

**NATURAL SCIENCE DATABASE:
RESOURCE MANAGEMENT AND PUBLIC HEALTH**

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ABSTRACT

The Natural Science Research Laboratory (NSRL) of the Museum of Texas Tech University is constructing the Natural Science Database (NSD) as a reference tool for wildlife biologists and academicians, but also as a reservoir of biological data to address public health issues. Database management software linked to Geographic Information Systems (GIS) will provide interactive queries and map production through a World Wide Web (WWW) interface. Wildlife data will include currently archived, but inaccessible, historical records for distribution of species and quality and quantity of habitat from a variety of sources. The NSRL currently has 50,000 cryopreserved tissue samples and a total holding of over 100,000 cataloged natural history specimens which will be included in NSD. Additional data will be included from other museums in Texas and from the Texas Department of Health (TDH), that collects specimens with the potential of possessing rabies or other human pathogens. The Natural Science Database will provide dynamic analysis and evaluation of factors influencing resource management and public health in a user friendly environment to anyone with internet access.

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AUTHOR LINE

The author line of this paper is uncharacteristically long. Most scientific papers are narrowly focused and restricted to a single discipline. The project described herein is just the opposite; it is multidisciplinary in scope and is made possible only through the contributions of a large team of scientists pooling their talents in a joint effort. The ultimate goal is to place the wealth of information in use across such agencies as the Museum of Texas Tech University, Texas Department of Health, and Texas Parks and Wildlife Department at the fingertips of the policy and decision makers in the state of Texas as well as the public at large. Former senator John T. Montford and his staff were critically important in identifying this need in Texas and addressing it through the state legislative process. John T. Montford now serves as the chancellor of TTU. The staff of the NSRL provided the base data and collections as well as demonstrated by example the usefulness of such a project. The NSRL has excellent working relationships with state agencies such as TPWD and TDH that were necessary for the successful completion of the project. The Texas Cooperative Fish and Wildlife Research Unit (TCFWRU) has provided GIS, remote sensing, global positioning system (GPS), and database development expertise to the process. TCFWRU has enjoyed strong support from the College of Agricultural Sciences and Natural Resources in which it operates at TTU. The College of Engineering has assisted with technology development including internet and computer programming resources. TDH has provided public health related data as well as expertise that otherwise would not have been available. TPWD, as the state natural resource management agency, is critical in the development of NSD. TPWD has historical natural resource data available from no other source and its continued support and involvement is crucial to the development of this project. This author line, with 23 authors from 13 disciplines representing 13 departments and agencies, reflects the strategic design of this project.

INTRODUCTION

Each year Texas spends millions of dollars on natural resource management, endangered species management, and public health issues related to human and animal interactions. Decisions and policy guiding these expenditures are best based upon verified scientific data. However, the lack of easily accessible, centrally available, and verifiable, scientific natural history data has made decision makers turn to other forms of information. Possibly the best source of such cataloged biological data are museum collections. In 1995 this need was identified and addressed by Texas leaders with a line item being added to the state budget for the development of the Natural Science Database (NSD). The NSD is to be developed by Texas Tech University. This paper describes progress during the first year of this challenging joint research effort to develop NSD.

The Natural Science Research Lab (NSRL) of the Museum of Texas Tech University (TTU) is coordinating Texas Tech's effort to develop NSD. The Texas Parks and Wildlife Department currently is developing a massive wildlife data set from historical records identified as the Texas Wildlife Database (TWD). The NSRL currently has 50,000 cryopreserved tissue samples and a total holding of over 100,000 cataloged natural history specimens. All specimens are cataloged in a well organized computerized database. This thorough collection lends itself well to serving as the base for the NSD. This collection is expanding with traditional collections as well as additions from Texas Parks and Wildlife Department (TPWD) and the Texas Department of Public Health. Moreover, each specimen has an almost infinite set of attributes that can be added to NSD including pictures, videos, measurements, anatomical descriptions, maps, geographic references, literature citations, etc.

The NSRL's current collection has served well, but was constructed to meet the needs of scientists and biologists. The ongoing technological development of computer software and hardware increase the potential of this collection. The NSD will be developed in a powerful relational database software environment that maximizes power, speed, and future flexibility. The database will be constructed for maximum interactivity, with links to Geographic Information Systems (GIS), statistical analysis software, and the internet. Online internet access via a World Wide Web (WWW) interface will allow easy interactive query and display of results in tabular as well as graphical and cartographic formats.

Although the construction of the NSD (combined with TPWD's TWD) will provide Texas decision makers, as well as the public at large, a user friendly method of accessing the most robust wildlife database ever constructed in Texas, the NSRL's current database has proven its usefulness through numerous studies. Several subsets of data have been extracted and utilized for studies of national importance. Sample data subsets have also been developed as tests for NSD construction. One important utilization of the NSRL's collection was to develop information about the recently discovered deadly human infection caused by hantavirus.

FOUR CORNERS DISEASE

When the mysterious Four Corners Disease (hantavirus pulmonary syndrome) occurred in 1993, several questions arose concerning the origin of the emerging virus. Museum collections provided some immediate resources to this important health issue. One concern expressed in the media was the possibility that Four Corners Disease had resulted from some escaped military biological warfare product. If this were true then implications would be decidedly different than if the disease had occurred in situ for many years affecting people at such a low frequency that a causal pattern was not

detectable. During the decade preceding this outbreak, rodent tissue samples of heart, liver, and kidney had been archived in several collections across the USA. TTU and University of New Mexico (NMU), in cooperation with Dr. T. Yates, housed large numbers of widely dispersed geographic samples of the deer mouse (Peromyscus maniculatus), which is known to carry one of the viruses (Sin Nombre virus) that cause hantavirus pulmonary syndrome.

Examination of these archived specimens (skin, skeleton, and cryopreserved tissues including brain, liver, heart, and lungs) clearly demonstrated several significant points. First, the hantavirus was present in the oldest specimen present, which eliminated the possibility that this was a recent release from a military installation. Second, the virus was widely distributed across the USA, ranging from Canada to Mexico. Third, a collection of deer mice were obtained by lifting bales of hay with a tractor during which time students were exposed to massive amounts of dust from the habitat of deer mice. These bales contained several individuals of mice that were hantavirus positive. The significance of this third point is that not all people exposed to the hantavirus infected mice, droppings, dust, etc. contract the disease (Baker, 1994).

Since the first recognized outbreak of hantavirus pulmonary syndrome (HPS), more than 145 cases have been confirmed in the US (CDC unpublished data). Most of these cases were caused by Sin Nombre virus (SNV). At least six cases have been due to non-SNV viruses: two were caused by New York virus (NYV); three by Bayou virus (BAYV); and one by Black Creek Canal virus (BCCV) (Hjelle, et al., 1995; Khan, et al., 1996; Hjelle, et al., in press; Khan, et al., 1995). SNV- and NYV-associated HPS are characterized by adult respiratory distress syndrome. In contrast three patients with infections due to either BAYV or BCCV had both the typical pulmonary syndrome and acute renal insufficiency (Duchin, 1994; Khan, et al., 1996; Hjelle, et al., in press)

Hantaviruses are known to occur worldwide. At least 20 species of the virus have been described; each is closely associated with a single species or genus of rodents (Mertz, et al., in press). Seven North American hantaviruses have been described; at least four are pathogenic to man: SNV, associated with the deer mouse (Peromyscus maniculatus); BAYV, associated with the rice rat (Oryzomys palustris); NYV, associated with white-footed mice (Peromyscus leucopus); and BCCV, associated with the cotton rat (Sigmodon hispidus) (Childs, et al., 1999; Torrez-Martinez, et al., 1995; Song, et al., 1994; Rollin, et al., 1995). Three North American hantaviruses have not (yet?) been associated with human disease: Prospect Hill virus (PHV), associated with the meadow vole (Microtus pennsylvanicus); El Moro canyon virus (ELMCV), associated with the western harvest mouse (Reithrodontomys megalotis); and the Muleshoe virus (MULEV), also associated with the cotton rat (Sigmodon hispidus) (Lee, et al., 1982; Hjelle, et al., 1994; Rawlings, et al., submitted). MULEV was first detected in Texas.

Collaborators involved with the development of NSD are further investigating the interaction or potential interaction between hantaviruses and humans. Cryopreserved tissue samples now held at the NSRL that would allow studies such as those conducted on the deer mouse (Peromyscus maniculatus) to be expanded to other rodents. New, more detailed animal (vector) range maps, such as those produced by the Texas Gap Analysis project, combined with medical records organized in a spatial context, population statistics, and other pertinent layers of data hold the possibility of predicting the occurrences of the animal reservoirs of these viruses and their level of interaction with the human population. It is also possible that cultural and environmental factors with the potential of impacting this interaction, such as agricultural practices, drought, etc., could be predicted. These predictive models allow decision makers to play “what if” scenarios before making key decisions that could affect public health.

The biological collections utilized to help evaluate the human health risk of hantavirus were not collected with this purpose in mind; however, this case alone proved that having archived libraries of biological data can be invaluable. If these collections were not available in such a way as to provide tissues for immediate analysis, other more costly and time consuming analyses would have to be used. The next public health scare similar to the hantavirus outbreak could be 1 day or 20 years away. In such a case, these collections have the potential to help save money, time, lives, or all three.

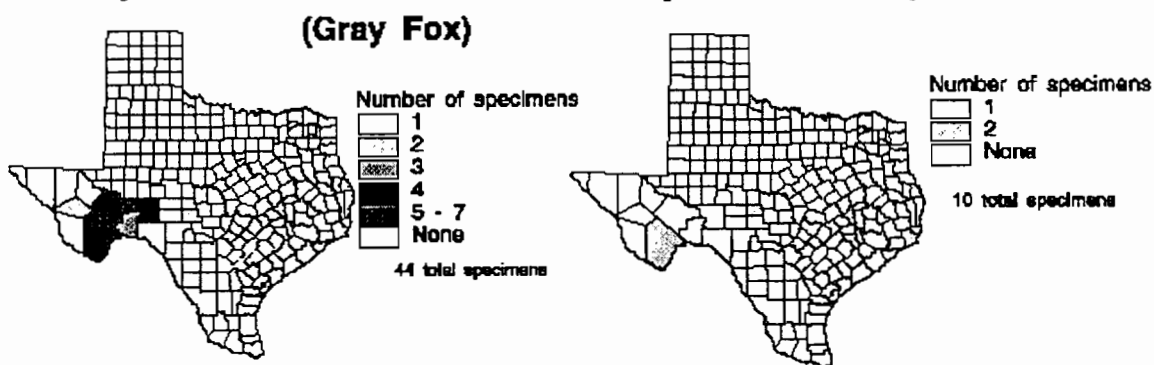
TEXAS FOX DATA

The data for foxes illustrates several points concerning museum collections and biological data bases. There are three species of foxes (Davis and Schmidly, 1994) known from Texas, and these charismatic animals are among the most prominent of the Texas carnivores. Additionally, foxes are a major component of the fur trade industry. Therefore, it might be expected that these species are well represented in museum collections. However, as can be seen in Figure 1 the total number of specimens in the TTU collection is 82 (44 Urocyon cinereoargenteus, 10 Vulpes velox, 25 V. vulpes and 3 V. macrotis). Additionally, these limited collections are concentrated around centers of human and animal interaction. This point is substantiated by the fact that most of the specimens in the collection are salvaged highway-killed animals, rather than animals taken in an effort to determine the biodiversity of the state.

In discussing museum collections with administrators, public officials, and scientists, the view often is expressed that the times of systematic collections has passed, but our perspective differs from this conclusion. For many species such as foxes, there simply is not an adequate representation of classically prepared species to adequately understand and document the biodiversity present in the state of Texas. Although classically prepared specimens are useful for many studies, collections prior to 1980 do not have associated

frozen tissue samples. Frozen tissue samples are necessary for molecular studies, to document presence or absence of disease, and to estimate levels of contaminants and pollutants in the environment. Further, by making a systematic study of specimens, we can document for future generations of Texans the biological conditions that existed during the sampling period.

Urocyon cinereoargenteus Vulpes velox (Swift fox)



Vulpes vulpes (Red Fox) Vulpes macrotis (Kit fox)

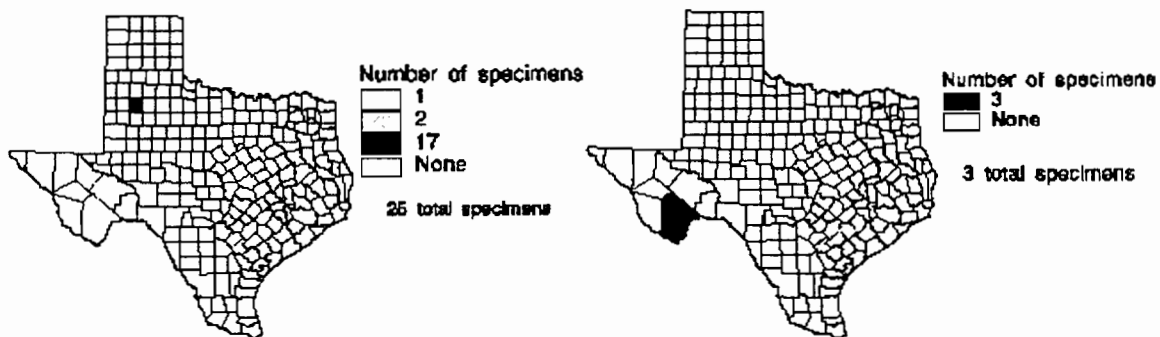


Figure 1. Distribution of foxes in Texas by species as represented in the Texas Tech Museum, Natural Science Research laboratory collection.

Although we use foxes as an example to document the under-representation of biological data in museums, the situations described above are not unique to foxes. In fact, with the exception of coyotes and bobcats, all of the carnivores are inadequately represented in collections. Smaller secretive taxa such as weasels, spotted skunks, mink, otters, etc., and larger, harder to prepare taxa such as raccoons, beavers, nutria, and muskrat are also under represented. If an emerging virus or new disease was discovered in any of these

taxa, specimens in current museum collections would be insufficient to provide for reliable analyses. Even for established diseases, such as rabies or distemper, new evidence from molecular studies has established that there are a variety of strains in mammalian fauna. It will be difficult to sort out these various strains of diseases collections.

The hantavirus data sets included one of the most commonly represented species (*Peromyscus maniculatus*) in most systematic collections. The point is that museums need to establish an adequate example of specimens with associated tissue samples. This type of well-designed systematic collection will provide society with an adequate database to efficiently address these questions concerning biodiversity, disease, pollutants and contaminants, and management.

INCIDENCE OF RABIES AMONG BATS IN TEXAS

In 1951, a 43-year-old Texas woman died from rabies presumably acquired from a bat bite. This was the first documented human case of rabies linked to a bat (Sulkin and Greve, 1954; Brass, 1994; Clark, 1994). Since then, bats have been found to be a major reservoir for the rabies virus, especially in the New World (Constantine, 1988).

Because of their association with rabies, hundreds of bats annually are tested for rabies by the Texas Department of Health. Since 1993, following testing, that agency has been sending these bats to biologists at TTU for identification. Data regarding the year and county from which bats were collected, as well as the incidence of positives and negatives, were analyzed using GIS. This resulted in the production of maps depicting spatiotemporal trends in the incidence of rabies among bats in Texas from 1993 to the present (Figure 2.). Although there are obvious sampling biases in bats submitted to health departments (Constantine, 1988; Schmidly, 1991; Brass, 1994), these results are nonetheless instrumental in understanding the prevalence and distribution of enzootic rabies in bats (Brass, 1994).

FUTURE IMPLICATIONS

The NSD will be able to address current biological and public health issues not previously possible. User interface and flexibility will provide this data set with the power to provide unique forms of data to answer increasingly difficult questions and develop better solutions to more challenging problems. Interaction with GIS software allows museum collections and attribute data to be analyzed in a spatial and temporal context. GIS clearly reveals patterns across a landscape that were formerly lost in tables

and graphs. These patterns (thematic layers) can be combined with other geographic layers of information such as land use, range maps, and satellite images. to develop new layers of information. Some of these patterns, unrecognizable to the naked eye, become apparent only when revealed by computer algorithms. While GIS is only an additional tool, it expands the capability of NSD and provides cartographic output, which is often a more powerful delivery medium than traditional methods.

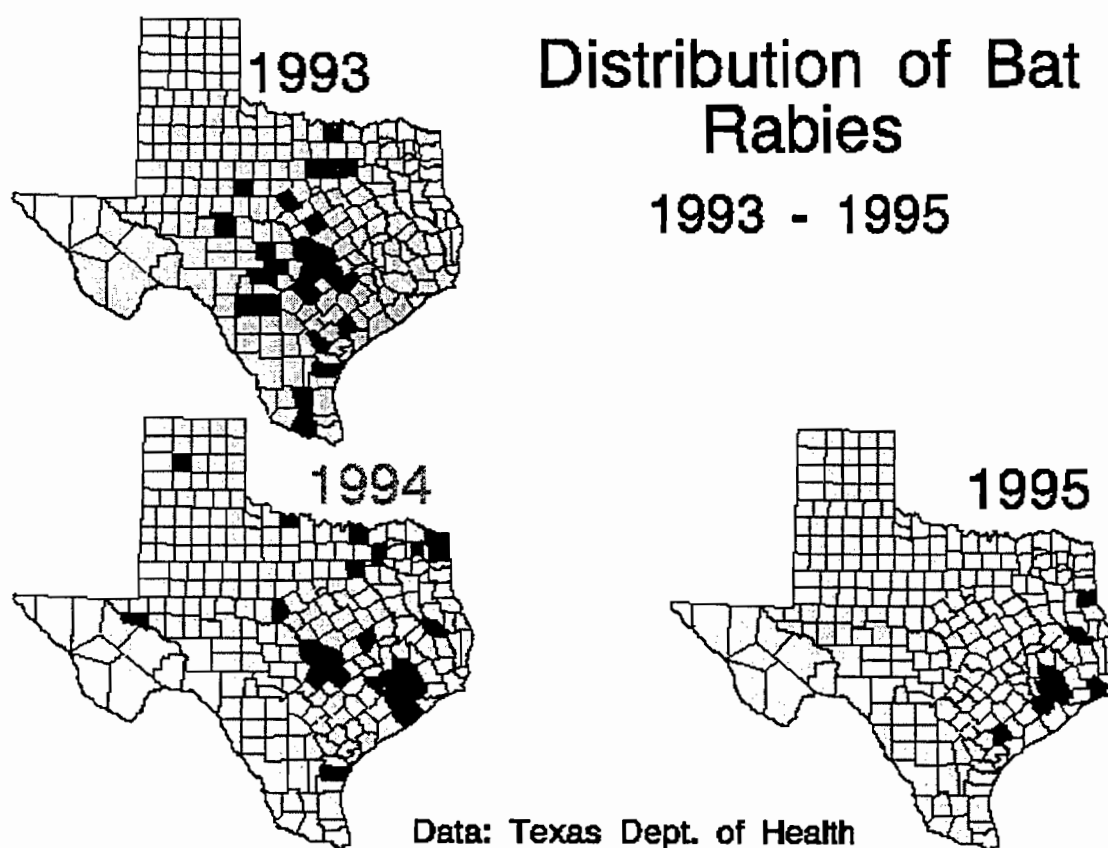


Figure 2. Distribution of the incidence of rabies among bats in Texas from 1993 through 1995.

Another and potentially even more powerful development is the utilization of the internet and the World Wide Web (WWW). To keep abreast of the latest changes in NSD and other similar efforts at Texas Tech University please visit the WWW home pages of the NSRL at <http://www.nsrl.ttu.edu/> or the TCFWRU at <http://www.tcru.ttu.edu/tcru/> respectively. The possible implications of data delivery and interaction via the WWW are almost unlimited. Access and queries of the database are instantaneous and measured

in minutes as opposed to days or weeks. The audience becomes truly worldwide. Potential for online collaboration among separate institutions and organizations becomes more feasible. It is possible to develop a central WWW access point for multiple collections. Among the implications are potential negative consequences. Data security is a major concern. Access will have to be limited to certain areas without being obtrusive. Public health issues may need strict access control.

CONCLUSION

The NSRL's collection has proven to be a valuable database, with many important applications. The NSD is now elevating this collection to new heights through improved collections, access, analyses, and data delivery. The NSD has the potential to best preserve and document the historical and future biodiversity of Texas through biological collections. Properly archived specimens collected at regular intervals provide a snapshot in time of the vertebrates and their associated potential human pathogens. This thorough database will be accessible to all Texans, will provide online queries and analyses in numerous formats including GIS, and results of these analyses will be available in many formats. The interdisciplinary team approach has proven to be the only way of successfully conducting the project.

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