK	OSAGE CO.	6.6 mi E Pawhuska
UO 13665	OK	POTTAWATOMIE CO.	Shawnee
UO 13795	OK	POTTAWATOMIE CO.	Shawnee
CHAS 12175	OK	TULSA CO.	Tulsa (Red Fork)
LACM 66841	TX	?	Galveston
USNM 205192	TX	ANDERSON CO.	Beaver Creek Ranch Near Alba
TCWC 18274	TX	ANDERSON CO.	7 mi E Alpine
STRECK 12128	TX	ANDERSON CO.	1 mi E Alpine

UMMZ 126902	TX	ANDREWS CO.	Montalba, 6.5 km NW of, Camp Bette Perot
UTEP 15610	TX	ANDREWS CO.	1 mi E Bethel Community Center
UNM 12074	TX	ANDREWS CO.	12.4 mi SW Andrews
UNM 12073	TX	ANDREWS CO.	?
MWSU 2878	TX	ARCHER CO.	Target rd, 3.3 rd mi SSE jct with FMRD 181 on STHY 115, then 1.2 mi E on Target
MWSU 2875	TX	ARCHER CO.	?
LSUMZ 9275	TX	BLANCO CO.	Hwy 16, 1 mi S Poteet
ASC 3886	TX	BORDON CO.	8 mi SE Seymour
TCWC 20417	TX	BRAZOS CO.	GAIL - 3 MI. S ON ST. 669
TCWC 27375	TX	BRAZOS CO.	Edwards Plateau
KU 61017	TX	BRAZOS CO.	Near Finfeather Lake
TCWC 3237	TX	BRAZOS CO.	11 mi ENE College Station
TCWC 17509	TX	BRAZOS CO.	College Station
TCWC 3236	TX	BRAZOS CO.	College Station
UTA 22284	TX	CHEROKEE CO.	Mt. Selman, on US Hwy 69
MWSU 2869	TX	CLAY CO.	5 mi NE Dean
MWSU 2870	TX	CLAY CO.	?
MWSU 2868	TX	CLAY CO.	E Jentch Rd, 3 km E jct US Hwy 281, 1.9 km S Wichita Falls
UTA 22285	TX	CLAY CO.	?
ASC 12383	TX	COKE CO.	18 MI. NW of Robert Lee Courthouse on HWY 208
ASC 12387	TX	COKE CO.	16 MI. NE of Robert Lee Courthouse on HWY 277.
KU 82092	TX	COKE CO.	18 MI. NW of Robert Lee Courthouse on HWY 208.
ASC 12381	TX	COKE CO.	2 mi W Robert Lee
ASC 12385	TX	COKE CO.	12 MI. N of Robert Lee Courthouse on HWY158 - 1 MI. N ON 2059
ASC 12382	TX	COKE CO.	11 MI. NW of Robert Lee Courthouse on HWY 208
ASC 12386	TX	COKE CO.	19 MI. NW of Robert Lee Courthouse on HWY208
ASC 12504	TX	COKE CO.	12 MI. NE of Robert Lee courthouse on Old Sanco Rd.
ASC 12384	TX	COKE CO.	10 MI. N of Robert Lee courthouse on Old Sanco Rd.
ASC 12485	TX	COKE CO.	1/2 MI. N of Robert Lee Courthouse on Old Sanco Rd.
TCWC 332	TX	COLORADO CO.	Altair
TCWC 335	TX	COLORADO CO.	6 mi N Eagle Lake
TCWC 334	TX	COLORADO CO.	6 mi N Eagle Lake

TCWC 184	TX	COLORADO CO.	7 mi N Eagle Lake
STRECK 4441	TX	COLORADO CO.	6 mi NE Eagle Lake
ASC 5611	TX	CONCHO CO.	5.0 mi W Millersview on FM 765
TCWC 69961	TX	CONCHO CO.	5 MI. W Doole - FM 765
TCWC 68741	TX	CONCHO CO.	0.3 mi E jct Hwy 765 and 83 on FM 765
TCWC 68743	TX	CONCHO CO.	?
TCWC 71170	TX	CONCHO CO.	2.1 mi N, 1.4 mi E Millersview on Co Rd.
TXAI 4127	TX	DUVALL CO.	5 mi W Benavidez
BYU 41651	TX	ECTOR CO.	E Odessa
LACM 66842	TX	ECTOR CO.	?
KU 82094	TX	EDWARDS CO.	12 mi NE Carta Valley
STRECK 5356	TX	FALLS CO.	2 mi S Stranger mt.
TNHC 29257	TX	GALVESTON CO.	Davis mtns.; Fort Davis
UTA 2291	TX	GALVESTON CO.	Galveston Island.
TNHC 29254	TX	HARRIS CO.	Hockley, 3 mi N.
LACM 66843	TX	HARRIS CO.	?
TNHC 29251	TX	HARRIS CO.	Just S of Prairie Dog Town Fork of Red River on FM 657
TCWC 185	TX	HARRIS CO.	Barker Park, near jct Tx Hwy 6 and FM 1093
TNHC 17059	TX	HOWARD CO.	Coahoma, School Campus
TNHC 21898	TX	HOWARD CO.	Sundown - 4 MI. NE
TCWC 20243	TX	HOWARD CO.	Big Spring, 5 mi NE.
UTEP 11005	TX	HUDSPETH CO.	US Hwy 62-180, 11.9 rd mi W jct w/Ranch rd 2775
UTEP 10489	TX	HUDSPETH CO.	USHY 62/180, 22 Rd Mi E Hueco Inn, 7.3 RD MI W Jct with HWY 2317
TNHC 29253	TX	HUDSPETH CO.	10 mi NE Big Springs
UTEP 6237	TX	HUDSPETH CO.	E Side of Hueco Mtns., on Hueco Inn Rd (=Pinon Rd) 5.4 MI N Jct w/USHY 62/180
UTEP 16126	TX	HUDSPETH CO.	Cypress, 3 mi N.
UTEP 11483	TX	HUDSPETH CO.	USHY 62/180, 9 MI E Hueco
USNM 279156	TX	IRION CO.	Stinnett, 9 mi E on Bugbee Ranch.
TCWC 55449	TX	KAUFMAN CO.	3 mi (by school rd) N crossing of Balcones Creek (Creek = Bexar-Kendall Co. Line)
TNHC 29256	TX	LEON CO.	2 mi. E Staton
CAS 9919	TX	MARTIN CO.	Eagle Pass

USNM 001249	TX	MAVERICK CO.	Waco
STRECK 10034	TX	MCLENNAN CO.	17th and Eastover, Colorado City, TX.
STRECK 6551	TX	MCLENNAN CO.	Waco
ASC 5238	TX	MITCHELL CO.	Stephen F. Austin Experimental Forest
CAS 102328	TX	NACAGDOCHES	Fort Stockton
USNM 005185	TX	PECOS	*AMARILLO (NEOTYPE)
KU 82093	TX	REAGAN CO.	2 mi E Big Lake
ASC 4939	TX	REAGAN CO.	?
USNM 001247	TX	REEVES CO.	13 mi NW Pecos, W of Pecos River, on US Hwy 285
STRECK 1581	TX	REEVES CO.	Pecos
USNM 005083a	TX	ROBERTSON CO.	Co. Rd, 10 mi SE Ballinger
STRECK 7444	TX	ROBERTSON CO.	*WHEELOCK (PARATYPE)
USNM 005083d	TX	ROBERTSON CO.	*WHEELOCK (TYPE)
USNM 005083c	TX	ROBERTSON CO.	*WHEELOCK (PARATYPE)
TCWC 69968	TX	RUNNELS CO.	Henderson, Route 4, Box 4071
TCWC 68732	TX	RUNNELS CO.	5 mi (airline) N jct FM 2133/Hwy 67
UTA 15842	TX	RUSK CO.	3.6 mi SE Post
UTA 2092	TX	SCURRY CO.	13 km NW Tyler on St Hwy 110
UTA 22286	TX	SMITH CO.	White House
UTA 15833	TX	SMITH CO.	W of Tyler, Spur 364 and Greenbriar Rd (FM 164)
NMSU 1953	TX	SMITH CO.	SW of Tyler, Noonday
UTA 15832	TX	SMITH CO.	5 mi W San Isidra at La Gloria
UTA 15835	TX	SMITH CO.	Lindale, Route 5, Box 225B
UTA 15834	TX	SMITH CO.	2.4 km N Tyler, ca 1 km W US Hwy 271, Hardy Rd at Pine Springs Drive
UTA 22287	TX	SMITH CO.	W shore Lake Tyler; Camp Tyler
UTA 22288	TX	SMITH CO.	11 km W Tyler off New Harmony Rd
KU 82095	TX	TOM GREEN CO.	City Farm
ASC 5068	TX	TOM GREEN CO.	San Angelo - Adjacent to Country Club
STRECK 5912	TX	TOM GREEN CO.	Christoval
STRECK 3943	TX	TOM GREEN CO.	25 mi N Del Rio
ASC 341	TX	TOM GREEN CO.	San Angelo Res. area
ASC 647	TX	TOM GREEN CO.	2 mi W San Angelo; N Concho Lake
ASC 5052	TX	TOM GREEN CO.	NORTH CONCHO LAKE

ASC 5015	TX	TOM GREEN CO.	San Angelo - 8 MI. NW, FM RD. 2288 - 1 MI. OFF US. 87.
ASC 5317	TX	TOM GREEN CO.	Vicinity of 3 Rivers Res.; Approx. 10 MI. SW San Angelo
ASC 5271	TX	TOM GREEN CO.	5 N San Angelo, N Concho
ASC 340	TX	TOM GREEN CO.	HWY87, N. Concho Lake, North Shore
ASC 12520	TX	TOM GREEN CO.	Water valley, Schovajsa Farm on North Concho River
ASC 1367	TX	TOM GREEN CO.	W of San Angelo ResevoirTX

Heterodon nasicus nasicus

SPECIMEN	STATE	COUNTY	LOCATION
UCM 52183	CO	?	?
USNM 008756	CO	?	Eastern Colorado
UMMZ 116958	CO	ARAPAHOE CO.	3.7 mi W Byers
UTA 2014	CO	ARAPAHOE CO.	Cherry Creek Reservoir
UCM 19713	CO	ARAPAHOE CO.	Denver
CAS 4024	CO	BACA CO.	15 mi S & 8 mi W Pritchett
UCM 31198	CO	BACA CO.	Ca. Springfield
USNM 009524	CO	BENT CO.	Fort Lyon
UCM 17827	CO	CHEYENNE CO.	11 mi SW Kit Carson
CM 39294	CO	CHEYENNE CO.	Firstview, 15 mi S
UCM 1218	CO	CHEYENNE CO.	10 mi S Firstview
AMNH 108157	CO	CHEYENNE CO.	22.4 mi. W Cheyenne Wells
UCM 17790	CO	CHEYENNE CO.	10 mi S Kit Carson
UCM 19714	CO	CROWLEY CO.	17 mi N Ordway
UCM 6719	CO	DENVER CO.	Denver
CAS 101897	CO	EL PASO CO.	13 mi E Fountain
CAS 102249	CO	EL PASO CO.	13 mi E Fountain
UNM 4804	CO	EL PASO CO.	Colorado Springs
CAS 102084	CO	EL PASO CO.	13 mi E Fountain
CAS 101918	CO	EL PASO CO.	13 mi E Fountain

CAS 102132	CO	EL PASO CO.	13 mi E Fountain
CAS 102157	CO	EL PASO CO.	13 mi E Fountain
CAS 101872	CO	EL PASO CO.	13 mi E Fountain
CAS 102104	CO	EL PASO CO.	13 mi E Fountain
CAS 102278	CO	EL PASO CO.	13 mi E Fountain
UCM 48458	CO	ELBERT CO.	6.5 mi S Agate
UCM 56093	CO	ELBERT CO.	Rattlesnake Creek, 4.25 mi W Agate
UCM 19715	CO	HUERFANO CO.	Lathrop State Park
UCM 47788	CO	HUERFANO CO.	4 mi S Walsenburg on Hwy 85-87
UMMZ 68585	CO	KIOWA CO.	Near Haswell
AMNH 108158	CO	KIOWA CO.	1.5 mi N Eads?
UCM 9735	CO	KIOWA CO.	1 mi E Eads
KU 6645	CO	KIT CARSON CO.	Near Stratton
UCM 1371	CO	KIT CARSON CO.	8 mi S Statton, Landsman creek
UCM 25577	CO	LARIMER CO.	2.5 mi N of Masonville
UCM 13889	CO	LAS ANIMAS CO.	23 mi E Trinidad
UCM 25641	CO	LINCOLN CO.	16.8 mi N of Arriba
UMMZ 73385	CO	LOGAN CO.	25 mi W Sterling
UCM 4063	CO	LOGAN CO.	5 mi S Sterling
UCM 56101	CO	MOFFAT CO.	at US 40, 10 mi W of Maybell
UCM 11792	CO	MORGAN CO.	Muir Spring
UCM 20511	CO	MORGAN CO.	1 mi S and .5 mi E Fort Morgan
UCM 17876	CO	OTERO CO.	La Junta
UCM 247	CO	OTERO CO.	15 mi S La Junta
UCM 6745	CO	PHILLIPS CO.	11 mi S Holyoke
UMMZ 62438	CO	PROWERS CO.	Lamar
UCM 1219	CO	PROWERS CO.	Lamar
CAS 9778	CO	PROWERS CO.	3 mi S Holly
UMMZ 62437	CO	PROWERS CO.	20 mi S Holly
CAS 13329	CO	PUEBLO CO.	33 mi SW Fowler
KU 19604	CO	SEDGEWICK CO.	Near Julesburg
LACM 103441	CO	WASHINGTON CO.	15 mi E Anton
UMMZ 62664	CO	WASHINGTON CO.	?
UMMZ 62663	CO	WASHINGTON CO.	Akron

KU 82085	CO	WELD CO.	12 mi SE Greeley
KU 82086	CO	WELD CO.	Greeley
USNM 028459	CO	WELD CO.	7 mi N Hudson
FMNH 46154	CO	YUMA CO.	23 mi NW St. Francis, KS
KU 20801	CO	YUMA CO.	?
AMNH 14575	CO	YUMA CO.	?
FMNH 46155	CO	YUMA CO.	Laird
CAS 9779	CO	YUMA CO.	Wray
UMMZ 35129	IA	CLAY CO.	?
UMMZ 35127	IA	CLAY CO.	?
UMMZ 35128	IA	CLAY CO.	?
UMMZ 35125	IA	CLAY CO.	?
UMMZ 35126	IA	CLAY CO.	?
UMMZ 55162	IA	DICKINSON CO.	Little Sioux River near Milford
KU 52223	KS	BARBER CO.	1 mi W Sharon Springs
KU 45394	KS	BARBER CO.	4 mi N Retma
FMNH 95170	KS	BARBER CO.	Abilene
CM 5432	KS	BARTON CO.	?
USNM 099825	KS	BARTON CO.	?
KU 55337	KS	BARTON CO.	3 mi N & 1 mi E Sharon
KU 174615	KS	CHEYENNE CO.	9.3 km S & 9.6 km W St. Francis
BYU 20738	KS	CHEYENNE CO.	8.3 km S St. Francis
KU 174614	KS	CHEYENNE CO.	5.5 mi S & .75 mi E Hale
KU 174618	KS	CHEYENNE CO.	15.4 km N St. Francis
KU 174617	KS	CHEYENNE CO.	9.6 km N Wheeler
KU 174616	KS	CHEYENNE CO.	7 mi W of Cheyenne Wells
KU 20314	KS	CLARK CO.	19.3 km W & 1.6 km N St. Francis
KU 20313	KS	COMANCHE CO.	Stephenson Ranch
INHS 5296	KS	DICKENSON CO.	Kas-Okla border S of Winfield
FMNH 18140	KS	DICKINSON CO.	?
CHAS 5296	KS	DICKINSON CO.	Abilene
FMNH 18141	KS	DICKINSON CO.	?
UTEP 5556	KS	EDWARDS CO.	KINSLEY, 3 MI S
UTEP 5557	KS	EDWARDS CO.	KINSLEY, 9 MI S

FHSU 1406	KS	ELLIS CO.	1.5 mi SW Hays
KU 176742	KS	ELLIS CO.	S of Hays
FHSU 2647	KS	ELLIS CO.	?
FHSU 3708	KS	ELLIS CO.	1.5 mi W Hays
FHSU 2767	KS	ELLIS CO.	12 mi N Hays
FHSU 483	KS	ELLIS CO.	Hays
FHSU 485	KS	ELLIS CO.	6 mi N Ellis
FHSU 6174	KS	ELLIS CO.	?
FHSU 482	KS	ELLIS CO.	1.5 mi SE Hays
FHSU 2766	KS	ELLIS CO.	1.5 mi SW Hays
FHSU 481	KS	ELLIS CO.	?
CAS 9981	KS	FINNEY CO.	Near Garden City, 1 mi S, 3 mi E
CAS 9980	KS	FINNEY CO.	Near Garden City, 2 mi E, 11 mi N
USNM 086913	KS	FINNEY CO.	Garden City, 6 mi N of
CAS 9920	KS	FORD CO.	4 mi SE Dodge City
CAS 9925	KS	FORD CO.	3 mi SE Dodge City
CAS 9971	KS	FORD CO.	8 mi NW Dodge City
CAS 9924	KS	FORD CO.	9 mi SE Dodge City
CAS 9921	KS	FORD CO.	12 mi NE Dodge City
CAS 9970	KS	FORD CO.	3 mi SE Dodge City
KU 55341	KS	FORD CO.	?
CAS 9923	KS	FORD CO.	5.5 mi SE Dodge City
CAS 9922	KS	FORD CO.	1.5 mi SE Dodge City
KU 55340	KS	FORD CO.	?
USNM 004761	KS	GEARY CO.	Fort Riley
USNM 007813	KS	GEARY CO.	Fort Riley
KU 55343	KS	GOVE CO.	?
KU 1713	KS	GRAHAM CO.	?
KU 021862	KS	GRANT CO.	?
CAS 9972	KS	GRAY CO.	3 mi SE Cimarron
CAS 9973	KS	GRAY CO.	3 mi SE Cimarron
FHSU 5245	KS	GREELEY CO.	8.2 mi N & 4 mi E Tribune
FHSU 1468	KS	HAMILTON CO.	?
USNM 056129	KS	HAMILTON CO.	4.8 mi N & 2.1 mi E Coolidge

CHAS 10060	KS	HAMILTON CO.	6 mi W Syracuse
FHSU 5244	KS	HAMILTON CO.	Hamilton Co. State Lake
FMNH 95169	KS	HARPER CO.	3.5 mi SE Danville
KU 020787	KS	HASKELL CO.	SW of Santana, Cimarron River
KU 20787	KS	HASKELL CO.	?
CAS 9975	KS	HODGEMAN CO.	8 mi S Jetmore
CAS 9974	KS	HODGEMAN CO.	8 mi S Jetmore
FHSU 1621	KS	JEWELL CO.	?
KU 21421	KS	KIOWA CO.	Rizeau Ranch
AMNH 68909	KS	LOGAN CO.	Vincent Ranch
CAS 9775	KS	LOGAN CO.	McAllister
CAS 9774	KS	LOGAN CO.	McAllister on Hwy 40
KU 20304	KS	LOGAN CO.	6 mi S Oakley
UMMZ 91519	KS	MEADE CO.	8 mi S & 6.5 mi W Meade
UMMZ 91520	KS	MEADE CO.	Meade Co. State Lake
KU 23301	KS	MEADE CO.	17 mi SW Meade
USNM 310957	KS	MEADE CO.	13 mi SW Meade
CM 119849	KS	MEADE CO.	Stump Arroyo
UMMZ 91517	KS	MEADE CO.	.5 mi W State Park
CAS 9139	KS	MEADE CO.	14 mi SW Meade
UMMZ 122281	KS	MEADE CO.	14 mi SW Meade
UMMZ 107955	KS	MEADE CO.	Meade
UMMZ 90182	KS	MEADE CO.	8 mi W Meade
AMNH 62849	KS	MEADE CO.	14 mi SW Meade
UMMZ 96063	KS	MEADE CO.	Meade
UTEP 5558	KS	MORTON CO.	ELKHART. 8.2 MI N
FHSU 5235	KS	MORTON CO.	10.1 mi N & 3 mi W Elkhart
FHSU 5233	KS	MORTON CO.	5.6 mi N Elkhart
FHSU 5239	KS	MORTON CO.	5.6 mi N Elkhart
CAS 10008	KS	NORTON CO.	Near Big Creek
FHSU 484	KS	OSBORNE CO.	2.5 mi N Alton
KU 174663	KS	OTTAWA CO.	12 km E & 2 km N Wells
TCWC 25315	KS	PHILLIPS CO.	4 mi W of Kirwin
CAS 9976	KS	PHILLIPS CO.	?

FHSU 6195	KS	PHILLIPS CO.	22 mi E Norton
TCWC 25316	KS	PHILLIPS CO.	Kirwin National Wildlife Refuge, 2 mi W of Kirwin
USNM 044367	KS	PRATT CO.	?
KU 55342	KS	PRATT CO.	Cairo
USNM 089144	KS	PRATT CO.	Pratt
KU 1711	KS	RAWLINGS CO.	27 mi W Atwood
KU 1714	KS	RAWLINGS CO.	McDonald
KU 1715	KS	RAWLINGS CO.	McDonald
AMNH 36741	KS	RILEY CO.	Manhattan
USNM 307543	KS	ROOKS CO.	Stockton
FHSU 3692	KS	RUSSELL CO.	5 mi N, 1 mi W Gorham
KU 1712	KS	RUSSELL CO.	?
KU 1710	KS	RUSSELL CO.	?
UTEP 5555	KS	SALINE CO.	Bavaria
FMNH 28458	KS	SALINE CO.	NEW CAMBRIA, 4 MI N
UTEP 5554	KS	SEDGWICK CO.	VIOLA, 4 MI N
KU 179174	KS	SEWARD CO.	7.7 km E Liberal
KU 106341	KS	SHERIDAN CO.	?
USNM 056130	KS	SHERIDAN CO.	15 mi E & 15 mi S Hoxie
CAS 9773	KS	SHERMAN CO.	1 mi E, 3 mi S Kanorado
FMNH 38120	KS	SHERMAN CO.	Goodland
KU 41836	KS	SHERMAN CO.	5 mi W Ruleton
KU 1706	KS	STAFFORD CO.	16 mi N, 4 mi E Stafford
KU 55339	KS	STAFFORD CO.	?
KU 3570	KS	STAFFORD CO.	Little Salt Marsh
KU 1707	KS	STAFFORD CO.	Little Salt Marsh
KU 41835	KS	STAFFORD CO.	?
KU 003570	KS	STAFFORD CO.	Little Salt Marsh
KU 55338	KS	STAFFORD CO.	?
INHS 10060	KS	SYRACUSE	Syracuse
CAS 9982	KS	THOMAS CO.	8 mi N Oakley
KU 3569	KS	TREGO CO.	7 mi W Wakeeney
KU 2715	KS	TREGO CO.	?
FHSU 2825	KS	TREGO CO.	12 mi S Collyer

KU 3643	KS	TREGO CO.	12 mi S Collyer
FHSU 1522	KS	TREGO CO.	12 mi S Collyer
CAS 10009	KS	TREGO CO.	12 mi S Ogallah
KU 82087	KS	TREGO CO.	Cedar Bluff Dam
KU 3655	KS	TREGO CO.	Cedar Bluff Reservoir
KU 003569	KS	TREGO CO.	?
CAS 9772	KS	WALLACE CO.	Sharon Springs
CAS 9771	KS	WALLACE CO.	Sharon Springs
UMMZ 67391	KS	WASHINGTON CO.	?
FHSU 3571	KS	ELLIS CO.	.5 mi S & 2 mi W Hays
CM 71963	MN	WABASHA CO.	Weaver Bottoms
CM 71962	MN	WABASHA CO.	1.8 mi N of Weaver, Rd. 84
CM 61646	MN	WABASHA CO.	Weaver Bottoms
CM 73901	MN	WABASHA CO.	1.8 mi N of Weaver, Hwy 84, Larry Guzas Farm
CM 61645	MN	WABASHA CO.	1.8 mi N of Weaver, Rd. 84
CM 61647	MN	WABASHA CO.	1.8 mi N of Weaver, Rd. 84
CAS 12918	MO	HOLT CO.	Dielstadt
KU 82088	MO	HOLT CO.	2 mi W Craig
CHAS 12918	MO	HOLT CO.	2 mi W Craig ????????
USNM 260839	MT	?	Yellowstone River, Above Powder River
USNM 009323	MT	?	Milk River
MTSU 1624	MT	?	?
UMMZ 49816	MT	?	?
USNM 009127	MT	?	Big Muddy River
USNM 001265	MT	?	Yellowstone, 80 mi up
USNM 001278	MT	?	Yellowstone Rier, Above Powder River
USNM 260841	MT	BIG HORN CO.	Crow Agency
AMNH 23086	MT	BIG HORN CO.	Fort Custer
USNM 260842	MT	BIG HORN CO.	Sarpy Creek
USNM 059768	MT	BIG HORN CO.	Fort Custer
USNM 014531	MT	BIG HORN CO.	Harding
USNM 260840	MT	BIG HORN CO.	5 mi NW Hardin
UMMZ 57043	MT	BIG HORN CO.	Fort Custer
USNM 260843	MT	BIG HORN CO.	Fort Custer

MTSU 6020	MT	BIG HORN CO.	Fort Custer
KU 130278	MT	CARTER CO.	6 mi S & 4.5 mi W Camp Crook
UMMZ 49817	MT	GARFIELD CO.	Jordan
MTSU 1634	MT	HILL CO.	Hingham
MTSU 1607	MT	MCCONE CO.	NE of Circle
MTSU 1632	MT	MCCONE CO.	Circle
MTSU 1599	MT	MUSSELSHELL CO.	Musselshell
MTSU 6000	MT	PHILLIPS CO.	?
USNM 054434	MT	POWDER RIVER CO.	Powderville
MTSU 1628	MT	SHERIDAN CO.	Big Muddy Creek
MTSU 3343	MT	SHERIDAN CO.	Medicine Lake
USNM 044346	MT	YELLOWSTONE CO.	Billings
USNM 053085	ND	?	Davison, Sand Hills 6 mi S of
KU 94321	ND	BILLINGS CO.	1 mi S & 1 mi W Medora
KU 94324	ND	BILLINGS CO.	1 mi S & 1 mi W Medora
UNM 7410	ND	BISMARCK	2mi W & 1 mi N Bismarck
UMMZ 74346	ND	CRANSVILLE	N Cransville
MTSU 6311	ND	GOLDEN VALLEY CO.	?
FMNH 15993	ND	MANDAN	Mandan
FMNH 15994	ND	MANDAN	Mandan
UMMZ 56911	ND	MEDORA	Medora
UMMZ 54463	ND	MEDORA	11 mi S Medora
UMMZ 56910	ND	MEDORA	Medora
UMMZ 74343	ND	MINOT	Minot
USNM 049602	ND	RICHLAND CO.	Hankinson
KU 18060	ND	SARGENT CO.	Near Havanna
UMMZ 74345	ND	TURTLE MTS.	Turtle mts., L. Metigoshe
USNM 260837	NE	?	Pole Creek
USNM 001222	NE	?	Platte River
USNM 001229	NE	?	?
USNM 001217	NE	?	?
USNM 001270	NE	?	North Kearney, W of
USNM 004795	NE	?	Platte River
USNM 001237	NE	?	Platte River

USNM 001275	NE	?	Platte River
USNM 001276	NE	?	Platte River
USNM 004625	NE	?	?
USNM 012750	NE	?	Platte River
USNM 260836	NE	?	Pole Creek, 310 R.
USNM 260835	NE	?	Platte River
USNM 004619	NE	?	Platte, Forks of
USNM 001234	NE	?	South Platte
USNM 001216	NE	?	?
FMNH 33799	NE	AGATE	Agate ???
FMNH 35010	NE	AGATE	Agate ???
FMNH 33741	NE	AINSWORTH	13 mi W Ainsworth
USNM 197617	NE	ANTELOPE CO.	Creighton, 3 mi S + 2.5 mi E of
KU 1718	NE	BANNER CO.	Harrisburg
CM 19887	NE	BOYD CO.	N of Bristow, Fort Randall Church
TCWC 63514	NE	BROWN CO.	Long Pine
USNM 021268	NE	BROWN CO.	Long Pine
USNM 021266	NE	BROWN CO.	Valentine National Wildlife Refuge, Mink Lake Valley
USNM 021267	NE	BROWN CO.	Niobraru Valley Preserve Headquarters
KU 45188	NE	CHERRY CO.	Welker Lake
KU 45189	NE	CHERRY CO.	1 mi S Crookston
FMNH 35815	NE	CHERRY CO.	11 mi E Kennedy
USNM 307544	NE	CHERRY CO.	11 mi E Kennedy
USNM 307545	NE	CHERRY CO.	4 mi NW Gavin
UMMZ 78119	NE	CUSTER CO.	14 mi N Oberlin
CAS 9983	NE	DECATUR CO.	Chappell
INHS 7308	NE	DEWEL CO.	5 mi W Parks on US 34
CAS 9777	NE	DEWEL CO.	3 mi E Chappell
CAS 9776	NE	DEWEL CO.	Chappell
FMNH 38119	NE	DUNDY CO.	Oshkosh
INHS 8443	NE	DUNDY CO.	Parks
CM 58620	NE	GARDEN CO.	Hackberry Lake
UMMZ 74724	NE	HACKBERRY LAKE	10 mi E O'Neil
UMMZ 67408	NE	HOLT CO.	?

FMNH 46153	NE	HOLT CO.	1 mi S Newark
UMMZ 67392	NE	HOLT CO.	10 mi E O'Neil
LACM 103442	NE	KEANNEY CO.	2 mi E Ogallala
KU 14167	NE	KEITH CO.	12 mi N Springview
KU 49452	NE	KEYA PAHA CO.	15 mi N North Platte
CAS 9999	NE	LINCOLN CO.	5 mi N North Platte
CAS 9998	NE	LINCOLN CO.	ROSE, 14 MI (BY USHY 183) S
CAS 10000	NE	LINCOLN CO.	15 mi N North Platte
FHSU 717	NE	LOUP CO.	20 mi N North Platte
UTEP 9409	NE	LOUP CO.	11 mi NW Burwell
CAS 10001	NE	MCPHERSON CO.	N side Platte River
LACM 103443	NE	MCPHERSON CO.	18 mi W of Tryon
KU 52224	NE	MERRICK CO.	3 mi S Ord
AMNH 36735	NE	ORD	4 mi N Antioch
UMMZ 79697	NE	SHERIDAN CO.	Sand Hills
UMMZ 79696	NE	SHERIDAN CO.	4 mi N Antioch
USNM 001225	NE	SHERMAN CO.	4 mi W Halsey
USNM 015340	NE	SHERMAN CO.	Sand Hills
USNM 260834	NE	SHERMAN CO.	Sand Hills
FHSU 1600	NE	THOMAS CO.	?
KU 45187	NE	THOMAS CO.	10 mi S, 16 mi E Thedford
UNM 11340	NM	BERNADILLO CO.	Montessa Park; S of Albuquerque
UNM 424	NM	BERNADILLO CO.	Albuquerque W of Rio Grande
UNM 32876	NM	BERNADILLO CO.	Near Alameda W of Rio Grande
UNM 32078	NM	BERNADILLO CO.	Albuquerque, Sunset Memorial Golf Course, 1/4 mi W of 16th tee
UNM 15900	NM	BERNADILLO CO.	Bel Aire, Albuquerque just NE of Fairgrounds
UNM 7611	NM	BERNADILLO CO.	2 mi W Rio Grande
UNM 390	NM	BERNADILLO CO.	6.5 mi N Las Lunas on State 45
UNM 8382	NM	BERNADILLO CO.	Albuquerque, Sunset Memorial Golf Course, 1/4 mi W of 16th tee
UNM 25664	NM	BERNADILLO CO.	8-9 mi NE UNM , Albuquerque
UNM 18028	NM	BERNADILLO CO.	Hwy 448 between us 66 & Alameda cutoff.
UNM 4190	NM	BERNADILLO CO.	Near Hermosa; Albuquerque
UNM 32878	NM	BERNADILLO CO.	5 mi N & 2 mi W Albuquerque
UNM 393	NM	BERNADILLO CO.	N of Santa Fe; St. Rd. 45 @ I-25

UNM 4740	NM	BERNADILLO CO.	4 mi.S Albuquerque
UNM 394	NM	BERNADILLO CO.	Candelaria Rd. NE Albuquerque
UNM 7610	NM	BERNADILLO CO.	6 mi SE Railroad tracks, Albuquerque US 54
UNM 392	NM	BERNADILLO CO.	5 mi N Gould ??????
UNM 8440	NM	BERNADILLO CO.	Sandia Base, Albuquerque
UNM 8409	NM	BERNADILLO CO.	Albuquerque
UNM 13430	NM	BERNADILLO CO.	9.3 rd mi SW Kenna
UNM 396	NM	BERNADILLO CO.	Albuquerque, West mesa housing edition, Paradise hills
UTEP 11917	NM	CHAVES CO.	38 mi. E Roswell
UNM 13922	NM	CHAVES CO.	6.2 mi N Roswell on US 285
UNM 15020	NM	CHAVES CO.	.25 mi. N Dexter, Pecos river bridge
AMNH 111173	NM	CHAVES CO.	6.3 mi W Caprock (Lea Co.)
UNM 26571	NM	CHAVEZ CO.	Between Correo & Laguna on Hwy 66
UNM 391	NM	CIBOLA CO.	So. edge of Springer
CM 11576	NM	COLFAX CO.	.25 mi W Colfax on rd to Dawson
UNM 30915	NM	COLFAX CO.	US 60/84 at 2.6 mi W of center of St. Vrain
UNM 19741	NM	COLFAX CO.	40 mi E of Taos, Sangre De Cristo Mtns, Cimarron Canyon.
UNM 36860	NM	CURRY CO.	56.4 mi N Roswell on Hwy 285
UNM 36887	NM	CURRY CO.	14.0 km W & 1.5 km S of center of Clovis
UNM 35797	NM	DE BACA CO.	Deming
UTEP 6333	NM	DON AÑA CO.	WAR RD, 0.5 ME E DONA ANA CAMP
USNM 022137	NM	DONA ANA CO.	1 mi S of Chaves Co. line on SH 2
NMSU 3128	NM	DONA ANA CO.	Las Cruces
FMNH 102685	NM	DONA ANA CO.	Corralitos ranch rd, 7.0 mi NW jct with IH-10 (T22S,R1W,NW1/4,Sec.31)
NMSU 2229	NM	DONA ANA CO.	Corralitos ranch rd, 7.4 mi NW jct with IH-10 (T22S,R1W,NW1/4,Sec.36)
USNM 100893	NM	DONA ANA CO.	Jornada Experimental Range
STRECK 8237	NM	GUADALUPE CO.	9 mi E & 7 mi S Santa Rosa
UNM 30877	NM	GUADALUPE CO.	11.5 mi N Lincoln County Line on US 285
CM 69085	NM	GUADALUPE CO.	Hwy 156, 17 mi. E Santa Rosa
STRECK 8239	NM	GUADALUPE CO.	16 mi SE Vaughn
UNM 15491	NM	GUADALUPE CO.	15 mi S Vaughn on US 285
CM 69086	NM	GUADALUPE CO.	15 mi NE Vaughn

UNM 4741	NM	GUADALUPE CO.	9.5 mi N & 2 mi W Roy
UNM 19370	NM	GUADALUPE CO.	4 mi SE Vaughn on US 285
UNM 19371	NM	GUADALUPE CO.	Vaughn
UAZ 24943	NM	GUADALUPE CO.	9.1 mi (by US 54) SW Santa Rosa
STRECK 8238	NM	GUADALUPE CO.	Vaughn
UNM 7133	NM	HARDING CO.	6 mi N of Roy on NM Hwy 39
UNM 19744	NM	HARDING CO.	Hwy 39, 3 rd. mi N Mosquero Creek Bridge
UNM 50643	NM	HARDING CO.	HWY 338, 16.5 MI S JCT WITH IHY 10
NMSU 2014	NM	LEA CO.	15 mi WNW Jal
UNM 4191	NM	LEA CO.	18 mi N Jal
UNM 52708	NM	LINCOLN CO.	NM Hwy 247, 25 mi SE Corona
UNM 56215	NM	MORA CO.	Hwy 506, S end Crow Flats (T25S,R18E,S27,SE1/4)
NMSU 6324	NM	OTERO CO.	County RD 7 ("Piñon rd"), 2.7 RD MI NNE Texas State line
UTEP 2865	NM	OTERO CO.	Crow Flats, Kitchen Well (T25S,R18E,S12,NE1/4)
UTEP 8674	NM	OTERO CO.	Hwy 506, S end Crow Flats (T25S,R18E,S11,NW1/4)
UNM 32390	NM	QUAY CO.	N end Tucumcari Lake, (R31E,T11N,SW1/4,Sec7)
UNM 15522	NM	QUAY CO.	Near Portales
UNM 48093	NM	QUAY CO.	1.5 mi. W Hassell
INHS 10125	NM	QUAY CO.	Hwy 39, 8 mi SE Jct 39 & US 54
CHAS 10125	NM	QUAY CO.	USHY 70, 3.8 mi SW Portales - DOR
KU 13793	NM	ROOSEVELT CO.	Melrose Bombing Range, 6 mi S & 9 mi E Tolar
UNM 56155	NM	ROOSEVELT CO.	St. rd 371, 7 mi S of Farmington
UNM 32875	NM	ROOSEVELT CO.	Melrose Bombing Range, 15.3 mi S & 10.3 mi E Tolar
UNM 56075	NM	ROOSEVELT CO.	11 mi E Rogers on St rd. 235
UTEP 11916	NM	ROOSEVELT CO.	St. rd 371, 7 mi S of Farmington
UNM 36933	NM	SAN JUAN CO.	N side of Morgan Lake, dirt rd into lake
UNM 36932	NM	SAN JUAN CO.	1 mi. S and .5 mi. E Rio Ranch Estates
UNM 56397	NM	SAN JUAN CO.	Cabra Spring
USNM 032744	NM	SAN MIGUEL CO.	1 mi. S and .5 mi. E Rio Ranch Estates
UNM 15201	NM	SANDOVAL CO.	Corrales
UNM 15598	NM	SANDOVAL CO.	Corrales
UNM 50032	NM	SANDOVAL CO.	NM Hwy 22; 2 mi S Pena Blanca
UNM 37821	NM	SANDOVAL CO.	Dump on rte 46, 0.3 mi E of rte 528 (T12N,R3E,S15)
UNM 15202	NM	SANDOVAL CO.	3.2 mi N I-25 on NM Hwy 22 near Santo Domingo Pueblo exit

UNM 49564	NM	SANDOVAL CO.	San Ildefonso
UNM 22378	NM	SANDOVAL CO.	Airport rd, 0.5 mi E of Santa Fe Country Club
UNM 48491	NM	SANTA FE CO.	Tesuque, Dr. Phil Schultz's place
USNM 008415	NM	SANTA FE CO.	St. Rd. 14, 7 mi S of US 85 SW of Santa Fe
UNM 32877	NM	SANTA FE CO.	.25 mi S Pueblo
USNM 004863	NM	SANTA FE CO.	St. Rd. 14, 4 mi S of US 85 SW of Santa Fe
UNM 45326	NM	SANTA FE CO.	On St. Hwy 41, 5.0 rd mi S jct with Hwy 285 (ca 25 air miles S Santa Fe)
UNM 32879	NM	SANTA FE CO.	1mi S Otto on NM 41
UNM 53339	NM	SANTA FE CO.	Santa Fe
UNM 33123	NM	SANTA FE CO.	2 mi N of Galisteo on NM 41
UNM 189	NM	SANTA FE CO.	Santa Fe
UNM 32880	NM	SANTA FE CO.	8 mi SE Santa Fe, just W of US Hwy 285, El Dorado
UNM 36934	NM	SANTA FE CO.	St. Rd. 14, 3 mi S of Jct US 85; S of Santa Fe
UTEP 16099	NM	SANTA FE CO.	46.0 rd mi N Small Missle Range gate on WSMR Rd 7
UNM 40657	NM	SANTA FE CO.	STHY 27, 3.5 rd mi S Hillsboro (32 deg 52'53 N, 107 deg 32'48 W)
NMSU 6577	NM	SIERRA CO.	1 meter W of gate at Black Butte, Sevilleta NWR
TCWC 9446	NM	SOCORRO CO.	6 mi E Bernardo on US 60
UNM 8319	NM	SOCORRO CO.	1 mi. N Bernardo.
UNM 13429	NM	SOCORRO CO.	3 mi SE Clines Corner on US 285
UNM 33134	NM	SOCORRO CO.	Bosque Del Apache NWR, SE corner unit 9, N part of refuge
UNM 54624	NM	SOCORRO CO.	Sevilleta NWR, 1 mi W Los Pinos Mtns.
UNM 56203	NM	SOCORRO CO.	Bosque Del Apache Wildlife Refuge
UNM 50021	NM	SOCORRO CO.	.5 mi E Bosque Del Apache Wildlife Refuge on rt 1 (US 85)
UNM 56147	NM	SOCORRO CO.	1 mi N Claunch on NM Hwy 14
UNM 56040	NM	SOCORRO CO.	9 mi E Magdalena
UNM 50259	NM	SOCORRO CO.	1 mi S Vequita
UNM 54113	NM	SOCORRO CO.	.5 mi E Bosque Del Apache Wildlife Refuge on rt 1 (US 85)
AMNH 66294	NM	SOCORRO CO.	6 mi W Encino
UNM 33133	NM	SOCORRO CO.	24.9 rd mi E NM Hwy 1 on US Hwy 380 (San Antonio)
NMSU 5690	NM	SOCORRO CO.	Near Bernardo
UNM 12084	NM	SOCORRO CO.	.75 mi N of RR tracks on NM rt 1, Bosque Del Apache NWR
UNM 7201	NM	TORRANCE CO.	Tucumcari
UNM 94	NM	TORRANCE CO.	5.8 mi N Encino, along US Hwy 285

UNM 52779	NM	TORRANCE CO.	6 mi W Encino
UNM 7202	NM	TORRANCE CO.	NM Hwy 42, 11.0 rd mi NW Cloverdale (21.8 rd mi NW Corona jct US Hwy 54)
UNM 51988	NM	TORRANCE CO.	15 rd mi E Willard (jct US Hwy 60/NM Hwy 421 on US Hwy 60)
LACM 74101	NM	TORRANCE CO.	Hwy 54, 3 mi NE Tucumcari
NMSU 6629	NM	TORRENCE CO.	11 mi S, 25.3 mi W Clayton
UNM 44983	NM	UNION CO.	1.5 mi N Belen
UNM 45010	NM	UNION CO.	11 mi S, 25.3 mi W Clayton
UNM 50428	NM	UNION CO.	11 mi S, 25.3 mi W Clayton
UNM 45010	NM	UNION CO.	11 mi S, 25.3 mi W Clayton
UNM 44983	NM	UNION CO.	3.7 mi S Seneca on NM Hwy 18
UNM 145	NM	VALENCIA CO.	Sandoval, 30 mi N of Hwy 66
UNM 53338	NM	VALENCIA CO.	5 mi ESE Belen, on NM Hwy 47
UNM 32075	NM	VALENCIA CO.	7.5 mi S Belen on St. rd 6
UNM 26182	NM	VALENCIA CO.	Coralitos Ranch Rd.
UNM 18220	NM	VALENCIA CO.	6 mi. SE Belen, St. rd. 6
UNM 23	NM	VALENCIA CO.	5 mi E Belen on Hwy 6
UNM 13339	NM	VALENCIA CO.	Approx. 10 mi ESE Belen on rd to J.F. Kennedy Campground
UNM 20628	NM	VALENCIA CO.	Approximately 1 mi. S I-state Bridge at St. Rd. 40.
UNM 18219	NM	VALENCIA CO.	Belen
UNM 8	NM	VALENCIA CO.	4 mi E Belen on Hwy 6
UNM 48785	NM	VALENCIA CO.	E. of Los Lunas
UO 9180	OK	ALFALFA CO.	9 mi N Driftwood
UO 9179	OK	ALFALFA CO.	Salt Fork
KU 33619	OK	ALFALFA CO.	4 mi S Salt Plain D???
UO 26845	OK	ALFALFA CO.	3.5 mi E Cherokee
CM 60454	OK	ALFALFA CO.	St. Hy. 11, 0.5 mi E of jct with St. Hy. 38, 29 mi E Alva
UO 9098	OK	ALFALFA CO.	3.5 mi E Cherokee
UO 25871	OK	ALFALFA CO.	3.5 mi E Cherokee
UO 9128	OK	ALFALFA CO.	2 mi S Carmen
KU 21061	OK	BEAVER CO.	Near Gate
CAS 10011	OK	BEAVER CO.	15 mi S Beaver
UO 13694	OK	BEAVER CO.	1 mi S State Line
UO 34465	OK	BECKHAM CO.	?

UMMZ 44644	OK	BLAINE CO.	Canton
CM 44644	OK	BLAINE CO.	?
USNM 011817	OK	CADDO CO.	Old Fort Cobb
USNM 011816	OK	CADDO CO.	Old Fort Cobb
FMNH 25418	OK	CANADIAN CO.	?
UO 26016	OK	CIMARRON CO.	Norman
UO 4898	OK	CIMARRON CO.	7 mi S Boise City
UNM 50739	OK	CIMARRON CO.	Black Mesa
UO 4919	OK	CIMARRON CO.	11 mi W Boise City
UMMZ 77548	OK	CIMARRON CO.	1 mi W Boise City
UO 5285	OK	CIMARRON CO.	7 mi S Boise City
UTA 2093	OK	CIMARRON CO.	1 mi N of Kenton
UO 4899	OK	CIMARRON CO.	2 mi E Wheelers ??
UMMZ 133527	OK	CIMARRON CO.	7 mi S Boise City
UO 3700	OK	CUSTER CO.	?
UO 493	OK	CUSTER CO.	Drumwright
UO 3699	OK	CUSTER CO.	El Reno
UO 19689	OK	CUSTER CO.	Weatherford
UO 19685	OK	HARPER CO.	Near Gate
UO 24974	OK	HARPER CO.	Gate
UO 20253	OK	OKLAHOMA CO.	.2 mi N Edmond
UO 4726	OK	TEXAS CO.	8+ mi SSE Guymon
UNM 20886	OK	TEXAS CO.	8+ mi SSE Guymon
UO 4863	OK	TEXAS CO.	7+ mi SE Guymon
UO 4864	OK	TEXAS CO.	8+ mi SSE Guymon
UO 4862	OK	TEXAS CO.	3 mi NE Hooker, on US Hwy 54
UO 25391	OK	TILLMAN CO.	4.2 mi W Frederick
UO 25392	OK	TILLMAN CO.	4.2 mi W Frederick
UO 19905	OK	WOODS CO.	10 mi SW Alva
UO 9701	OK	WOODS CO.	2.5 mi W Edith
UO 9642	OK	WOODS CO.	1.5 mi W Edith
KU 6614	OK	WOODS CO.	12 mi W Alva
UO 8535	OK	WOODS CO.	3 mi S Wyanoke
UO 5417	OK	WOODWARD CO.	11 mi SW Freedom

CAS 10010	OK	BEAVER CO.	5 mi N Beaver
FMNH 7885	SD	BATTLE CREEK CANYON	Battle Creek Canyon, SW part of State
FMNH 7886	SD	BATTLE CREEK CANYON	Battle Creek Canyon, SW part of State
KU 129660	SD	BENNETT CO.	9 mi S Martin
USNM 021269	SD	BRULE CO.	Chamberlain
USNM 048814	SD	CHARLES MIX CO.	Lake Andes
USNM 307546	SD	CODINGTON CO.	Watertown, NW of, MCM illon Lake
KU 129659	SD	CUSTER CO.	5.75 mi N & 5.75 mi E Custer
KU 129599	SD	CUSTER CO.	2.5 mi N & 5 mi E Wind Cave
CHAS 14247	SD	DEWEY CO.	8 mi S White Horse
KU 129658	SD	FALL RIVER CO.	5 mi W Minnekahta
CHAS 14246	SD	HAAKEN CO.	20 mi S Eagle Butte
KU 68784	SD	HARDING CO.	2 mi W Camp Crook
KU 130306	SD	HARDING CO.	4 mi S, 7 mi W Ladner
UTEP 8462	SD	HUGHES CO.	ON OIL RD. 1 MI NE PIERRE
UMMZ 76496	SD	KADOKA	Kadoka
UMMZ 76497	SD	KADOKA	Kadoka
STRECK 4371	SD	PENNINGTON CO.	6 mi NW Scenic
AMNH 36790	SD	PENNINGTON CO.	4 mi N Wall
KU 98353	SD	POTTER CO.	Whitlock's Crossing
KU 98352	SD	POTTER CO.	Whitlock's Crossing
CHAS 11313	SD	TODD CO.	Hidden Timber
UMMZ 78120	SD	TRIPP CO.	Dog Ear Lake
KU 17425	SD	TRIPP CO.	4 mi S Colome
KU 94323	SD	WASHABOUGH CO.	10 mi N, 4 mi E Potato Cave
UNM 36936	SD	WASHABOUGH CO.	3 mi E of Potato Creek
KU 94322	SD	WASHABOUGH CO.	20 mi N Long Valley
INHS 7566	TX	ARMSTRONG CO.	Lake Diversion
USNM 044351	TX	ARMSTRONG CO.	Claude, .4 mi inside east city limits on Hwy 287
USNM 044352	TX	ARMSTRONG CO.	Washburn
TNHC 10273	TX	ARMSTRONG CO.	?
TCWC 54078	TX	BAYLOR CO.	Palo Duro State Park
KU 82090	TX	BRISCOE CO.	Fork of Red River, Hwy 256
UTA 15840	TX	CROSBY CO.	White River Lake

MWSU 2865	TX	CROSBY CO.	White River Lake
UTA 15837	TX	CROSBY CO.	White River Lake
UTA 15839	TX	CROSBY CO.	?
UTA 15838	TX	CROSBY CO.	White River Lake
UTA 15836	TX	CROSBY CO.	White River Lake
USNM 104667	TX	DALLAM CO.	Dalhart, 6 mi NE of
USNM 104666	TX	DALLAM CO.	Dalhart, 7 mi NE of
LSUMZ 27526	TX	DALLAM CO.	4 mi NW Perico
TNHC 17032	TX	DAWSON CO.	Lamesa, 10 mi E.
KU 1709	TX	DAWSON CO.	6 mi NE Lamesa
TNHC 17033	TX	DAWSON CO.	Lamesa, 10 mi E.
UTEP 15955	TX	EL PASO CO.	NE El Paso, DOR on Stan Roberts Rd., 1/2 mi E Power [illegible]
AMNH 71010	TX	GARZA CO.	2 mi W Galveston
AMNH 1010	TX	GARZA CO.	11 mi E Post
FMNH 23373	TX	GRAY CO.	Goliad, Vicinity of Mission Rosario
TCWC 4586	TX	HALE CO.	5 mi S Plainview
ASC 670	TX	HALE CO.	SE of Seguin on FM rd 466.
UTA 15841	TX	HALL CO.	3 mi SW Bruce
CAS 10012	TX	HALL CO.	4.5 MI. N PETERSBURG - JOE BOYD FARM
UAZ 24945	TX	HARTLEY CO.	4 me SE Hockley
ASC 4744	TX	HOCKLEY CO.	McAllen
CM 118665	TX	HOCKLEY CO.	4.7 mi N Levelland on US 385
ASC 1529	TX	HOCKLEY CO.	WITHERALL, 3 MI. E, 3.5 MI. N
ASC 4745	TX	HOCKLEY CO.	SYMER, 6 MI. N; 2.5 MI. E
TNHC 10908	TX	HUTCHINSON CO.	Stinnett, 9 mi E on Bugbee Ranch.
TNHC 10504	TX	HUTCHINSON CO.	Stinnett, 9 mi E on Bugbee Ranch.
TNHC 10782	TX	HUTCHINSON CO.	Stinnett, 9 mi E on Bugbee Ranch.
TNHC 10835	TX	HUTCHINSON CO.	USHY 62/180, 5.8 RD MI W JCT WITH RMRD 2317
STRECK 10252	TX	HUTCHINSON CO.	?
TNHC 10996	TX	HUTCHINSON CO.	Stinnett, 9 mi E on Bugbee Ranch.
MWSU 2867	TX	HUTCHINSON CO.	Stinnett, 9 mi E on Bugbee Ranch.
TNHC 11406	TX	HUTCHINSON CO.	Stinnett, 9 mi E on Bugbee Ranch.
TNHC 10809	TX	HUTCHINSON CO.	Stinnett, 9 mi E on Bugbee Ranch.
TNHC 10576	TX	HUTCHINSON CO.	Boyer

UTA 1063	TX	LUBBOCK CO.	17 mi N Stanton
UNM 17783	TX	LUBBOCK CO.	Staton/Slaton?
UNM 13428	TX	LUBBOCK CO.	7 MI. SW AIRLINE ON SLIDE ROAD - DOR
ASC 4061	TX	LUBBOCK CO.	Lubbock, vacant lot on Quacker
ASC 4014	TX	LUBBOCK CO.	LUBBOCK - 7 MI. W ON 34TH STREET
USNM 032746	TX	POTTER CO.	2.7 mi S Marfa
STRECK 3792	TX	RANDALL CO.	Amarillo
UNM 33116	TX	RANDALL CO.	6 miles SE Amarillo
TNHC 11774	TX	RANDALL CO.	15 mi S Canyon
TNHC 11777	TX	RANDALL CO.	STILES, 11.7 MI. NW
KU 16713	TX	ROBERTS CO.	9 mi N Hearne
UNM 42233	TX	STONEWALL CO.	Near Tule Canyon
UMMZ 69005	TX	SWISHER CO.	Dryden, 25 mi N.
MWSU 2872	TX	WICHITA CO.	6 mi W Burkburnett
MWSU 2876	TX	WICHITA CO.	4 mi N Wichita Falls
MWSU 2873	TX	WICHITA CO.	5 mi NE Wichita Falls
TCWC 8779	TX	WICHITA CO.	7 mi W Wichita Falls
MWSU 2871	TX	WICHITA CO.	Vernon
MWSU 2877	TX	WICHITA CO.	Lake Kickapoo
STRECK 4078	TX	WILBANGER CO.	Bustanante on TX 16
KU 27834	WY	CAMPBELL CO.	2 mi N, 7 mi W Spotted Horse
KU 27833	WY	CAMPBELL CO.	2 mi S & 1.5 mi W Rocky Point
CM 105619	WY	FREMONT CO.	2.6 mi W Shoshoni on US 26
KU 79687	WY	LARAMIE CO.	5 mi W Carpenter
KU 79686	WY	LARAMIE CO.	5 mi W Carpenter
AMNH 46388	WY	NIOBRARA CO.	10.1 mi S Mule Creek Jct.
KU 79688	WY	NIOBRARA CO.	Lusk

APPENDIX D

Taxonomic Characters

The following characters were recorded for each specimen of Heterodon examined. Not all of these characters were included in the final anaysis.

1. Ventrals - Counts of ventrals follow the method of Dowling (1951a).
2. Azygous Scales - Count includes the azygous scale posterior to the rostral scale and the accessory azygous scales (Fig. IV-1).
3. Azygous position - The position of the posterior border of the single azygous scale in relation to the frontal scale was scored a 0 if the azygous scale does not extend to the frontal scale and a 1 if the azygous scale extends to the frontal scale.
4. Loreal scales - The number of loreal scales were counted for the left and right sides of the head (Fig. IV-1).
5. Postnasal - Orbitals - If the loreal scales separated the postnasal scales and the orbitals then a 1 was scored. If the postnasals contacted the orbitals then a 0 was scored.
6. Orbitals - The # of orbital scales surrounding the eye were counted for the left and right side (Fig. IV-1).
7. Dorsal Blotches - The number of dorsal blotches were counted from the back of the head to the vent for the left and right sides.
8. Tail Dorsal Blotches - The number of tail dorsal blotches were counted from the vent to the end of the tail for the left and right sides.

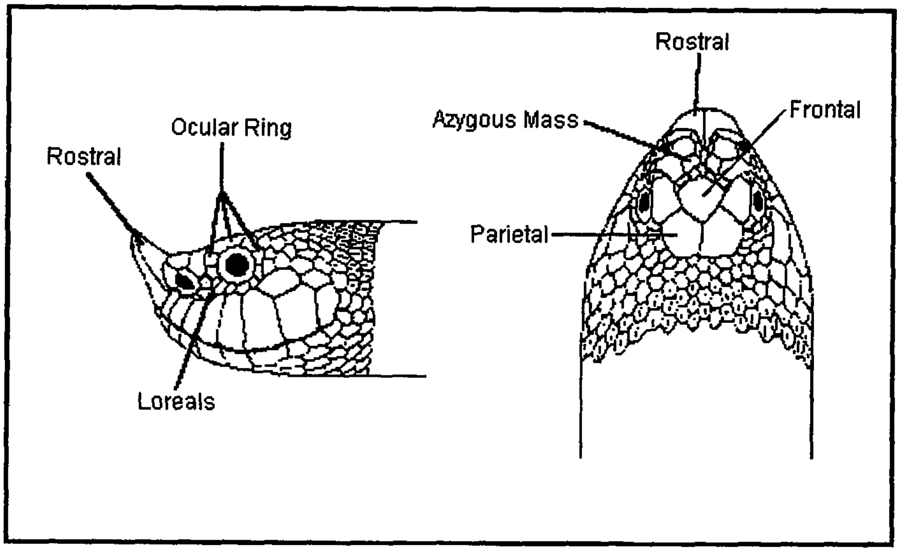


Figure IV-1: Heterodon nasicus head scutellation.

9. Lateral Blotches - The number of lateral blotches were counted from the back of the head to the vent for the left and right sides.

10. Tail Lateral Blotches - The number of tail lateral blotches were counted from the vent to the end of the tail for the left and right sides.

11. 1st Dorsal Blotch - The nature of the first dorsal blotch. A 0 was scored for a single transverse blotch, a 1 was scored for a transverse blotch that seems anterio-posteriorly constricted, a 2 was scored for a pair of blotches, and a 3 was scored for any unusual configurations of blotches (included y and v shaped blotches as well as unpaired blotches).

12. CON M-1 - Connection of the Middle prong of the nuchal blotch with the 1st dorsal blotch. A 0 was scored if there was now connection and a wide separation, a 1 was scored if the middle prong came close to the dorsal blotch but there was no connection, and a 2 was scored for specimens that had the middle prong connected to the first dorsal blotch.

13. BF & PF - Between Frontal and Prefrontal. A 0 was scored if the prefrontals contacted the frontal scale and a 1 was given if the accessory azygous scales separated the prefrontals from the frontal scale.

14. 3-PDB - Character of 3-pronged nuchal blotch. A 0 was scored if the 3-pronged dark pattern was absent, a 1 was scored if the middle prong of the pattern was absent or there was only a trace of it, and a 2 was scored if the 3-pronged dark mark was complete.

15. Head Length (mm) - This measurement was taken from the posterior end of the

suture between the parietal scales to the tip of the rostral scale.

16. Head Width (mm) - The width of the head was taken between the top of the eyes.
17. Parietal Length (mm) - The maximum length of the parietal perpendicular to the anterior border of the parietal scale was taken. The right side of the head was used in measurement.
18. Parietal Width (mm) - The maximum width of the parietal across the posterior edge of the parietal scale was taken. The right side of the head was used in meas
19. Frontal Length (mm) - The maximum length of the frontal scale was taken.
20. Frontal Width (mm) - The maximum width of the frontal scale was taken.
21. Rostral Scale Front Height - The dorsal measurement of the rostral scale from the mid-posterior end to the mid-anterior end was taken. This measurement follows from Edgren 1952a (Fig. IV-2).
22. Rostral Scale Straight Height - The lateral measurement of the rostral scale from the most mid-posterior portion on the dorsal side to the ventral side of the rostral scale was taken. The measurement forms a right angle from the plane of the ventral surface of the rostral scale to the mid-posterior portion of the rostral scale on the dorsal side. This measurement follows from Edgren 1952a (Fig. IV-2).
23. Rostral Width - The width of the rostral scale, best measured underneath at the points where it contacts the supralabial scales, was taken.
24. Rostral Position - The anterior-posterior position of the posterior border of the rostral scale with respect to internasals was scored. A 0 was given if the posterior border of the rostral scale extended to the anterior half of the internasal (including the

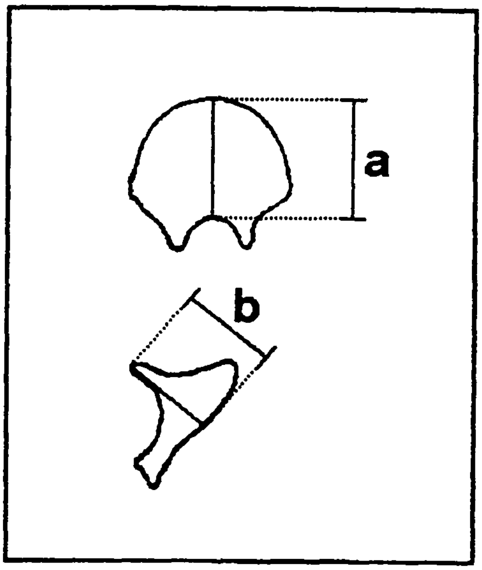


Figure IV-2: Measurements taken on the rostral plates of specimens of Heterodon. The rostral front height (a) and the rostral straight height (b).

middle) and a 1 was given if the posterior portion of the rostral scale extended beyond the middle of the internasal scales.

25. Venter Color - The venter coloration was scored a 0 if it is light with no dark blotches, a 1 if it is light with only a few dark blotches, a 2 if it has a lot of dark and a lot of white blotches, and a 3 if it is mostly dark with or without white blotches.
26. Anal Plate Color - A 0 was scored if the anal plate was dark and a 1 was given if the anal plate was light. A 0.5 was given if it was half and half.
27. Locality data including the state, county, specific data, longitude and latitude were recorded for distributions and for 2 and 3 dimensional graphs of specific characters.

APPENDIX E

The equation for the F-test for difference between two regression coefficients.

$$F = (b_1 - b_2)^2 / (((\sum x_1^2 + \sum x_2^2) / ((\sum x_1^2)(\sum x_2^2)))(s^2_{Y*X}))$$

Where s^2_{Y*X} is the weighted average s^2_{Y*X}. Since there are only two groups, the formula can be written as:

$$s^2_{Y*X} = (\sum d^2_{Y*X(1)} + \sum d^2_{Y*X(2)}) / (n_1 + n_2 - 4)$$

Compare F with $F_\alpha[1, n_1 + n_2 - 4]$.

F = Calculated F distribution.

b_1 and b_2 = slope of regression lines for each group.

$\sum x_1^2$ and $\sum x_2^2$ = Sum of squares for group 1 (x_1) and group 2 (x_2).

s^2_{Y*X} = this is the weighted average of s^2_{Y*X} which is the unexplained variance of each group.

$\sum d^2_{Y*X(1)}$ and $\sum d^2_{Y*X(2)}$ = Unexplained sum of squares for group 1 (Y*X(1)) and group 2 (Y*X(2)).

$n_1 + n_2$ = sample size.

APPENDIX E (cont.)

The equation for the F-test for differences between k regression coefficients.

$$F = (\sum[x^2_i(b - b)^2] / (k - 1)) / s^2_{Y*X}$$

---

k = the number of groups being compared (3 in this case).

b = the slope of the line.

$b = (\sum\sum xy) / (\sum\sum x^2)$ = the common slope.

$\sum xy$ = Sum of the product of squares.

$\sum x^2_i$ = The sum of squares for the *i*th group.

$s^2_{Y*X} = (\sum\sum d^2_{Y*X}) / (\sum a\text{-}2k)$This is the weighted average of s^2_{Y*X} which is the unexplained variance of each group.

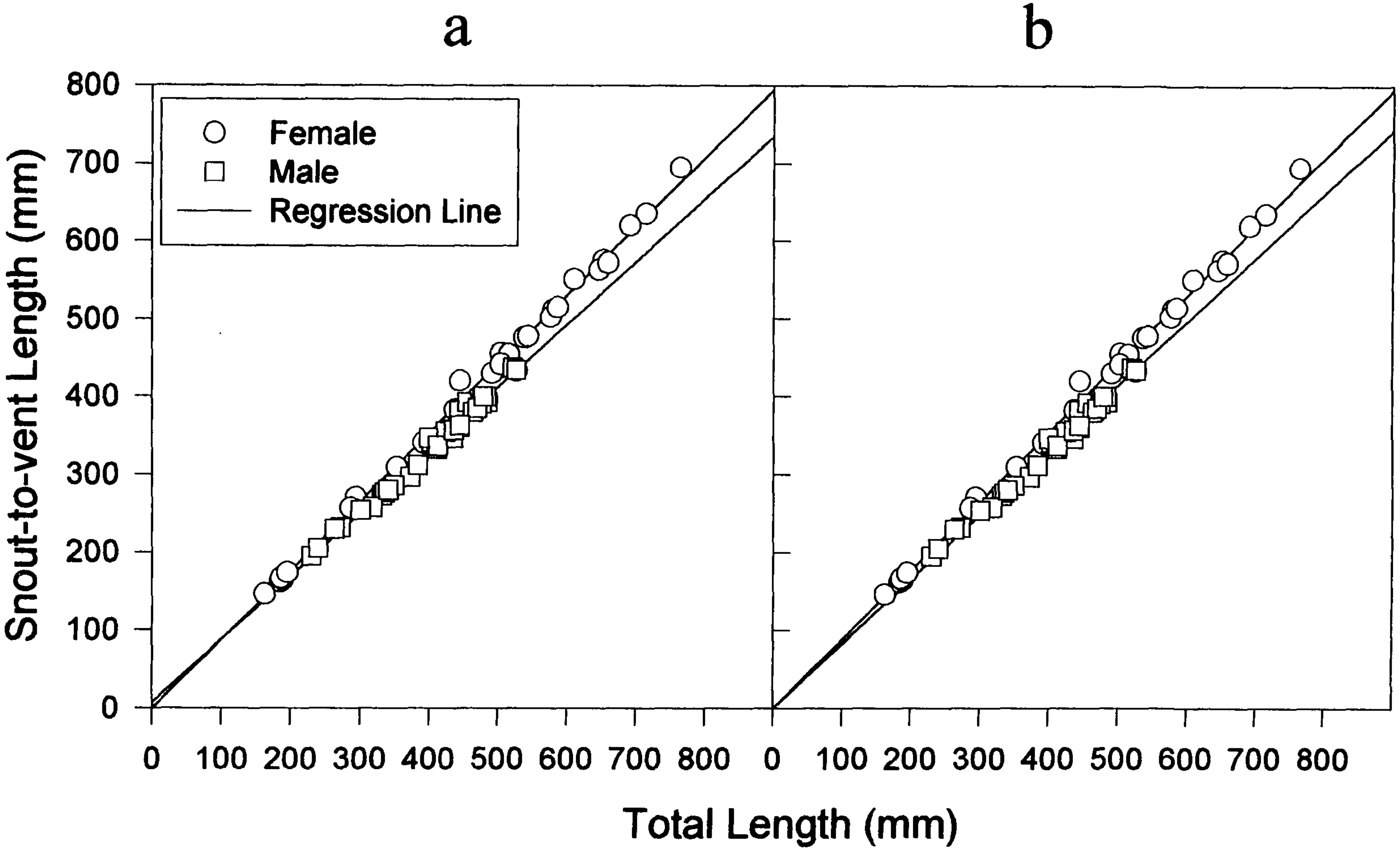
$\sum d^2_{Y*X}$ = The unexplained sum of squares.

a = The number of groups.

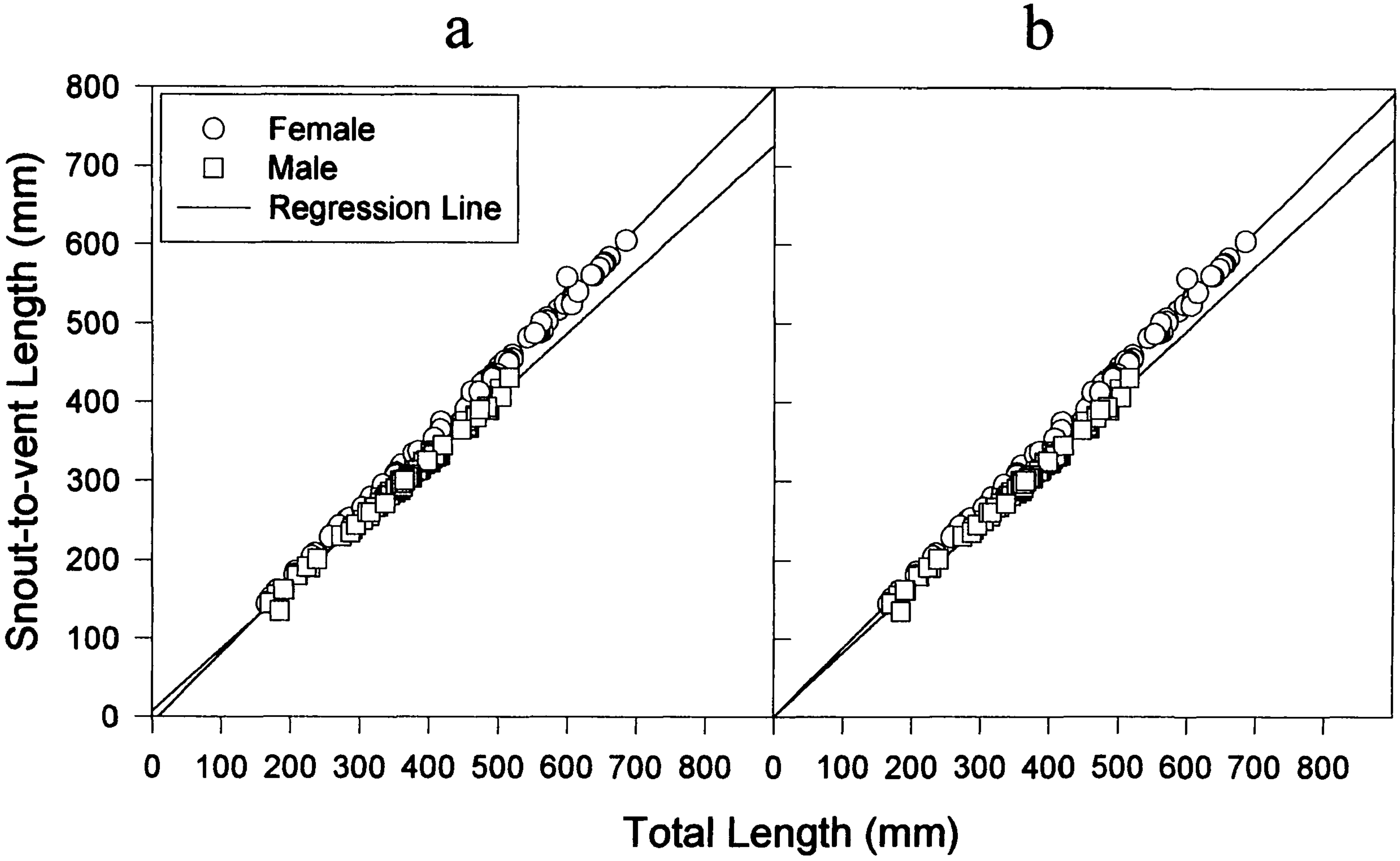
APPENDIX F

Scatterplot graphs of sexually dimorphic characters for _Heterodon_ _nasicus_ _gloydi_ and _H_. _n_. _kennerlyi_.

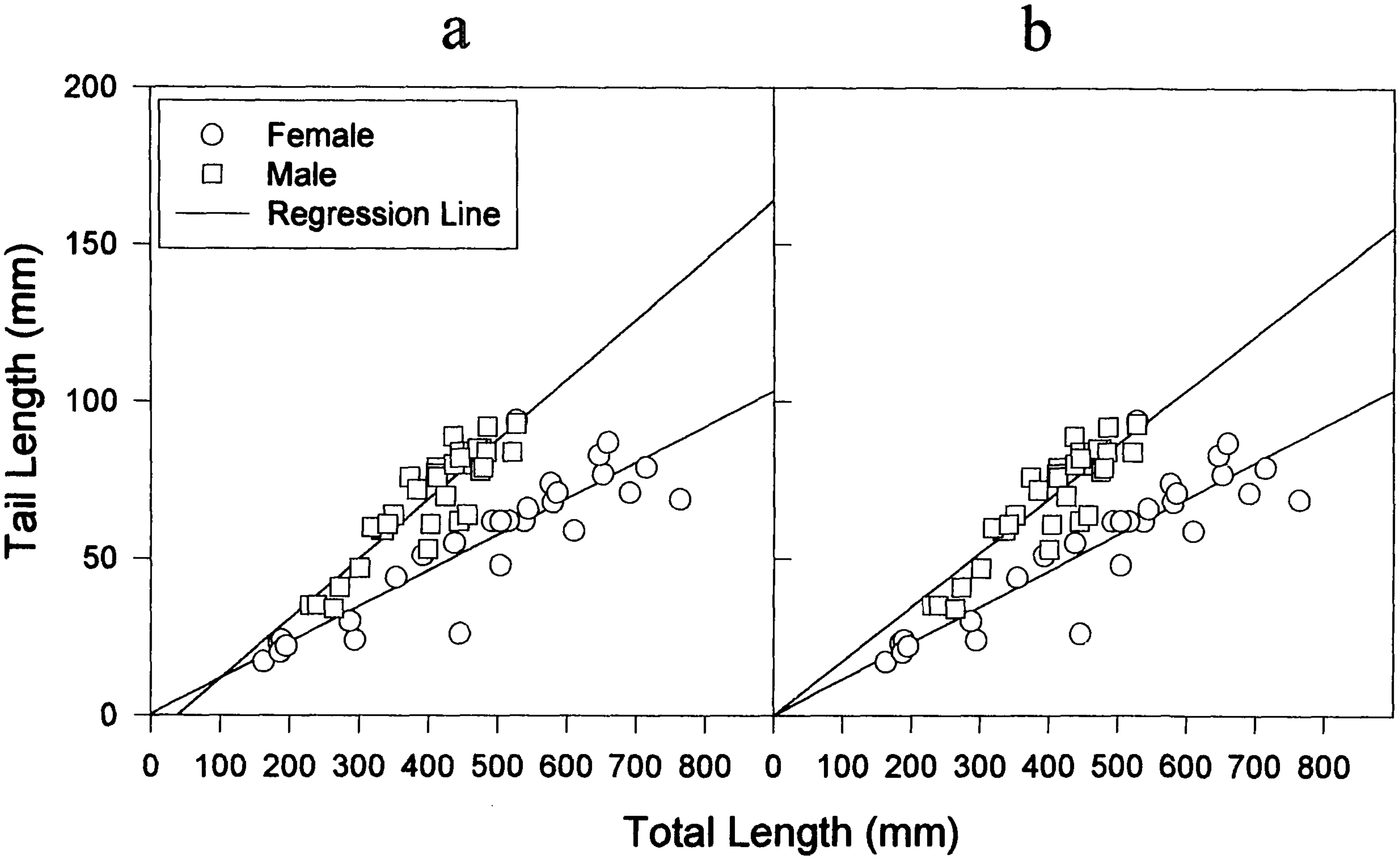
Scatterplot graph of the total length (TOTL) (mm) on the snout-to-vent length (SVL) (mm) for Heterodon nasicus gloydi. Open circles represent females and open squares represent males. The two graphs are graphed from the same data. Graph (a) uses the calculated Y-intercept to construct the regression line and graph (b) has the regression line constructed with the Y-intercept set equal to 0.


a
b
Female
Male
Regression Line
Snout-to-vent Length (mm)
0
100
200
300
400
500
600
700
800
Total Length (mm)
0
100
200
300
400
500
600
700
800

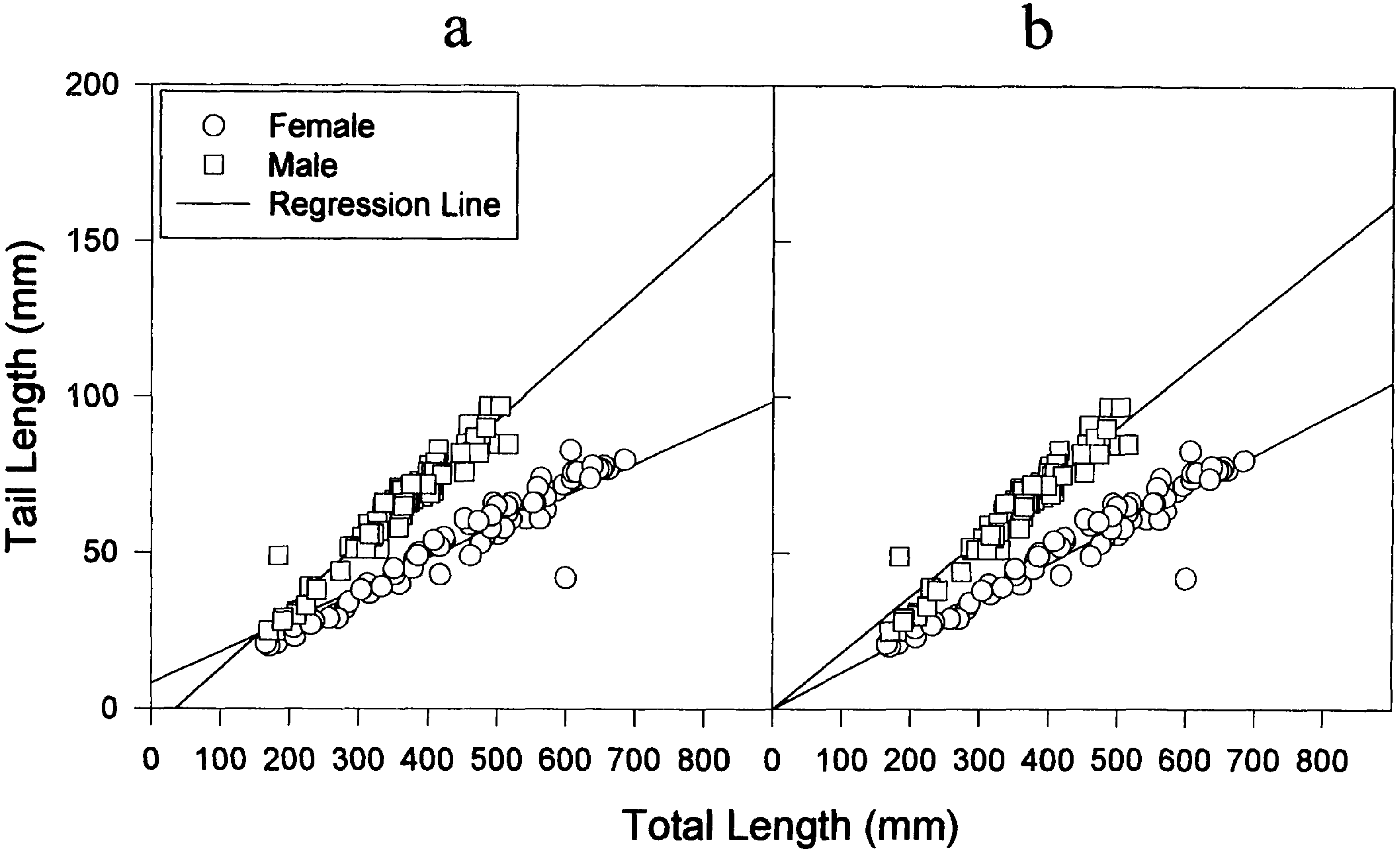
Scatterplot graph of the total length (TOTL) (mm) on the snout-to-vent length (SVL) (mm) for Heterodon nasicus kennerlyi. Open circles represent females and open squares represent males The two graphs are graphed from the same data. Graph (a) uses the calculated Y-intercept to construct the regression line and graph (b) has the regression line constructed with the Y-intercept set equal to 0.


a
b
Female
Male
Regression Line
Snout-to-vent Length (mm)
0
100
200
300
400
500
600
700
800
Total Length (mm)
0
100
200
300
400
500
600
700
800
0
100
200
300
400
500
600
700
800

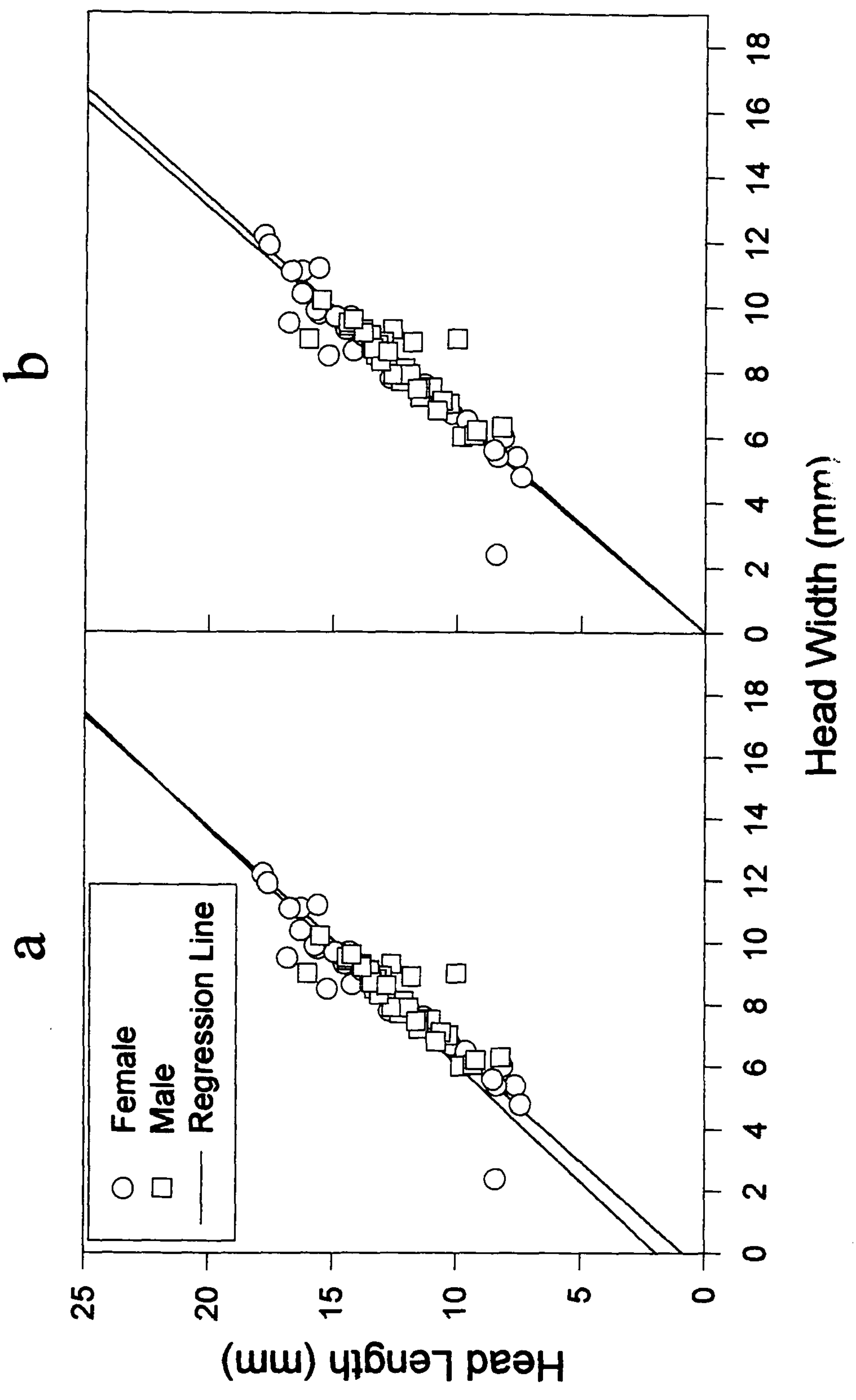
Scatterplot graph of the total length (TOTL) (mm) on the tail length (TL) (mm) for Heterodon nasicus gloydi. Open circles represent females and open squares represent males. The two graphs are graphed from the same data. Graph (a) uses the calculated Y-intercept to construct the regression line and graph (b) has the regression line constructed with the Y-intercept set equal to 0.


a
b
Female
Male
Regression Line
Tail Length (mm)
0
50
100
150
200
Total Length (mm)
0
100
200
300
400
500
600
700
800

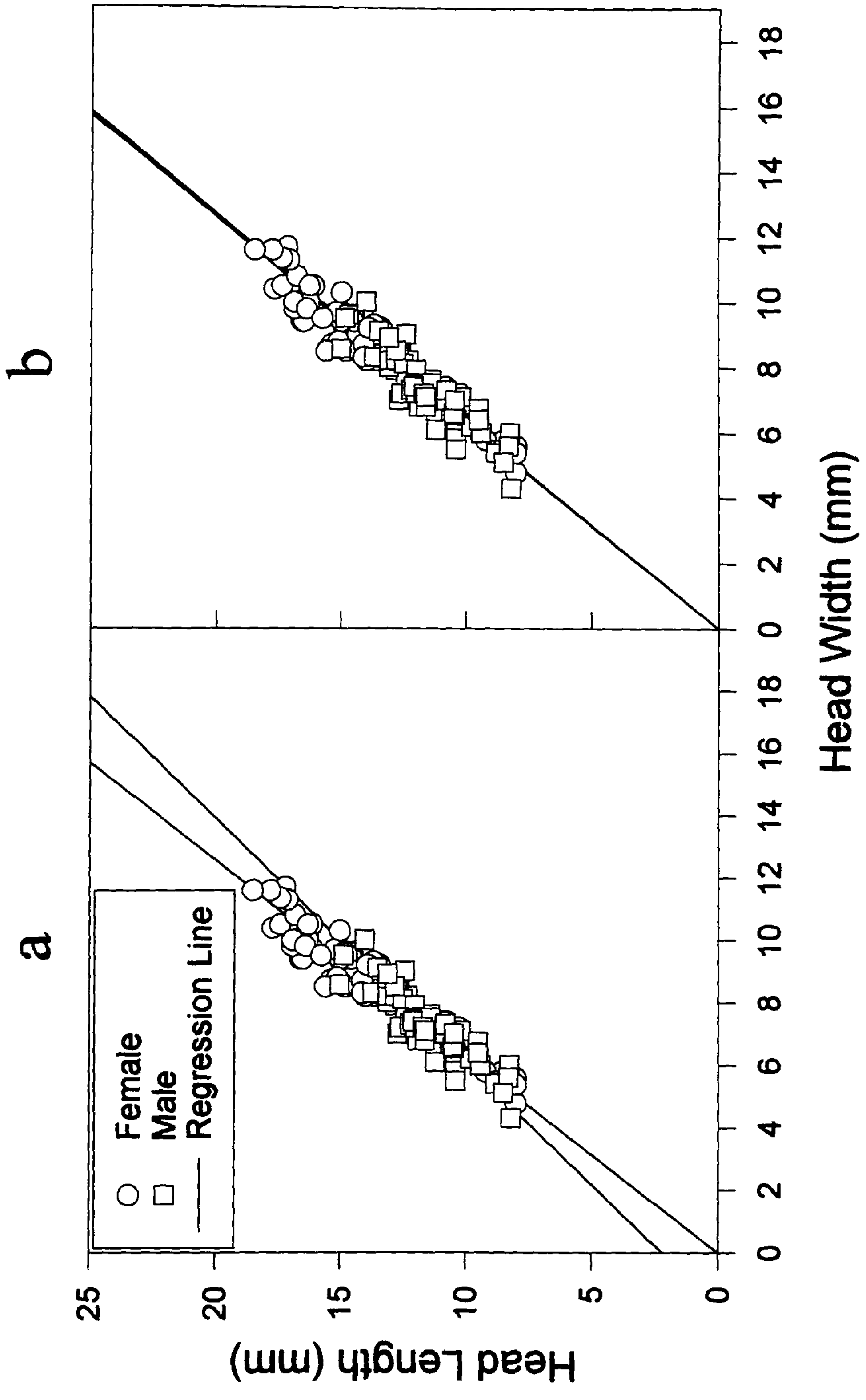
Scatterplot graph of the total length (TOTL) (mm) on the tail length (TL) (mm) for Heterodon nasicus kennerlyi. Open circles represent females and open squares represent males. The two graphs are graphed from the same data. Graph (a) uses the calculated Y-intercept to construct the regression line and graph (b) has the regression line constructed with the Y-intercept set equal to 0.


a
b
Female
Male
Regression Line
Tail Length (mm)
0
50
100
150
200
Total Length (mm)
0
100
200
300
400
500
600
700
800

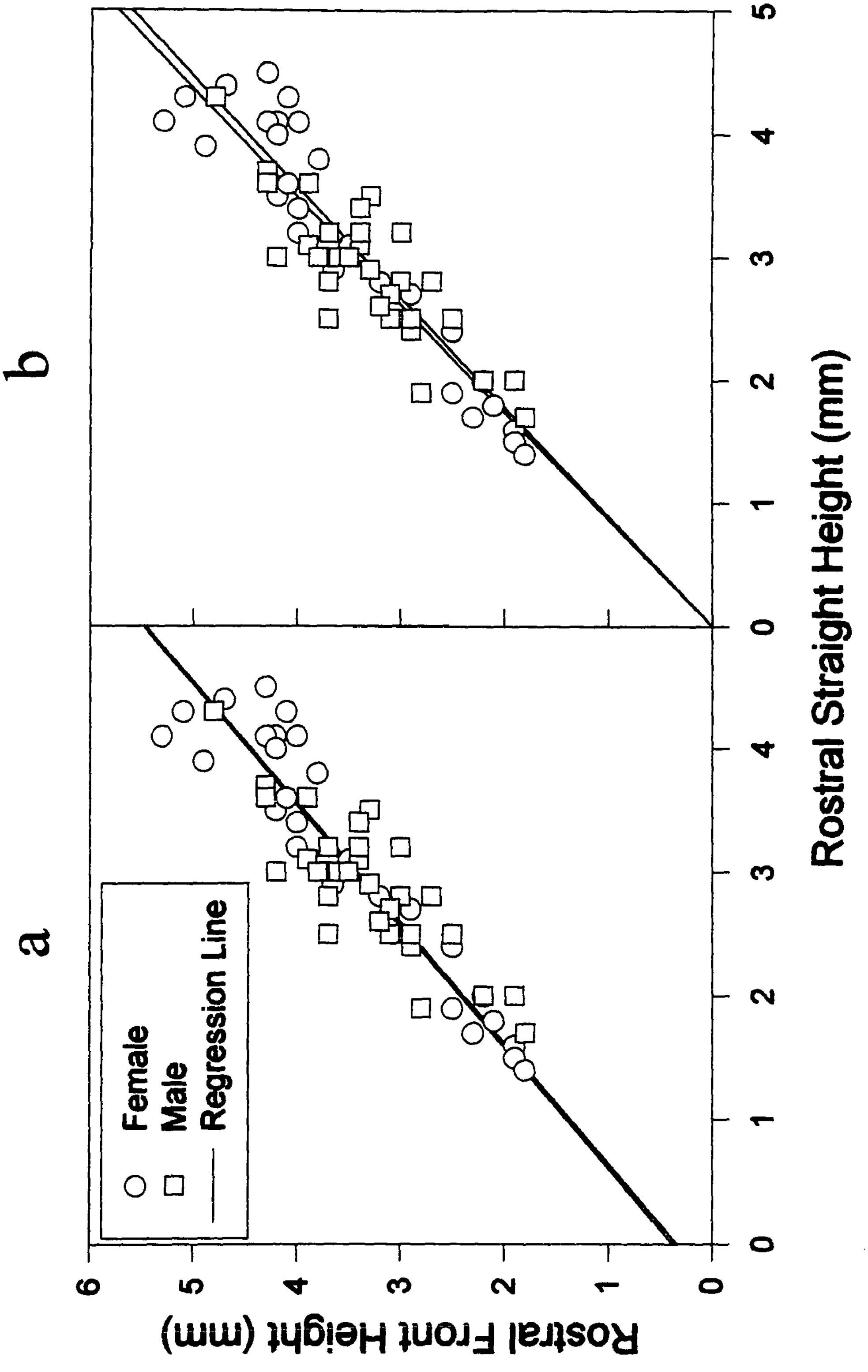
Scatterplot graph of the head width (HW) (mm) on the head length (HL) (mm) for Heterodon nasicus gloydi. Open circles represent females and open squares represent males. The two graphs are graphed from the same data. Graph (a) uses the calculated Y-intercept to construct the regression line and graph (b) has the regression line constructed with the Y-intercept set equal to 0.


a
b
Female
Male
Regression Line
Head Length (mm)
Head Width (mm)
0
5
10
15
20
25
0
2
4
6
8
10
12
14
16
18

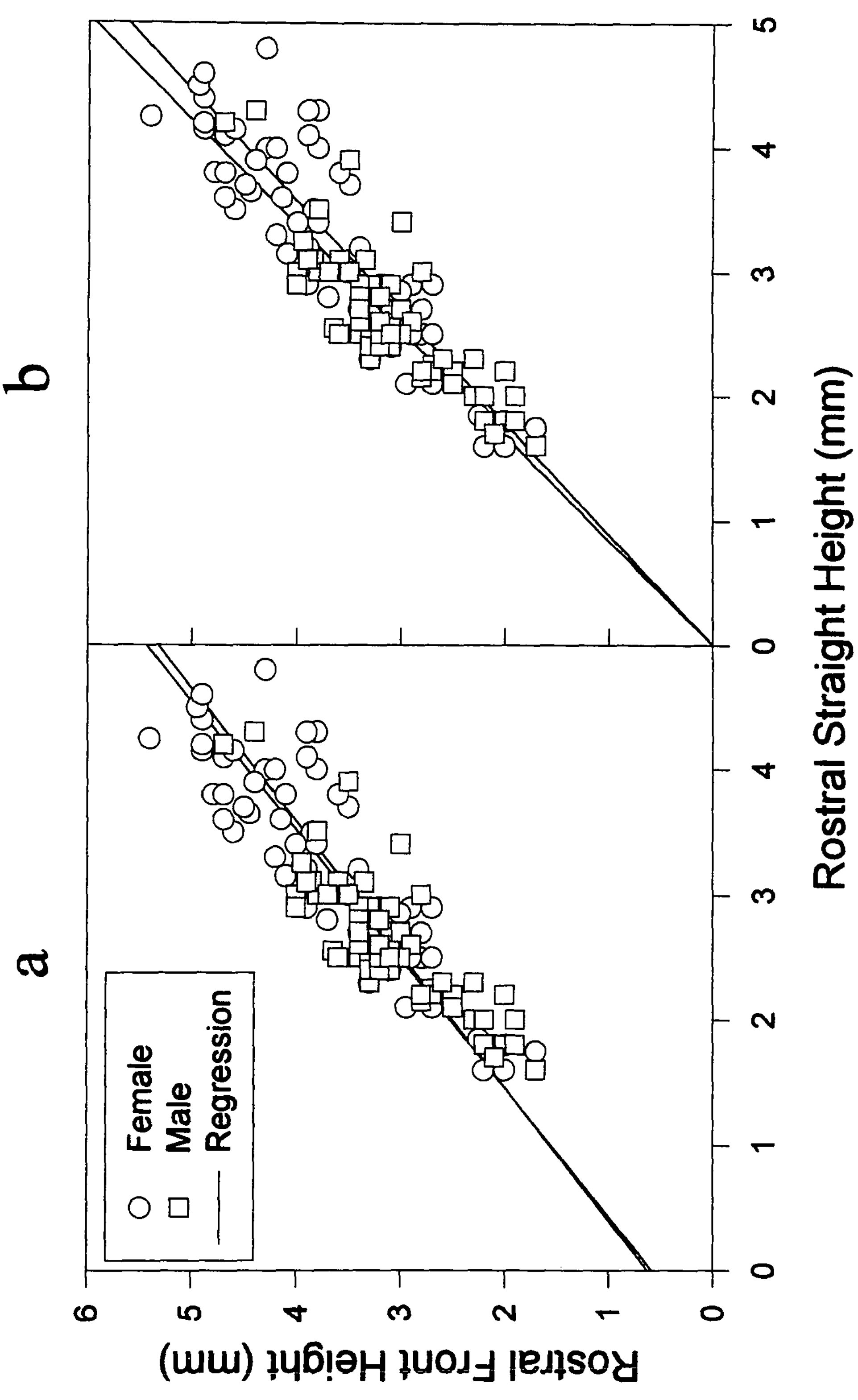
Scatterplot graph of the head width (HW) (mm) on the head length (HL) (mm) for Heterodon nasicus kennerlyi. Open circles represent females and open squares represent males. The two graphs are graphed from the same data. Graph (a) uses the calculated Y-intercept to construct the regression line and graph (b) has the regression line constructed with the Y-intercept set equal to 0.


a
b
Female
Male
Regression Line
Head Length (mm)
Head Width (mm)
0
5
10
15
20
25
0
2
4
6
8
10
12
14
16
18

Scatterplot graph of the rostral front height (ROSFH) (mm) on the rostral straight height (ROSSH) (mm) for Heterodon nasicus gloydi. Open circles represent females and open squares represent males. The two graphs are graphed from the same data. Graph (a) uses the calculated Y-intercept to construct the regression line and graph (b) has the regression line constructed with the Y-intercept set equal to 0.


a
b
Female
Male
Regression Line
Rostral Front Height (mm)
0
1
2
3
4
5
6
Rostral Straight Height (mm)
0
1
2
3
4
5

Scatterplot graph of the rostral front height (ROSFH) (mm) on the rostral straight height (ROSSH) (mm) for Heterodon nasicus kennerlyi. Open circles represent females and open squares represent males. The two graphs are graphed from the same data. Graph (a) uses the calculated Y-intercept to construct the regression line and graph (b) has the regression line constructed with the Y-intercept set equal to 0.


a
b
Female
Male
Regression
Rostral Front Height (mm)
0
1
2
3
4
5
6
Rostral Straight Height (mm)
0
1
2
3
4
5
0
1
2
3
4
5

APPENDIX G

The sample size (n), mean ($\bar{x}$), and standard deviation (Sd) for the separate sexes of each subspecies for all the sexually dimorphic meristic variables (DB, TDB, LB, TLB, VENT, and SC) including the sum of these variables (DB+TDB, LB+TLB, and VENT+SC).

	Sample size	Mean	Standard deviation
Dorsal Blotches			
H. n. nasicus ♀	210	41.78571	3.776886
H. n. nasicus ♂	217	37.65438	3.902206
H. n. gloydi ♀	59	35.69492	4.727959
H. n. gloydi ♂	82	31.39024	4.429854
H. n. kennerlyi ♀	126	36.38095	4.063215
H. n. kennerlyi ♂	114	33.04386	3.947421
Tail Dorsal Blotches			
H. n. nasicus ♀	90	11.60000	1.733996
H. n. nasicus ♂	94	14.68085	1.990368
H. n. gloydi ♀	27	9.88889	2.258886
H. n. gloydi ♂	45	11.46667	2.436465
H. n. kennerlyi ♀	85	9.34118	1.637019
H. n. kennerlyi ♂	91	11.29670	1.816557
Dorsal Blotches + Tail Dorsal Blotches			
H. n. nasicus	180	52.64444	5.167174
H. n. nasicus ♀	88	53.26136	4.953796
H. n. nasicus ♂	92	52.05435	5.323314
H. n. gloydi	71	44.32394	7.042270
H. n. gloydi ♀	27	46.44444	6.818151
H. n. gloydi ♂	44	43.02273	6.933198
H. n. kennerlyi	172	45.47674	5.006958
H. n. kennerlyi ♀	85	46.16471	4.888877
H. n. kennerlyi ♂	87	44.80460	5.057436

	Sample size	Mean	Standard deviation
Lateral Blotches			
H. n. nasicus ♀	59	42.00000	3.508610
H. n. nasicus ♂	64	37.37500	4.452572
H. n. gloydi ♀	31	35.38710	4.638085
H. n. gloydi ♂	36	30.00000	4.579457
H. n. kennerlyi ♀	83	33.25301	4.140418
H. n. kennerlyi ♂	75	36.54667	3.783286
Tail Lateral Blotches			
H. n. nasicus ♀	62	2.580645	1.66496
H. n. nasicus ♂	64	5.000000	12.37509
H. n. gloydi ♀	28	2.214286	1.70744
H. n. gloydi ♂	37	2.756757	1.58825
H. n. kennerlyi ♀	74	0.864865	0.92639
H. n. kennerlyi ♂	88	0.852273	1.09900
Lateral Blotches + Tail Lateral Blotches			
H. n. nasicus	120	42.62500	5.047776
H. n. nasicus ♀	59	44.57627	4.107199
H. n. nasicus ♂	61	40.73771	5.182990
H. n. gloydi	64	34.78125	5.559116
H. n. gloydi ♀	28	37.32143	5.270839
H. n. gloydi ♂	36	32.80556	5.001825
H. n. kennerlyi	156	35.67949	4.434450
H. n. kennerlyi ♀	74	37.37838	4.248135
H. n. kennerlyi ♂	82	34.14634	4.043351

	Sample size	Mean	Standard deviation
Ventral Scales			
H. n. nasicus ♀	159	146.4843	4.875482
H. n. nasicus ♂	169	137.0888	3.986337
H. n. gloydi ♀	50	144.3600	5.472603
H. n. gloydi ♂	70	133.9714	4.913665
H. n. kennerlyi ♀	114	142.3509	3.396986
H. n. kennerlyi ♂	106	132.3113	3.071724
Subcaudal Scales			
H. n. nasicus ♀	163	35.60736	3.601158
H. n. nasicus ♂	169	45.50296	3.132252
H. n. gloydi ♀	53	33.32075	3.646777
H. n. gloydi ♂	74	42.74324	4.003631
H. n. kennerlyi ♀	118	31.37288	3.123653
H. n. kennerlyi ♂	107	41.39252	2.619798
Ventral Scales + Subcaudal Scales			
H. n. nasicus	314	182.0382	6.157554
H. n. nasicus ♀	150	181.7800	6.234640
H. n. nasicus ♂	164	182.2744	6.095685
H. n. gloydi	116	177.1638	7.183246
H. n. gloydi ♀	46	177.7174	6.006156
H. n. gloydi ♂	70	176.8000	7.882470
H. n. kennerlyi	214	173.7897	4.275455
H. n. kennerlyi ♀	111	173.8108	4.248023
H. n. kennerlyi ♂	103	173.7670	4.325492

CURRICULUM VITAE

Curtis Michael Eckerman was born on January 1, 1970 in San Angelo, Texas. The first son of Michael Alan Eckerman and Margaret Louise Eckerman, he graduated from St. Joseph's Catholic High School, Victoria, Texas, in the spring of 1988 and entered Angelo State University, San Angelo, Texas, with a Carr scholarship in the fall of 1988 and transferred to Texas A&M University in the fall of 1989. While pursuing a bachelor's degree in Fish and Wildlife Sciences, he worked as a research assistant with Dr. [illegible] Dixon in Herpetology from 1990 until he graduated in 1992. He was involved in conservation projects involving the Houston toad, Bufo houstonensis, and the Concho Water Snake, Nerodia harteri paucimaculata. He was also part of a study of timber harvesting effects on the east Texas herpetofauna.

In the fall of 1993, he entered the graduate school at the University of Texas at El Paso. As a graduate student, Curtis was a laboratory instructor for a variety of subjects including General Biology, Human Biology, Ecology, Zoology, Human Anatomy and Physiology, and Field Biology. He has given presentations to the Southwestern Association of Naturalists, The Texas Herpetological Society, and the El Paso Herpetological Society. He also has given over 50 presentations to local grade school and high schools on various subjects of herpetology, entomology and ecology. Curtis is interested in general zoology with research interests in herpetology, entomology and evolutionary biology.

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