AN ASSESSMENT OF SPECIES AND SUBSPECIES OF *ZAPUS* IN WYOMING

A. Bowe and G.P. Beauvais, Wyoming Natural Diversity Database (University of Wyoming)

17 November 2012

Suggested citation: Bowe, A. and G.P. Beauvais. 2012. An assessment of species and subspecies of Zapus *in Wyoming. Report prepared for the USDI Fish and Wildlife Service - Wyoming Field Office by the Wyoming Natural Diversity Database - University of Wyoming, Laramie, Wyoming.*

INTRODUCTION

Two species of jumping mouse occupy Wyoming: western jumping mouse (*Zapus princeps*), and meadow jumping mouse (*Z. hudsonius*). The former is assumed to occupy mesic environments in all mountain ranges in the state except the Black Hills, and ranges downward into foothills and adjacent basin/ prairie environments along stream corridors. Three subspecies of *Z. princeps* are assumed to occupy the state: *Z. p. utahensis* in mountains along the Utah and Idaho borders; *Z. p. idahoensis* in the remaining western mountains; and *Z. p. princeps* in the Bighorn, Laramie, Sierra Madre, and Medicine Bow ranges (Long 1965, Hall 1981, Clark and Stromberg 1987).

The meadow jumping mouse, *Z. hudsonius*, is assumed to occupy mesic environments in and near the Black Hills, and also in and near the Laramie Mountains. Current range maps for Montana (Foresman 2001; see also Montana Natural Heritage Program maps at www.mtnhp.org, and USGS Gap Analysis maps at www.gap.uidaho.edu/NorthwestGAPSpeciesviewer/) suggest *Z. hudsonius* occupies much of the southeast corner of that state, extending as far west as the Pryor Mountains, which in turn suggests possible occupation of northeastern Wyoming as far west as the Bighorn Mountains and possibly even the eastern front of the Absaroka Mountains. Two subspecies of *Z. hudsonius* likely occupy the state: *Z. h. campestris* in the northeast, and *Z. h. preblei* in the southeast (Long 1965, Clark and Stromberg 1987, King et al. 2006). In an opposite elevational pattern to *Z. princeps*, *Z. hudsonius* is assumed to primarily occupy mesic environments in prairie and foothills regions, with occasional extensions into the montane zone along stream corridors. *Zapus hudsonius* is also assumed to have a stronger preference for riparian and wetland environments than *Z. princeps*, and any forays into adjacent uplands are thought to be short in both distance and time (Long 1965, Clark and Stromberg 1987, Ryon 1999, Schorr 2003).

Research and management interest in Wyoming *Zapus* increased substantially with the listing of *Z. h. preblei* as Threatened under the U.S. Endangered Species Act (ESA) in 1998, and has increased further with the potential for accelerated petroleum development within the range of *Z. h. preblei* in Wyoming (see http://nrgcoalition.org/basins/wyoming-niobrara-energy/resources/). Following the initial listing, it became clear that distinguishing the two species from one another in areas of sympatry in southeast Wyoming was difficult, and perhaps impossible, under field conditions. Modern genetic analyses can clearly distinguish the species, and have been applied to many recently-captured specimens as well as a few older ones (Ramey et al. 2005, King et al. 2006). However, conclusive species assignment of many older Wyoming *Zapus* observations by these means is impossible given the lack of preserved tissue. Furthermore, genetic testing of all current *Zapus* observations may not be possible given the permitting required for tissue collection from ESA-listed taxa, the expertise and materials necessary for tissue collection and preservation, and the expense of tissue delivery and laboratory operations.

Total length (TL) of *Zapus* specimens has been used to distinguish the two species in Wyoming, with adults >225mm TL keying to *Z. princeps* and adults <225mm TL keying to *Z. hudsonius* (Clark and Stromberg 1987). This measurement may be useful for sorting large groups of specimens, but is not 100% accurate when applied to any single specimen. Furthermore, it may be misleading when applied to individuals that have not attained full adult dimensions. Similarly, the two species appear to segregate generally by elevation, with *Z. princeps* typically occurring above *Z. hudsonius* (Clark and

Stromberg 1987, Armstrong et al. 2011). But we now know of several specific situations in which the reverse pattern holds, and it appears that the two species overlap across a relatively broad elevation zone in southeastern Wyoming. Both TL and elevation-of-observation may be potentially useful indicators of species identity – especially given the ease with which they can be applied in the field - but they clearly require more study and refinement as predictive tools.

Other measurements have been developed to identify Wyoming *Zapus* to species, but none have proven 100% accurate and thus are best used as indicative, rather than conclusive, of species identity. An early analysis of mitochondrial DNA by Riggs et al. (1997) classified some specimens to species. Conner and Shenk (2003) developed a discriminant function based on multiple skull measurements that suggested *Z. princeps* skulls are, on average, larger than those of *Z. hudsonius* in this region. The same researchers examined a dental character - anterior median tooth-fold of M3 – that is also suggestive of species identity.

The current state of knowledge of the ranges of *Z. princeps* and *Z. hudsonius* in southeastern Wyoming is substantially complicated by the diversity of species identification techniques applied to various observations over time, and the uncertainties specific to each technique. Furthermore, attempts to organize Wyoming *Zapus* information to-date have revealed numerous instances in which original observation data was lost or altered as specimens and tissue samples were exchanged between various researchers, laboratories, museum collections, and other data repositories.

This project sought to clarify the state-of-knowledge of Wyoming *Zapus* via a comprehensive review, cross-referencing, and compilation of as many observation records of Wyoming *Zapus* as possible. We gave special attention to attributing each record with accurate geographic coordinates of the site of original observation, and all information relevant to species identification. We then used records of known species identity - i.e., those that underwent genetic analyses via Ramey et al. (2005) or King et al. (2006) – as a basis for evaluating the accuracy of six indicative measures of species identity. Where sample size allowed, we re-framed indicative measures as quantitative models predicting species identity. Finally, we synthesized all information and models into a weight-of-evidence determination of species identity for as many observations as possible in our dataset, resulting in range maps for *Z. princeps* and *Z. hudsonius* in Wyoming.

This project was supported by the USDI Fish and Wildlife Service (Ecological Services, Cheyenne, Wyoming), the Wyoming Game and Fish Department (WGFD), and the Office of the Governor of Wyoming. It follows an initial project that developed an annotated bibliography of scientific literature addressing Wyoming *Z. hudsonius* in general, and with special relevance to managers and project operators involved with petroleum development within the purported range of *Z. h. preblei* in particular (Bowe and Beauvais 2011). The report and products from the initial project, as well as those from the project presented here, are available on the web site of the Wyoming Natural Diversity Database (WYNDD; University of Wyoming): www.uwyo.edu/wyndd

METHODS

<u>Consolidation and attribution of *Zapus* observation records for Wyoming:</u> Data compilation started with a download of records of Wyoming *Zapus* observations from the WYNDD central database, which was the most complete collection of such records in existence at the start of this project. Importantly, efforts preceding this project ensured that the WYNDD download included observation records collected by the WGFD up to 2009. Records of *Zapus* observations collected by the WGFD from 2009 – 2011 were brought into the project by a separate effort. The WYNDD download was converted to an MS Excel spreadsheet, and initially contained several records that each represented multiple individual *Zapus* observed at single sites. Such records were expanded into multiple records, one for each individual *Zapus*. This same procedure was applied to all other record sets brought into the project. Several attribute fields were added to the original table in order to accurately track specimen characteristics (e.g., ID number, gender, body measurements; see Appendix A). Also, a suite of fields was added pertaining to any species identification techniques applied to each specimen. When newly-acquired record sets contained information that required documentation in new attribute fields, we added those fields to all records in the set and populated them as best we could, given the available information.

We contacted data managers at several major sources of mammal specimen and observation data and requested downloads of Wyoming *Zapus* records (Table 1). All records we received were cross-checked against all others in our collection, with special attention to observation/ collection locations and dates in order to identify and eliminate duplicate records. In cases where the same record was discovered in multiple sources, we collapsed the duplicates into only one record and ensured that all source-specific attributes were captured in that record. Importantly, we also cross-referenced each record against information in Riggs et al. (1997), Conner and Shenk (2003), Ramey et al. (2005), and King et al. (2006), with attention to sample/ specimen identification codes, to ensure proper attribution of species assignments from those efforts to individual records.

We attributed each record with locational coordinates that best represented the actual site of field observation, and also a map precision value that best represented the likely error associated with those coordinates. In some cases, exact coordinates and map precision values were reported in the original record documentation. In other cases, locations were reported in narrative form and were unaccompanied by any estimates of map precision. Our methods for deriving specific locational coordinates and map precision values for records in the latter situation are outlined in Appendices A and B. Manual digitization and other spatial operations required by these methods were conducted with the ArcMap (version 9.3; ESRI Inc.) software package and Google Earth (Google, Inc.) application.

We additionally attributed records with an elevation value that best represented the elevation of the actual observation site. For each record, an elevation value was derived by overlaying the locational coordinates on a digital elevation model (DEM; Gesch et al. 2002). Some records were accompanied by an elevation reported in the original documentation. Our review of such records suggested that most reported elevation values were rather coarse estimates made in the field, possibly without map assistance. Thus, we replaced the reported values with those derived from the DEM overlay on the assumption that the latter were more accurate.

We also attributed each record with a standardized elevation value, which was the raw elevation of the observation site adjusted for latitude. Ecological zones occupy lower elevation bands at more northerly latitudes, a phenomenon most easily observed in the negative relationship between elevation of upper tree-line and latitude. To account for this phenomenon, and for the possibility that *Zapus* are responding to "ecological elevation" rather than raw elevation, we attributed each record with standardized elevation, which was the elevation of the observation site adjusted to account for a loss of 130m (426.5 feet) per degree of latitude north of 41 degrees (the latitude of the Colorado/ Wyoming border). This follows the global estimates of Korner (1998), and also closely matches the estimates of Knight (1994) for Wyoming.

Assessing evidence of species identity : Once *Zapus* records were compiled, attributed, and quality-checked, we assessed the species identity of the individual represented in each record. We assumed that species assignments by either Ramey et al. (2005) or King et al. (2006) were completely accurate, and thus records of individuals identified to species by those efforts were attributed accordingly. This provided a set of records of confirmed species identities with which we evaluated the accuracy of less conclusive, but potentially still valuable, measures of species identity. We recognized six such indicative measures. Four pertained to the observed *Zapus* individual: genetic analysis of Riggs et al. (1997); skull morphology analysis of Conner and Shenk (2003); anterior medial tooth-fold on M3 following Conner and Shenk (2003); and specimen TL following Clark and Stromberg (1987). Two pertained to the observation site: major river basin encompassing the site; and elevation of site (including both raw and standardized elevation). Importantly, the latter two measures could be derived for almost all records, given that almost all records were attributed with locational coordinates.

The analysis of Riggs et al. (1997) and the skull morphometry of Conner and Shenk (2003) each produced a prediction of either *Z. hudsonius* or *Z. princeps*, providing a straightforward comparison of each of those measures to the confirmed identity via a standard 2x2 confusion matrix. Total length and elevation could be treated in the same manner provided a cut-point on each measure that separated *Z. hudsonius* from *Z. princeps*. We used 225mm as the TL cut-point between the species (*Z. hudsonius* <225mm), following Clark and Stromberg (1987). We used 7500 feet as the elevation cut-point (*Z. hudsonius* <7500 feet), which generally agreed with the opinions of local and regional mammalogists familiar with *Zapus* spp. We recognized that both TL and elevation would be amenable to more precise logistic regression modeling, and thus did not apply more intensive research to the selection of these cut-points in this phase of the project.

The tooth-fold analysis of Conner and Shenk (2003) suggested that whereas the presence of a tooth-fold was indicative of *Z. hudsonius*, its absence was not reliable indication of either species. Thus we anticipated deriving only a 1x2 confusion matrix for this measure.

Finally, based on previously published range maps (Long et al. 1965, Hall 1981, Clark and Stromberg 1987) and preliminary mapping of observation records, it was apparent that *Z. hudsonius* was likely the only *Zapus* species potentially occupying the Little Missouri, Belle Fourche, Cheyenne, and Niobrara River basins in the state. Conversely, *Z. princeps* was likely the only *Zapus* species occupying the Yellowstone, Snake, Bear, Green, and Little Snake River basins, and the Great Divide Basin. However, both taxa were either known or strongly suspected to occupy portions of the North Platte, South Platte, Powder, Tongue, and Bighorn River basins. Thus, we anticipated deriving a 3x2 confusion matrix for this measure in which records encompassed by the latter five basins would be assigned no species prediction.

We anticipated that for most indicative measures there would be relatively few records that had corresponding confirmed species identities - i.e., relatively few specimens that had been evaluated by the indicative measure and also by either Ramey et al. (2006) or King et al. (2006). In cases of low sample size, we did no further modeling or evaluation beyond the confusion matrix.

In cases where we felt we had a large enough sample of records, we derived logistic regression models to more finely assess the degree to which an indicative measure predicted species identity. Logistic regression models were built in S-Plus (version 6.1; Insightful Corp.). Input records were a subset of all records possessing both confirmed identity and the target indicative measure. The subset included records whose observation sites were at least 1000m apart (i.e., we eliminated from the subset records that were closer than 1000m). In cases where we could have chosen more than one record to represent a cluster of records <1000m apart, we preferentially selected the record with the most recent date of observation. This spatial de-clustering was necessary because we assumed that our full sample of observation records would be spatially biased towards particularly heavily-sampled sites, and thus we wanted to avoid biasing the resulting models towards attribute values from over-sampled sites. Said differently, we de-clustered the records to approximate a more spatially-random distribution of input values for modeling.

Each logistic regression model was validated with a confusion matrix in which input records were classified to species by the model. Records were classified using a probability cut-point between predicted *Z. hudsonius* and predicted *Z. princeps* as the mid-point between the average predicted probabilities for the known-identity records for each species. Selecting a cut-point in this manner helped balance the predictive error of the model when used as a classification tool – i.e., model predictions were not biased towards either species.

We then used all indicative measures, as refined by logistic regression modeling where appropriate, to assign a final prediction of species identity to each record that did not already have a confirmed species identity. Our protocol assigned a point to either *Z. princeps* or *Z. hudsonius* according to the conclusion of each indicative measure relevant to the record. The points were summed after all indicative measures were scored, resulting in point totals for *Z. princeps* and *Z. hudsonius* for each record. The species category with the most points was assigned as the identity of the individual *Zapus* represented by that record. For records with equal points between species categories, species identity was assigned as "unknown *Zapus*".

The magnitude of the difference between the point totals was used as an ordinal measure of certainty in the species identification. Records for which one species category had only one or two more points than the other were labeled "possible" – e.g., a record evaluated by four indicative measures of which three indicated *Z. princeps* and one indicated *Z. hudsonius* was attributed "possible *Z. princeps*". Records for which one species category had >2 points than the other were labeled "likely" – e.g., a record evaluated by three indicative measures of which all three indicated *Z. hudsonius* was attributed "likely *Z. hudsonius*".

Mapping of *Zapus* observation records for Wyoming: Records were initially mapped as points, symbolized to represent their confirmed, likely, possible, or unknown species affiliations. However, species' ranges are often not well depicted by point-maps, primarily because un-sampled area usually dominates such maps and provides viewers no information on occurrence across more meaningful landscapes. To address this, WYNDD has begun mapping species' ranges in Wyoming by 10-digit hydrologic units (HUCs; Simley and Carswell 2009), an approach that appears to be increasingly adopted by other organizations such as the USGS (e.g., Prior-Magee et al. 2007) and Wyoming Game and Fish Department (Wyoming Game and Fish Department 2010). The 10-digit scale has proven to be a useful compromise for mapping at the state and regional scales, and appears to provide the best balance between the extreme precision of point-maps and gross over-mapping of coarse "field guide" style range maps.

All 10-digit HUCs in Wyoming that encompassed records of confirmed *Z. princeps* were attributed as such. Then, remaining unattributed HUCs that encompassed records of likely *Z. princeps* were attributed accordingly. Finally, any remaining unattributed HUCs that encompassed records of possible *Z.princeps* were attributed accordingly. A similar procedure was used to separately attribute HUCs as to the presence of encompassed *Z. hudsonius* records. We assumed that several HUCs would encompass records of both species, and thus attributed HUCs separately per species in order to construct accurate species-specific maps. The species maps were each produced by symbolizing HUCs, using color, to indicate differences between the known, likely, and possible levels of identification. Also, in each map, all records of unknown *Zapus* were indicated not by HUC attribution, but rather only by symbolized points.

RESULTS

Consolidation and attribution of *Zapus* observation records for Wyoming: At the time of this analysis we had received and organized 1892 records of Wyoming *Zapus* observations from 20 different sources (Table 1). Attributes of records in this set are described in Appendix A. Note that this record set is under continual revision and updating. Future examinations of the set will reveal different record totals, and possibly slightly different attributes.

Assessing evidence of species identity: Twenty-seven of the 1892 records had confirmed species affiliations via Ramey et al. (2005), whereas 195 had confirmed species affiliations via King et al. (2006). The latter set included 34 records that were not included in the original King et al. (2006) study but that were evaluated by the same methods via tissue samples collected by and submitted to the King laboratory by WGFD. The species identity of one record was evaluated by both Ramey et al. (2005) and King et al. (2006), for a total of 221 records (11.7% of the total) with confirmed species identities (Table 2). One-hundred-fifty represented confirmed *Z. princeps*; 71 represented confirmed *Z. hudsonius*.

Regarding the six indicative measures of species identity, 1875 records could be attributed with major river basin of occurrence, and 1847 with a reliable elevation (and thus also standardized elevation) of the observation site. Far fewer records could be attributed with the remaining four indicative measures (Table 2). All six indicative measures appeared to have some ability to correctly predict species identity but, as anticipated, our ability to finely assess the predictive power of most such measures was hampered by low sample sizes (Table 3).

We produced logistic regression models predicting species identity with TL, and with elevation of the observation site. We initially assessed the possibility of constructing a separate TL model for adult specimens only, but quickly concluded that such partitioning of the data would reduce an already-tenuous sample size (16 records following spatial filtering) to an unacceptably low level. Based on all 16 records attributed with TL and confirmed species identity, the logistic regression model correctly classified 68.8% of the confirmed *Zapus* records based on a cut-point probability of 0.55, which corresponded to a TL of 213mm (Figure 1a).

We produced separate logistic regression models for elevation of observation site, and for standardized elevation of observation site. Whereas the model using standardized elevation as a predictor correctly classified 71.2% of the confirmed records to species (cut-point probability 0.622, corresponding to 6896 feet standardized elevation), the model using raw elevation correctly classified 76.3% of the confirmed cases (cut-point 0.606, 6407 feet elevation; Figure 1b). Given its higher classification success and greater ease of interpretation, we used the latter model in the remainder of this project.

Our record scoring procedure considered the results of Riggs et al (1997), skull morphometry of Conner and Shenk (2003), tooth-fold assessment of Conner and Shenk (2003), and major river basin of occurrence as shown in Table 3. The procedure considered TL and elevation of occurrence as refined by the logistic regression models and cut-points shown in Figure 1. After scoring was completed, in addition to the 150 (7.9% of the total 1892) records representing confirmed *Z. princeps* and 71 (4.2%) representing confirmed *Z. hudsonius*, our dataset included: 20 (1.0%) records of likely *Z. princeps*; 1305 (69.0%) of possible *Z. princeps;* 4 (0.2%) of likely *Z. hudsonius*; and 184 (9.7%) of possible *Z. hudsonius*. Note that the dataset also encompassed 158 (8.4%) records of unknown *Zapus* (Figures 2 and 3).

Mapping of *Zapus* observation records for Wyoming: Figures 2 and 3 show the geographic distributions of the records in our dataset, symbolized by confirmed or predicted species identity. Thirteen HUCs encompass confirmed, likely, or possible records of both species; only four HUCs encompass confirmed records of both species. Most such “dual species” HUCs lie along the Laramie Mountains, although two HUCs in the former set are in the Bighorn basin along the North Fork and South Fork of the Shoshone River, and one HUC in the former set is on the Bighorn Mountains in the vicinity of the town of Buffalo (Clear Creek).

DISCUSSION

--- The compilation of records resulting from this project is arguably the most comprehensive collection of Wyoming *Zapus* data in existence, but it must be viewed as a work continually in-progress. New observation records are continually being recorded and added to the set; older observation records from minor sources may come to light; and more detailed examination of existing records may reveal duplicates that require collapsing into single records. The database will be continually expanded, updated, and improved by WYNDD staff into the future as new information becomes available.

--- Within the purported range of *Z. h. preblei* (southeastern Wyoming), all confirmed *Z. hudsonius* records are on or near the eastern front of the Laramie Mountains. No confirmed, likely, or possible record of *Z. hudsonius* falls west of the crest of the Laramie Mountains. Many confirmed *Z. princeps* records (as well as many likely and possible *Z. princeps* records) fall to the west of this range. In combination with the suggested elevation cutoff between the two species of 6407 feet (Figure 1b), this suggests that the Shirley Basin/ Laramie Valley vicinity may be occupied only by *Z. princeps*. The eastern slope and eastern base of the Laramie Mountains supports both species.

--- The several confirmed, likely, and possible *Z. hudsonius* records in and near the Black Hills of northeastern Wyoming concur with the general understanding of the distribution of *Z. h. campestris* in the state. The lack of *Zapus* records mapping to the Niobrara, Cheyenne, and upper Powder River basins suggests very little connectivity between *Z. h. preblei* in southeastern Wyoming and *Z. h. campestris* in northern Wyoming.

--- Records of likely and possible *Z. hudsonius* on the eastern front of the Bighorn Mountains suggest that *Z. h. campestris* may extend to that area, which would agree with Montana range maps for the subspecies. Furthermore, the possible *Z. hudsonius* records mapping to the Shoshone River in the Bighorn Basin suggests possible occupation of that region as well.

--- In 2012 WYNDD collected *Zapus* observation records, and tissue samples, from upper Rock Creek, upper Medicine Bow River, and the Little Laramie River. Genetic results following the methods of King et al. (2006) are expected by January 2013 for these samples. These results will add confirmed *Zapus* points and HUCs in portions of eastern Carbon County and western Albany County that currently encompass no *Zapus* records. Note that this same effort sought, but failed, to document *Zapus* on the lower Sweetwater and lower Medicine Bow Rivers.

--- In 2012 the WGFD attempted to document *Zapus* at several sites on and near the main stem of the North Platte River from, roughly, the Nebraska/ Wyoming border upstream to the town of Casper. No *Zapus* were captured during this trapping effort. In the same season the WGFD captured a single *Zapus* from one site on the North Laramie River. A tissue sample was collected from the trapped individual and has been submitted for genetic analysis following the methods of King et al. (2006). Genetic results are expected by January 2013. These results will be added to the database, alongside the 2012 WYNDD results described above.

LITERATURE CITED

Armstrong, D.M., J.P. Fitzgerald, and C.A. Meaney. 2011. Mammals of Colorado. Second edition. Denver Museum of Nature and Science and University Press of Colorado. Boulder, Colorado.

Bowe, A. and G.P. Beauvais. 2011. Literature compilation: Preble's meadow jumping mouse (*Zapus hudsonius preblei*) in Wyoming, with attention to potential effects of petroleum development. Report prepared for the Wyoming Game and Fish Department and USDI Fish and Wildlife Service – Wyoming Field Office by the Wyoming Natural Diversity Database – University of Wyoming, Laramie, Wyoming.

Clark, T.W. and M.R. Stromberg. 1987. Mammals in Wyoming. University of Kansas Museum of Natural History. Lawrence, Kansas.

Conner, M.M. and T.M. Shenk. 2003. Distinguishing *Zapus hudsonius preblei* from *Zapus princeps princeps* by using repeated cranial measurements. Journal of Mammalogy 84:1456-1463.

Foresman, K.R. 2001. The wild mammals of Montana. American Society of Mammalogists Special publication No. 12.

Gesch, D., Oimoen, M., Greenlee, S., Nelson, C., Steuck, M., and Tyler, D. 2002. The National Elevation Dataset. Photogrammetric Engineering and Remote Sensing. 68:5-11.

Hall, E.R. 1981. The mammals of North America. Volume 2. John Wiley and Sons, Inc. New York, New York.

King, T.L., J.F. Switzer, C.L. Morrison, M.S. Eackles, C.C. Young, B. Lubinski, and P. Cryan. 2006. Comprehensive genetic analyses reveal evolutionary distinction of a mouse (*Zapus hudsonius preblei*) proposed for delisting from the U.S. Endangered Species Act. Molecular Ecology 15:4331–4359.

Knight, D. 1994. Mountains and plains: the ecology of Wyoming landscapes. Yale University Press. New Haven, Connecticut.

Körner, C., 1998. A re-assessment of high elevation treeline positions and their explanation. Oecologia 115:445–459.

Long, C.A. 1965. The mammals of Wyoming. University of Kansas Museum of Natural History Publication 14:349-472.

Prior-Magee, J.S., K.G. Boykin, D.F. Bradford, W.G. Kepner, J.H. Lowry, D.L. Schrupp, K.A. Thomas and B.C. Thompson (editors). 2007. Southwest Regional Gap Analysis Project final report. U.S. Geological Survey-Gap Analysis Program. Moscow, Idaho.

Ramey, R.R., H.P. Liu, C.W. Epps, L.M. Carpenter, and J.D. Wehausen. 2005. Genetic relatedness of the Preble's meadow jumping mouse (*Zapus hudsonius preblei*) to nearby subspecies of *Z. hudsonius* as inferred from variation in cranial morphology, mitochondrial DNA, and microsatellite DNA: implications for taxonomy and conservation. Animal Conservation 8:329-346.

Riggs, L.A., J.M. Dempcy, and C. Orrego. 1997. Evaluating distinctness and evolutionary significance of Preble's meadow jumping mouse: phylogeography of mitochondrial DNA non-coding region variation. Final Report submitted to Colorado Division of Wildlife, 13 pp. + appendices.

Ryon, T.R. 1999. Travel distance and movement patterns of the Preble's meadow jumping mouse (*Zapus hudsonius preblei*) at the Rocky Flats Environmental Technology Site. Journal of Colorado-Wyoming Academy of Science 31:12.

Schorr, R.A. 2003. Meadow jumping mice (*Zapus hudsonius preblei*) on the U.S. Air Force Academy, El Paso County, Colorado: populations, movement and habitat from 2000-2002. Report prepared for U.S. Air Force Academy – Natural Resources Branch by the Colorado Natural Heritage Program – Colorado State University, Fort Collins, Colorado.

Simley, J.D. and W.J. Carswell Jr. 2009. The National Map—Hydrography. U.S. Geological Survey Fact Sheet 2009-3054.

Wyoming Game and Fish Department. 2010. Wyoming Game and Fish Department State Wildlife Action Plan. Wyoming Game and Fish Department. Cheyenne, Wyoming.

TABLES

Table 1. Major sources of observation records of *Zapus* in Wyoming. Record tallies include duplicate records (i.e., the same records existing in different sources). Note that the first source – "Wyoming Natural Diversity Database Biotics Records" – incorporated *Zapus* observation records collected by the Wyoming Game and Fish Department prior to 2009.

Collection Name	**Abbreviation**	**No. records**	**Source**
Wyoming Natural Diversity Database Biotics Records	WYNDD	1287	WYNDD
Kansas University Museum of Natural History	KUMNH	487	MANIS
National Museum of Natural History, Smithsonian Institution	USNM	229	MANIS
Division of Mammals, Museum of Southwestern Biology, Albuquerque, NM.	MSB	129	ARCTOS
University of Michigan Museum of Zoology (UMMZ) - Mammal specimens	UMMZ	61	MANIS
Wyoming Game and Fish Dept. – Nongame Program *Zapus* captures, 2009-2011	WGFD	130	WGFD
University of Wyoming Vertebrate Collection	UWyo	43	UWyo
MVZ Mammal Catalog	MVZ	19	ARCTOS
American Museum of Natural History (AMNH) - Mammals	AMNH	15	MANIS
Museum of Texas Tech University (TTU) - Mammal specimens	TTU	6	MANIS
University of Alaska Museum, Mammal Collection	UAM	5	MANIS
MCZ-Harvard University Provider - MCZ Mammalogy Collection	MCZ	4	MANIS
University of Colorado Museum of Natural History - Mammal Collection	UCol	4	MANIS
University of Montana Division of Biological Sciences	UMont	4	UMont
Santa Barbara Museum of Natural History	SBMNH	3	MANIS
University of Nebraska State Museum - UNSM Vertebrate Specimens	UNSM	2	MANIS
Western New Mexico University Mammal Collection	WNMU	2	MANIS
James R. Slater Museum (PSM) - Terrestrial vertebrates	PSM	1	MANIS
Royal Ontario Museum - Mammal specimens	ROM	1	MANIS
Texas Cooperative Wildlife Collection (TCWC) - TCWC Vertebrate Collections	TCWC	1	MANIS

Table 2. Measures of species identity attributed to records of *Zapus* observations in Wyoming. Numbers in table cells indicate number of records.

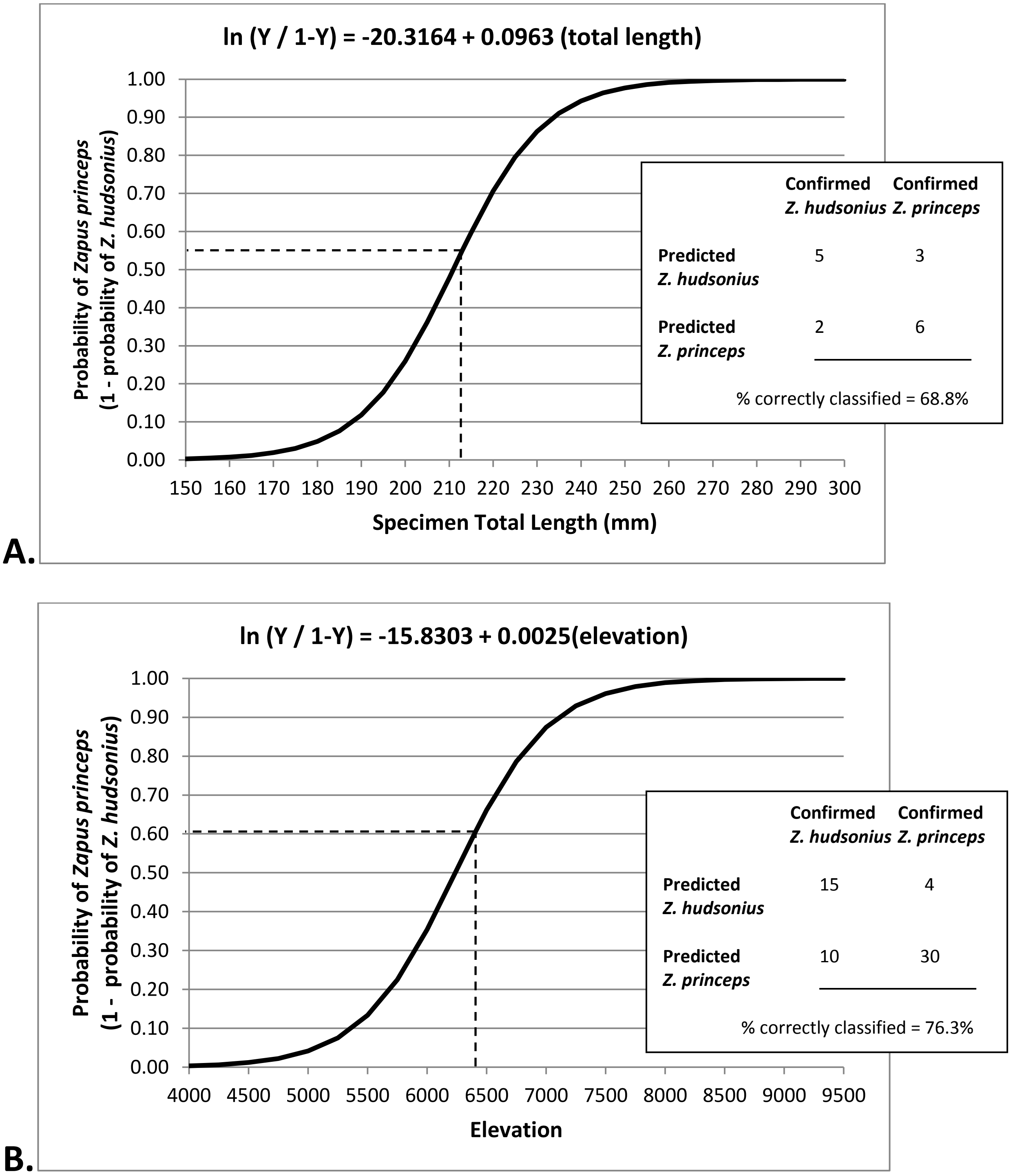
	Ramey et al. 2005 - genetics	King et al. 2006 - genetics	Major river basin	Riggs et al. 1997 – genetics	Conner and Shenk 2003 – skull morph.	Conner and Shenk 2003 – tooth-fold	Specimen total length	Elevation of obs. site
Ramey et al. 2005 – genetics	27							
King et al. 2006 – genetics	1	195						
Major river basin	26	195	1875					
Riggs et al. 1997 - genetics	1	0	11	11				
Conner and Shenk 2003 – skull morph.	11	2	62	0	67			
Conner and Shenk 2003 – tooth-fold	1	1	7	0	6	8		
Specimen total length	3	14	112	3	3	1	112	
Elevation of obs. site	24	194	1846	11	59	7	110	1847

Table 3. Confusion matrices showing success of each of 6 different measures in predicting the species identity of *Zapus* observation records in Wyoming. Numbers in the cells of the middle 2 columns indicate number of observation records for which species identity was known (based on techniques of Ramey et al. 2005 or King et al. 2006) and also predicted by the associated measure. The cut-point used to assign records to species via total length was <225mm = *Z. hudsonius*; >225mm = *Z. princeps*. The cut-point used for elevation of occurrence was <7500 ft = *Z. hudsonius*; >7500 ft = *Z. princeps.* See Figure 1 for a refinement of the latter 2 models.

	Confirmed *Z. hudsonius*	Confirmed *Z. princeps*	Overall success
MAJOR RIVER BASIN			
Predicted *Z. hudsonius*	6 (100%)	0	100%
Predicted either spp.	65	143	
Predicted *Z. princeps*	0	7 (100%)	
SKULL MORPHOMETRY			
Predicted *Z. hudsonius*	6 (100%)	1	91.7%
Predicted *Z. princeps*	0	5 (83.3%)	
TOOTH-FOLD			
Predicted *Z. hudsonius*	1 (100%)	NA	100%
Predicted *Z. princeps*	NA	NA	
RIGGS ET AL. 1997			
Predicted *Z. hudsonius*	1 (100%)	0	100%
Predicted *Z. princeps*	0	0	
TOTAL LENGTH			
Predicted *Z. hudsonius*	6 (85.7%)	6	56.2%
Predicted *Z. princeps*	1	3 (33.3%)	
ELEVATION			
Predicted *Z. hudsonius*	68 (61.3%)	1	79.7%
Predicted *Z. princeps*	43	105 (99.0%)	

FIGURES

Figure 1. Logistic regression models predicting *Zapus* species identity with (a) specimen total length and (b) elevation of observation site. Dotted lines show cut-point values used to classify records as shown in the confusion matrix. Cut-points were 0.552 (=213mm) for total length; 0.606 (=6407ft) for elevation.



	Confirmed *Z. hudsonius*	**Confirmed *Z. princeps***
Predicted *Z. hudsonius*	5	3
Predicted *Z. princeps*	2	6

% correctly classified = 68.8%

	Confirmed *Z. hudsonius*	**Confirmed *Z. princeps***
Predicted *Z. hudsonius*	15	4
Predicted *Z. princeps*	10	30

% correctly classified = 76.3%

Figure 2. Distribution of observation records of *Zapus princeps* in Wyoming. Records are indicated by point-symbols, and also by 10-digit hydrologic units (HUCs) encompassing the points, as shown in the map legend. Point-symbols for confirmed records are depicted on top of point symbols for likely and possible records; thus, some underlying symbols are obscured. HUCs encompassing confirmed records are symbolized as such, regardless of other record types encompassed. Remaining HUCs encompassing likely records are symbolized similarly; finally, remaining HUCs encompassing possible records are symbolized as such. Note that species identity was "confirmed" only when determined via the methods of either Ramey et al. (2005) or King et al. (2006). Red question marks indicate observations of *Zapus* spp. unaccompanied by specimen or location measurements that provided any insight on species identity.

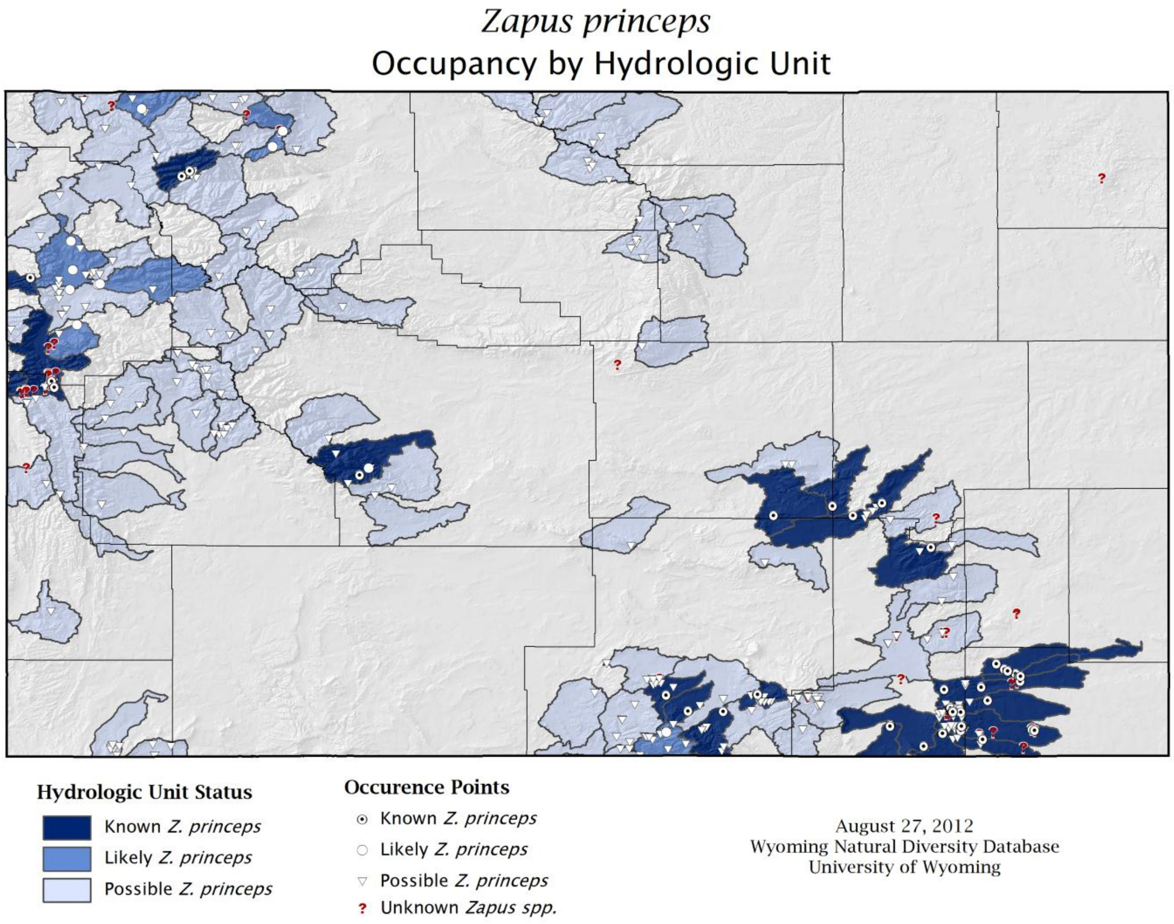
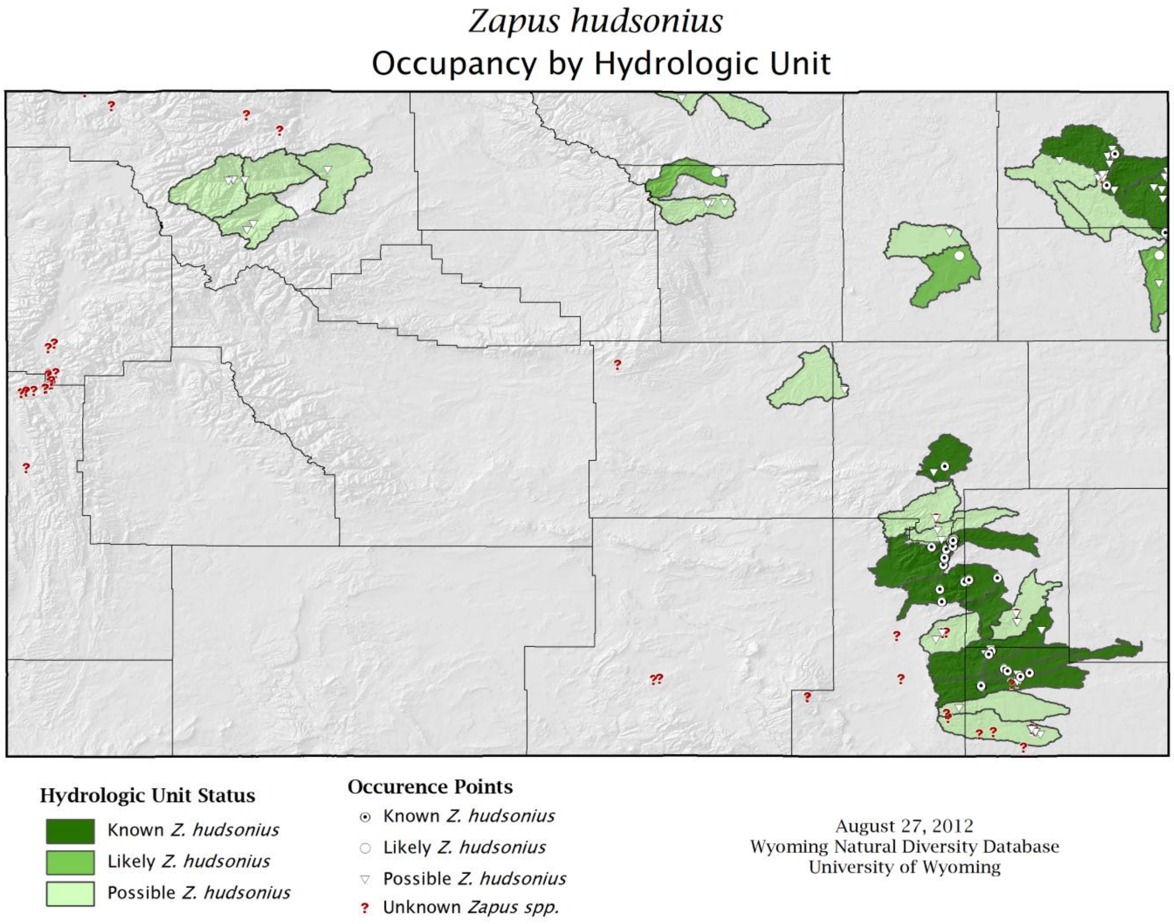


Figure 3. Distribution of observation records of *Zapus hudsonius* in Wyoming. Records are indicated by point-symbols, and also by 10-digit hydrologic units (HUCs) encompassing the points, as shown in the map legend. Point-symbols for confirmed records are depicted on top of point symbols for likely and possible records; thus, some underlying symbols are obscured. HUCs encompassing confirmed records are symbolized as such, regardless of other record types encompassed. Remaining HUCs encompassing likely records are symbolized similarly; finally, remaining HUCs encompassing possible records are symbolized as such. Note that species identity was "confirmed" only when determined via the methods of either Ramey et al. (2005) or King et al. (2006). Red question marks indicate observations of *Zapus* spp. unaccompanied by specimen or location measurements that provided any insight on species identity.



APPENDICES

Appendix A. Attributes appended to records of *Zapus* spp. observations in Wyoming.

1. Record Information
    a. **SpecID** - Unique Key used to identify each specimen record in the database. In the format ZPSP####.
    b. **ELCode -** Stands for Element Code. A unique 10 digit code for each organism, assigned by NatureServe and used by WYNDD and other state Natural Heritage Programs. The ELCodes and associated taxa used in this database are listed below. Note that there are no unique ELCodes assigned to individual subspecies of *Z. princeps*.
        - *Zapus hudsonius*: AMAFH01010
        - *Zapus hudsonius preblei*: AMAFH01011
        - *Zapus hudsonius campestris*: AMAFH01013
        - *Zapus princeps*: AMAFH01020
    c. **Orig_Scientific Name** – Scientific name of the reported individual, as originally reported.
    d. **Orig_Common Name** – Common name of the reported individual, as originally reported.
    e. **Orig_Obs_Date** - Date on which the capture or observation was made in the field, as originally reported.
    f. **Norm_Obs_Date** - Date on which the capture or observation was made in the field, converted into a standardized entry in the form of mm/dd/yyyy. Note that "1/1/yyyy" is used when only the year was originally reported.
    g. **Observer** - Individual(s) or organization responsible for making the first-hand capture or observation in the field, as originally reported.
    h. **Obs_Type** – A general classification for the source, formality of the protocol, and estimated reliability of the observation or record. Uses the WYNDD-derived standard entries of: Specimen; Observation: Non-WYNDD expert; Observation: WYNDD staff; Survey: non-WYNDD expert; Survey: WYNDD staff; Survey: WYNDD experts; WOS: not reviewed; Literature: unspecified).
    i. **Obs_Data** – A text description of the results of the overall trapping survey or detection effort that resulted in the capture or observation of the reported individual. If the individual is 1 of 5 trapped at that location and date, the Obs_Data description might read "5 individuals (2 male, 2 female, 1 unknown) trapped in 750 trap nights". This text description would be the same for all 5 separate records resulting from such a survey.
    j. **Type of Detection**– A code referring to the basic nature of the overall trapping, survey, or other detection effort resulting in the reported individual. Entries include: O = Observed only; T = Trapped but no specimen collected; C = specimen Collected; S = tissue Sample taken.
    k. **Record_Notes** - Additional notes about the record. I.e., information added from other sources, modifications made to original text, apparent discrepancies or errors.

    l. **Orig_References** - Source from which the record was obtained. Should be in the form of a short citation (e.g., Bowe 2012), which links to the full citation via the References table.

2. Specimen Information
    a. **Alt_Spec_ID** - Any additional names, codes, or ID numbers associated with the individual *Zapus* referenced in the record.
    b. **Specimen Type** - Type of specimen collected: none, ear punch, blood sample, skin, skull, skeleton, organs, full specimen.
    c. **Orig_Gender** – Gender of the reported individual, as originally reported.
    d. **Norm_Gender** – Gender of the reported individual converted to a standardized entry: male, female, unknown.
    e. **Orig_Measurements** - All morphological measurements associated with the observed individual, including lengths of body parts and weight, as originally reported.
    f. **Total_Length (mm) –** Entire length (nose to tip of tail) of the reported individual, in millimeters.
    g. **Torso_Length (mm)** – Length of the head and body (nose to base of tail) of the reported individual, in millimeters.
    h. **Tail_Length (mm)** – Length of the tail of the reported individual, in millimeters.
    i. **HindFoot_Length (mm)** – Length of the hind foot of the reported individual, in millimeters.
    j. **Ear_Length (mm)** – Length of the ear of the reported individual, in millimeters.
    k. **Weight (g)** – Weight of the reported individual, in grams.
    l. **Orig_Age** – Age of the reported individual, as originally reported.
    m. **Norm_Age** – Age of the reported individual, converted to a standardized entry: A (adult), U (unknown), SubA (Subadult), Juv (Juvenile), Embryo (embryo removed from a pregnant female).
    n. **Orig_Reproductive Status** - Information on the reproductive status of the reported individual, as originally reported.
    o. **Norm_Reproductive Status** – Information on the reproductive status of the reported individual, converted to a standardized entry: NotRepro, active, pregnant, lactating, Testes Scrotal, embryos, unknown.
    p. **Toothfold** -Presence or absence of an anterior median toothfold as determined by the methods of Conner and Shenk 2003.
    q. **Specimen_Location** - Location where the specimen is currently housed or was last known to be housed. See Museum_Collections table for abbreviations. “NA” is used for records not associated with a specimen.
    r. **Specimen_Notes** – Additional notes about the reported individual. May refer to individuals with injuries or other unusual attributes; specimens that were lost or destroyed; analytical fate of tissue samples; etc.

3. Location Information. *See Appendix B for additional details on how* Zapus *spp. records were assigned spatial coordinates and map precision values.*
    a. **Locator(TRS)** - Township/Range/Section (Public Land Survey System) description of the location where the individual was observed in the field. Format = TTT N RRR W Sec #. Note that fractions of sections are included in the Locator_Notes field.
    b. **Locator_Notes** – Additional notes about the information in the Locator field, including ½ sections, ¼ sections, and ¼ ¼ sections.
    c. **Orig_Location_Description** - Description of the location where the individual was observed in the field, taken from the original report or data source. Usually a text description; e.g., name of watershed or drainage.
    d. **Orig_X_Coord** – Spatial coordinate corresponding to the east-west position of the location where the individual was observed in the field, as originally reported. E.g., units of longitude, units of UTM easting.
    e. **Orig_Y_Coord** - Spatial coordinate corresponding to the north-south position of the location where the individual was observed in the field, as originally reported. E.g., units of latitude, units of UTM northing.
    f. **Orig_Datum** – Datum associated with the original X and Y coordinates, as originally reported.
    g. **Orig_Elev** - Any estimate of the elevation of the location where the individual was observed in the field, as originally reported.
    h. **Orig_Map_Precis** - Any estimate of the mapping precision associated with the original X and Y coordinates, as originally reported.
    i. **Orig_Location_Notes** – Additional notes on the location where the individual was observed in the field, as originally reported.
    j. **Orig_Mapping_Notes** – Additional information about the process of mapping the point defined by Orig_X_Coord and Orig_Y_Coord. Includes any assumptions or changes made; problems with projections; etc. May be taken straight from the original source, or alternatively from mappers working with the data after original reporting.
    k. **Orig_Habitat** - Any information about the habitat in which the reported individual was captured or observed, as originally reported.
    l. **X_Coord(Int)** – East-west geographic coordinate derived from the original location information. This field represents an intermediate step between the original location information and the final derived latitude. Unstandardized.
    m. **Y_Coord(Int)** – North-south geographic coordinate derived from the original location information. This field represents an intermediate step between the original location information and the final derived longitude. Unstandardized.
    n. **Derivation(Int)** – How the intermediate X and Y coordinates were derived. Typically, either transcribed from the original report or plotted based on location description in either ArcGIS or GoogleEarth.
    o. **Datum(Int)** – Datum in which the intermediate coordinates were reported.

p. **Map_Comments(Int)** – Any intermediate comments about the mapping procedure. Typically includes additional details about how the intermediate coordinates were derived.

q. **Final_Latitude** - The final estimate of the latitude of the location from which the individual was reported in the field, standardized to decimal degrees in NAD83/WGS1984.

r. **Final_Longitude** - The final estimate of the longitude of the location from which the individual was reported in the field, standardized to decimal degrees in NAD83/WGS1984.

s. **Final_Derivation** - How the values in the Final_Latitude and Final_Longitude field were obtained. Entries "Original" or "From WYNDD Biotics" indicate that the values were verbatim from the original dataset. "GoogleEarth" indicates that the point was plotted using the GoogleEarth application and the original location information (typically in text form; e.g., "3 mi south 10 mi W town of Wamsutter"). "TRS via ArcMap" indicates that the coordinates were obtained by plotting original Public Land Survey System information in ArcMap 9.3. In some cases the coordinates needed to be converted from UTM or degree-minute-seconds into decimal degrees. Such conversions were performed with a conversion tool developed by the Montana State University Research Coordination Network, and designated as "Converted via Montana State University". NAD 27 to NAD 83 conversion was performed in ArcGIS and reported as "Converted via ArcGIS". A few points were plotted using the US Geological Survey's Geographic Names Information System "GNIS".

t. **Final_Datum** - The datum in which the Final_Latitude and Final_Longitude were generated. All points from GoogleEarth are in World Geodetic System of 1984 ("WGS84") and almost all other values were converted to North American Datum of 1983 ("NAD83"). "Unknown" values occur when the geographic coordinates were taken from the original database, but no datum information was included. Note that the NAD83 and WGS1984 are basically indistinguishable inside the continental U.S.

u. **Final_Precision** – Final estimate of the mapping precision associated with the point defined by Final_Latitude and Final_Longitude. When the coordinates were copied verbatim from the original database (Final_Origin = Original), the estimate of precision originally accompanying these values was copied verbatim as well. See Appendix B for additional details.

v. **Final_Elev –** Elevation at the point defined by Final_Latitude and Final_Longitude. Derived via overlay of the point defined by Final_Latitude and Final_Longitude on the National Elevation Dataset; reported in meters.

w. **Final_County** – Name of the county encompassing the point defined by Final_Latitude and Final_Longitude.

x. **Final_Mapping_Notes** – Additional comments about the final mapping procedure or results including any discrepancies in the data.

y. **Basin_Name** – Name of the major river basin encompassing the point defined by Final_Latitude and Final_Longitude. Basins were defined in accordance with the USDI Geological Survey Level 6 Hydrologic Unit Codes.

4. Identification Information
    a. **Original_ID_Method** – Method used to determine the species and/ or subspecies identity of the specimen as it appears in the original report. Possible values include "unknown" and "unknown – assumed field visual".
    b. **Long1965_ID** - Species or subspecies identification as it appears in Long 1965.
    c. **Clark&Stromberg1987_ID -** Species or subspecies identification as it appears in Clark and Stromberg 1987. Identifications were assigned to all points older than 1987 which were in close proximity to points appearing in range maps from Clark and Stromberg 1987.
    d. **Tag_ID** - Species or subspecies identification as it appears on the original specimen tag.
    e. **Field_Visual** – Species or subspecies identification based on visual examination of the individual in the field, according to the original observer or other sources that examined the relevant record or specimen.
    f. **Habitat (incl Elev)** - Species or subspecies identification based on the habitat in which the individual was found (e.g., vegetation type, elevation, distance to water), according to the original observer or other sources that examined the relevant record or specimen.
    g. **Geography** - Species or subspecies identification based on the location where the individual was found, according to the original observer or other sources that examined the relevant record or specimen.
    h. **King_Genetics** – Species or subspecies identification made using the genetic analysis developed by King et al. 2006.
    i. **Ramey_Genetics** - Species or subspecies identification made using the genetic analysis developed by Ramey et al. 2005.
    j. **Malaney_Genetics** - Species or subspecies identification made using the genetic analysis developed by Malaney et al. 2011.
    k. **DFA** - Species or subspecies identification made using the discriminant function analysis developed by Conner and Shenk 2003.
    l. **Toothfold_ID** – Species or subspecies identification based on the presence or absence of an anterior median toothfold, as determined by the methods of Conner and Shenk 2003.
    m. **Riggs_Genetics** - Species or subspecies identification made using the genetic analysis delevoped by Ramey et al. 2005.
    n. **Total_Length_ID** - Species or subspecies identification made based on the total length of the reported individual, according to the original observer or other sources that examined the relevant record or specimen.
    o. **Other** - Notes on any other identification methods that might have been used in specimen identification, and their result.

    p. **ID_Sources** – A list of references pertaining to the identification of the specimen.
    q. **ID_Notes** - Additional notes about the identification of the observed individual. May refer to particular conflicting conclusions; uncertainties in character presence or measurement; pending analyses; etc.
    r. **Bowe_Beauvais_2012_ID** – Species ID as derived by the final analysis presented in Bowe and Beauvais 2012. Values are either *Zapus hudsonius* or *Zapus princeps*.
    s. **Bowe_Beauvais_2012_Certainty -** Certainty of the species ID derived by the final analysis of Bowe and Beauvais 2012. Values are Known, Likely, or Possible.

5. WYNDD_Data. *The primary purpose of this family of fields is to help link records that were contributed to the database from the WYNDD central database back to their original 2011 conformations. Most users of the* Zapus *spp. database may not find this information useful.*
    a. **Obs_Description** – Description of the basic character of the observation or record.
    b. **Number of Individuals** – Number of *Zapus* spp. individuals to which the record refers. Note that some original WYNDD records refered to >1 individual *Zapus* spp.
    c. **FID_2011** – Internal feature number for each WYNDD record.
    d. **OBS_ID _2011**- Unique identification number for the Observation assigned by WYNDD.
    e. **DATA_SENS_2011** – Indication of whether a record is Sensitive ("Y") or not (“N”) according to the WYNDD Sensitive Data Policy (2011). Records that are sensitive because of data donor or private land considerations are distributed from the WYNDD database at the township scale. Records that are sensitive for biological reasons are distributed at the precise scale, depending on the requester.
    f. **ID_CONFIRM_2011** – Indication of whether the identification of the reported individual was confirmed (“Y”) or not (“?”) by WYNDD experts, circa 2011.
    g. **ID_NOTES_2011** – Provides details on records in which ID_CONFIRM_2011 = “?”.
    h. **ORIG_SHAPE_2011** – Geometric shape (point, line, or polygon) used to represent the 2011 record spatially.
    i. **SOURCE_ID_2011** – Unique identification number for the WYNDD Source Feature corresponding to the record, circa 2011. The same value may repeat across several unique records as multiple observations can be contained by one original Source Feature record.
    j. **EO_ID_2011** - Unique identification number for Element Occurrence records encompassing the observation record, circa 2011.
    k. **EO_NUM_2011** - Unique identification number for Element Occurrence records encompassing the observation record, circa 2011.
    l. **INDEPEN_SF_2011** – An indication of whether the original record was (“Y”) or was not (“N”) represented as an Independent Source Feature incorporated into an Element Occurrence in the WYNDD database, circa 2011.
    m. **DESCRIPTOR_2011** - Brief description of population and type of observation in the original WYNDD record.
    n. **ID_CONFIRM_NEW_2011** –An updated version of the “ID_CONFIRM” field.
    o. **ID_NOTES_NEW_2011** - An updated version of the “ID_NOTES_NEW” field.

6. References
    1. **Full_Citation** – The full, formal citation for a given reference.
    2. **Full_Citation …ctd** – A continuation of the full citation field for citations which exceed MS Access's 255 character limit.
    3. **Short Citation** –The shortened form of the full citation (usually "Author year"). The short citation is also the file name of the corresponding .PDF of the full document, if such a document is available in the WYNDD Zapus .PDF Library.
    4. **Taxon_Discussed** – The relevant species or subspecies referenced. Abbreviations include: "ZP" = *Zapus princeps;* "ZT" = *Zapus trinotatus;* "ZH" = *Zapus hudsonius;* "ZHP" = *Zapus hudsonius preblei*; "ZHC" = *Zapus hudsonius campestris;* "ZHI" = *Zapus hudsonius intermedius;*"ZHL" = *Zapus hudsonius luteus;* "NZ" = *Neozapus spp*.; "Zapus" = *Zapus* spp. in general, and typically referring to several taxa; "NA" = document does not directly reference *Zapus*.
    5. **Subject_Keywords** – Key topics discussed in the reference (e.g., range, habitat, human impacts).
    6. **Available? –** Location and availability of the full document represented by the reference. "PDF" indicates that an electronic copy is available in the WYNDD Zapus .PDF Library. "On file at WYNDD" indicates that WYNDD owns a hard copy of the reference. "On file at CNHP?" indicates that the reference was obtained from CNHP and it is believed they have a hard copy on file. "No" indicates a reference which has been cited, but could not be located.
    7. **Ref_Notes** – Additional notes about the reference or its contents.

Appendix B. Protocols used to derive map precision values for records of *Zapus* spp. observations in Wyoming.

Protocols used to assign _geographic coordinates_ and _map uncertainty distances_ to each record of observed *Zapus* spp. in Wyoming were intended to preserve as much of the locational information contained in the original records as possible.

The four procedures outlined here progress from finer- to coarser-scale information. Each record was evaluated in this order; i.e., first evaluated for precise coordinates; if none, then TRS information; if none, then text information.

We made no attempt to interpret whether the reported coordinates or precision values were reported by the original observers, or were later added or modified by other personnel.

1. For records including precise geographic coordinates: The field location of *Zapus* spp. detection for many records was reported as lat/long coordinates in dd/mm/ss format, or in decimal degrees. More recent records were accompanied by UTM coordinates.

> _Location_ - Record was mapped as a point defined by the finest reported coordinates, verbatim. All points were mapped in decimal degrees and converted to North American Datum of 1983 (NAD83) using a conversion tool developed by the Montana State University's Research Coordination Network.
>
> _Uncertainty_ – Uncertainty distance was the distance, in meters, corresponding to the last non-zero digit in the coordinate system (i.e., we interpreted ending zeroes as expressions of uncertainty).

2. TRS: The field location of *Zapus* spp. detection for some records was reported as Township/ Range/ Section, sometimes including ¼ section and ¼ ¼ section, or very occasionally ½ section.

> _Location_ – Record was mapped as a point at the center of the finest spatial unit described, verbatim. TRS units were plotted manually in ArcGIS 9.3, in NAD83.
>
> _Uncertainty_ - Uncertainty distance was assigned as the distance, in meters, from the center to the corner of the finest spatial unit described. Township = 6828m; Sec = 1138m; ¼ sec = 569m; ¼ ¼ sec = 284m.

3. Text description of a vector from another mapped feature: The field location of *Zapus* spp. detection for many records was provided in text form, for example "30 MI W, WAMSUTTER". In these cases we assumed that such notation specified a point at the given distance, along the given true compass bearing, from the given feature. Dual distances, such as "9 MI EAST 2 MI N, BAGGS", defined points at the end of two additive vectors. In cases where the text description included a vague reference to an additional mapped feature, such as "9 MI SOUTH, DUBOIS (JAKEY'S CREEK), we did not use the additional feature to modify the location because the intent and meaning of the additional feature notations are not knowable with any consistency. In the given example, JAKEY'S CREEK may have been noted to simply ID the watershed of observation; or perhaps because the observer could see

JAKEY'S CREEK from the observation point; or perhaps because the observation was made precisely in the creek itself. The exception to this rule is when a location was specifically mentioned as having been mapped along a linear feature. E.g., "10 mi. E. of Carter *along* UP Railroad" or "2 mi N of Colorado Boundary *on* HWY 287" (emphasis added). In such cases the distance was mapped along the reference feature rather than a straight line path.

> *Location* - Record was mapped as a point at the end of all vectors described in the text entry, verbatim. When plotting points from a town, major landmarks were used as starting points including post offices, town halls, major crossroads, or in the case of very small towns, the approximate center of town. Most locations were plotted in GoogleEarth, a GIS freeware. For more obscure localities, the U.S. Geological Survey's Geographic Names Information System (GNIS) was used to identify reference points.
>
> *Uncertainty* - Uncertainty distance was assigned as distance, in meters, as follows:
>
>> If a location and vector were reported:
>>
>>> For records where distance is reported to nearest mile: 6828m (equivalent to Township-level precision, as described above).
>>>
>>> For records where distance is reported to nearest 0.1 mile or finer: 1138m (equivalent to Section-level precision, as described above).
>>
>> If just a location was reported:
>>
>>> For records mapping to a city or feature (> 1 mile across): 6828m (equivalent to Township-level precision, as described above).
>>>
>>> For records mapping to a small town or feature (<1 mile across): 1138m (equivalent to Section -level precision, as described above).
>>
>> If multiple locational features were reported:
>>
>>> For records mapping the intersection of two features (roads, rivers, etc): 1138m (equivalent to Section -level precision, as described above).
>>
>> If measured along a feature (e.g., river, road, railroad):
>>
>>> For records where distance was reported to nearest mile: 6828m (equivalent to Township-level precision, as described above).
>>>
>>> For records where distance was reported to nearest 0.1 mile or finer: 1138m (equivalent to Section-level precision, as described above).
>>
>> If a precise junction was reported: 569m (equivalent to ¼ section precision, as described above).

If an exact street address was reported: 284m (equivalent to ¼ ¼ section precision, as described above).

4. Unmappable Features: The field location of the detection of a *Zapus* spp. was considered unmappable for one of four reasons:

- Locational information defined too large of a geographic area. This included text descriptions consisting only of stream or road names, names of mountain ranges, and similarly large features with no supplemental information (e.g., "Wind River Mountains"; "Spring Creek"; "Yellowstone Park").

- The locational feature described in the record could not be found. Some locales or topographic features have had multiple names over time, and changes and previous names are not always recorded or known with certainty. Errors in original handwriting or transcription might also cause difficulties in identifying a feature.

- The locational feature described in the record corresponded to multiple separate features of the same name. If multiple locations or features with the same name were located and there was no additional information available for clarification, the feature was considered unmappable to avoid making potentially false assumptions.

- No location information was included in or associated with the record.