EXPLORING RED-TAILED HAWK MIGRATION USING STABLE ISOTOPE ANALYSIS AND DNA SEXING TECHNIQUES

by

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The following individuals read and discussed the thesis submitted by student Kara Clare Donohue, and they also evaluated her presentation and response to questions during the final oral examination. They found that the student passed the final oral examination, and that the thesis was satisfactory for a master's degree and ready for any final modifications that they explicitly required.

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GENERAL INTRODUCTION

The following two chapters present my studies of the use of 1) stable isotopes in feathers to determine the origins of migratory red-tailed hawks (*Buteo jamaicensis*) and 2) morphometrics and DNA to determine the sex of red-tailed hawks based on in-hand measurements. Data for these studies were collected at fall migration sites throughout the western United States. My first objective was to use stable isotope technology to determine origins of red-tailed hawks caught during the migration period and then to use those origins and passage dates to examine migration patterns in hatch-year red-tailed hawks. My second objective was to use morphological measurements of red-tailed hawks of known sex to produce a mechanism for non-invasive, in-hand sexing of individual red-tailed hawks using Discriminant Function Analysis (DFA). The results of these studies will be of interest to anyone interested in migration ecology, stable isotope technology, red-tailed hawks, or techniques to determine the sex of free-living birds.

Stable Isotope Notation and Analysis

Atoms of an element all have the same number of protons, but the neutron number may vary. These different forms of the same element are referred to as isotopes. Some isotopes spontaneously decay and are called radioactive isotopes. Atoms that do not decay are called stable isotopes (Campbell and Reece 2005). Carbon (C), nitrogen (N), sulfur (S), hydrogen (H), and oxygen (O) all have stable isotopes, which can be measured precisely a mass spectrometer. Isotopic ratios change in predictable ways as

these elements cycle through the biosphere. Delta (δ) values are measures of the amount of heavy and light isotopes in a sample. Increases in these values denote increases in the amount of the heavy isotope components and decreases in these values denote decreases in the amount of heavy isotope components (Peterson and Fry 1987). δD symbolizes deuterium, or hydrogen isotopes. Isotope ratios of elements such as carbon and nitrogen in an organism are dependent on factors such as the types of plants an organism is feeding on or whether an organism is in a marine or terrestrial environment. In contrast, δD values are geographically linked, not diet-dependent, and therefore have strong potential for use as geographic markers (Kelly and Finch 1998).

The ratio of the heavy and light isotopes in a sample (R_{sa}) can be measured by a mass spectrometer and compared to a standard (R_{std}). The primary standard for hydrogen isotopes is Vienna Standard Mean Ocean Water (V-SMOW) (Lajtha and Marshall 1994). Differences in ratios are calculated by:

$\delta = (R_{sa} - R_{std})/R_{std} \times 1000.$

Study Species: Red-Tailed Hawk (*Buteo jamaicensis*)

The red-tailed hawk belongs to the genus *Buteo*, a group of stout-bodied, broad-winged raptors (Preston 2000). They are one of the most widespread and commonly observed birds of prey in North America. Red-tailed hawks range from central Alaska south to Panama and east to the Virgin Islands. They commonly inhabit open areas interspersed with patches of trees or structurally similar features such as power poles and towers. Their diet includes a wide variety of small to medium sized mammals, birds, and snakes, with occasional insects and fresh carrion (Preston and Beane 1993). The sexes are similar in appearance, with considerable overlap in size (Palmer 1988).

Up to 16 subspecies of red-tailed hawks are recognized, with a breeding range extending from Alaska down into Central America and spanning North America from coast to coast (Figure 1.1). Their winter range overlaps some of the breeding range, with most individuals vacating the northernmost part of the range in the fall (Preston and Beane 1993).

Dispersal in red-tailed hawks is not well studied. Newly fledged birds remain in the parental territory for 18 to 70 days (Johnson 1973; Petersen 1979). Premigratory movements can include northern or lateral as well as southern movements except in the northernmost populations (Luttich et al. 1971). For example, in Wisconsin, five of six red-tailed hawks banded as nestlings were recovered during the hatch year. Four traveled at least 100 km, the farthest going 3,000 km south of the natal territory. One was recovered 184 kilometers to the northeast (Petersen 1979).

The migratory pattern of red-tailed hawks is complex and varies annually with the weather. Most birds breeding in northern regions migrate southward, remaining there for 3-5 months. However, even in harsh winters some northern birds remain near their breeding territories year-round. Similarly, many mid-latitude (45-50 degrees N) breeding birds remain within or near the breeding range throughout the winter (Preston and Beane 1993), and even northward movements are not uncommon (Brinker and Erdman 1985). Approximately 95% of fall migratory movements at western interior sites occur between 23 August and 2 November (Preston and Beane 1993). Because it is not usually possible to determine the sex of migrant red-tailed hawks, it is not known whether the timing of migration consistently differs between males and females (Preston 2000). However, juveniles generally migrate earlier than adults (Haugh 1972; Geller and Temple 1983).

When females do return to the breeding grounds they show a high degree of nest site fidelity (Janes 1984). Male breeding site fidelity has not been documented, to the best of my knowledge, but is expected in red-tailed hawks as is seen in other buteos such as Swainson's hawk (*Buteo swainsoni*) (England et al. 1997) and red-shouldered hawk (*Buteo lineatus*) (Crocoll 1994). However, more study is needed with banded pairs during the breeding season to confirm male breeding site fidelity in red-tailed hawks.

The expanded range of red-tailed hawks in recent years (Preston and Beane 1993) is related to deforestation in the east and fire suppression in the west, both of which produce a patchwork of woodland and large open areas. Red-tailed hawks decline in areas where this patchwork is replaced by large expanses of either unbroken woodland or treeless landscape (Preston and Beane 1993).

Juvenal plumage is well developed at the time of first flight and is retained through winter into the following spring. All molt in migrating red-tailed hawks occurs on the breeding grounds and is suspended during migration and winter (Palmer 1988).

I chose the red-tailed hawk for my study species for a variety of reasons. First, because red-tailed hawks are widespread and abundant, one can obtain a sufficient sample size. Second, species at higher trophic levels may show less variation in stable isotope levels through the incorporation of components of the chemical environment into their tissues. Third, migratory raptors are considered indicator species of ecosystem health (Bildstein 2001; Newton 1979). By monitoring red-tailed hawks at migration sites, it may be possible to use red-tailed hawks as an indicator of changes in the environment in which they live. Lastly, despite being well studied in other aspects of

their natural history, red-tailed hawk migration patterns are still poorly understood. Stable isotope technology can provide evidence for interpreting migratory movements.

Overview of Chapter One and Two

Chapter One entails determining origins and examining patterns of migrating and dispersing red-tailed hawks. Stable isotope technology has the potential to shed light on the movements of migratory species and to help us better understand their population dynamics. In addition to stable isotope analysis, feathers were collected for sex determination using Polymerase Chain Reaction (PCR) in order to examine differences in the movements of males and females.

In Chapter Two, I use red-tailed hawks of known sex, along with various morphological measurements, to build models for sex determination in the field. Red-tailed hawks currently cannot be sexed outside of the breeding season using in-hand morphological measurements. The ability to sex red-tailed hawks in the hand will aid studies in which gender is an important variable.

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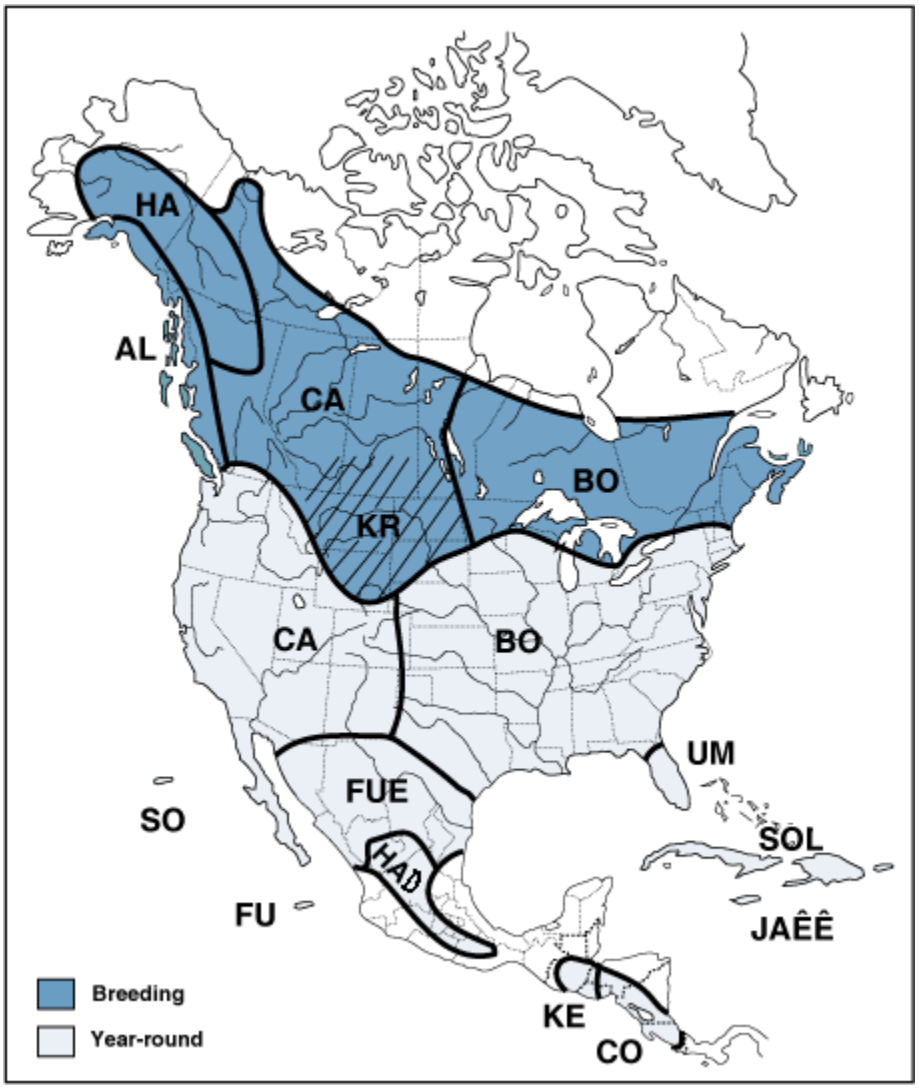

Figure 1.1 Approximate breeding distribution of red-tailed hawk races: HA = *harlani*, AL = *alascensis*, CA = *calurus*, KR = "kriderii," BO = *borealis*, FUE = *fuertesi,* SO = *soccorroensis*, HAD = *hadropus*, FU = *fumosus*, UM = *umbrinus*, SOL = *solitudinus*, JA = *jamaicensis*, KE = *kemsiesi*, CO = *costaricensis* (Preston and Beane 1993).

CHAPTER ONE:

USING STABLE ISOTOPE TECHNOLOGY TO PREDICT ORIGINS OF MIGRATING AND DISPERSING RED-TAILED HAWKS

Abstract

Understanding the movements of migratory birds and connecting the different stages of their annual cycle is necessary for the conservation and management of migratory bird species. Stable isotope technology has the potential to shed light on the movements of migratory species and to help us better understand their population dynamics. Several studies use stable hydrogen isotopes in particular to predict origins of birds sampled during migration or in winter. However, recent work on stable hydrogen isotopes in feathers (δD_f) draws into question the utility of this technology in estimating origins of migrants. My objective was to determine whether stable hydrogen isotope analysis is a useful technique to estimate the origin of red-tailed hawks (*Buteo jamaicensis*) migrating through monitored migration sites in the western United States. I used the base map created by Lott and Smith (2006) to predict origins from the δD_f values and looked for relationships between that estimated origins of migrants and year of capture, sex, and passage date. In addition, I compared δD_f signatures with the signatures predicted by the base map for breeding locations of adult birds outfitted with satellite telemetry units and for a recaptured bird banded as a nestling. Predicted origins

were frequently both to the north and south of migration monitoring stations and covered large areas. Identifiable migration patterns existed only at the Goshutes Mountains site where individuals from lower latitudes migrated through earlier than individuals from higher latitudes and during one season when females migrated through later than males. Smaller sample sizes may have contributed to a lack of patterns at the other migration sites. The satellite telemetry individuals and recaptured juvenile did not match up to predicted signatures in most cases. The broad possible source areas for migrating red-tailed hawks in the fall rendered this technique ineffective for determining breeding locations or natal origins using my procedures. Furthermore, the concerns raised regarding using this technology for conservation and management suggest other techniques, such as satellite telemetry, may provide more reliable results.

Introduction

Bird Movements

Organisms exhibit various types of movements that can affect individual fitness and can have consequences for populations and communities. Most movements occur within the home range of an organism (Dingle 1996). However, two types of movement, dispersal and migration, occur outside of the home range and can alter the distribution and abundance of individuals (Clobert et al. 2001). Understanding these movements is important for the conservation and management of migratory bird species, could facilitate the protection and management of habitats utilized by dispersing and migrating individuals (Holmes and Sherry 1992; Hobson et al. 2001; and Webster et al. 2002).

"Bird migration is…the regular seasonal movement from breeding areas to resting grounds (often winter quarters) and back" (Berthold 2001). Through these seasonal

movements, birds can exploit temporarily abundant resources and avoid times or locations of resource scarcity (Kerlinger 1995).

Birds generally exhibit one of three different migration patterns: complete, partial, or irruptive. In complete migration, all individuals leave the breeding range. Irruptive migrants, many of which are food specialists (Kerlinger 1995), make seasonal movements in some years, while remaining in the breeding areas in other years. Red-tailed hawks are partial migrants, with most individuals vacating the northern portion of the breeding range while most remain on the breeding grounds in mid and southern latitudes (Preston and Beane 1993).

Migration and Conservation Biology

Studying the different stages of an organism's annual cycle helps to understand its life history (Webster et al. 2002). Because many migrants move long distances, efforts to protect and manage migrants need to be focused not only on the breeding grounds, but also on staging areas and wintering areas, making migrants particularly at risk for decline (Berthold 2001). The link between breeding and nonbreeding areas is termed migratory connectivity (Webster et al. 2002), and establishing this link is important because conservation efforts in one part of a species' range may prove ineffective if population declines occur in other parts. Currently, movements of many migratory species are poorly understood, but understanding them is crucial to modeling population dynamics (Hobson et al. 2003). In order to design successful conservation strategies, information is required concerning population processes and the role of migrants in ecosystems throughout their annual cycle (Dhondt & Matthysen 1993; Nur 1993).

Raptors in particular, pose a problem for assessing population status during the breeding season due to their large home ranges and low breeding densities (Fuller and Mosher 1987; Titus et al. 1989). Because of these traits, monitoring raptor populations during the breeding season can be extremely labor-intensive and costly. Counts of migrating raptors offer an alternative index for studying population status. Large numbers of migrating raptors concentrate along the tops of mountain ridges, the margins of deserts, and the edges of large bodies of water each fall (Mueller and Berger 1967; Hoffman 1985; Meehan et al. 2001). Raptor study sites have been established at many areas of concentration (Kerlinger 1989; Bildstein 2006) where researchers observe, count, and in some cases trap raptors that come from different areas of the continent and these data can provide important information for assessing population index trends (Bednarz et al. 1990; Titus and Fuller 1990; Bildstein et al. 2008).

Unfortunately, the absence of morphological markers that identify geographically distinct subpopulations of raptors, and that allow for linking of breeding and wintering populations, impedes our understanding of year-round population dynamics and hinders development of appropriate conservation strategies (Chamberlain et al. 1997). The use of raptor migration counts to monitor populations is limited in that the origin of individual migrants cannot be determined (Meehan et al. 2001). Mark-recapture techniques on long distance dispersers and migrants, while useful in theory, often are ineffective because of the low probability of recapture of marked birds (Hobson et al. 2001). Nevertheless, capture and banding has been the primary method for investigating the origins of migrating raptors, even though raptors banded during migration are encountered during the breeding season at low rates (Hobson and Wassenaar 2001). Moreover, methods such

as banding and radio telemetry are not applicable for tracing the movements of most species (Hobson 1999).

More recently, molecular and chemical techniques such as stable isotope analysis have been used to investigate bird origins and movements. Stable isotopes are naturally variable in the environment. Distinct patterns in rainfall across North America provide a strong latitudinal gradient in deuterium, the stable isotope of hydrogen, over much of the continent. As latitude increases, the relative abundance of deuterium decreases (Hobson and Wassenaar 1997). This pattern is affected by changes in topography. For example, high-latitude, low elevation areas and lower-latitude, high-elevation areas can have similar δD_p values.

Deuterium values in consumer tissue reflect those in local precipitation averaged over plant growing seasons (Kelly and Finch 1998). This procedure relies on the fact that feathers are metabolically inert following synthesis and so maintain an isotopic record indicating an area where the feathers were synthesized (Hobson 1999). Chamberlain et al. (1997) provided the first evidence that hydrogen isotopic ratios of feathers are largely fixed once feathers are fully formed. The use of intrinsic stable isotopic markers in bird feathers has revealed promising new directions for linking migratory birds and other wildlife to areas of origin (Hobson and Wassenaar 2001). For example, Meehan et al. (2001) found stable-hydrogen isotope analysis to be an effective method to determine the natal origins of migrating raptors. Lower costs and less effort and time were required than the band-encounter method.

Despite the early promise shown in using deuterium to predict origins of migrants, several recent studies have drawn attention to untested assumptions and

unresolved methodological issues with the technique (Norris et al. 2006; Rocque et al. 2006; Langin et al. 2007; Smith et al. 2008; Smith et al. 2009). For example, Langin et al. (2007) point out three assumptions underlying the use of δD_f to predict origins of migratory birds. First, it is assumed the relationship between δD_p and δD_f is constant among species and across populations. Second, the δD_f value for birds growing in feathers at the same location should be similar regardless of age, sex, or feather type. Third, variation in δD_f by season or year is assumed to be small for any given molt location. Studies on shorebirds (Rocque et al. 2006), raptors (Smith and Dufty 2005; Smith et al. 2008), and on annual variation in δD_p (Farmer et al. 2008) suggest problems with these assumptions. Methodological issues such as consistency in sample preparation (e.g, feather cleaning, Paritte and Kelly 2009) and the conditions of measurement (e.g., within and between automated runs and laboratories, Smith et al. 2009) raise additional concerns with using δD_f to predict origins of migratory birds.

Study Goals

The purpose of my study was to investigate whether stable isotope analysis is a useful technique to estimate the North American latitude of origin of red-tailed hawks migrating through monitored migration sites in the western United States. Due to potential problems with stable isotopes to determine the origins of adult raptors (Meehan et al. 2003; Smith and Dufty 2005), feathers were collected primarily from hatch year birds with the exception of adult red-tailed hawks outfitted with satellite telemetry units. The estimated origins determined by the δD_f were then used to test for relationships

between the estimated origin of the migrant and year of capture, sex, and passage date through the migration monitoring station.

Lott and Smith (2006) created a map of estimated North American raptor δD_f. This model was used in my study to estimate the natal/breeding origins of red-tailed hawks migrating through western migration sites during autumn. Furthermore, HawkWatch International (HWI) placed satellite telemetry units on red-tailed hawks at each of their fall migration banding sites and tracked them to their breeding areas the following spring. Assuming strong nest site fidelity of red-tailed hawks, I compared the data gained from the telemetry units with results from stable isotope analysis of the feathers taken from those same birds.

Methods

Feather Collection

Feather samples were collected at four HawkWatch International sites (Goshute Mountains, Bonney Butte, Chelan Ridge, and Manzano Mountains) and at the Idaho Bird Observatory (Table 1.1). During the fall migration season of 2002 and 2003, I obtained three to five breast feathers from all red-tailed hawks captured at the migration monitoring stations. All sites utilize a variety of trapping techniques including bow nets, dho-ghaza nets, and mist nets (Bloom 1987). Captured individuals received numbered United States Geological Survey aluminum leg bands and standard morphological measurements were taken. Feathers were placed in envelopes with location, date, band number, age, measurements, and collector recorded on the envelope. Sex was assigned to individuals based on the equations described in Donohue and Dufty (2006).

Stable Isotope Analysis

The feather cleaning protocol was suggested by Dr. Len Wassenaar at the Stable Isotope Laboratory at the National Hydrology Research Centre (Environment Canada, Saskatoon, Saskatchewan). All feathers were cleaned at Boise State University in a 2:1 chloroform to methanol solution and dried for 48 hr in a fume hood. Feathers were clipped in the same location (i.e., along the distal rachis) and samples weighing 0.35 (± 0.01) mg were packaged in silver capsules. The capsule was sealed and placed in a tray for transportation. The sample name, date, and final weight were recorded and samples were sent out to the Stable Isotope Laboratory for analysis. The protocol for stable isotope analysis is similar to Kelly et al. (2001) and is based on Sharp et al. (2001). Stable hydrogen isotope composition of the feather samples was measured relative to the composition of a standard in a mass spectrometer (Nier 1947; McKinney et al. 1950). The samples were pyrolized into their separate gas components (Wassenaar and Hobson 2003). Sample and reference gases were measured simultaneously in the mass spectrometer. A comparison of isotopic frequencies between sample and reference gas reveals the isotopic composition of the sample relative to the reference gas (Brand 1996).

Statistical Analyses

To test for differences between isotopic signatures at a site based on year and sex, a two-way analysis of variance (ANOVA) was performed on each site with the independent variables being year and sex and the response variable isotopic signature. For the Idaho Bird Observatory, sex could not be determined because of a lack of the necessary morphometric data, therefore an ANOVA was performed excluding sex as a variable.

I used analysis of covariance (ANCOVA) to examine migration patterns related to differences in passing date and sex based on the δD_f value (or assumed location of origin) at each site. Before running ANCOVAs for each site by year, I tested for an interaction between date of passage and sex. If there was no interaction, I ran ANCOVAs to test for a sex effect. This was followed by a comparison between δD_f and passage date using a linear regression. For the Idaho Bird Observatory, only the comparison between δD_f and passage date was made. The analyses were run using JMP IN 6 statistical software.

Base Map

I used a "base map" (Lott and Smith 2006, Figure 4) of North American raptor δD_f that incorporates regional variation in raptor δD_f values to map the potential origins of sampled red-tailed hawks. All feather samples used to create this base map were obtained from nestlings or birds in juvenile plumage that were assumed to be in or near their natal territory at the time of collection.

Generating Stable Isotope Estimates of Origins

For each migration monitoring station the measured δD_f values from each migration monitoring station were plotted using the Lott and Smith (2006) base map with a ± 8‰ (parts per mil), for these authors found the mean difference between predicted and measured δD_f values to be (mean ± SD) 0.1 ± 8‰. For each δD_f value on the base map, I calculated the percentage of individual birds from for each site, by year, whose range of estimated δD_f values included this value, creating a relative frequency histogram. For example, 11 out of 32 samples (34%) from the Goshute Mountains in 2003 had δD_f values of either -118‰ or -119‰. Samples were divided into four classes

of abundance (common: >33% of all samples per δD_f value; fairly common: 17 – 33% of all samples per δD_f value: uncommon: 8 – 16% of all samples per δD_f value: and rare: <8% of all samples per δD_f value. I assigned a color to each category and then displayed each color on the base map of North American raptor δD_f to produce a spatial histogram of the relative contribution of different source populations from the sample from each site by year. This approach was recommended by Lott and Smith (2006) for skewed distributions, such as sites where migrants include locally dispersing birds. Some samples were found to have δD_f values representing origins south of the migration monitoring station at which an individual was captured, suggesting dispersal movements. Discussion of the resulting histograms will be confined to core source areas defined as contributing ≥17% (common and fairly common abundance classes) of the birds in a sample.

Satellite Telemetry and Foreign-Recapture Red-Tailed Hawks

I collected and analyzed breast feather samples from seven adult and hatch-year red-tailed hawks captured and outfitted with satellite telemetry units at the Chelan Ridge, Goshute Mountains, and Manzano Mountains sites during the fall migration season. HawkWatch International tracked these individuals and provided the subsequent breeding season locations. These breeding season locations were plotted on the base map (Lott and Smith 2006) and the feather stable hydrogen isotope signatures were compared to the isotope signature predicted for the breeding season location on the base map. An additional hatch-year red-tailed hawk was banded and had a feather removed elsewhere as a nestling and was recaptured in the Goshutes. The feather was analyzed for its isotope signature and compared to the predicted isotope signature for its banding location.

Calibration of Samples

Lott and Smith (2006) found that feathers reanalyzed several months after first analysis had significantly different δD_f values than when originally analyzed. They determined that one should reanalyze a subset of the feathers used to create the base map during each lab session in future studies in order to calibrate the feather samples from that study to the base map. In addition, Smith et al. (2009) discovered poor relative accuracy and repeatability in repeated measurements of δD analyzed in different lab sessions within the same lab. In April 2005, 20 of my previously analyzed (February 2005) red-tailed hawk samples were reanalyzed along with a subset of the feathers used by Lott and Smith (2006) to create their base map. A simple regression equation was created using the reanalyzed δD_f values as the response variable and the δD_f values from the initial analysis as predictor variable. The equation was developed to standardize δD_f values in order to use the base map for plotting origins of red-tailed hawks analyzed in this study.

Results

Feather Collection

A total of 222 individuals were analyzed for stable hydrogen isotope signatures. One feather was required to obtain a sufficient sample for stable isotope analysis. Feather samples came from all five migration monitoring stations and both the 2002 and 2003 fall migration seasons (see Table 1.2).

Calibration Equation

The following simple regression equation was used to calibrate my red-tailed hawk isotope signatures to the base map created by Lott and Smith (2006):

Adjusted $\delta D_f = 1.04(\text{Original } \delta D_f) + 12.75$

$F_{1, 28} = 1478.3$, $P < 0.001$, R-squared = 0.98

Migration Monitoring Station Relationships

None of the migration monitoring stations showed significant differences between years or between the sexes (Bonney Butte $F_{1,61} = 0.86$, $P = 0.3582$, $F_{1,61} = -2.58$ $P = 0.1134$ Table 1.3; Goshute Mountains $F_{1,68} = -0.27$, $P = 0.6034$, $F_{1,68} = 1.54$, $P = 0.2192$ Table 1.4; Manzano Mountains $F_{1,30} = 0.20$, $P = 0.6594$, $F_{1,30} = -0.03$, $P = 0.8591$ Table 1.6; Chelan Ridge $F_{1,18} = 0.023$, $P = 0.8856$, $F_{1,18} = -0.83$, $P = 0.3736$ Table 1.7; IBO $F_{1,22} = -0.04$, $P = 0.8544$ Table 1.8). No significant interaction between year and sex was found for Bonney Butte ($F_{1,61} = 0.005$, $P = 0.9445$), Manzano Mountains ($F_{1,30} = -0.01$, $P = 0.9245$), or Chelan Ridge ($F_{1,18} = -0.85$, $P = 0.3698$). However, the interaction between year and sex was significant for the Goshutes Mountains site (ANOVA: $F_{1,68} = 6.76$, $P = 0.0114$) (Table 1.5). In 2002, female red-tailed hawks originated from lower latitudes than male red-tailed hawks at that trapping station than in 2003.

The relationship between δD_f and date of capture did not vary between the sexes for 2002 or 2003 at Bonney Butte, Goshute Mountains, Manzano Mountains or Chelan Ridge (Table 1.9), so I proceeded with the ANCOVA to test for differences between the sexes. On any given day in 2002 or 2003 (Table 1.10), captured males and females from Bonney Butte, Manzano Mountains and Chelan Ridge possessed, on average, similar δD_f values, suggesting that for hatch-year red-tailed hawks there is no differential migration

of the sexes through these sites. In the Goshute Mountains for any given day in 2002, captured males possessed δD_f values significantly lower than females, suggesting that hatch-year males from a particular breeding area were migrating through earlier in the season than hatch-year females (Table 1.10). However, this difference in δD_f was absent in 2003, suggesting similar temporal migration patterns for male and female hatch-year birds through this site (Table 1.10).

The linear regressions comparing δD_f values and passage date were not significant for 2002 or 2003 at Bonney Butte, Manzano Mountains, Chelan Ridge or IBO (Table 1.11). This result suggests there was no clear migration pattern at these four sites during these seasons. In the Goshute Mountains, δD_f values declined with passage date (Table 1.11). In other words, individuals from lower latitudes pass through the Goshutes site earlier in the season than individuals from higher latitudes.

Stable Isotope Estimates of Origin

I present, below, the estimated origins of hatching-year red-tailed hawks from each migration monitoring station.

Bonney Butte, Oregon

For estimates of red-tailed hawk origins from Bonney Butte during 2002 and 2003 by δD_f values depicted in histograms, see Figure 1.3. The most frequent values correspond to Alaska, western British Columbia, western Washington, western Oregon, and California (Figures 1.4 and 1.5). Additional, but less prominent, contributions to the migrant sample in 2002 and 2003 correspond to central California and central British Columbia (Figures 1.4 and 1.5).

Goshute Mountains, NV

For estimates of red-tailed hawk origins from the Goshute Mountains during 2002 and 2003 by δD_f values depicted in histograms, see Figure 1.6. The most frequent values correspond to Alaska, British Columbia, western Alberta, eastern Washington, eastern Oregon, Idaho, and western Montana (Figures 1.7 and 1.8). Additional, but less important, contributions to the migrant sample in 2002 and 2003 correspond to Yukon Territory, Nevada, Utah, Arizona, and California (Figures 1.7 and 1.8).

Manzano Mountains, NM

For estimates of red-tailed hawk origins from the Manzano Mountains during 2002 and 2003 by δD_f values depicted in histograms, see Figure 1.9. The most frequent values correspond to Alaska, central Montana, Alberta, southwestern Northwest Territories, New Mexico, and Mexico (Figures 1.10 and 1.11). Minor contributions to the migrant sample in 2002 and 2003 correspond to parts of Wyoming, Colorado, Montana, Alberta, and southwestern Northwest Territories (Figures 1.12 and 1.13).

Chelan Ridge, WA

For estimates of red-tailed hawk origins from Chelan Ridge during 2002 and 2003 by δD_f values depicted in histograms, see Figure 1.12. These values correspond to Alaska, British Columbia, Washington, Idaho, Oregon, California (excluding the Central Valley), and most of Nevada and Utah (Figures 1.13 and 1.14). Additional small contributions to the migrant sample correspond to central Alberta and parts of central Washington, central Oregon, southern Idaho, Nevada, and eastern California (Figures 1.13 and 1.14).

Idaho Bird Observatory, ID

For estimates of red-tailed hawk origins from Lucky Peak during 2002 and 2003 by δD_f values depicted in histograms, see Figure 1.15. These values correspond to Alaska, eastern and northern British Columbia, western Alberta, Washington, Oregon, western Montana, Yukon Territories, southern California, southern Utah, northern and central Arizona, and southern Nevada (Figures 1.16 and 1.17). Small contributions to the migrant sample in 2002 and 2003 correspond to southern Idaho, southeastern Oregon, Wyoming, Nevada, northern Utah, and scatter locations in British Columbia, Alberta, and Saskatchewan (Figures 1.16 and 1.17).

Satellite Telemetry and Red-tailed Hawks of Known Origin

Results of the comparison of isotope signatures determined from feathers collected during migration from red-tailed hawks outfitted with satellite telemetry units with their predicted feather isotope signature (Lott and Smith 2006 base map) are presented in Table 1.12. In their description of the origins of migrants, Lott and Smith (2006) determined a map accuracy of ± 8‰. Two out of the eight satellite telemetry and known origin red-tailed hawks fell within ± 8‰ of their predicted δD_f value. Red-tailed hawk number 1 (RT1) is the foreign recapture from the Goshutes site banded as a nestling in Laguna Beach, CA. This is the only individual in this group that's natal territory location was known prior to capture during migration. The predicted δD_f value was 59‰ greater than the actual δD_f value. For the rest of the satellite telemetry red-tailed hawks, the predicted δD_f value was lower, ranging from 3‰ to 36‰ less, than the actual δD_f value (Table 1.12). Individuals captured at Chelan Ridge exhibited low

differences between predicted and actual δD_f values, while the individuals captured at the Goshutes Mountain site had the two greatest differences between predicted and actual δD_f values. See Figure 1.19 for the plotted locations of each bird on the Lott and Smith (2006) base map.

Discussion

The results of this study provide little useful information for predicting origins of migrating red-tailed hawks in the western United States. Potential source locations consisted of large bands covering much of western North America, frequently including areas north as well as south of the migration monitoring stations. Several factors potentially contributed to the low level of precision in the results. Lack of ability to restrict potential source areas for red-tailed hawks, use of the Lott and Smith (2006) base map, and recurring δD_p values in western North America contributed to the broad predicted source areas, while problems with the technique itself, as discussed by others (Smith et al. 2008; Farmer et al. 2008; Paritte and Kelly 2009; Smith et al. 2009, add citations}call into question the utility of this technique, at least with raptors. Each of these factors is discussed in detail below.

Stable Isotope Estimates of Origin

Red-tailed hawks utilize a variety of habitats during the breeding season. Therefore, using GIS to eliminate potential source areas by habitat, as has been done in other studies (Lott and Smith 2006; Meehan et al. 2004), was not possible. For migration monitoring stations such as Bonney Butte and Chelan Ridge, which lie within 185 and 340 kilometers, respectively, of the Pacific Ocean, potential source areas may include

coastal populations. A marine component to an individual's diet will likely elevate the δD_f value to a level higher than other individuals living further away from the coast at similar latitudes (Lott et al. 2003). That is, average δD of ocean water is approximately 0‰, while average δD of growing season precipitation in North America ranges from -140 to -20‰ (Lécuyer et al. 1998). Feeding on marine prey would translate into higher δD values in an individual's tissue and distort the relationship between latitude and δD_f (Lott et al. 2003) by producing an estimate that errs in a southerly direction. Stable sulfur isotopes have been used to identify birds exposed to marine water (Hobson et al. 1997; Caccamise et al. 2000; Knoff et al 2001; and Lott et al. 2003). Marine sulfate has greater δS^{34} values than terrestrial materials or waters (Michener and Schell 1994). By identifying the marine contribution to feather isotope ratios, marine influenced samples can be removed for a more accurate model of the relationship between δD_p and δD_f (Lott et al. 2003). Breeding red-tailed hawks rarely live right on the coast. Potential sources of prey with a marine influence might include least tern (*Sterna antillarum*) chicks, clapper rails (*Rallus longirostris*), American coots (*Fulica americana*), and various waterfowl. However, P. Bloom (pers. comm.), who has spent a considerable amount of time studying red-tailed hawks in California, has seen no evidence of red-tailed hawks taking any kind of marine prey. Based on this information, it seems likely that few, if any, red-tailed hawks caught at Bonney Butte or Chelan Ridge would have a marine influence on their δD_f values. The absence or infrequent occurrence of δD_f values below -40‰ at either site further suggests a lack of red-tailed hawks passing through these sites with a marine influence to their diet.

I considered restricting discussion of potential source areas for migration monitoring stations to within the flyway in which they occur. Hoffman et al. (2002) showed that accipiters and, to a lesser extent, red-tailed hawks in the west exhibit high fidelity to three migration flyways: Pacific Coast, Intermountain, and Rocky Mountain. Similarly, most red-tailed hawks banded along the central coast of California tend to remain along the Pacific Coast (Scheuermann 1996, 1997; Acuff 1998, 1999). Of red-tailed hawks trapped at Golden Gate Raptor Observatory in California during fall migration, most band recoveries occurred south of the site of capture within the Pacific flyway in California (Hull et al. 2009). However, Bloom (1985) found first-year dispersal in red-tailed hawks to be variable, and some young birds banded in southern California moved extensively and in a variety of directions.

To examine whether hatch-year red-tailed hawks stay within a flyway during migration, I acquired band recovery data from the Bird Banding Laboratory (USGS Patuxent Wildlife Research Center) of all hatch-year red-tailed hawks banding during the breeding season (presumably close to their natal area) and recaptured or recovered during the ensuing fall. As found by Bloom (1985), southern California birds move in various directions, leaving the Pacific Flyway (Figure 1.19). Several band recoveries showed movements across flyways (Figure 1.20). Therefore, I did not find sufficient evidence to restrict red-tailed hawks potential origins to within the flyway they were captured on migration.

With no justification to limit (by habitat or flyway) potential source areas for migrants passing through a given migration monitoring station, each station has large potential source areas due to recurring δD_p values in the mountainous west. For example,

western Alaska shares similar δD_p values with Idaho. A red-tailed hawk from the Central Valley of California could share a similar δD_f value with a red-tailed hawk from southern New Mexico. Farmer et al. (2008) showed that inter-annual variation in the δD_p values make it difficult to accurately assign an individual to sites separated by less than 12º of latitude (or 53‰). In other words, two samples differing by less than 53‰ cannot be said to originate from different latitudes. As a result, potential source areas have low resolution and provide little information of conservation value.

In addition, all stations with the exception of the Goshutes have common potential source areas (i.e., areas with the same δD_p value) both to the north as well as to the south. This may be due to dispersing birds frequently passing through migration sites or could suggest a lack of reliability in stable hydrogen isotope values for red-tailed hawks. Additional use of satellite telemetry would improve our knowledge of the movements of red-tailed hawks by providing high resolution information on the movements of individual birds.

The base map created by Lott and Smith (2006) utilized feathers from 12 raptor species, rather than just from red-tailed hawks. Their purpose for creating the base map was to provide researchers studying any of these 12 species with the capability to predict natal origins of birds captured during migration or winter. However, given that current research has revealed several technical issues with using stable hydrogen isotopes to predict origins of migratory birds (Rocque et al. 2006; Langin et al. 2007; Smith et al. 2008; Smith et al. 2009), it may be necessary to create base maps built only on red-tailed hawks of known origin. However, regardless of potential improvements to accuracy, a base map created from only red-tailed hawk feathers would still have low resolution from

recurring δD_p values due to the pattern of Deuterium in precipitation. For example, birds from Alaska would still share signatures with birds in California, Idaho, and Montana.

Even if it were possible to resolve the issues associated with recurring δD_p values in western North America, several other problems with this technology remain unresolved. For instance, choice of feather tract as well as location within a single feather provides significantly different δD_f values (Smith et al. 2008). Similarly, feather samples analyzed in different sessions or in different laboratories also differ significantly in δD_f values (Smith et al. 2009). The process chosen for sample preparation may also contribute to the accuracy of the results. Paritte and Kelly (2009) found the regime chosen for cleaning feathers may affect the δD_f value. In Japanese quail (*Coturnix japonica*), δD_f values were enriched approximately 40‰ when they cleaned feathers with 2:1 chloroform:methanol, as was used in this study. Although my results do not indicate a uniform enrichment, it is possible the cleaning regime changed the δD_f values in some unknown way.

Satellite Telemetry and Foreign Recapture Red-tailed Hawks

The estimated origins of the foreign recapture and satellite telemetry birds included the actual natal or breeding location in two of eight (25%) instances. RT2 and RT3 are the two individuals whose breeding locations fell within the range of the δD_f predicted values. It is possible these birds originated from a region that contains more accurate predictors than the other individuals. Both birds spent the breeding season in the same general area along the border between Washington and Canada.

For individuals that fell outside of the range of the δD_f predicted values a variety of explanations may apply, including: 1) an effect of natal dispersal distance on the δD_f value (natal dispersal), 2) an analogous effect of breeding dispersal distance on the δD_f value (breeding dispersal), and 3) the inadequacy of stable isotopes to describe the origins of adult raptors (isotope inadequacy), which includes variation in stable isotope ratios within and between feathers from the same track (feather variation) and the influence of coastal locations (coastal influence). The δD_f values of all satellite telemetry red-tailed hawks were based on the collection of feathers grown during the previous summer. However, the δD_f predicted values were based on the location of the bird, as determined by satellite telemetry, the summer following capture. Therefore, it is possible these individuals exhibited natal or breeding dispersal movements between years, changing their location from one summer to the next. Furthermore, stable hydrogen isotopes signatures in adult red-tailed hawks may differ from juveniles from the same location as was found in other raptor species. For example, Meehan et al. (2003) found that adult Cooper's hawks (*Accipiter cooperii*) had higher δD_f values than their nestlings and the degree to which adult δD_f values differed from those of their nestlings varied from location to location. Similarly, Smith and Dufty (2005) found that adult northern goshawks (*Accipiter gentilis*) exhibited higher δD_f values relative to their nestlings, but in a predictable manner. More research is needed to determine if red-tailed hawk adults differ from their nestlings consistently. Even excluding the potential differences between adult and juvenile red-tailed hawks, other issues with this technique need to be resolved. For example, in a study on biological variation in the stable-hydrogen isotope content of raptor feathers, Smith et al. (2008) found significant differences in the feather δD

measurements between adjacent locations of the same feather. Furthermore, feathers from the same tract (i.e., contour feathers) showed small, but significant differences in feather δD. This is a complication for isotope research since it would not be possible to know how any given contour feather selected from an individual varied from other contour feathers without additional analyses.

RT1 was banded as a juvenile in its place of origin near the coast in southern California and a feather was subsequently taken during the ensuing migration period. The stable isotope signature, which was outside of the range of the δD_f predicted value, could result from a coastal influence brought about by the inclusion of marine prey in its diet. However, this should have increased the δD_f value, and RT1 had a stable isotope signature much lower than predicted. Therefore, it is likely that marine prey did not factor into the δD_f value for this individual.

Twelve different raptor species were used to create the base map I used to determine the origins of red-tailed hawks in this study. Some of these species, such as the falcons and accipiters, may have a stronger coastal influence due to diet than is likely in red-tailed hawks, causing the base map to predict a more positive δD_f value than would actually be expected in red-tailed hawks. Falcons and accipiters frequently take more avian prey than red-tailed hawks and could incorporate a heavier coastal influence into the stable isotope signatures of their feathers through the consumption of shorebirds, waterfowl and other coastal species. If one ignores the coastal effect and considers instead the predicted values in low altitude areas near where RT1 originated, then predicted values drop to between -39 and -23 δD_f. (Figure 1.18). However, this still represents a difference of 22‰ between predicted and actual values.

RT4 also was a young bird and exhibited a stable isotope signature outside of the predicted range. This could have resulted from natal dispersal. Little is known about dispersal in red-tailed hawks; however, studies in southwestern Idaho (Steenhof et al. 1984) and southern California (Peter Bloom, pers. comm.) suggest that red-tailed hawks tend to return to breed in the general area of their natal origin.

For RT2, RT3, RT5, RT6, RT7 and RT8, all adult birds, explanations involving breeding dispersal and isotope inadequacy could apply. Considering that female red-tailed hawks are thought to show strong breeding site fidelity (Janes 1984), breeding dispersal for after second-year individuals (RT2, RT6, and RT8) is unlikely. However, for second-year individuals (RT5) and after hatch-year individuals that may have been second-year individuals (RT2 and RT7), it is possible that dispersal, most likely in the form of natal dispersal, explains the difference seen between the actual signature and predicted signature exists. Rarely are red-tailed hawks observed breeding as juveniles (less than two years old; possessing a brown tail) (Henny and Wight 1972; Wiley 1975), so second-year birds may still be in the process of natal dispersal.

Conclusions

Concerns about stable isotope analysis were raised by Meehan et al. (2003). They argue that it may not be possible to use hydrogen stable isotope analysis of feathers to determine the origins of adults of large-bodied species, such as red-tailed hawks. They present three hypotheses to explain the difference seen between adult birds and their nestlings: 1) feathers grown early in the breeding season may be influenced by the consumption of migrant avian prey exhibiting greater δD values than that found in the local growing-season precipitation, 2) feathers grown earlier in the season might be

grown using winter energy reserves acquired at lower latitudes, and 3) during incubation and/or higher level of hunting activity, adults may use panting to dissipate heat (evaporative cooling) which potentially could lead to enrichment of heavy hydrogen stable-isotopes in the body water pool. Smith and Dufty (2005) further explored these hypotheses and suggest evaporative cooling may be the most likely explanation. Molting during the breeding season could coincide with increased frequency of evaporative cooling, which in turn could have an enriching effect on feather stable isotope composition. Therefore, there is a suite of unresolved technical issues with stable isotope analyses. These issues may or may not be restricted to raptors, but until they are resolved it will be difficult to predict origins of red-tailed hawks and other birds of prey and have a high level of confidence in the accuracy of those predictions.

At some migration monitoring stations biologists might encounter different populations from year to year, as suggested by the significant interaction between sex and year for the Goshutes Mountain site. In 2002, males came from higher latitudes than females on average, but in 2003 there was no significant difference. Data from the Goshutes suggest red-tailed hawks exhibit chain migration through that station, but no other site showed a correlation between passage date and δD_f value. Small sample sizes from sites could have contributed to the inability to detect any migratory patterns at the other stations.

Future studies utilizing stable isotope technology will require further examination of potential problems with using stable isotopes to predict the origins of migrating birds, and of raptors in particular. Although some studies have had success using stable isotopes to determine migratory passerine origins (Paxton et al. 2007; Clegg et al. 2003;

Wassenaar and Hobson 2001), studies involving shorebirds have experienced problems similar to those seen with raptors (Rocque et al. 2006; Wunder et al. 2005). As suggested by Lott and Smith (2006), standardizing methodology in order to make studies comparable is of the utmost importance. The type of feather sampled needs to be the same in order to compare studies. Smith et al. (2008) and Kelly et al. (2001) found that flight feathers possessed lower δD values than contour feathers. Furthermore, feather samples should be analyzed during the same session within the same laboratory. Feather samples analyzed at different times and in different labs have shown poor accuracy and repeatability (Smith et al. 2009). Lott and Smith (2006) also suggest comparative studies should use the same models for δD_p estimates for feather-collection sites.

The results of this study indicate that caution must be exhibited when using this technology and researchers should interpret stable isotope data in light of the problems that have been identified previously. For example, confirmatory studies, using birds of known origin, would be valuable in indentifying species or taxa where stable isotope analysis of feathers produces reliable data. And in the case of red-tailed hawk, additional use of satellite telemetry might shed light on life history parameters, such as natal dispersal and migratory movements that would facilitate the interpretation of stable isotope data.

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Table 1.1 Collection locations and land managers for sampled red-tailed hawks.

Migration Monitoring Station	Location	Coordinates
Goshute Mountains	Northeastern Nevada Bureau of Land Management	40º 25.417’ N, 114º 16.276’ W
Bonney Butte	North Central Oregon Mount Hood National Forest	45º 15’ 46.8” N, 121º 35’ 31.2” W
Chelan Ridge	Eastern Cascade Mountains Washington State	48º 01’12.8” N, 120º 05’38.4” W
Manzano Mountains	Central New Mexico Cibola National Forest	34º 42.25’ N, 106º 24.67’ W
Idaho Bird Observatory	Southwestern Idaho Boise National Forest	43º 41’36.84” N, 116º 05’43.08” W

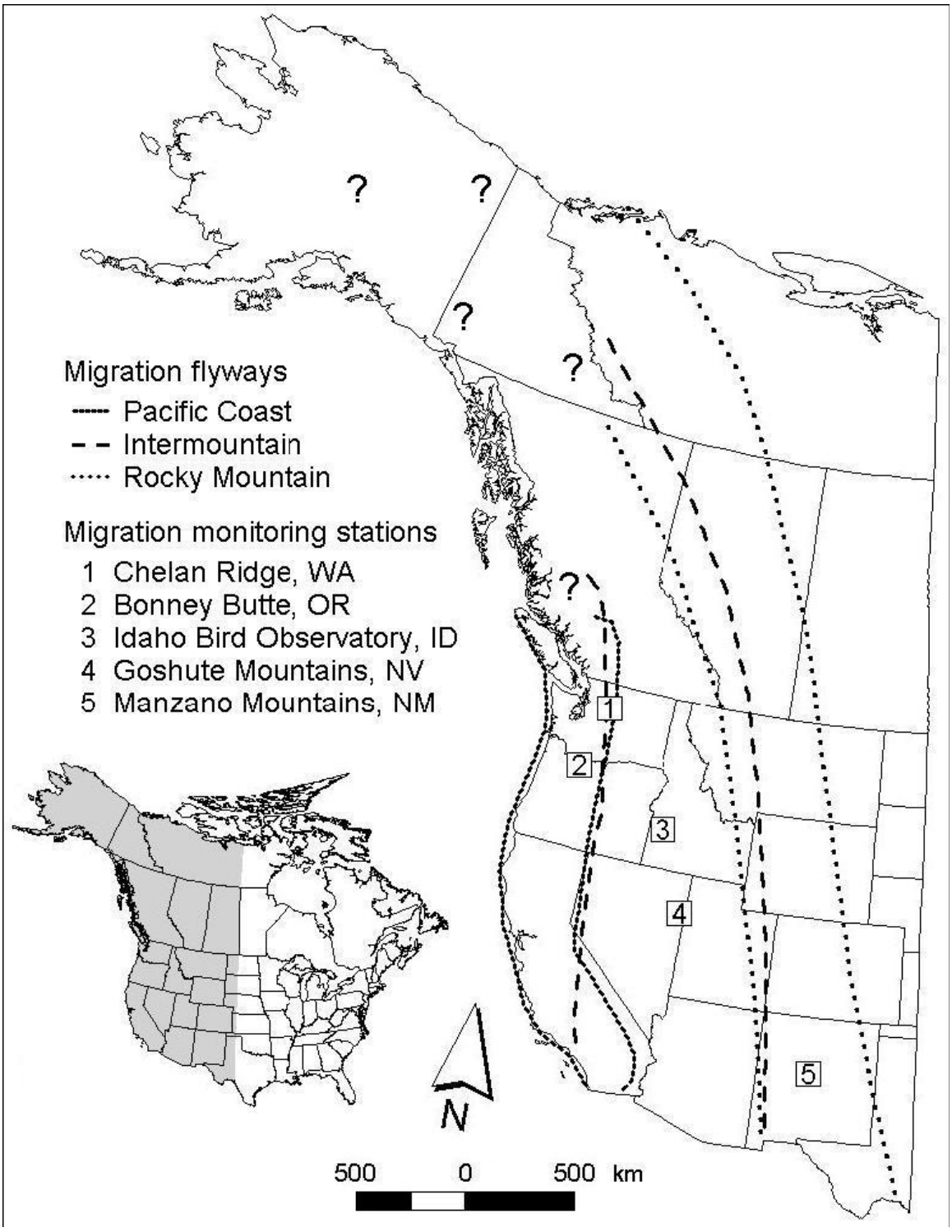

Figure 1.2 Locations of migration monitoring stations and migration flyways. Question marks at the northern ends of migration flyways represent areas where it is not known how the migration flyways are separated.

Table 1.2 Distribution of feather samples by migration monitoring site and year of capture.

Site Year	Bonney Butte	Chelan Ridge	Idaho Bird Observatory	Goshute Mountains	Manzano Mountains
2002	32	12	14	42	16
2003	35	10	10	32	19
Total feathers analyzed	67	22	24	74	35

Table 1.3 Bonney Butte ANOVA for hydrogen isotope signatures by year and sex.

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio	Prob > F
Model	3	1821.150	607.050	1.0068	0.3960
Error	61	36780.844	602.965		
Total	64	38601.994			

Parameter Estimates

Source	DF	Sum of Squares	F Ratio	Prob > F
Year	1	516.7353	0.8570	0.3582
Sex	1	1555.7319	2.5801	0.1134
Year x Sex	1	2.9445	0.0049	0.9445

Table 1.4 Goshute Mountains ANOVA for hydrogen isotope signatures by year and sex.

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio	Prob > F
Model	3	11591.332	3863.78	3.1313	0.0312
Error	68	83905.796	1233.91		
Total	71	95497.127			

Parameter Estimates

Source	DF	Sum of Squares	F Ratio	Prob > F
Year	1	336.1006	0.2724	0.6034
Sex	1	1897.2825	1.5376	0.2192
Year x Sex	1	8354.3468	6.7706	0.0114

Table 1.5 Goshute Mountains interaction between year and sex.

Level	Least Square Mean	Std Error
2002, Female	-79.2577	7.312
2002, Male	-111.4931	8.280
2003, Female	-96.7104	8.782
2004, Male	-85.2827	9.070

Table 1.6 Manzano Mountains ANOVA for hydrogen isotope signatures by year and sex.

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio	Prob > F
Model	3	377.454	125.82	0.0792	0.9708
Erro	30	47685.983	1589.53		
Total	33	48063.436			

Parameter Estimates

Source	DF	Sum of Squares	F Ratio	Prob > F
Year	1	314.90499	0.1981	0.6594
Sex	1	50.95262	0.0321	0.8591
Year x Sex	1	14.50017	0.0091	0.9245

Table 1.7 Chelan Ridge ANOVA for hydrogen isotope signatures by year and sex.

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio	Prob > F
Model	3	734.2414	244.747	0.6872	0.5715
Erro	18	6410.8602	356.159		
Total	21	7145.1016			

Parameter Estimates

Source	DF	Sum of Squares	F Ratio	Prob > F
Year	1	7.58787	0.0213	0.8856
Sex	1	296.48407	0.8324	0.3736
Year x Sex	1	301.43292	0.8463	0.3698

Table 1.8 Idaho Bird Observatory ANOVA for hydrogen isotope signatures by year.

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio	Prob > F
Model	1	39.885	39.89	0.0345	0.8544
Error	22	25457.709	1157.17		
Total	23	25497.595			

Parameter Estimates

Source	DF	Sum of Squares	F Ratio	Prob > F
Year	1	39.885288	0.0345	0.8544

Table 1.9 Homogeneity of slopes for migration monitoring stations by year.

Site Analysis	Bonney Butte	Goshute Mountains	Manzano Mountains	Chelan Ridge	Idaho Bird Observatory
Homogeneity of Slopes (2002)	$F_{1,28} = -0.11$, $P = 0.75$	$F_{1,38} = -0.16$, $P = 0.69$	$F_{1,12} = 1.17$, $P = 0.30$	$F_{1,8} = 1.74$, $P = 0.22$	N/A
Homogeneity of Slopes (2003)	$F_{1,29} = -0.005$, $P = 0.94$	$F_{1,28} = -0.006$, $P = 0.93$	$F_{1,15} = -0.005$, $P = 0.21$	$F_{1,6} = 0.0004$, $P = 0.98$	N/A

Table 1.10 ANCOVA for migration monitoring stations by year.

Site Analysis	Bonney Butte	Goshute Mountains	Manzano Mountains	Chelan Ridge	Idaho Bird Observatory
ANCOVA (2002)	$F_{1,29} = 3.13$, $P = 0.09$	$F_{1,39} = 5.20$, $P = 0.03$	$F_{1,13} = -0.14$, $P = 0.72$	$F_{1,9} = -0.72$, $P = 0.42$	N/A
ANCOVA (2003)	$F_{1,30} = -0.61$, $P = 0.44$	$F_{1,29} = -1.10$, $P = 0.30$	$F_{1,16} = 0.66$, $P = 0.43$	$F_{1,7} = -0.05$, $P = 0.83$	N/A

Table 1.11 Linear Regression for migration monitoring stations by year.

Site Analysis	Bonney Butte	Goshute Mountains	Manzano Mountains	Chelan Ridge	Idaho Bird Observatory
Linear Regression (2002)	$F_{1,30}$ = -0.15, P = 0.70	$F_{1,40}$ = -19.98, P = <0.0001	$F_{1,14}$ = -0.16, P = 0.70	$F_{1,10}$ = -0.004, P = 0.95	$F_{1,12}$ = -0.71, P = 0.42
Linear Regression (2003)	$F_{1,31}$ = -1.88, P = 0.18	$F_{1,30}$ = -16.08, P = 0.0004	$F_{1,17}$ = -0.59, P = 0.45	$F_{1,8}$ = -1.21, P = 0.30	$F_{1,8}$ = -0.34, P = 0.58

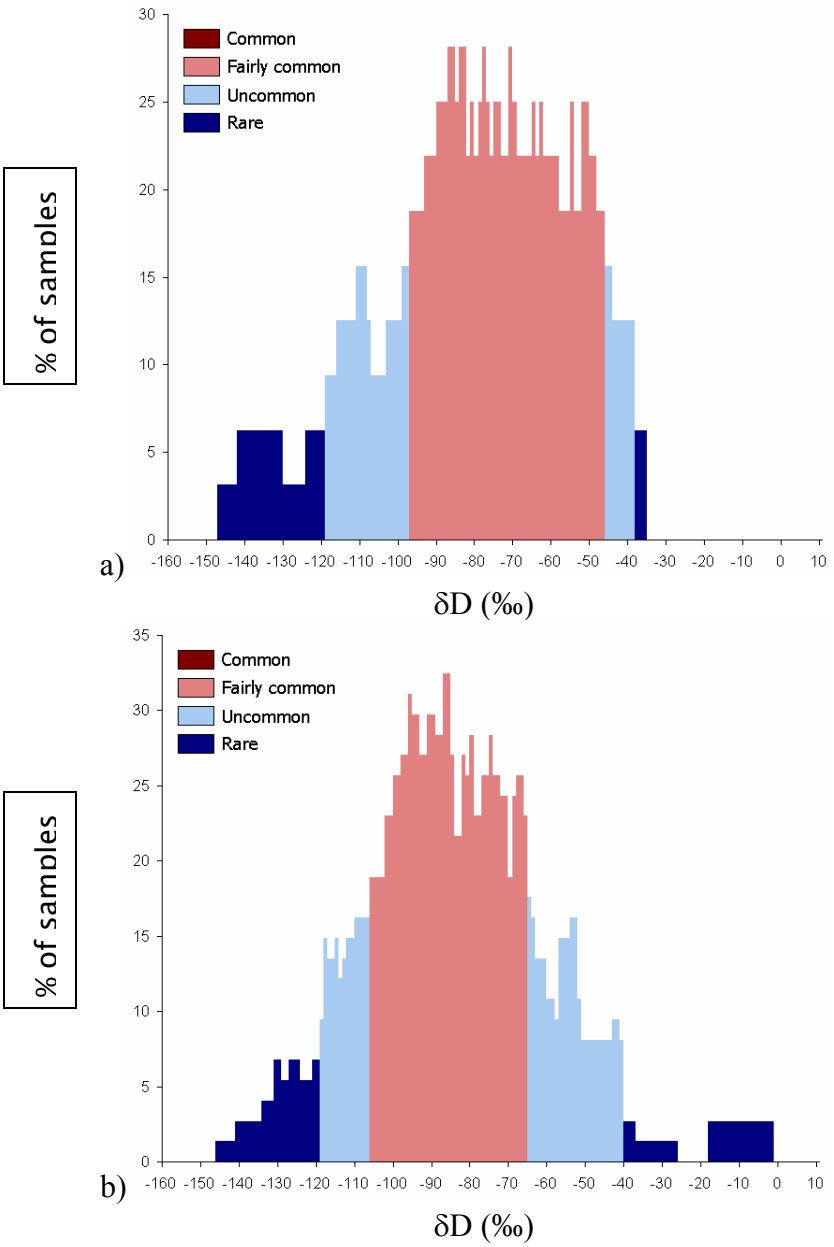

Figure 1.3 Relative frequency histogram of the stable-hydrogen isotope composition (δD) of red-tailed hawks captured at Bonney Butte, Oregon, during the fall migration season of a) 2002 (n = 32) and b) 2003 (n = 35). Common: >33% of all samples per δD_f value; fairly common: 17 – 33% of all samples per δD_f value: uncommon: 8 – 16% of all samples per δD_f value: and rare: <8% of all samples per δD_f value.

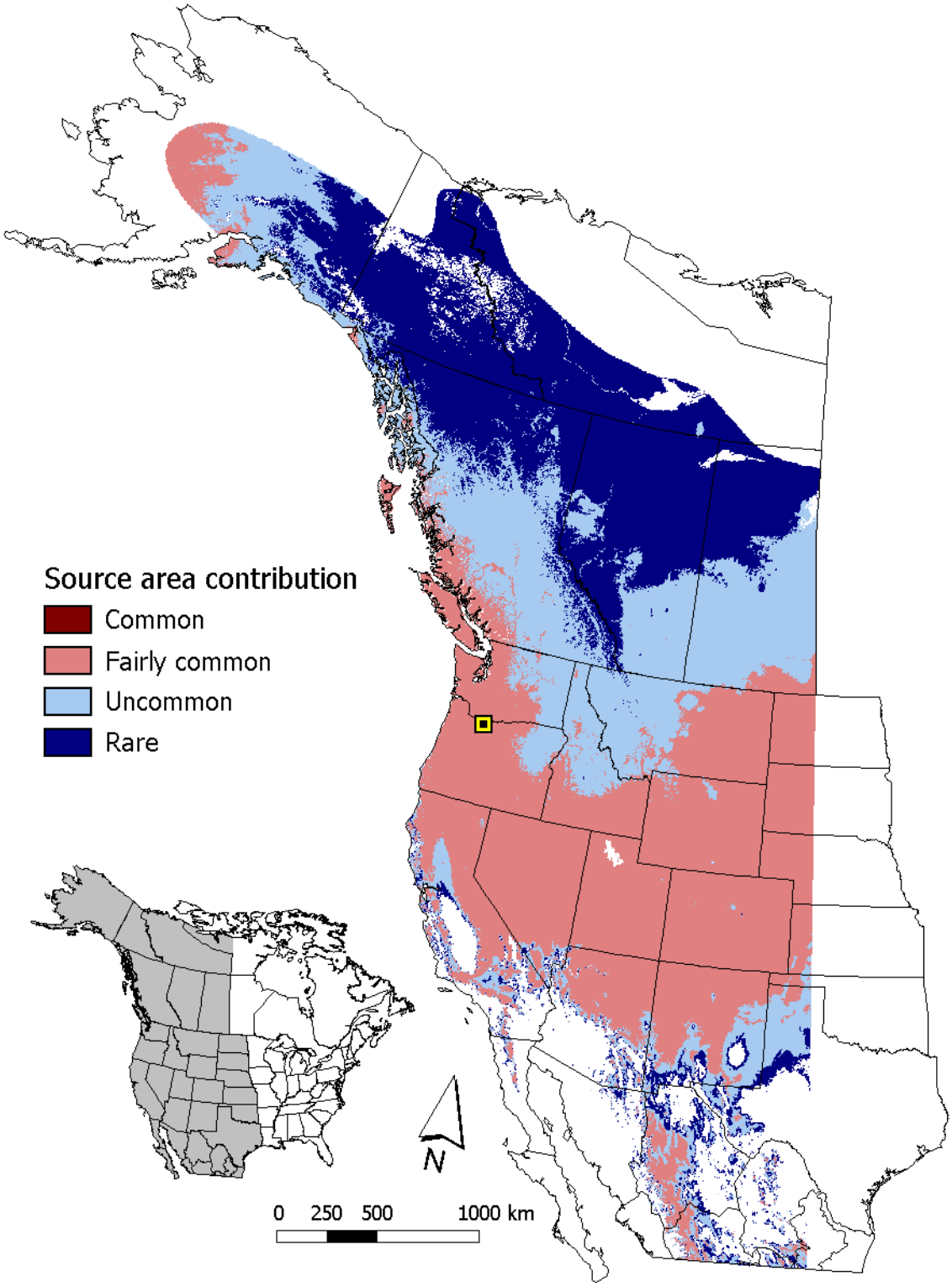

Figure 1.4 Estimated origins of red-tailed hawks captured at Bonney Butte, Oregon (square), during the fall migration season of 2002 (n = 32).

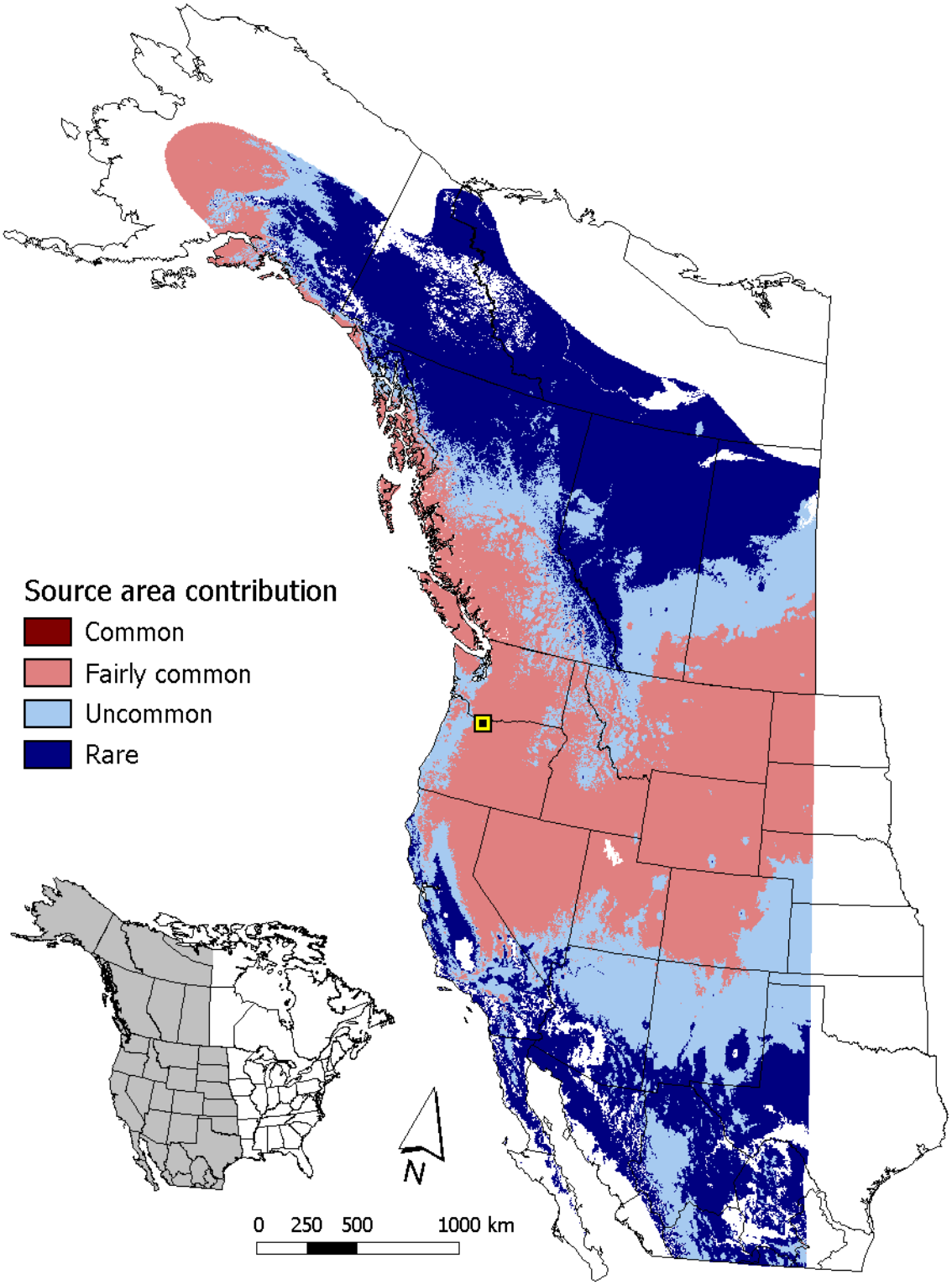

Figure 1.5 Estimated origins of red-tailed hawks captured at Bonney Butte, Oregon (square), during the fall migration season of 2003 (n = 35).

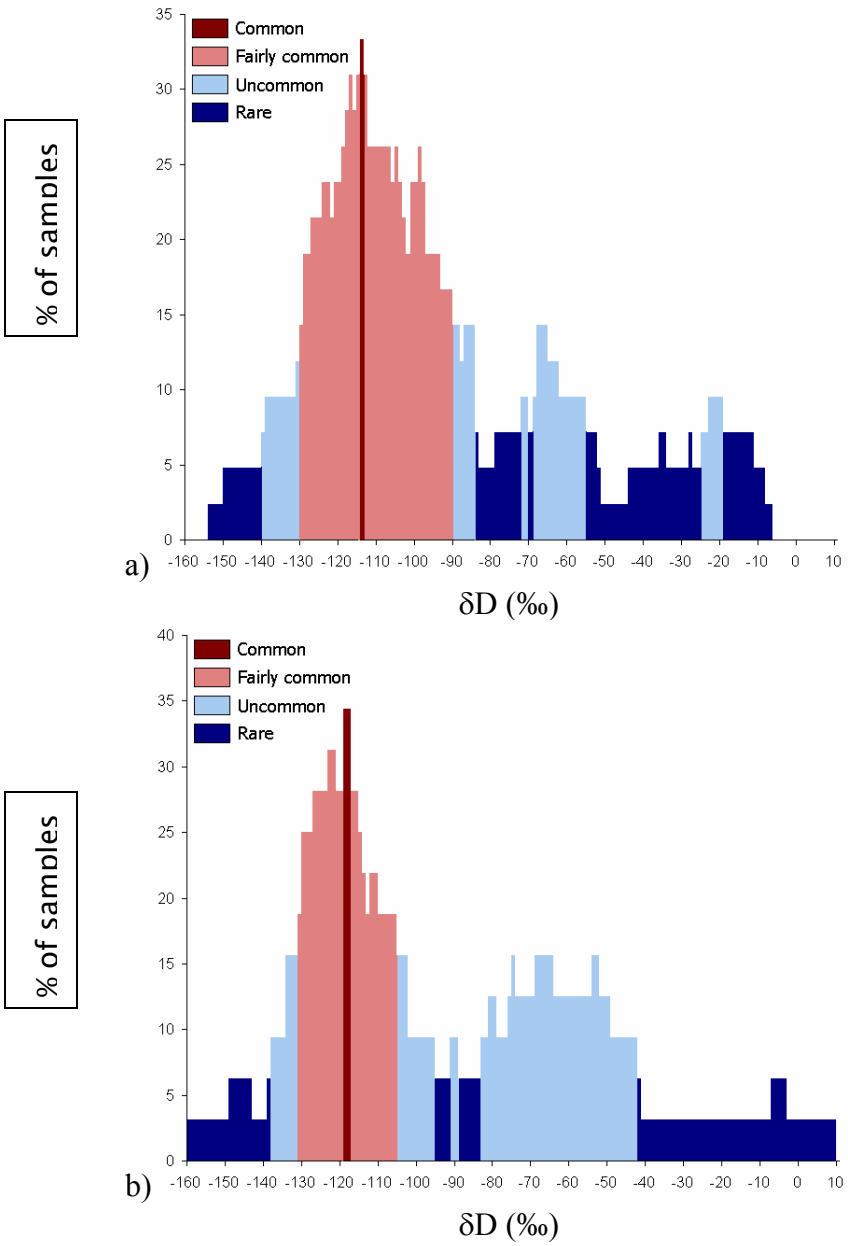

Figure 1.6 Relative frequency histogram of the stable-hydrogen isotope composition (δD) of red-tailed hawks captured at Goshute Mountains, Nevada, during the fall migration season of a) 2002 (n = 42) and b) 2003 (n = 32). Common: >33% of all samples per δD_f value; fairly common: 17 – 33% of all samples per δD_f value: uncommon: 8 – 16% of all samples per δD_f value: and rare: <8% of all samples per δD_f value.

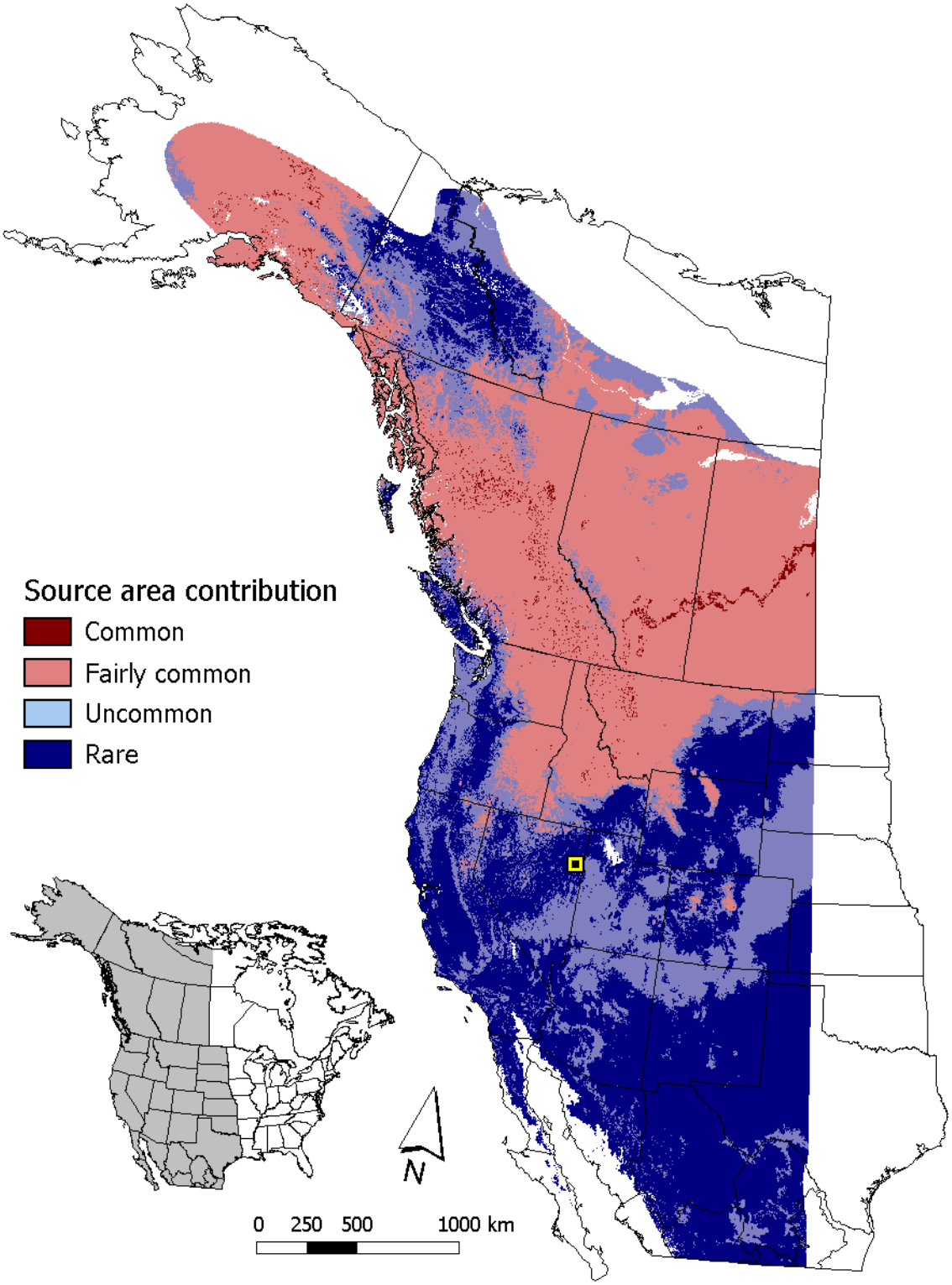

Figure 1.7 Estimated origins of red-tailed hawks captured at Goshute Mountains, Nevada (square), during the fall migration season of 2002 (n = 42).

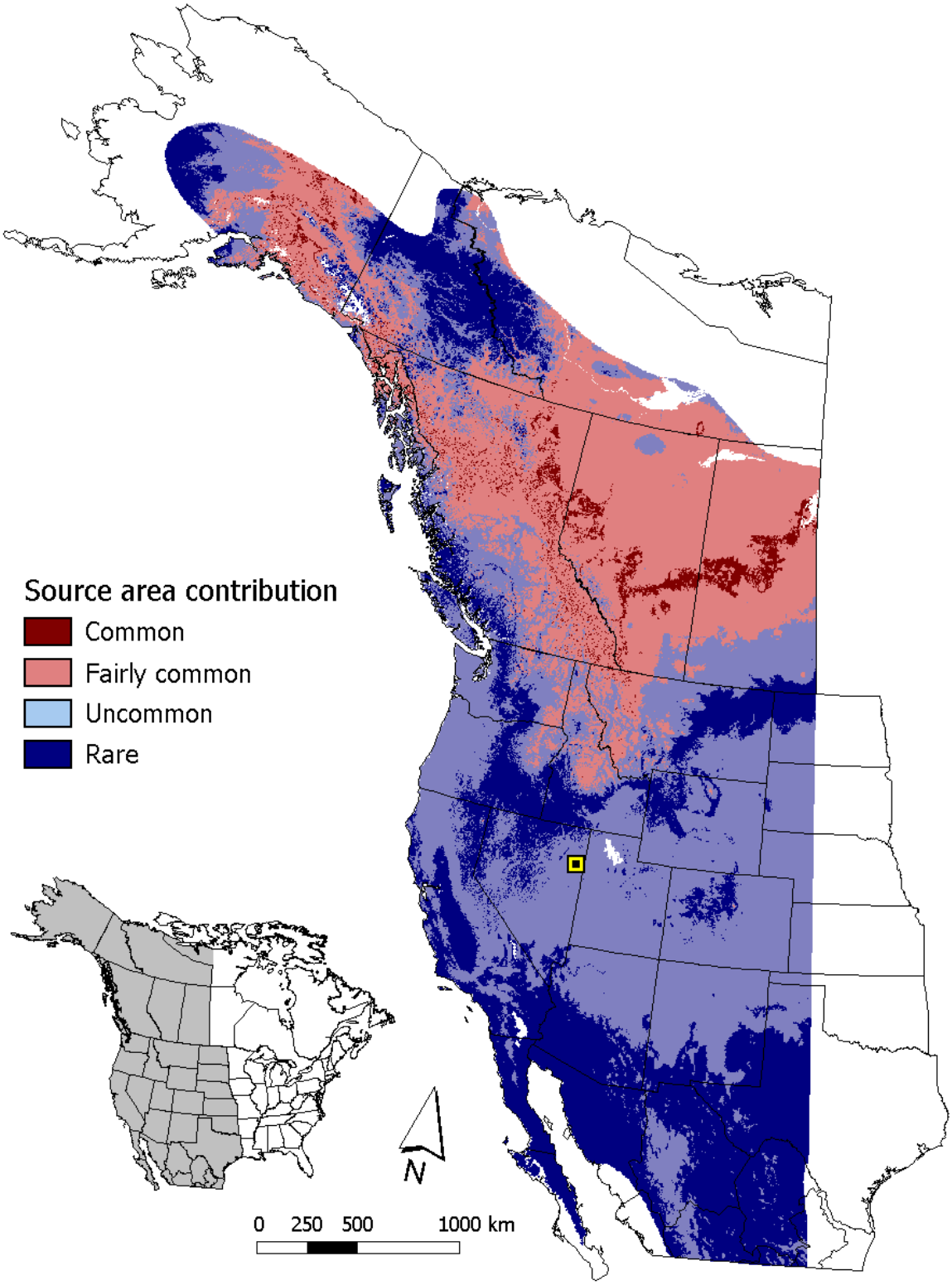

Figure 1.8 Estimated origins of red-tailed hawks captured at Goshute Mountains, Nevada (square), during the fall migration season of 2003 (n = 32).

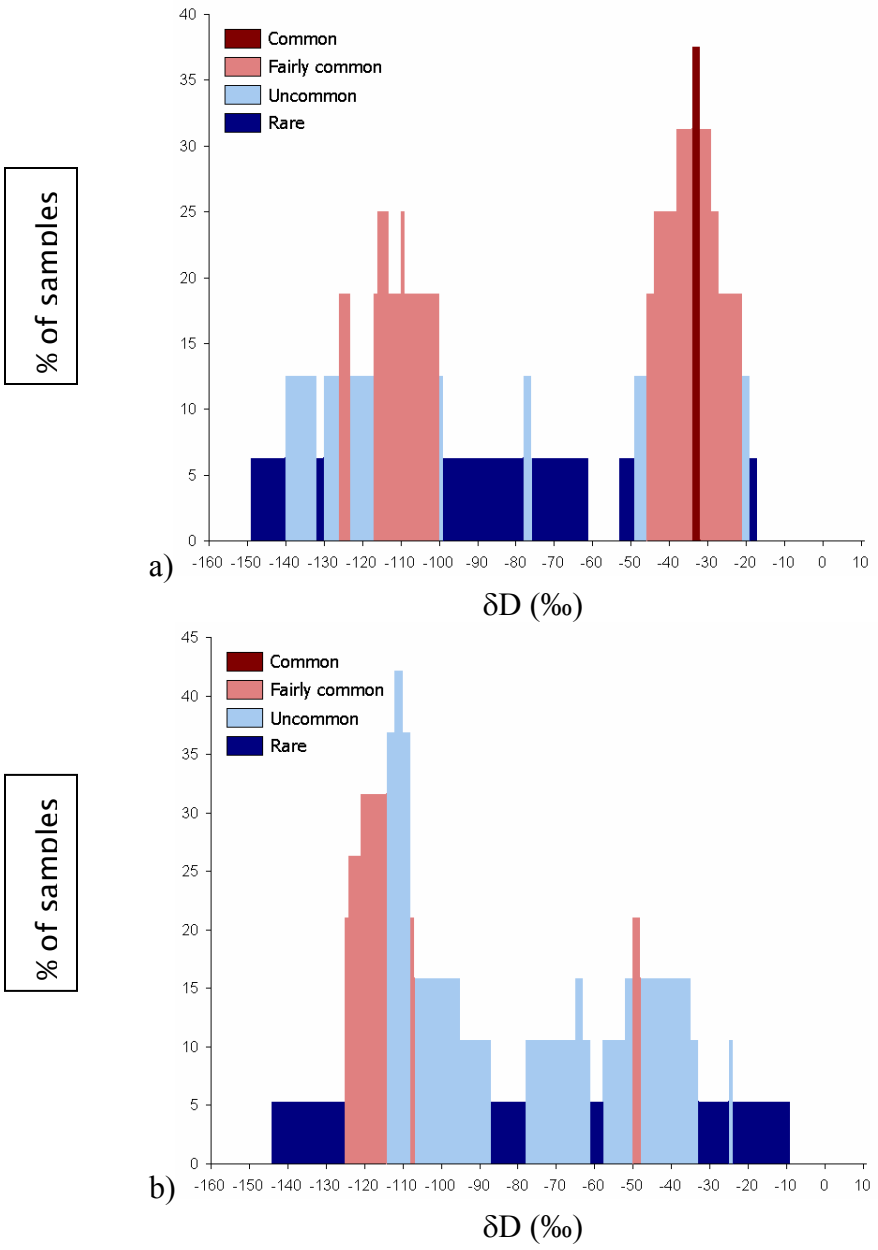

Figure 1.9 Relative frequency histogram of the stable-hydrogen isotope composition (δD) of red-tailed hawks captured at Manzano Mountains, New Mexico, during the fall migration season of a) 2002 (n = 16) and b) 2003 (n = 19). Common: >33% of all samples per δD_f value; fairly common: 17 – 33% of all samples per δD_f value: uncommon: 8 – 16% of all samples per δD_f value: and rare: <8% of all samples per δD_f value.

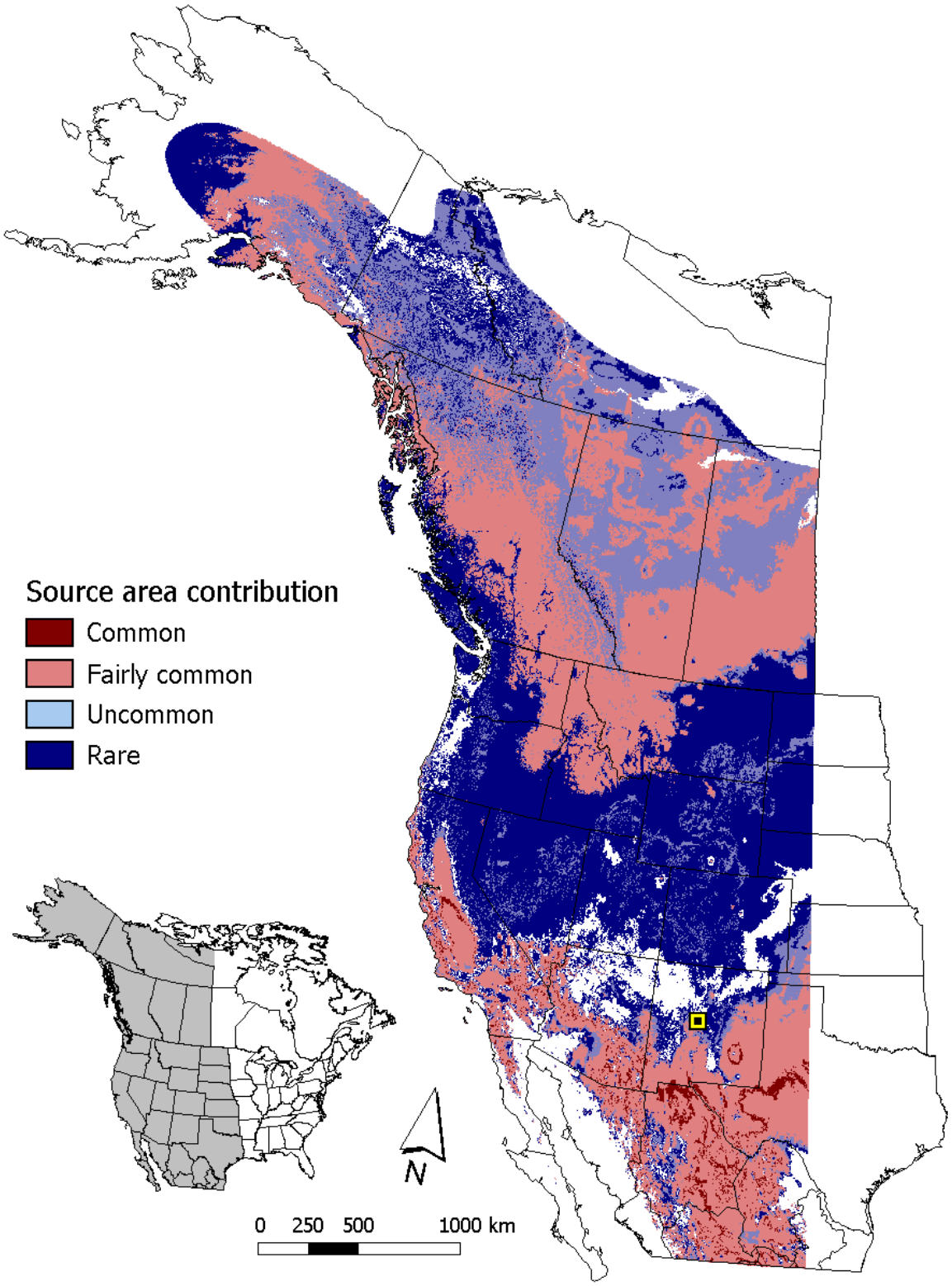

Figure 1.10 Estimated origins of red-tailed hawks captured at Manzanos Mountains, New Mexico (square), during the fall migration season of 2002 (n = 16).

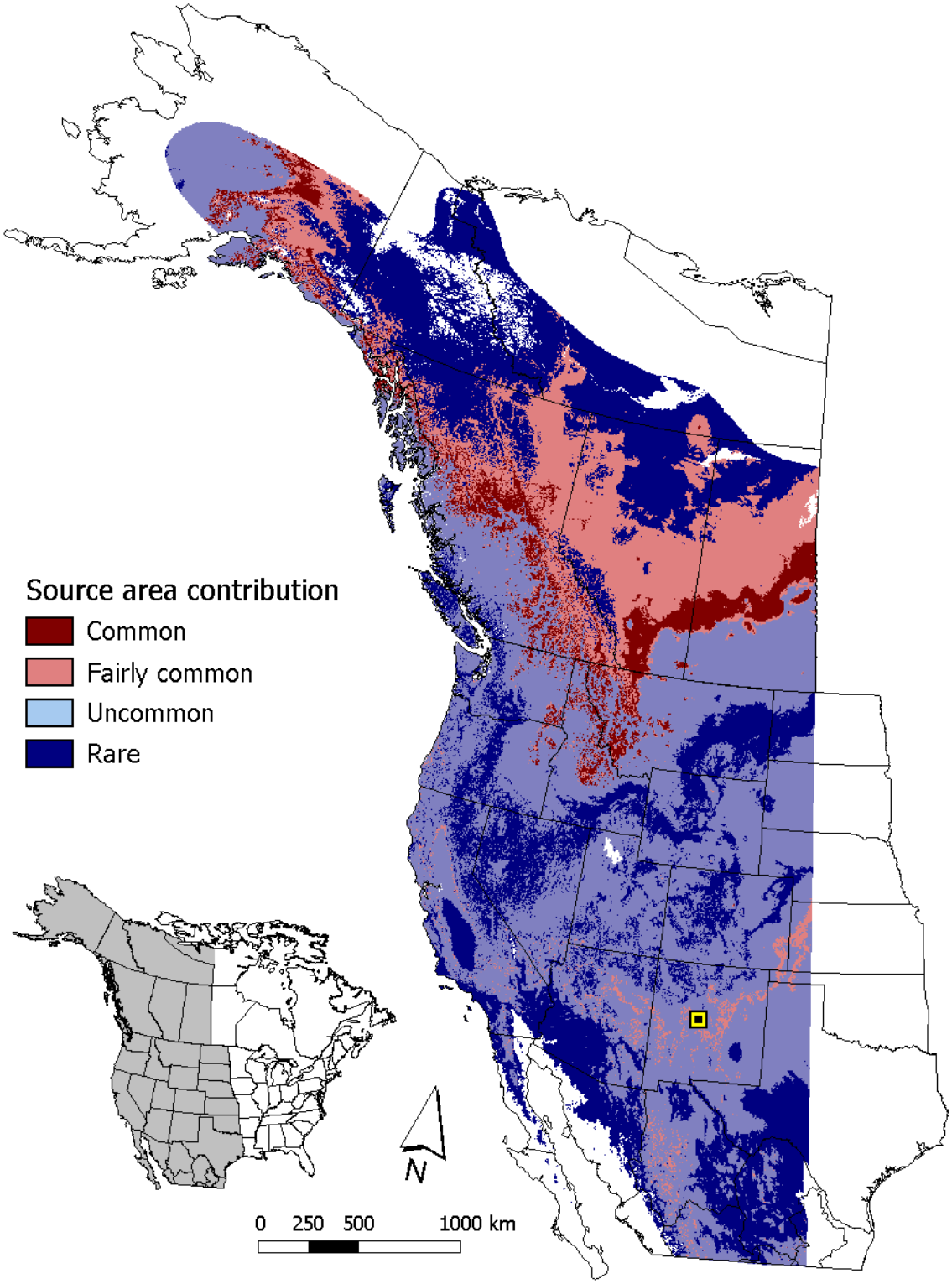

Figure 1.11 Estimated origins of red-tailed hawks captured at Manzanos Mountains, New Mexico (square), during the fall migration season of 2003 (n = 19).

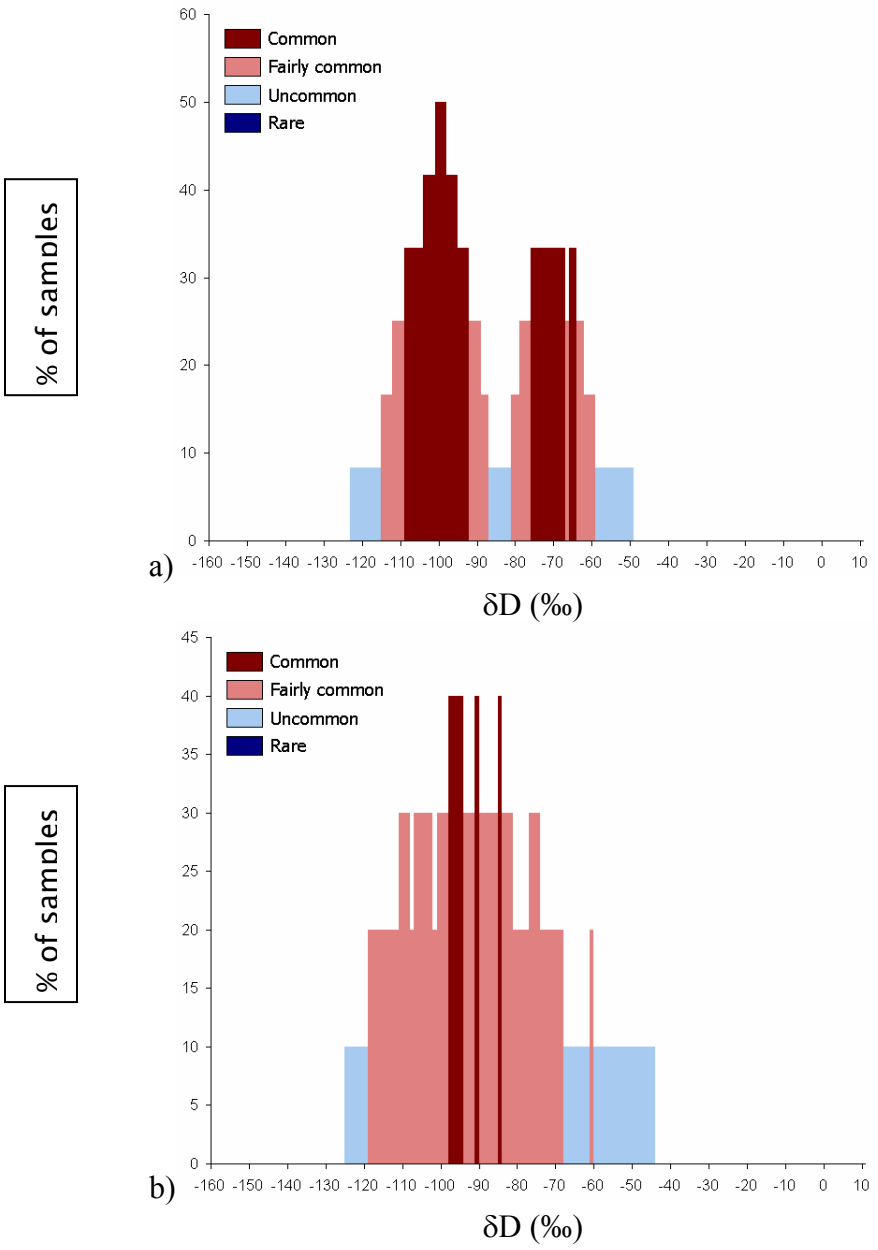

Figure 1.12 Relative frequency histogram of the stable-hydrogen isotope composition (δD) of red-tailed hawks captured at Chelan Ridge, Washington, during the fall migration season of a) 2002 (n = 12) and b) 2003 (n = 10). Common: >33% of all samples per δD_f value; fairly common: 17 – 33% of all samples per δD_f value: uncommon: 8 – 16% of all samples per δD_f value: and rare: <8% of all samples per δD_f value.

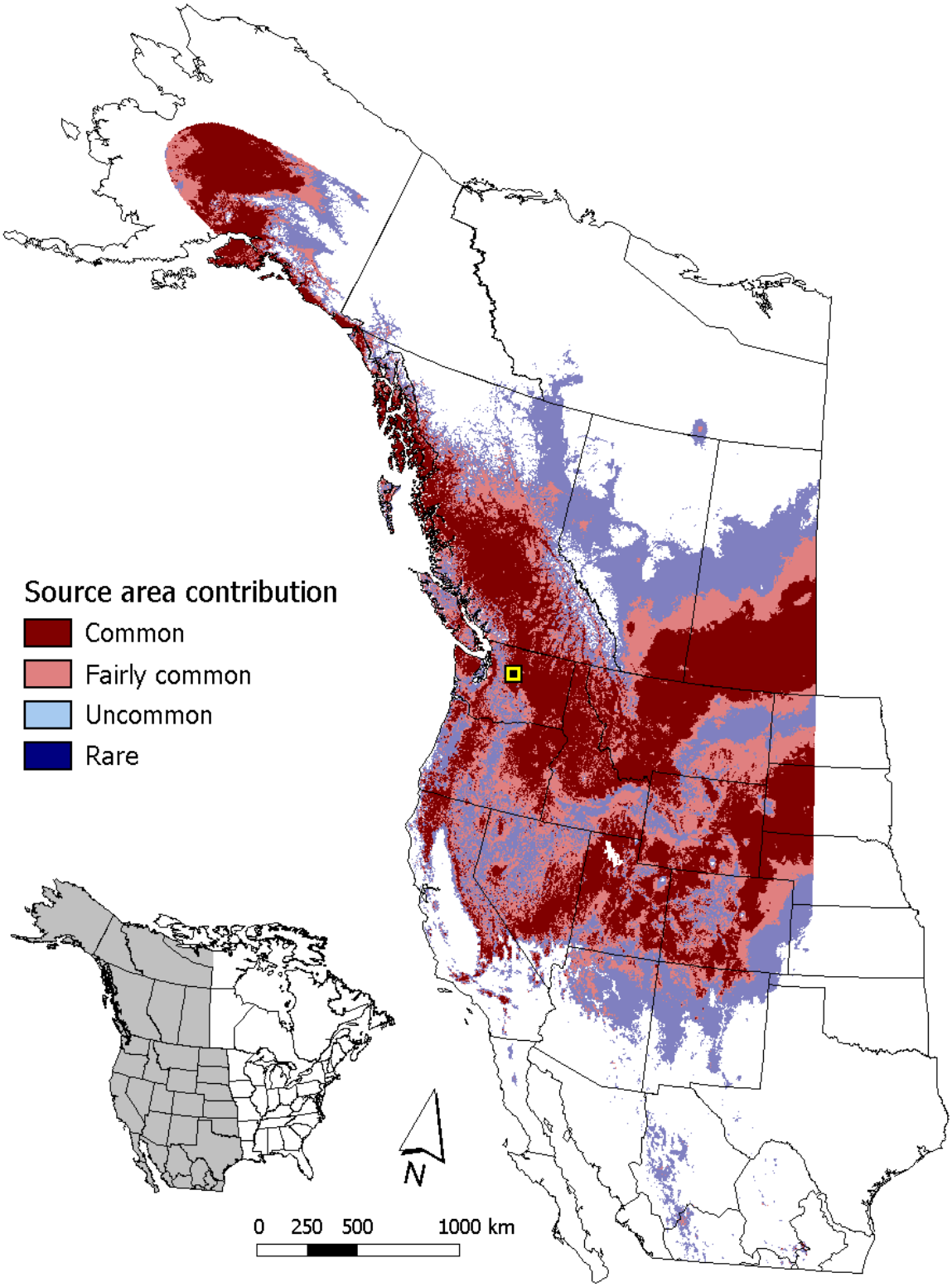

Figure 1.13 Estimated origins of red-tailed hawks captured at Chelan Ridge, Washington (square), during the fall migration season of 2002 (n = 12).

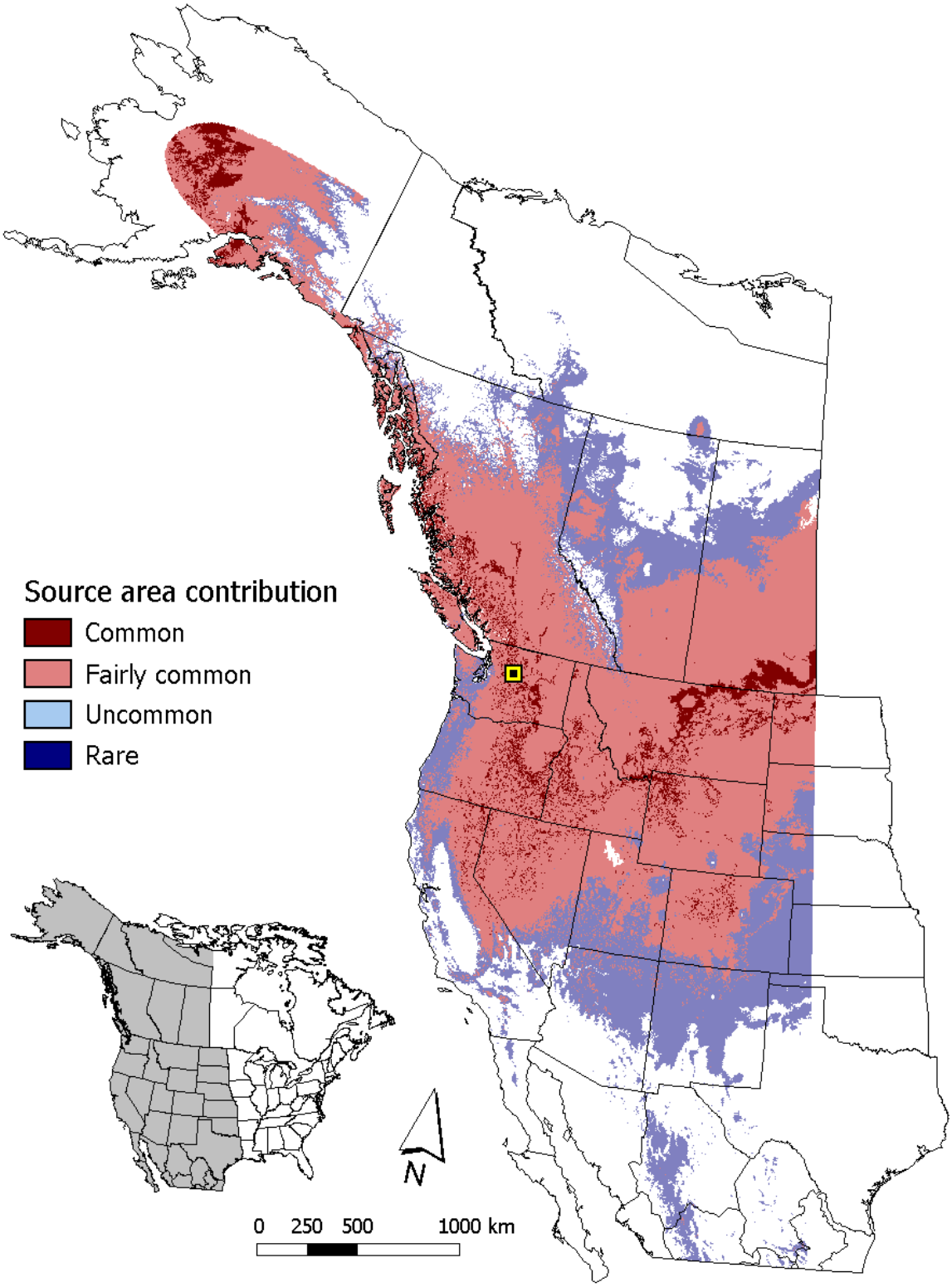

Figure 1.14 Estimated origins of red-tailed hawks captured at Chelan Ridge, Washington (square), during the fall migration season of 2003 (n = 10).

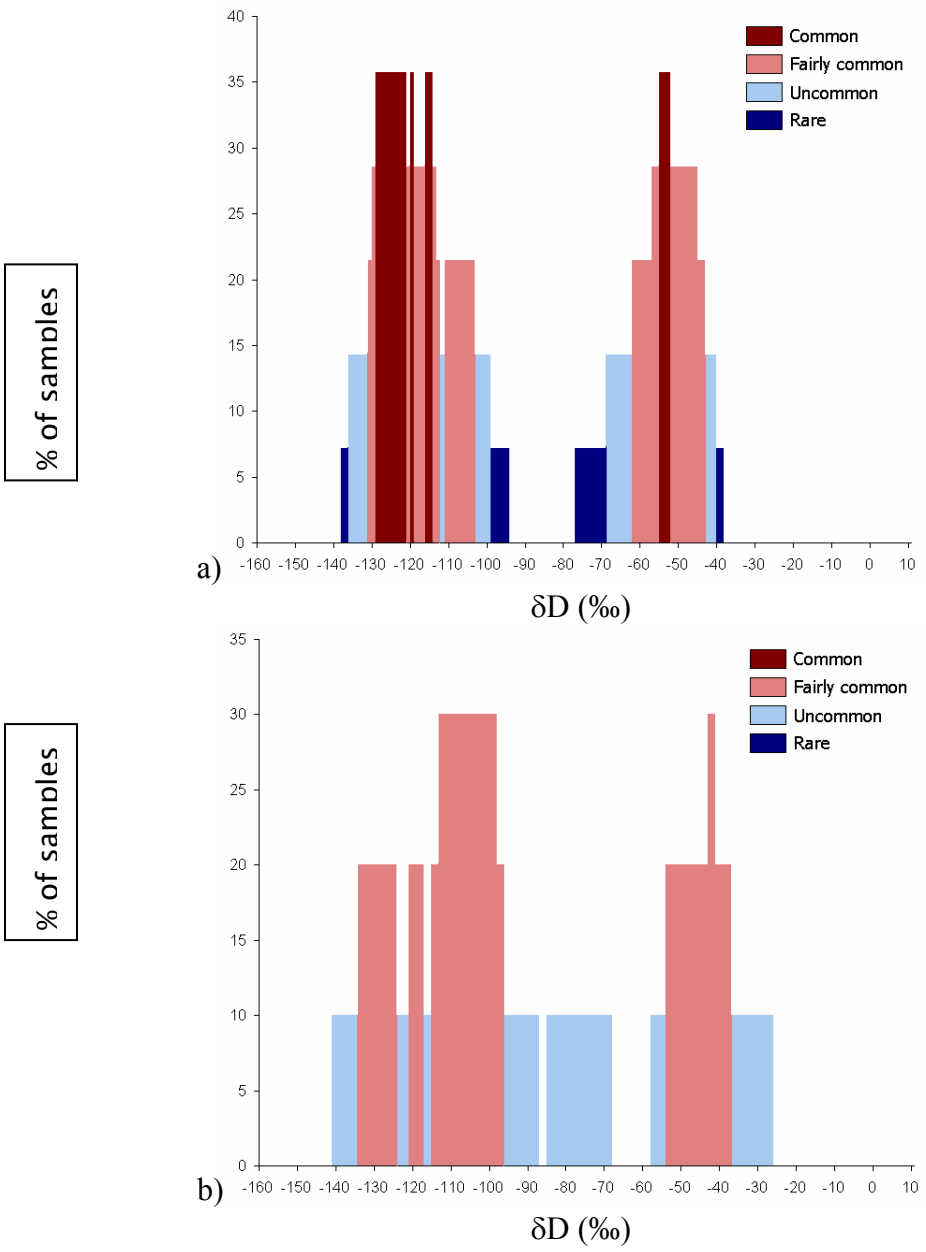

Figure 1.15 Relative frequency histogram of the stable-hydrogen isotope composition (δD) of red-tailed hawks captured at Idaho Bird Observatory, Idaho, during the fall migration season of a) 2002 (n = 14) and b) 2003 (n = 10). Common: >33% of all samples per δD_f value; fairly common: 17 – 33% of all samples per δD_f value: uncommon: 8 – 16% of all samples per δD_f value: and rare: <8% of all samples per δD_f value.

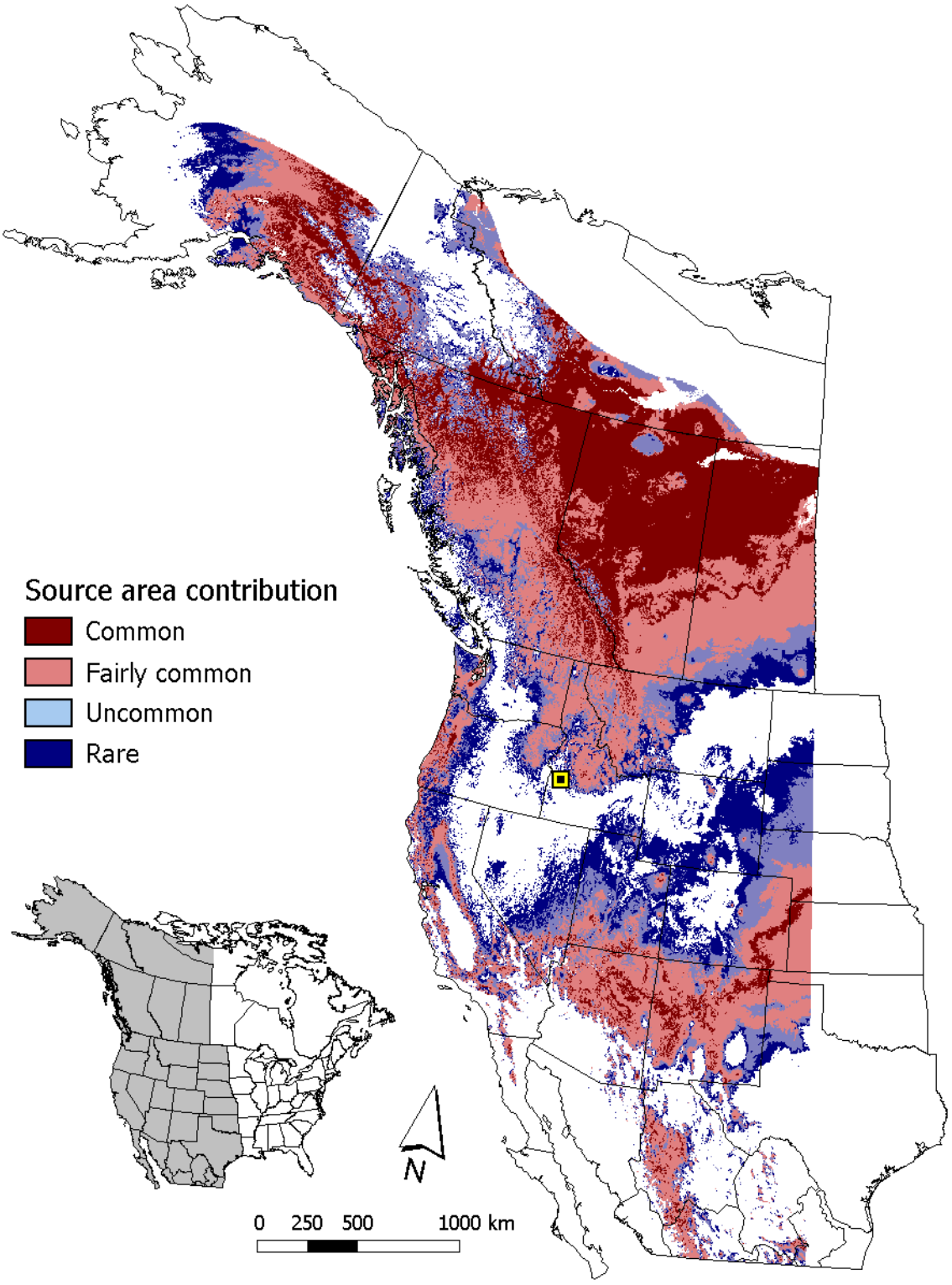

Figure 1.16 Estimated origins of red-tailed hawks captured at Idaho Bird Observatory, Idaho (square), during the fall migration season of 2002 (n = 14).

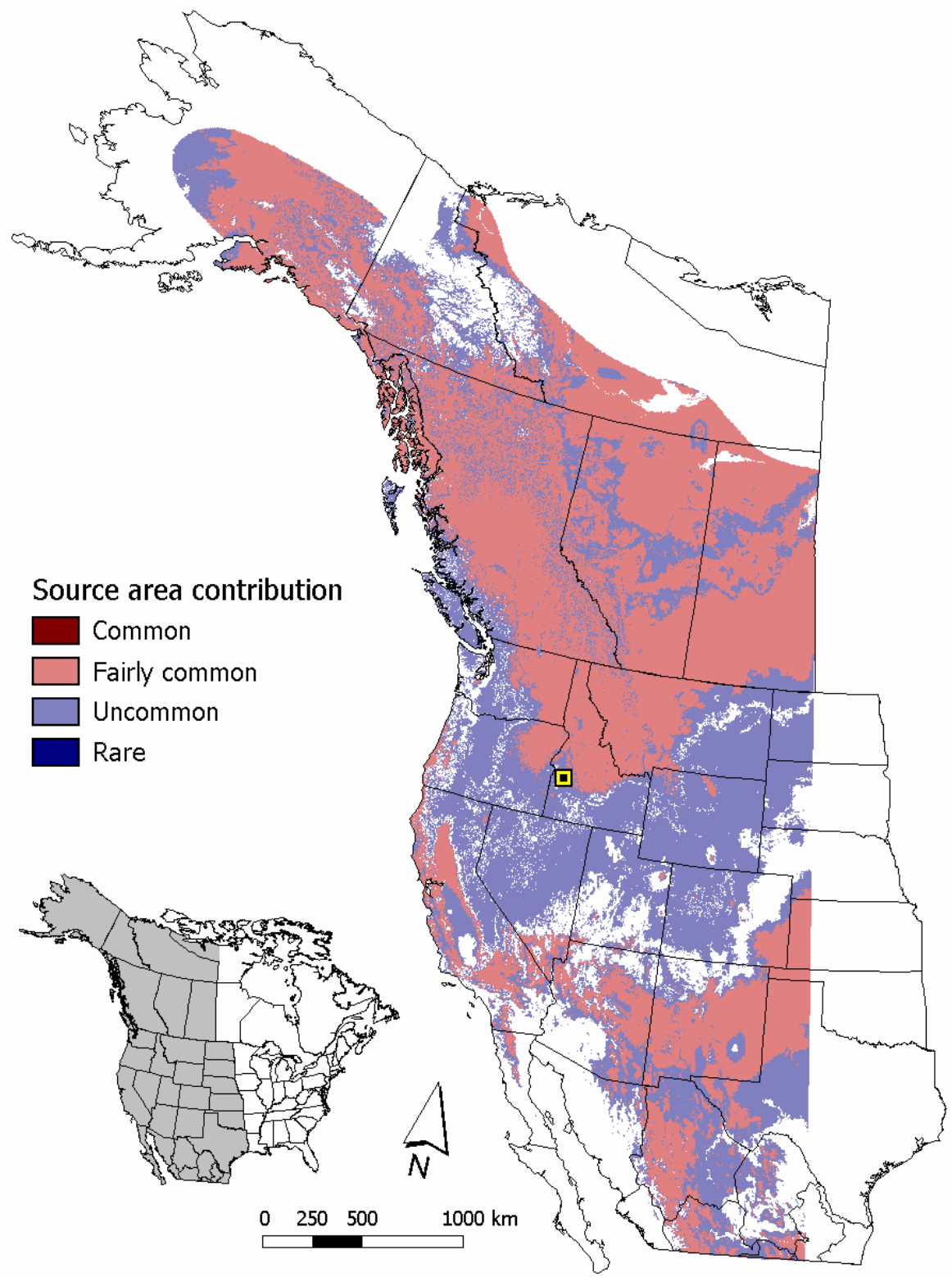

Figure 1.17 Estimated origins of red-tailed hawks captured at Idaho Bird Observatory, Idaho (square), during the fall migration season of 2003 (n = 10).

Table 1.12 Actual and predicted stable hydrogen signature of satellite telemetry and recapture red-tailed hawks.

Bird	T/R	Capture Location	Natal or breeding location (post-capture for telemetry birds, pre-capture for recapture birds)	Age, Sex	Predicted Signature (‰)	Actual Signature (‰)
RT1	R	GM	Laguna Beach, CA	HY,	-2*	-61
RT2	T	CR	Northcentral WA	AHY, F	-94	-91
RT3	T	CR	Southern BC	ASY, F	-100	-96
RT4	T	CR	East of Hampton Butte, OR	HY, F	-88*	-76
RT5	T	GM	Wallowa Mountains, northeast OR	SY, F	-107*	-71
RT6	T	GM	San Gabriel Mountains, southern CA	ASY, F	-46*	-60
RT7	T	MM	Between Albuquerque and Los Alamos, NM	AHY, F	-43*	-29
RT8	T	MM	Southwest of Durango, CO	ASY, F	-50*	-27

T = Telemetry, R = Recapture, GM = Goshute Mountains, CR = Chelan Ridge, MM = Manzano Mountains, HY = Hatch Year, SY = Second Year, AHY = After Hatch Year, ASY= After Second Year, F = Female, M = Male

*fall outside of the ± 8‰ accuracy of the Lott and Smith (2006) assessment of map accuracy in the description of the origin of migrants.

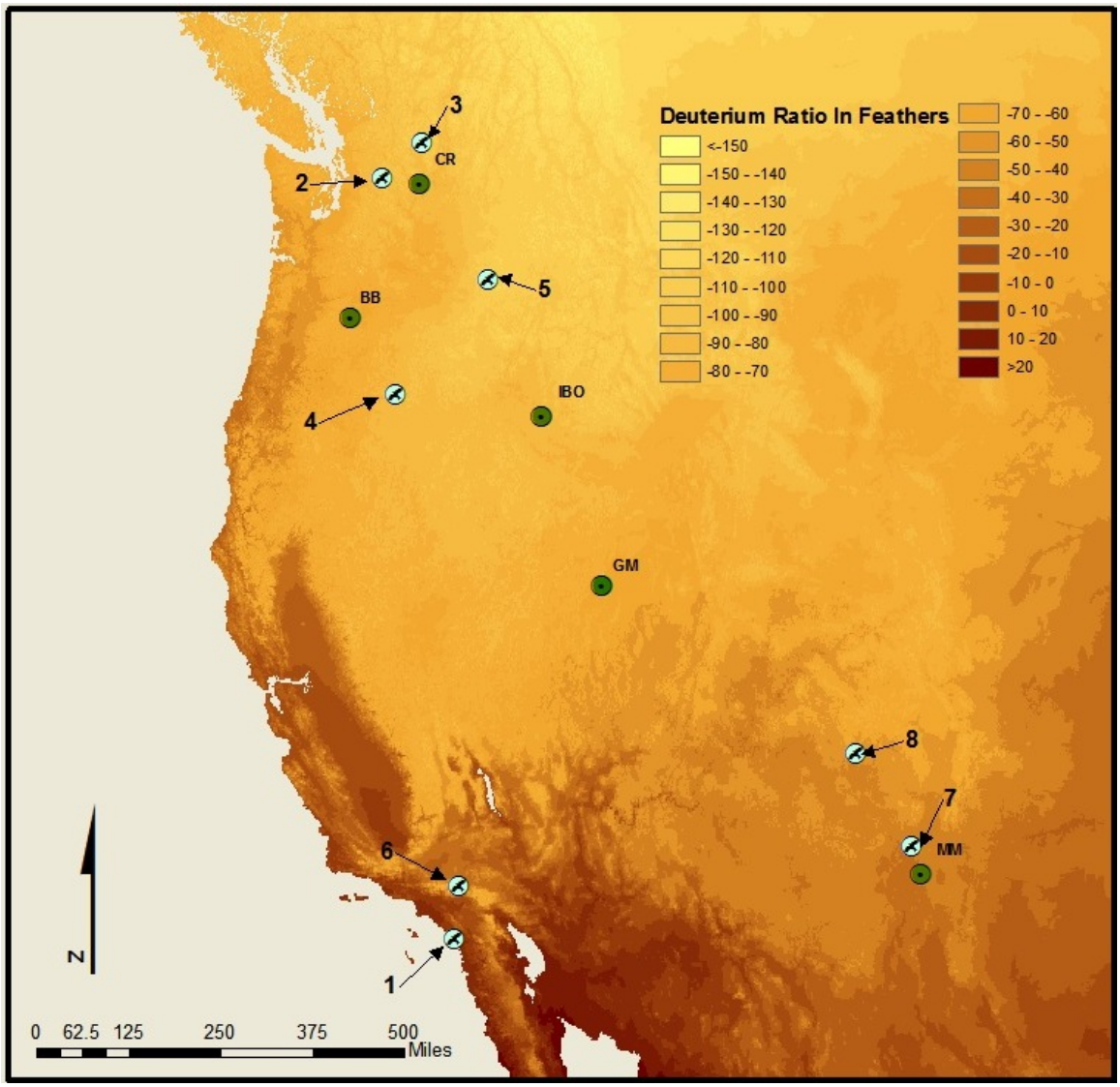

Figure 1.18 Known origin bird locations plotted on the Lott and Smith (2006) base map: 1 = RT1 in Laguna Beach, CA; 2 = RT2 in southern BC; 3 = RT3 in northcentral WA; 4 = RT4 east of Hampton Butte, OR; 5 = RT5 in the Wallowa Mountains of northeast OR; 6 = RT6 in the San Gabriel Mountains of southern CA; 7 = RT7 between Albuquerque and Los Alamos, NM; and 8 = RT8 southwest of Durango, CO. Site 1 = Chelan Ridge, Site 2 = Bonney Butte, Site 3 = Idaho Bird Observatory, Site 4 = Goshute Mountains, Site 5 = Manzano Mountains.

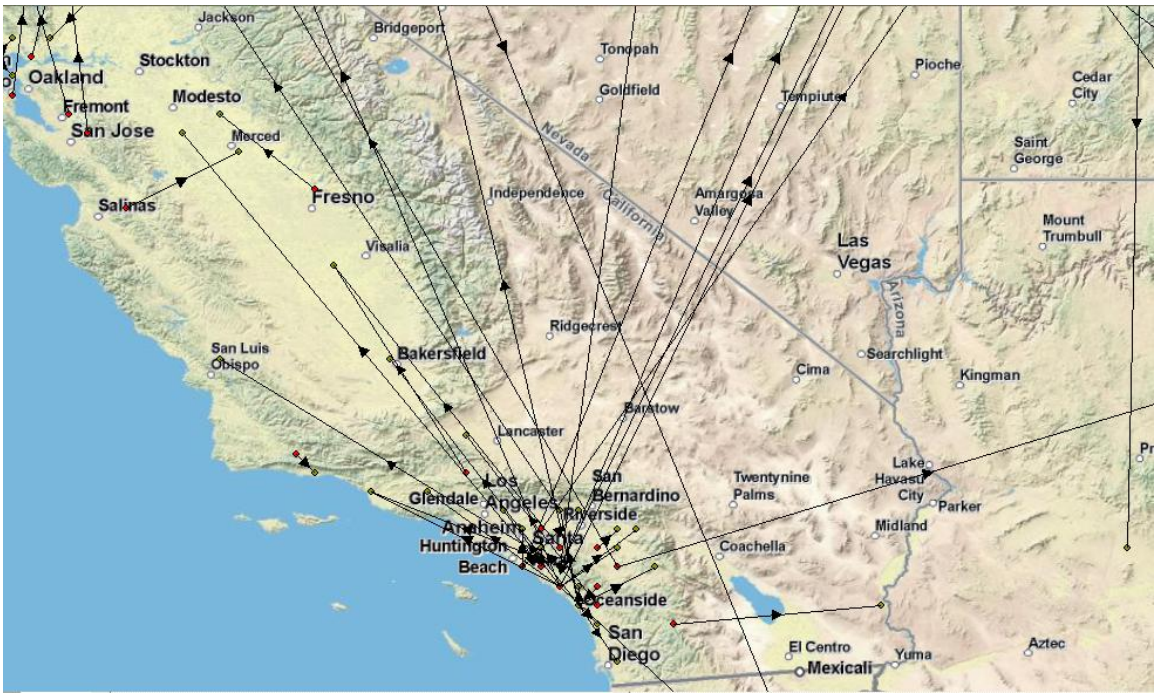

Figure 1.19 Red-tailed hawk band recapture/recovery data from southern California. All individuals were HY birds captured during the breeding season and then recaptured in the fall during the same year.

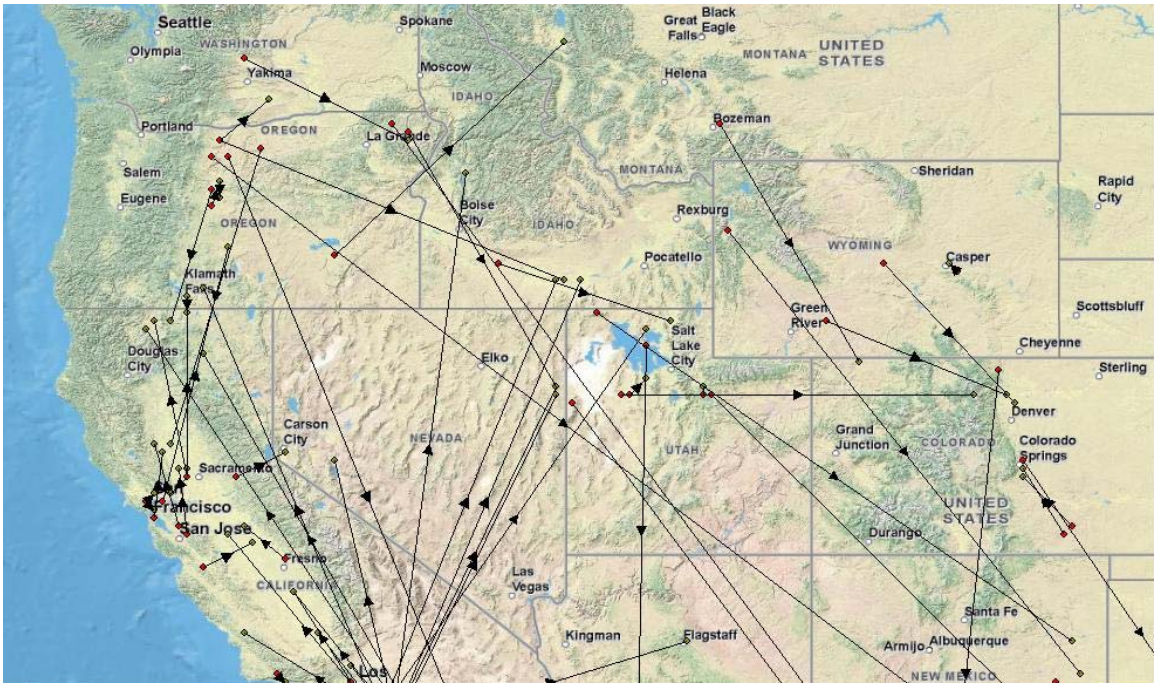

Figure 1.20 Red-tailed hawk band recapture/recovery data from western North America. All individuals were HY birds captured during the breeding season and then recaptured in the fall during the same year.

CHAPTER TWO:

SEX DETERMINATION IN THE WESTERN SUBSPECIES OF RED-TAILED HAWKS (*BUTEO JAMAICENSIS CALURUS*) USING DNA ANAYLSIS AND MORPHOMETRICS

Abstract

Currently the sex of red-tailed hawks (*Buteo jamaicensis*) cannot be determined by in-hand methods. Males and females do not differ in plumage and overlap in size. During migration, I collected feather samples and morphological measurements from birds at four sites in the western United States. Sex was determined for individual birds using sex-specific DNA markers and Polymerase Chain Reaction was used to identify these DNA markers. Through Discriminant Function Analysis, I created equations for determining the sex of red-tailed hawks using in-hand measurements based on the DNA-determined sexes. I formed two equations, one for adults, which was 98% accurate, and one for hatch-year birds, which was 97% accurate. Our results will aid future studies of intra- and intersexual differences in the western red-tailed hawk.

Introduction

Determining sex in natural populations is important for studying population dynamics, population structure, habitat use, behavior and mating systems, and for making

management decisions (Hughes 1998; Ito et al. 2003). Unfortunately, for many avian species it is difficult to determine sex from morphometrics and plumage (Ito et al. 2003). This is particularly true for several monomorphic raptor species. For example, red-tailed hawks (*Buteo jamaicensis*) lack plumage differences between the sexes, but show some sexual size dimorphism (Palmer 1988). However, the size differences between male and female red-tailed hawks have not been quantified in a manner useful for field situations. Although it is possible to determine the sex of individual birds by observing copulation and courtship behaviors (Catry et al. 1999), or by cloacal examination in some species (Boersma and Davies 1987; Gray and Hamer 2001), these methods are limited to the breeding season.

The red-tailed hawk has a wide distribution, ranging from central Alaska south to Panama and east to the Virgin Islands and is very common (Figure 1.1). The ability to determine the sex of individuals in the hand using simple measurements would greatly improve our effectiveness to study sex-specific movements and behaviors in this species. For example, sex determination is important in investigating research questions that address foraging behavior (Kelly and Wood 1996; Gonzalez et al. 2000; Noske 2003), dispersal (Brooke 1978), and migration patterns (Evans and Day 2001). One successful approach in sexing many bird species involves discriminant analysis using morphological measurements (Balbontin et al. 2001; Bertellotti et al. 2002; Quintana et al. 2003; Mizuta et al. 2004; Setiawan et al. 2004). Additionally, because females are heterogametic, sex in birds can be determined using a molecular technique, Polymerase Chain Reaction (PCR) amplification of DNA. Red-tailed hawks can be sexed by PCR (Norris-Caneda and Elliott 1998) and a particularly inexpensive technique was developed by Fridolfsson

and Ellegren (1999) for use with non-ratite birds. I developed a cost-effective and accurate method of sexing red-tailed hawks in the hand, based on discriminant analysis of morphometrics, which I verified with molecular techniques using feathers as the source of DNA (Griffiths and Tiwari 1995; Bello et al. 2001; Sacchi et al. 2004).

Methods

I collected feather samples during fall migration of 2002 and 2003 at four HawkWatch International (2240 South 900 East Salt Lake City, UT 84106) banding sites. These sites are in the Goshute Mountains, NV, Bonney Butte, OR, Chelan Ridge, WA, and Manzano Mountains, NM (Figure 2.1, Table 2.1).

Red-tailed hawks were captured using standard trapping techniques (Bloom, 1987) and banded with United States Geological Survey aluminum bands. In addition, the following morphological measurements were taken: body mass (g), and natural wing chord, tail, hallux, culmen, and tarsus length (all in mm). I measured natural wing chord with a ruler from the wrist of the wing to the tip of the longest flight feather without flattening the wing against the ruler (Figure 2.3a). Tail length was measured with a ruler between the two middle tail feathers, from the base of the feathers to the end of the longest feather (Figure 2.3b). Hallux talon length was measured with calipers from the base of the talon to the tip of the talon (Figure 2.3c). Culmen length was measured with calipers from the base of the culmen to the tip of the culmen (Figure 2.3d). Finally, tarsus length was measured with calipers from the front of the tarsometatarsal bone at the toe-joint to the end of the bone below the ankle-joint (Figure 2.3e).

For DNA sexing, three breast feathers were plucked from each bird and placed in a coin envelope with the band number, measurements, age, date, and capture site

information provided on the label. DNA was extracted from plucked breast feathers using a protocol provided by Dr. I. Lovette of Cornell University (Lovette et al. 2004) using the commercially available Qiagen DNeasy Kit®. I clipped small rings from the feather shaft tip (3-4 mm in length) and placed them in a 1.5 mL eppendorf tube. Scissors were dipped in ethanol and flamed over a Bunsen burner for sterilization between samples. Buffer ATL (180 uL) and Proteinase K (20 uL) were added, and each tube was vortexed for 1-2 seconds. Samples were spun for a few seconds in a centrifuge before being placed overnight in a water bath (55˚C). After removing the tubes from the water bath, 200 uL of buffer AL were added to each tube and the tubes were vortexed for 1-2 seconds. Tubes were then incubated on a heat block set to 70˚C for 10 minutes. Upon removal from the incubator, 200 uL of cold, 100% ethanol was added to each tube, after which tubes were vortexed for 1-2 seconds. The entire contents of the tubes were then pipetted into spin columns with wash tubes provided by the DNeasy kit and spun at 8000 rpm for 1 minute. After removing the spin columns from the centrifuge, they were placed in new wash tubes. Five hundred microliters of buffer AW1 were added to each spin column and then centrifuged for 1 minute at 8000 rpm. Wash tubes again were replaced and 500 uL of buffer AW2 was added to each spin column. The spin columns were spun for 3 minutes at 14000 rpm. Spin columns were then placed in labeled 1.5 mL eppendorf tubes for storage. Buffer AE (60uL) was applied to the spin column membrane and after sitting for 1 minute, tubes were then spun for an additional minute at 8000 rpm. At the end of this, spin columns were discarded and tubes were capped and stored in a freezer.

Genetic sex was determined following the method described by Fridolfsson and Ellegren (1999) using primers 2550 and 2718. I prepared a master mix of Promega 1X buffer, 1.5 mM of 10X MgCl2, 200 uM of each dNTP, 4pM of each primer, and 0.5 units of Promega *Taq* polymerase for a total of 10 uL for amplification. Thermal cycling consisted of an initial denaturing step of 120 s at 94˚C, followed by repeated denaturing, annealing, and extension steps for 30 cycles of 30 s at 94˚C, 30 s at 50˚C, and 30 s at 72˚C, with a final extension step of 300 s at 72˚C. Samples were then placed in a 2% agarose gel containing 10 uL ethidium bromide and electrophoresis was run in 0.5X TBE at 70V for approximately 75 min. Gels were visualized under UV light and photographs were taken of all successful runs. Female sex was assigned if both the CHD-Z and CHD-W bands were present, and male sex was assigned if a single CHD-Z band was present.

I employed SAS statistical software (SAS Institute 1999) to perform a MANOVA on both age and sex. Because adult birds might differ from hatch-year birds in measurements, a MANOVA was run on age class. Subsequently, I conducted separate Discriminant Function Analyses (DFA) on adult and hatch-year birds, along with backward elimination to determine the most useful variables for determining sex using in-hand measurements. Various combinations of measurements were run in the DFA to account for differences in the types of measurements taken at other banding sites.

Sex was successfully determined by PCR for 175 red-tailed hawks, 100 from the Goshute Mountains, 26 from Chelan Ridge, 21 from Bonney Butte and 28 from the Manzano Mountains. Three birds had missing measurements and were eliminated from the analyses. An additional hatch-year male was excluded from analyses. This bird was an extreme outlier in wing chord, hallux and culmen and perhaps was transcribed

incorrectly from the data sheet to the feather envelope. The remaining 121 hatch-year birds and 50 adult birds were used to produce a discriminant function with morphometrics.

Results

Adults differed significantly from hatch-year birds by mass, culmen, and tail measurements (Table 2.2), so adult and hatch-year birds were treated separately in all further analyses. A MANOVA run on sex class demonstrated that females were significantly larger than males in all measurements of adult and hatch-year birds (Tables 2.3 and 2.4).

Backward elimination of variables following discriminant analysis selected wing chord and mass as significant morphological measurements for distinguishing between the sexes in adult birds, and this produced the following equation: 0.166 x wing chord + 0.026 x mass = Z. If $Z > 94.902$, then the bird is female; if $Z \leq 94.902$, then it is male. This equation accurately assigned sex to 98% of the 50 adult red-tailed hawks whose sex was determined by PCR. The one misclassified bird was a female with an exceptionally small wing chord measurement of 381 mm. This bird may have been mismeasured, because the mean (± SE) wing chord measurement for a *B. j. calurus* female is 412 mm ±14.9 (Preston and Beane 1993). See Figure 2.2a for the distribution of males and females based on their discriminant scores.

Backward elimination of variables following discriminant analysis selected body mass, wing chord, hallux, and culmen as significant morphological measurements for discriminating between the sexes in hatch-year birds. The following equation was

produced: 0.2 x wing chord + 0.011 x mass + 1.302 x hallux + 1.356 x culmen = Z. If Z > 160.933, then the bird is female; if Z ≤ 160.933 then it is male. This equation accurately assigned sex to 97% of the 121 hatch-year red-tailed hawks of known sex. The four misclassified birds consisted of two females with short wing chords, a female with a short culmen, and a female with measurements close to male and female sizes. See Figure 2.2b for the distribution of males and females based on their discriminant scores.

Additional equations are given in Tables 2.5 and 2.6, along with their accuracy (all > 90%), using only wing chord and mass, which I provide because some banders do not take measurements requiring calipers.

Discussion

I assume no red-tailed hawk subspecies except *calurus* significantly contributed to data used for this study. This assumption is based on *alascensis* being a year-round resident in its range (Alaska and Canada) and red-tailed hawks showing fidelity to migration flyways in the west (Hoffman et al. 2002; Scheuermann 1996, 1997; Acuff 1998, 1999). *Harlani* sampled at the migration sites were eliminated from the data when identified. Few *harlani* are captured at these migration sites; however, it is possible a small number were misidentified and included in the data for this study.

The DNA sexing technique unambiguously sexed individual birds for use in discriminant analyses, confirming the usefulness of plucked feathers for extracting DNA, as shown elsewhere (Griffiths and Tiwari 1995; Bello et al. 2001; Sacchi et al. 2004). Plucking feathers does not require special training and the feathers do not require special storage, other than an envelope, making them extremely practical in remote field

situations such as those experienced at many migration monitoring sites. The discriminant functions produced through morphometrics provided an inexpensive and highly accurate method of sexing red-tailed hawks in the hand. These results should greatly aid future studies concerning this species.

The ability to determine the sex of individual red-tailed hawks in the hand will be valuable in future studies addressing intersexual and intrasexual differences. For example, in-hand sex determination may facilitate investigation of sex differences in dispersal patterns (Brooke 1978), heritability differences in morphology (Jensen et al. 2003), molt intensity and chronology (Craigie and Petrie 2003), foraging niche partitioning (Gokula et al. 1999; Marsden and Sullivan 2000; Pryzbylo and Merila 2000), foraging strategies (Kelly and Wood 1996; Gonzalez et al. 2000; Noske 2003), prey composition and size (Overskaug et al. 2000; Lee and Severinghaus 2004), migration patterns and sex ratios (Evans and Day 2001), winter spacing patterns (Ohsako 2001), parasite load (Freeman et al. 2001), dominance and aggressive behavior (Tarvin and Woolfenden 1997; Jones and Hunter 1999), and vocalizations (Bretagnolle et al. 1998).

A potential problem in using the discriminant function equations for sexing red-tailed hawks is individual variation among investigators in taking the measurements. There may also be differences in measurement techniques among and within sites. However, given that the data in this study were collected by as many as 30 volunteer banders at four different locations, accuracy rates consistently greater than 90% suggest that the sexing technique is robust.

Due to concerns about consistent measurement techniques and because they are used relatively rarely, many other potentially useful morphometric measurements were

not examined in the study. For example, other studies have used forearm length (Ferrer and De Le Court 1992), tarsal width (Shepard et al. 2001), and bill depth (Bortolotti 1984) to successfully determine sex in raptor species. However, these measurements are not commonly taken at migration sites in North America and might have proved difficult to teach to the numerous volunteers at four different sites. Therefore, I chose to use a smaller number of frequently collected measurements. However, other additional measurements may be useful in sex determination of birds not easily sexed by commonly taken measurements.

Because all sampling sites were located in the western United States, these equations may only be applicable to studies examining the western red-tailed hawk subspecies (*B. j. calurus*). Other subspecies may not be accurately sexed due to differences in morphological characters. For example, the average wing chord measurement for *B. j. calurus* females is 412 ± 14.9 mm and is 386.8 ± 11.4 mm for males, and the mean tail length measurement is 237.3 ± 11.3 mm for females and 224.2 ± 7.9 mm for males. The eastern subspecies, *B. j. borealis*, is smaller than *B . j. calurus* (Preston and Beane 1993). Future research should assess the need to develop in-hand sexing techniques for the other subspecies of red-tailed hawk.

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Table 2.1 Collection locations for sampled red-tailed hawks.

HawkWatch Site	Location	Coordinates
Goshute Mountains	Northeastern Nevada Bureau of Land Management Land	40º 25.417’ N, 114º 16.27’ W
Bonney Butte	North Central Oregon Mount Hood National Forest	45º 15’ 46.8” N, 121º 35’ 31.2” W
Chelan Ridge	Eastern Cascade Mountains Washington State	48º 01’ 12.8” N, 120º 05’ 38.4” W
Manzano Mountains	Central New Mexico Cibola National Forest	34º 42.25’ N, 106º 24.67’ W

Table 2.2 Results of MANOVA on adult and hatch-year age classes of red-tailed hawks.

Age (Wilks' Lambda F=27.88, d.f. 6,165, pvalue=<0.0001)	Weight Means (F=32.13, P=<0.0001)	Tail Means (F=42.57, P=<0.0001)	Culmen Means (F=6.56, P=0.0113)
Adult	1095±23	220±2	26.0±0.2
Hatch-year	943±14	233±1	25.3±0.2

Table 2.3 Results of MANOVA and mean body measurements of male and female adult red-tailed hawks.

Sex Adults	Weight	Hallux	Tarsus	Tail	Wing	Culmen
(Wilks' Lambda F=28.07, d.f. 6,43, pvalue=<0.0001)	(F=122.65, P= <0.0001	(F=71.94, P= <0.0001	(F=15.90, P= 0.0002	(F=40.35, P= <0.0001	(F=79.53, P= <0.0001	(F=16.40, P= 0.0002
Female	1266±134	31.5±1.8	88.9±3.1	227±10	415±15	27.0±2.1
Male	923±78	27.7±1.4	85.7±2.6	211±7	381±12	25.0±1.4

Table 2.4 Results of MANOVA and mean body measurements of male and female hatch-year red-tailed hawks.

Sex Hatch-year	Weight	Hallux	Tarsus	Tail	Wing	Culmen
(Wilks' Lambda F=72.46, d.f. 6,114, P=<0.0001)	(F=80.26, P= <0.0001	(F=180.99, P= <0.0001	(F=23.09, P= <0.0001	(F=42.46, P= <0.0001	(F=201.36, P= <0.0001	(F=113.35, P= <0.0001
Female	1022±116	30.5±1.2	88.2±3.6	238±12	407±12	26.2±1.2
Male	847±95	27.4±1.3	85.2±3.1	226±8	378±10	24.1±1.0

Table 2.5 Gender determination based on discriminant analysis, using only mass for adult birds and wing chord and mass hatch-year red-tailed hawks.

	Equation	Z score – male	Z score – female	Accuracy[a]
Adult	0.029 x mass	≤ 31.359	> 31.359	94%
Hatch-Year	0.227 x wing chord + 0.013x mass	≤ 100.981	>100.981	94.8%

[a] Compared to the results of gender determination based on DNA analysis.

Table 2.6 Gender determination based on discriminant analysis, using only wing chord for adult and hatch-year red-tailed hawks.

	Equation	Z score – male	Z score – female	Accuracy[a]
Adult	0.189 x wing chord	≤ 75.345	> 75.345	94%
Hatch-Year	0.24 x wing chord	≤ 94.218	> 94.218	93%

[a] Compared to the results of gender determination based on DNA analysis.

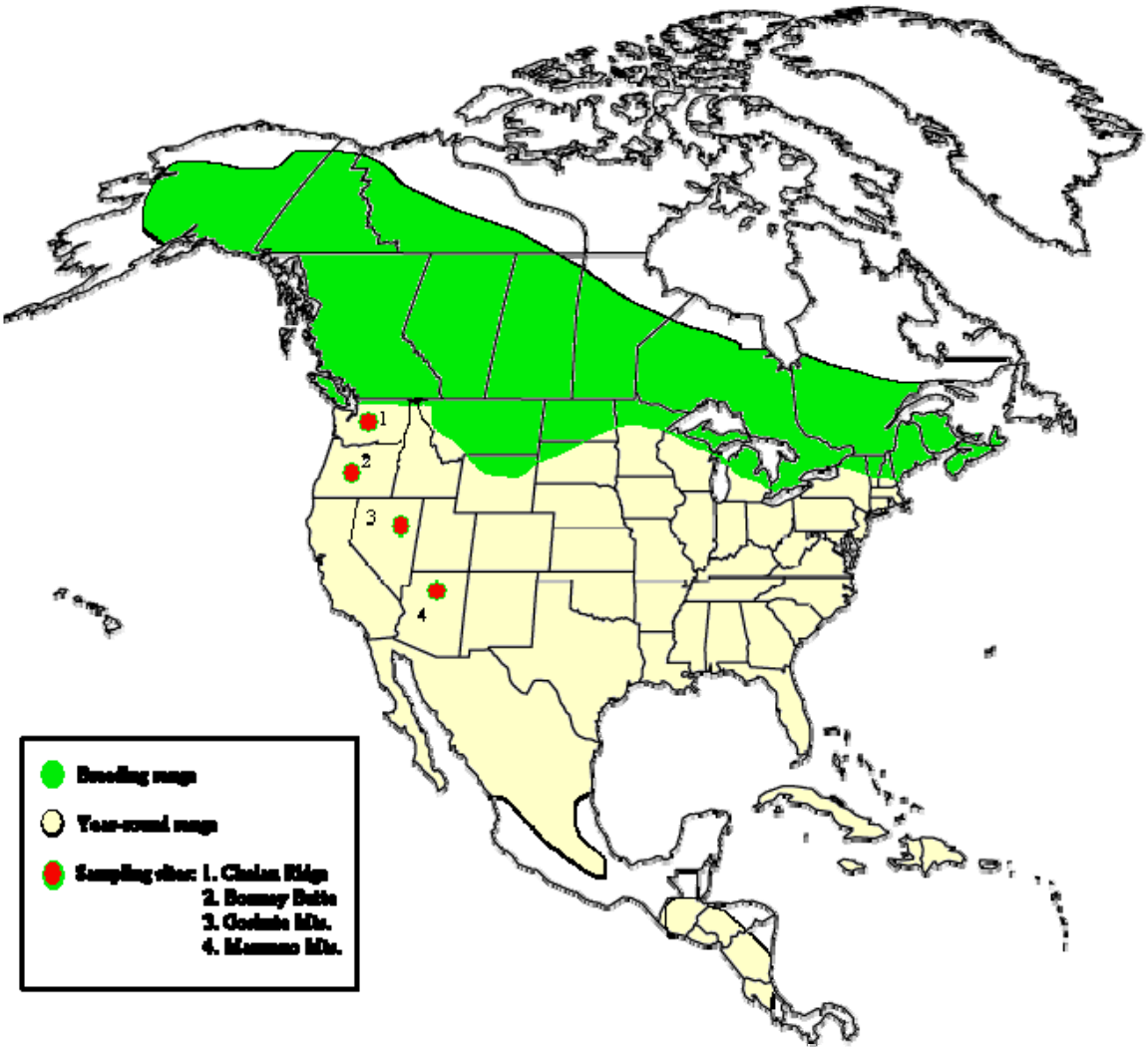


Figure 2.1 Breeding range of the red-tailed hawk and fall migration sampling sites (adapted from Johnsgard 1990).

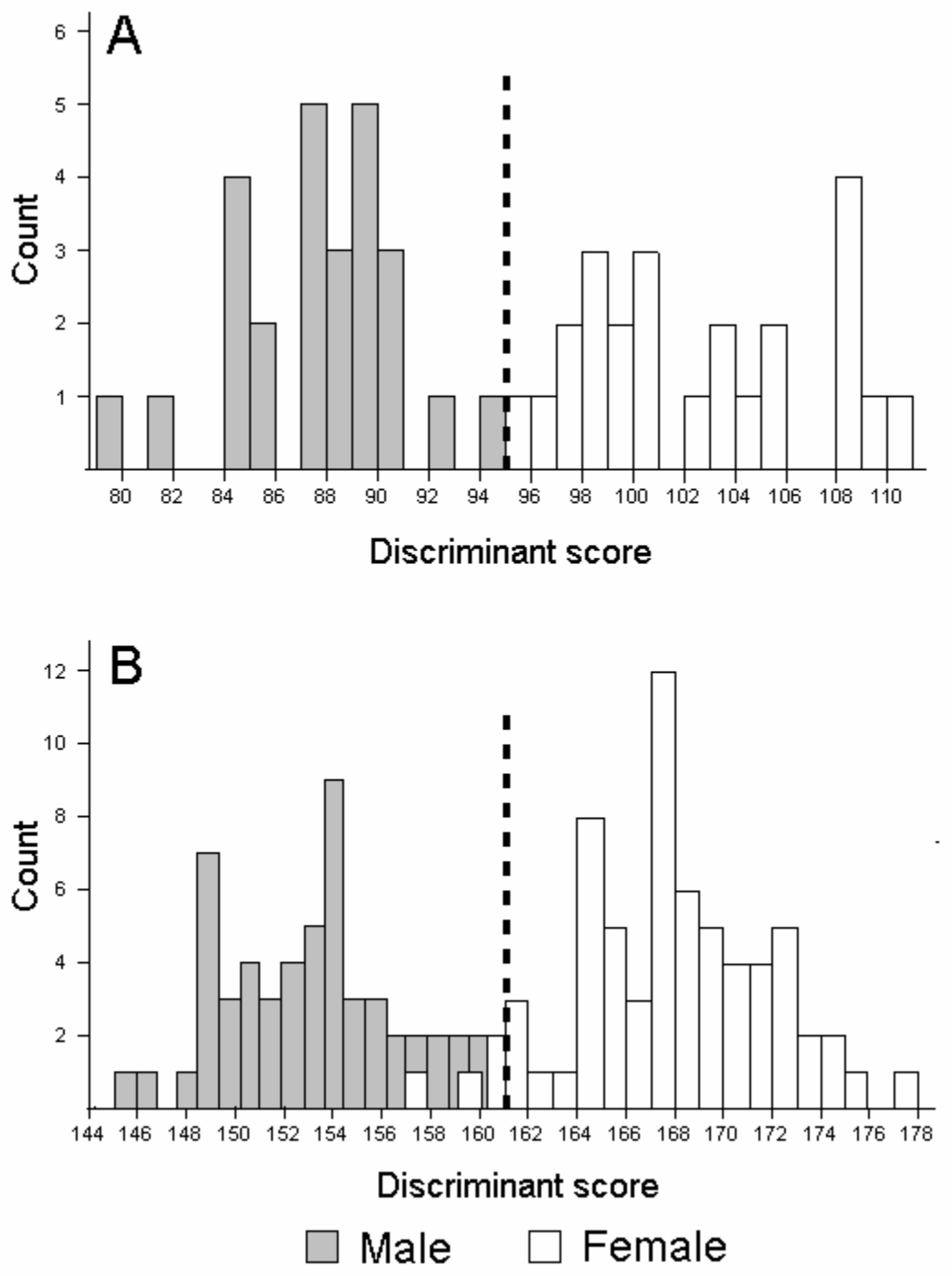
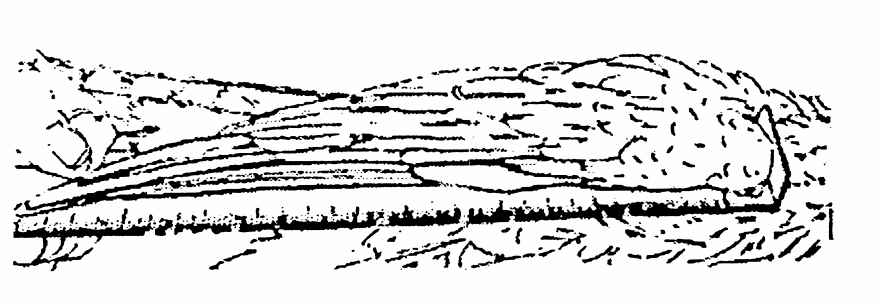
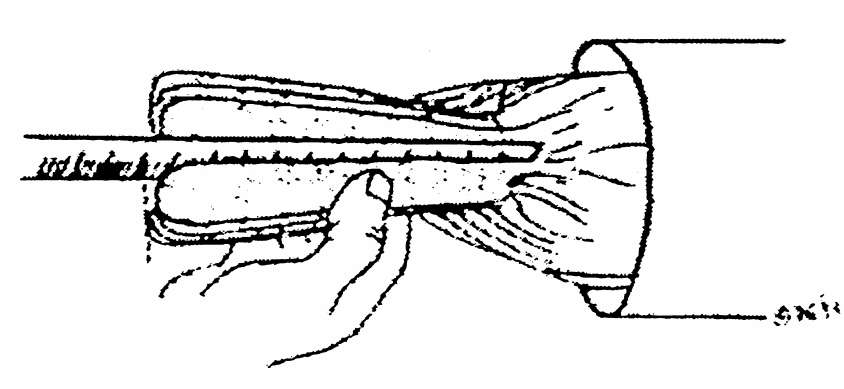


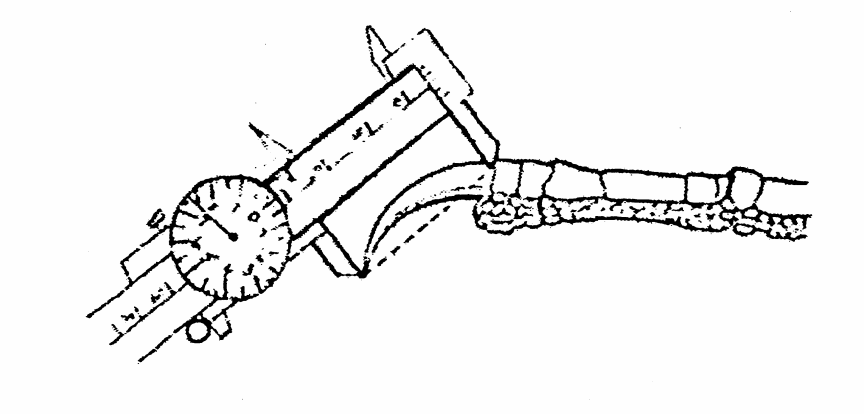
Figure 2.2 Distribution of adult males and females based on discriminant scores. The dotted line represents the cutoff score which males fall to the left of and females to the right. a) Distribution of adult males and females. b) Distribution of hatch-year males and females.



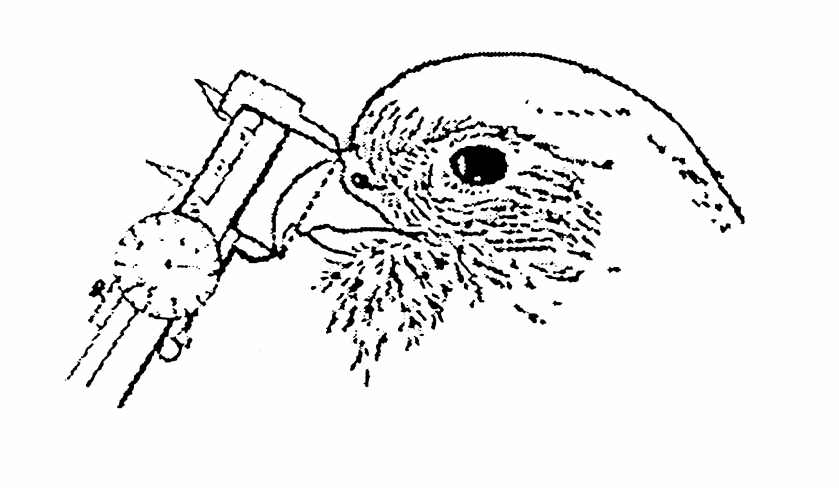
a. Wing chord



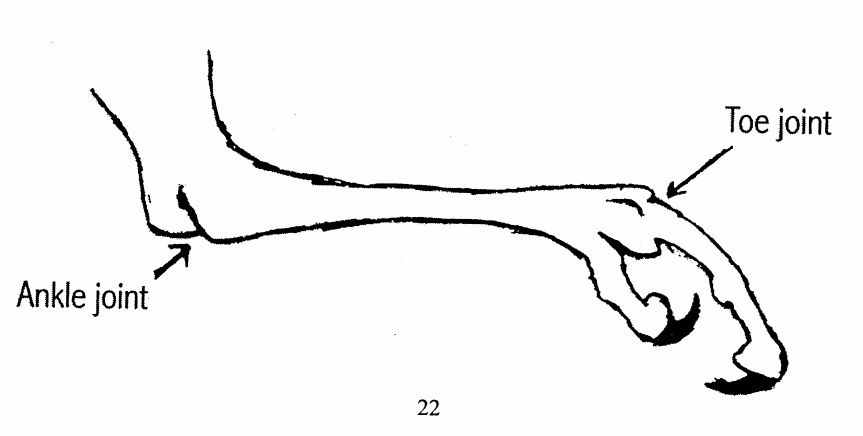
b. Tail length



c. Hallux



d. Culmen



e. Tarsus

Figure 2.3 Diagrams of measurements taken.

APPENDIX

Red-Tailed Hawk Measurements

Red-Tailed Hawk Measurements

ID #	Site	Date	Age	Weight	Hallux	Tarsus	Tail	Wing	Culmen	DNA sex
1	Goshutes	09/18/02	HY	1027	28.3	85.7	230	383	24.4	M
2	Goshutes	10/04/02	ASY	1417	35.9	91.4	232	425	27.3	F
3	Goshutes	09/13/02	HY	823	28.3	87.1	231	378	24.9	M
4	Goshutes	09/19/02	ASY	1170	31.4	88.4	207	410	22	F
5	Goshutes	10/05/02	HY	864	27	84.6	230	379	23.4	M
6	Goshutes	09/12/02	HY	1064	30.5	94.5	235	402	26.3	F
7	Goshutes	09/12/02	HY		26.5	84.7	229	373	23.2	M
8	Goshutes	09/14/02	HY	925	27.8	81.5	219	375	23.3	M
9	Goshutes	09/14/02	HY	817	29.3	88.1	238	403	26.8	F
10	Goshutes	09/15/02	ASY	938	27.4	87	217	376	24.4	M
11	Goshutes	09/25/02	SY	1462	32.2	94	219	399	27.6	F
12	Goshutes	09/02/02	ASY	876	28.2	85.5	220	397	26.8	M
13	Goshutes	09/23/02	HY	891	30.4	89.8	237	401	26.4	F
14	Goshutes	09/10/02	HY	1101	30.7	91.7	235	395	25.8	F
15	Goshutes	09/23/02	HY	840	27.9	83.1	230	382	27.8	M
16	Goshutes	10/15/02	HY	931	30	94.8	215	380	25.6	M
17	Goshutes	09/14/02	HY	741	25.3	82.3	223	380	23.4	M
18	Goshutes	10/15/02	ASY	936	28.2	89.8	203	406	25.6	M
19	Goshutes	10/15/02	ASY	1395	33.3	89.3	230	426	27	F
20	Goshutes	09/05/02	HY	1124	31.3	93.7	227	392	27.4	F
21	Goshutes	10/26/02	SY	1026	28.8	84.1	220	385	26	M
22	Goshutes	09/13/02	HY	1054	30.8	88.1	260	432	27.7	F
23	Goshutes	09/01/02	HY	992	32	89.6	225	396	26.4	F
24	Goshutes	08/29/02	HY	895	31	81.5	249	397	23.5	F
25	Goshutes	10/21/02	ASY	915	23.4	84.9	213	392	21.4	M
26	Goshutes	09/05/02	HY	1017	29.8	87.7	101	406	25.4	F
27	Goshutes	08/24/02	HY	883	27.5	80.5	223	370	22	M
28	Goshutes	10/09/02	ASY	1125	33.1	87.5	235	403	26.9	F
29	Goshutes	09/16/02	HY	999	30.2	87.8	239	402	26.9	F
30	Goshutes	09/30/02	HY	929	31.8	88	237	401	27.7	F
31	Goshutes	09/03/02	HY	1104	30.6	89.5	257	414	25.8	F
32	Goshutes	09/09/02	HY	1023	33.3	88.4	233	389	25.7	F
33	Goshutes	09/07/02	SY	1207	32.7	91.2	244	437	28.2	F
34	Goshutes	09/09/02	ASY	1406	33.5	89.1	246	434	28	F
35	Goshutes	09/26/02	HY	783	27	84.8	235	390	24.2	M
36	Goshutes	09/20/02	HY	1059	32.2	87.7	232	402	27	F
37	Goshutes	10/06/02	ASY	1380	31.5	89	230	430	28.1	F
38	Goshutes	10/06/02	HY	856	29	84.4	224	381	22.7	M
39	Goshutes	09/18/02	HY	925	29.5	87.9	241	411	28.2	F
40	Goshutes	10/26/02	HY	1059	27.9	85.8	230	371	23.8	M

ID #	Site	Date	Age	Weight	Hallux	Tarsus	Tail	Wing	Culmen	DNA sex
41	Goshutes	10/26/02	HY	1212	30.3	90.9	233	389	27.3	F
42	Goshutes	09/13/02	HY	1013	30.1	88.8	244	415	26.5	F
43	Goshutes	08/30/02	SY	875	28.3	89.9	211	372	25.5	M
44	Goshutes	10/09/02	ASY	975	27.1	85.6	206	371	24.7	M
45	Goshutes	08/29/02	HY	1013	29.5	86.7	236	399	26.8	F
46	Goshutes	10/21/02	ASY	1013	27	88.1	215	380	25.3	M
47	Goshutes	10/21/02	ASY	1008	29.4	81.5	219	386	27.2	M
48	Goshutes	09/05/02	HY	910	32.1	88	215	393	27.7	F
49	Goshutes	08/30/02	HY	1263	30.5	86.5	249	411	27	F
50	Goshutes	08/29/02	HY	1052	30.3	90.8	245	415	23.8	F
51	Goshutes	10/19/02	HY	1131	29.2	91.9	231	394	26	F
52	Goshutes	10/09/02	HY	951	28.7	81.9	229	395	26	F
53	Goshutes	09/22/02	HY	1011	29.3	85.5	227	403	25.7	F
54	Goshutes	09/15/02	HY	822	32.4	92.4	247	421	27.5	F
55	Goshutes	09/14/02	HY	967	30.1	91.2	243	393	27	F
56	Goshutes	10/24/02	HY	1035	27.2	87.6	234	391	24.7	M
57	Goshutes	10/22/02	HY	732	25.7	80.5	222	376	25.1	M
58	Goshutes	10/18/02	HY	1155	27.1	87.7	231	387	22.3	M
59	Goshutes	10/15/02	HY	765	27.8	81.9	232	377	25	M
60	Goshutes	10/15/02	HY	741	25.2	77	226	367	22.9	M
61	Goshutes	10/15/02	HY	863	28	85.9	230	386	23.7	M
62	Goshutes	10/13/02	HY	851	28.7	85.6	218	383	23.2	M
63	Goshutes	10/09/02	ASY	905	28	87.1	198	381	25.1	M
64	Goshutes	10/06/02	HY	877	25.4	84.9	234	391	23.6	M
65	Goshutes	10/05/02	HY	787	26.1	80.2	225	373	23.7	M
66	Goshutes	09/26/02	HY	898	28	84.8	220	385	24.7	M
67	Goshutes	09/03/02	HY	814	28.2	87.2	210	381	25.1	M
68	Goshutes	10/14/02	AHY	1131	28.4	89	220	390	25.7	M
69	Goshutes	10/08/02	HY	1041	30.2	85.4	240	406	28	F
70	Goshutes	10/07/02	ASY	1215	28.4	88.1	223	408	28.2	F
71	Goshutes	10/06/02	HY	975	31	89.9	241	401	26.7	F
72	Goshutes	10/06/02	HY	914	30.4	87.3	233	376	24.7	M
73	Goshutes	09/20/02	HY	1051	29	85	237	395	26.6	F
74	Goshutes	09/19/02	HY	935	30.4	89.3	236	410	25.7	F
75	Goshutes	09/18/02	HY	898	30.9	85.8	248	417	25.9	F
76	Goshutes	09/17/02	HY	882	27.8	86.4	238	400	25.6	F
77	Goshutes	09/17/02	HY	892	29.6	?	250	410	27.2	F
78	Goshutes	09/13/02	ASY	1214	30.8	85.6	229	409	28.5	F
79	Goshutes	09/11/02	HY	964	30.6	86.6	251	412	25.7	F
80	Goshutes	09/09/02	HY	1081	30.4	89.6	238	415	22.3	F
81	Goshutes	10/24/02	HY	880	27.3	85.3	216	359	24.4	M
82	Goshutes	10/13/02	HY	784	26.4	81.4	221	373	23.3	M
83	Goshutes	10/12/02	HY	853	26.5	83.7	228	369	24.1	M
84	Goshutes	10/11/02	HY	707	27.8	84.4	225	371	23.9	M
85	Goshutes	10/06/02	HY	950	29.1	86.9	213	365	25.5	M
86	Goshutes	10/04/02	HY	764	27	82.2	227	364	24	M

ID #	Site	Date	Age	Weight	Hallux	Tarsus	Tail	Wing	Culmen	DNA sex
87	Goshutes	09/30/02	ASY	948	28.1	86.9	219	396	26.7	M
88	Goshutes	09/21/02	HY	784	26.7	85.5	230	368	23	M
89	Goshutes	09/18/02	ASY	882	29.8	81.7	208	385	25.5	M
91	Goshutes	09/10/02	HY	820	28	87.2	230		24.7	M
93	Goshutes	09/19/02	HY	913	31.3	87.5	225	419	26.5	F
94	Goshutes	09/19/02	HY	701	28.5	84.8	222	373	24	M
95	Goshutes	09/19/02	HY	850	27.6	84.1	223	378	22.9	M
96	Goshutes	09/25/02	HY	726	27	85.4	225	385	24.9	M
97	Goshutes	08/26/02	HY	801	30.9	83.6	229	421	25.2	F
98	Goshutes	09/08/02	HY	971	32.3	85.2	233	394	26.7	F
101	Goshutes	09/10/02	HY	791	26.6	84.6	229	384	22.7	M
102	Goshutes	10/06/02	HY	1104	29.7	90.4	250	414	25.8	F
104	Goshutes	09/13/02	HY	749	27.4	82.3	227	380	25.4	M
105	Goshutes	09/22/02	HY	760	27.8	84.5	211	353	25	M
106	Goshutes	09/10/02	HY	826	27.7	90.1	239	396	24.8	M
107	Chelan	08/31/02	HY	752	27.5	80.3	232		22.9	M
108	Chelan	09/03/02	HY	884		94.7	219	385	22.5	M
109	Chelan	09/04/02	HY	1060	31.2	83.7	230	398	26.1	F
110	Chelan	09/05/02	HY	1057	31	80.6	236	425	27.7	F
117	Chelan	09/17/02	HY	886	32.5	86	250	420	27.6	M
118	Chelan	09/17/02	HY	1187	31.7	12.2	230	405		F
122	Chelan	09/21/02	HY	844	28.6	80.4	210	375	26.4	F
123	Chelan	09/21/02	HY	987	30.1	91.4	234	402	22	F
124	Chelan	09/23/02	HY	1036	29	85	231	390	24.2	F
125	Chelan	09/22/02	HY	853	27.9	86.1	206	352	24.9	M
128	Chelan	09/28/02	HY	771	27.3	82	212	361	23.1	M
129	Chelan	10/06/02	HY	1143	31.7	85.7	230	391	25.7	F
130	Chelan	10/09/02	HY	899	25.7	88.8	210	369	23.5	M
131	Chelan	10/10/02	HY	998	29	90	239	402	25.5	F
132	Chelan	10/16/02	HY	1242	33.6	96.5	232	420	26.6	F
133	Manzanos	09/06/02	HY	977	29.9	90.8	262	426		F
135	Manzanos	09/15/02	ASY	1281	33.8	92.3	227	415	26.6	F
140	Manzanos	09/20/02	HY	1270	30	87.1	239	408	26.7	F
141	Manzanos	09/21/02	HY	816	27.7	83.5	225	392	25.5	M
142	Manzanos	09/22/02	HY	928	27.2	87.3	241	402	26.1	F
143	Manzanos	09/22/02	HY	890	28.3	85	229	397	22.7	M
144	Manzanos	09/25/02	HY	1003	30.1	90.8	244	410	25.3	F
145	Manzanos	09/25/02	HY	840	27.2	87.2	231	388	22.7	M
146	Manzanos	09/26/02	ASY	962	23	84.7	213	385	25	M
147	Manzanos	09/26/02	HY	1009	32.7	88.3	240	417	25.6	F
148	Manzanos	09/29/02	ASY	1275	31.7	93	239	329	29.8	F
150	Manzanos	09/30/02	AHY	1100	31.1	90.3	245	445	21.4	F
151	Manzanos	10/01/02	HY	843	26.1	85.8	227	384	23.3	M
154	Manzanos	10/01/02	HY	828	26.7	88.9	228	384	23.9	M
155	Manzanos	10/02/02	HY	1027	31.1	91.1	242	413	27.2	F
156	Manzanos	10/02/02	HY	978	25.6	88.4	240	386	23.9	M

ID #	Site	Date	Age	Weight	Hallux	Tarsus	Tail	Wing	Culmen	DNA sex
157	Manzanos	10/02/02	HY	1086	29.9	90.5	235	407	27.3	F
159	Manzanos	10/04/02	HY	935	29.2	91.3	285	416	25.4	F
160	Manzanos	10/05/02	AHY	792	26.5	85	214	387	24	M
161	Manzanos	10/05/02	AHY	1192	30.2	86.7	226	412	26.4	F
162	Manzanos	10/05/02	HY	919	30.6	86.6	245	419	25.9	F
163	Manzanos	10/06/02	ASY	920	27.3	84.7	205	372	24.5	M
164	Manzanos	10/08/02	HY	886	29.9	82.8	237	413	27.1	F
165	Manzanos	10/08/02	HY	709	27.6	86.1	231	384	23.8	M
166	Manzanos	10/09/02	AHY	963	28.1	85.3	207	383	25.1	M
167	Manzanos	10/09/02	HY	833	27.7	84.2	234	386	23.5	M
168	Manzanos	10/11/02	HY	1027	31.3	96.1	232	426	27.6	F
169	Manzanos	10/13/02	HY	1143	31	96.3	251	421	27	F
170	Manzanos	10/15/02	HY	1270	30.6	86.7	239	420	25.6	F
171	Manzanos	10/18/02	AHY	966	26.7	88.4	210	383	26.7	M
172	Manzanos	10/20/02	HY	816	28.1	85.1	242	403	25	M
173	Manzanos	10/20/02	AHY	1175	29.9	89	234	407	28.8	F
174	Manzanos	10/20/02	HY	1028	30.3	90	249	428	27.4	F
175	Manzanos	10/21/02	ASY	1093	30.6	89.5	225	415	25.4	F
176	Manzanos	10/22/02	ASY	1244	30.8	88.1	242	426	28	F
178	Bonney	08/31/02	HY	1083	28.7	90.9	232	395	25.5	F
180	Bonney	08/31/02	HY	890	30.2	81.1	211	396	26.5	F
181	Bonney	08/31/02	HY	950	28.4	90.6	229	375	23.6	M
182	Bonney	08/31/02	HY	1288	23.1	82.8	236	392	26.9	F
187	Bonney	09/02/02	HY	817	26.8	90.1	231	378	25.2	M
195	Bonney	09/06/02	ASY	967	29.1	80.4	211		23	M
196	Bonney	09/06/02	ASY	955	28	87.4	210	385	25.2	M
201	Bonney	09/09/02	HY	883	27.7	88.5	231		25.1	M
202	Bonney	09/09/02	HY	964	28.4	85.2	222	395	24.3	M
203	Bonney	09/09/02	HY	724	27.2	89.9	221	378	24.7	M
224	Bonney	09/19/02	ASY	892	29.9	85.4	217	385	26.8	M
229	Bonney	09/22/02	HY	865	28.2	88	238	392	23.8	M
230	Bonney	09/23/02	HY	1020	31.6	90.1	242	395	25.5	F
231	Bonney	09/23/02	HY	804	29.7	85.2	225	368	24.1	M
233	Bonney	09/25/02	AHY	774	26.5	88.7	220	368	22.8	M
235	Bonney	09/26/02	ASY	1242	29.9	85.4	227	400	27.9	F
236	Bonney	09/26/02	AHY	1197	30.6	95.2	219	400	27	F
237	Bonney	09/26/02	AHY	839	26.1	81.5	222	378	23.4	M
238	Bonney	09/26/02	AHY	840	27.5	85	195	346	24.2	M
246	Bonney	09/27/02	AHY	903	26.2	81.1	203	368	24.3	M
250	Bonney	10/07/02	AHY	960	29.2	85.2	205	380	24.4	M
253	Bonney	10/11/02	AHY	1230	30.1	87.6	206	381	26.3	F
254	Bonney	10/11/02	AHY	853	27.2	83	210	376	23.1	M
259	Bonney	10/13/02	ASY	1279	30.4	90.4	222	413	28.9	F