

**DRAFT**



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# MEMORANDUM

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Date: January 22, 2001

To: The Honorable Chair and Members  
Pima County Board of Supervisors

From: C.H. Huckelberry  
County Administrator 

Re: **Comparisons of Ferruginous Pygmy-Owl mtDNA at Local and International Scales**

## I. Background

When the Board adopted the Sonoran Desert Conservation Plan in concept in March of 1999, Pima County initiated a pygmy-owl study series that included the broadest survey effort undertaken by any jurisdiction, telemetry and habitat assessments, and genetics studies. The survey effort was conducted by Dr. Lisa Harris and Mr. Russell Duncan, and the results were published in November of 1999 in a study entitled *Pygmy Owl Update*. The telemetry work and habitat assessments were conducted by a team of scientists led by Mr. Scott Richardson from the Arizona Game and Fish Department, and the results were published in July of 2000 in two studies entitled *Cactus Ferruginous Pygmy-Owl Investigations in Pima County*, and *Cactus Ferruginous Pygmy-Owl Habitat Selection*.

Today I am forwarding a study by Mr. Glenn Proudfoot entitled *Comparisons of Ferruginous Pygmy-Owl mtDNA at Local and International Scales*. Mr. Proudfoot, the leading pygmy-owl biologist in the United States, has worked for the last two years to gather and analyze the data that allows us to address issues regarding the genetic viability of ferruginous pygmy-owls in Arizona and to establish a framework for future management efforts. Texas A&M University co-funded this effort which included genetics analysis of ferruginous pygmy-owls within the United States and at the international scale. The results will be peer reviewed, submitted for publication in scientific literature, and deposited in the national GenBank. Follow up studies will be conducted as described in the text below.

## II. Method

Pages three through five describe the method used to make objective assessments based on analysis of the mtDNA genetic marker. DNA extractions were obtained from 95 ferruginous pygmy-owls: 14 from Arizona, 18 from Texas and 63 from Mexico. Greater detail on the methods employed to carry out the analysis can be found in the text and appendices of the attached study.

## III. Major Questions Addressed by the Study

The two major questions addressed by the Proudfoot study are (1) do populations of concern lack genetic variation relative to putative healthy populations, and (2) how unique are geographically distinct populations within a species of special concern?

#### **IV. Do Populations of Concern Lack Genetic Variation Relative to Putative Healthy Populations?**

##### **A. Description of the Issue**

Low genetic variation can result from inbreeding. The attached study states that "populations without genetic variation are considered in peril, owing to effects of low population numbers, inbreeding, or both." (p. 1) Because recessive deleterious characteristics are more likely to be expressed in the offspring of closely related individuals, continued inbreeding may lead to a loss of fitness within populations. When the overall population numbers are low, inbreeding depression may set the stage for extinctions.

At times, a population can pass through a "bottleneck" by dropping in numbers at a rapid rate, but withstand the potential effects of inbreeding depression that occur among small populations if the population rebounds quickly to a large number and maintains the size sufficient to restore normal levels of genetic variation for the species, or if by chance the founder population lacks deleterious alleles.

A small population effected by inbreeding depression might also avert extinction through special management, such as the re-establishment of travel corridors or facilitated immigration of unrelated individuals to the local inbred population at a rate that begins to reverse the inbreeding effects.

##### **B. Baseline information**

Among raptors, documented instances of inbreeding are rare, with less than two dozen known cases. This is a surprising baseline, given that local biologists have documented second generation inbreeding in northwest Tucson in just the two years that such data have been available.

##### **C. Study Findings in Arizona on the Issue of Low Genetic Variation**

The Proudfoot study found that "in comparison to Mexico, Arizona (e.g., northwest Tucson) ... [ferruginous pygmy-owls] have extremely low levels of average haplotype diversity." (p. 5) This translates roughly to mean that the ferruginous pygmy-owls in northwest Tucson lack genetic variation.

The study indicates that "given the extreme similarities within the Arizona (e.g., samples from northwest Tucson) ... population, it is possible that the population as a whole underwent [a] bottleneck sometime in the not-too-distant past." (p. 7)

The study goes on to warn that "if other genetic markers, such as microsatellites, show low level genetic variation, concern could be warranted. Genetic data play only one role in conservation policy and demographic data might indicate that the population [is] currently in peril and requires special management attention." (p. 7)

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### D. Significance of findings of low genetic variation in the northwest Tucson population for land management decision making

#### (1) Understanding of conditions prior to the Proudfoot study

In the Spring of 1999, there were 27 pygmy-owls identified in northwest Tucson. The northwest Tucson population is one of four geographically separated pygmy-owl populations documented in Arizona. The other three include: Altar Valley, Pinal County, and Organ Pipe Cactus National Monument.

As of July 2000, no exchange had been documented between the Eastern Pima County populations. Currently, northwest Tucson is subject to three levels of management prescription:

- Much of the area is within designated critical habitat;
- This area is within survey Zone 1 of the landowner take guidance based on the biological assumption that "pygmy-owls are present"; and
- The best science available is currently applied through Section 7 consultations in a manner that limits disturbance of habitat to 20%.

The demographic data indicates that owls on the northwest side are isolated and the numbers within this population are low. At 27 individuals, the population is barely half of the size called for by the simple conservation biology guideline that when a population slips below 50 individuals, the deck may be stacked against that population's survival.

#### (2) Understanding of conditions as a result of the Proudfoot study

The Proudfoot study now adds more difficulty to this dire situation with a finding that ferruginous pygmy-owls in northwest Tucson "have extremely low levels of average haplotype diversity." (p. 5)

Two years of data collection on mating among individuals in this area confirm that inbreeding is occurring at least to the second generation.

Survey efforts dating back through the 1990s tend to indicate that the population is not rebounding quickly to a size sufficient to restore normal levels of genetic variation for the species.

### E. Recommendations

Mr. Proudfoot suggests further study, and we will look to the biologists on the Recovery Team and employed by the United States Fish and Wildlife Service for advice about special management or other actions that are needed to avert extinction caused by the potential and perhaps foreseeable cascade of these circumstances.

## V. How Unique are Geographically Separated Populations within a Species of Concern?

### A. Description of the Issue

The ultimate viability of the pygmy-owl in Arizona will depend on our ability to avert local extinctions within the known population segments and to secure large landscapes and connecting corridors that allow the overall population to increase and the individual population segments to be connected through viable dispersal corridors. Within the four Arizona population segments, it is not common for dispersing pygmy-owls to fly from one population segment to another. This gives rise to the need for management attention at this scale. In Eastern Pima County we have two population segments: a population in Altar Valley, and an isolated population in Northwest Tucson. The Proudfoot study provides a comparison of the genetic make up of pygmy-owls within Arizona. It also compares Arizona pygmy-owls to those in Texas, and those in Mexico.

### B. Study Findings

The Proudfoot study states that "the low haplotypic diversity and distinct clade occurring in northwest Tucson suggests current separation between populations in northwest Tucson and populations in the Altar Valley, Sonora, and Sinaloa." (p. 6)

The study also establishes that pygmy-owls in Arizona are significantly different than pygmy-owls in Texas. On page 6 the study states: "Patterns of mtDNA variation provide strong evidence of two genetically distinct units, one in Arizona, Sonora and Sinaloa and the other in Texas and Tamaulipas, and regions of South-Central Mexico."

The study observes: "The separation of these two groups is probably the consequence of barriers to gene flow provided by the altitudinal Sierra Madre Occidental, because ferruginous pygmy-owls rarely occur above 1,300 m." (p. 6)

The study recommends: "there is a distinct difference between the Arizona and Texas populations and, thus, suggestive genetic reason based on mtDNA sequence variation to advocate separate management for the ferruginous pygmy-owl populations in the United States." (p. 7)

The study acknowledges that if some amount of geographic isolation exists between the Arizona and Mexico populations due to agricultural expansion, "the span of isolation [is] approximately 75 years (an extremely short time span in population genetic terms)." (p. 7)

In addition to finding significant distinctions between the Arizona and Texas pygmy-owls, the study states that "information obtained from this study (i.e., the 2.2 to 2.8% sequence divergence between the study group and the out group [from South America]) support [prior scholar's] suggestion to treat the North American 'population' as a distinct species." (p.8)

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### C. Significance of these findings for land management decision making

In 1997 the pygmy-owl was listed as endangered in Arizona as a Distinct Population Segment. The Texas population was not listed. The Distinct Population Segment rationale is based in part on the understanding that subspecies across administrative boundaries can not be relied upon to offset population declines in the United States for purposes of delisting. Therefore this study does not address the basis of the listing, but offers information about the potential to manage our way toward recovery given the potential for demographic support and genetic interchange.

The study data indicate that the distinct clade occurring in northwest Tucson suggests current separation between populations in northwest Tucson and populations in the Altar Valley, Sonora, and Sinaloa, once again bringing focus to northwest side issues.

The study establishes the Arizona and Texas pygmy-owls are distinct at the level of subspecies. It also confirms prior scholarship which indicated that the North American and South American pygmy-owls are distinct species. Accordingly, the management and recovery of Arizona pygmy-owl populations will not be assisted by these outlying populations.

### VI. Conclusion

In March of 1999 when the pygmy-owl genetics study was first proposed, it was assumed by some that a clear answer would arise from the data that determined our responsibility or our freedom from assisting in the complex and burdensome conservation and recovery efforts that are indicated by this listing. The results of the study show that the Arizona pygmy-owls are not related as a subspecies to pygmy-owls in Texas, nor to owls in the vast majority of Mexico, and they are not related as a species to owls in South America. The genetic connection to owls in the nearby state of Sonora, Mexico and perhaps to Sinaloa, might be less viable as a landscape connection given agricultural expansion during the past 75 years.

Pygmy-owls in northwest Tucson now deserve greater attention as a result of the Proudfoot study. Within Arizona, the northwest side pygmy-owls are in a distinct clade that suggests current separation between the Eastern Pima County population segments. We know that in addition to their low numbers and isolated status, ferruginous pygmy-owls in northwest Tucson "have extremely low levels of average haplotype diversity." Data collection on mating among individuals in this area confirm that inbreeding is occurring at least to the second generation. Inbreeding depression combined with demographic factors and ongoing habitat impacts in the area might set the stage for extinction of this population unless management actions are taken.

Mr. Proudfoot suggests further study, and we will look to the biologists on the Recovery Team and employed by the United States Fish and Wildlife Service for advice about whether special management or other actions that are needed to avert extinction caused by the potential and perhaps foreseeable cascade of these circumstances. The genetic neighbor tree found below is the portrait of the pygmy-owl family which maps out this complex undertaking that Mr. Proudfoot has performed so well during the last two years.

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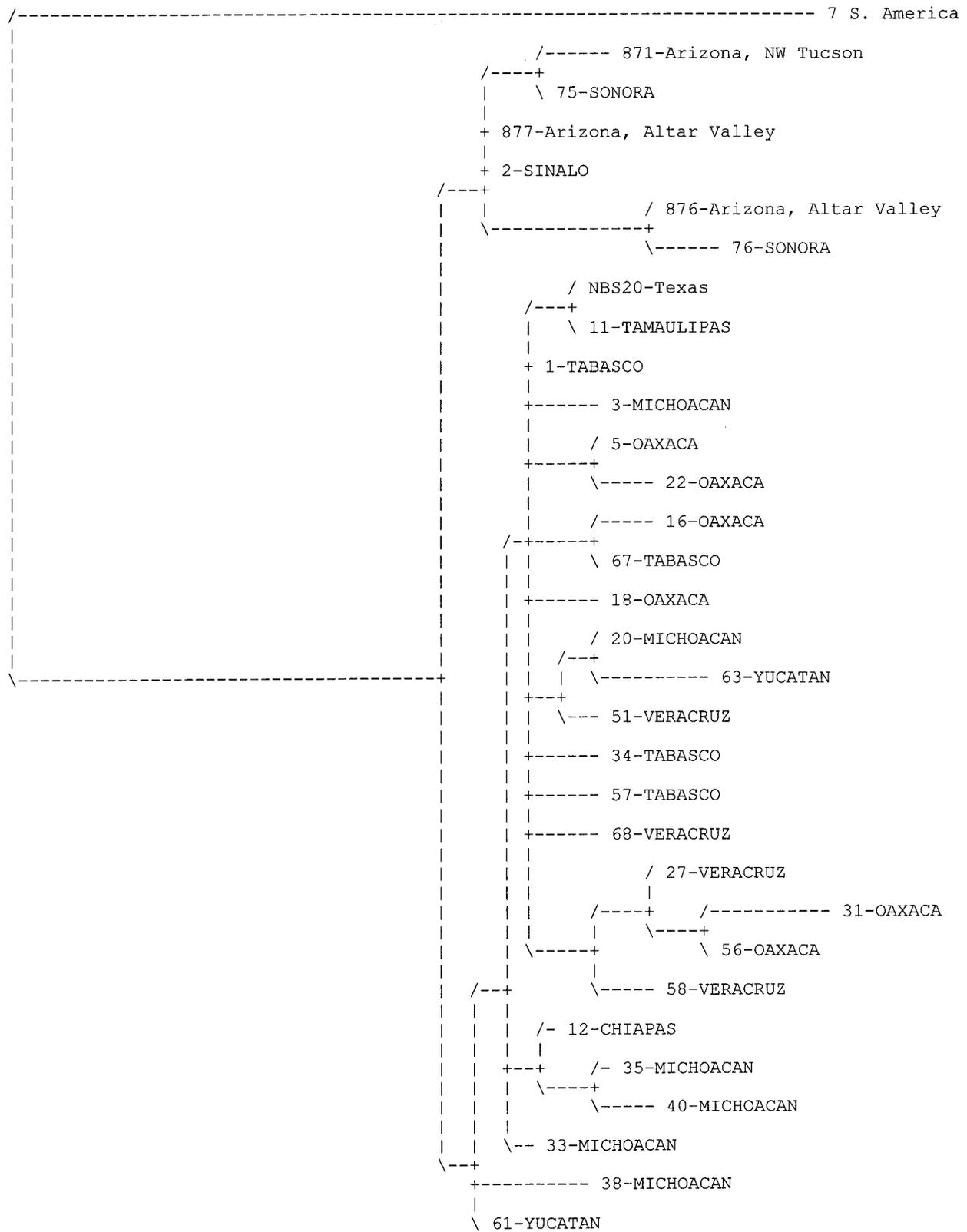


Figure 1. Haplotypic differentiation in Ferruginous Pygmy-Owls based on 899 bp of the cytochrome *b* gene, using Neighbor-joining analysis, PAUP 4.0. Geographic origin is given after sample number.



COMPARISONS OF FERRUGINOUS PYGMY-OWL mtDNA AT LOCAL AND  
INTERNATIONAL SCALES

for

Charles H. Huckelberry, County Administrator  
County Administrator's Office  
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as

Fulfilment of Contract Agreement  
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by

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Modern studies of species' conservation biology involve both demographic and genetic components (Barrowclough, 1992, Haig and Avise, 1995). Most genetic studies of populations attempt to address two primary questions: 1) Are the populations of concern lacking genetic variation relative to putative "healthy" populations? and 2) How unique are geographically distinct populations within a species of special concern? Populations without genetic variation are considered in peril, owing to the effects of low population number, inbreeding, or both (Haig and Avise, 1995). However, residual effects of bottlenecks, or phylogenetic inertia, can cause low levels of genetic variation in populations that are demographically healthy (i.e., the intrinsic rate of population increase is at 1.0 or above) (Ridley, 1993).

The second question relates to delimiting units for conservation priority. Genetically distinct populations might merit individual attention from conservation managers, because genetic differences are evidence of historical isolation. Therefore, genetically differentiated units are in effect the units of biodiversity that require management attention (Mortiz, 1994). Based on mitochondrial DNA (mtDNA) analysis, this paper addresses the necessity for special management of Ferruginous Pygmy-Owls (*Glaucidium brasilianum*, hereafter referred to as FEPO) in the United States.

Taxonomically, up to 15 subspecies of FEPO are recognized over their entire range, with as many as 4 subspecies (*G. b. ridgwayi* Sharpe, 1875: S. Texas south through e. Mexico along Atlantic slope to central Panama, *G. b. cactorum* van Rossem 1937: S. Arizona south to Nayarit, Mexico, *G. b. intermedium* Phillips, 1966: Pacific slope of Mexico from Nayarit south to Oaxaca, and *G. b. saturatum* Brodkorb, 1941: Pacific lowlands of Chiapas, Mexico, south into adjacent Guatemala) proposed for North American populations (Friedmann et al., 1950, Am. Ornithol. Union, 1957, Phillips, 1966, US Federal Register, 1997, Holt et al., 1999, König et al., 1999). König et al. (1999), however, suggest North American populations are not subspecies to FEPO in South America but are actually a distinct species (*G. ridgwayi*) with only 2 subspecies (*G. r. cactorum*: S. Arizona south to Nayarit and Jalisco, Mexico and *G. r. ridgwayi*: S. Texas south along Atlantic slope to Central America, Panama) occurring. Because only slight

differences in size (e.g., wing and tail length), pattern (e.g., streaking and coloration), and vocalization (which are broadly similar over entire range) have been used to characterize subspecies, evaluation of taxa is complicated and may require thorough taxonomic revision with molecular data (Proudfoot and Johnson, 2000). For this report, initial discussion will continue to use FEPO, the generally accepted term for North American populations.

Historically, the range of FEPOs included areas of southern Arizona and southern Texas, and extended south through Mexico to Chile, South America (Ridgway, 1914). During 1870-1920 FEPOs were thought to be fairly numerous in mesquite (*Prosopis spp.*) woodlands and cottonwood (*Populus spp.*) forests on the Salt, Verde, and Gila rivers in Arizona (Gilman, 1909, Millsap, 1987). Prior to 1920, FEPOs were considered common residents of mesquite brush, ebony (*Pithecellobium spp.*), and riparian areas in the Lower Rio Grande Valley of Texas. By the early 1970's more than 90% of this habitat was cleared for urban and agricultural expansion, reducing the population size of FEPOs (Oberholser, 1974).

In recent years, reports of FEPO sightings in the United States (US) have been infrequent (Monson and Phillips, 1981, Proudfoot and Johnson, 2000). In Arizona, the US Fish and Wildlife Service has listed the FEPO as endangered. The Texas Parks and Wildlife Department listed the FEPO as threatened in 1994, however, the proposed federal listing of the FEPO population in Texas was withheld (US Federal Register, 1997). In this study, we evaluate the genetic uniqueness between FEPO populations occurring in Arizona and Texas and compare these populations to those occurring in Mexico. The primary goal was to use genetic markers as a means of identifying potential management units with the FEPO.

## **METHODS**

Because my primary goal was to provide an objective assessment of geographic variation within the FEPO, we selected a mtDNA genetic marker. As indicated by several authors (Heidrich and Wink, 1994, Heidrich et al., 1995, König and Wink, 1995, Johns and Avise 1998),

mtDNA provides an effective marker for examining phylogeographic structure within species and has proven useful at several geographic scales (Zink, 1997).

Haplotype diversity in mtDNA was evaluated using sequences of >1000 bp fragment of the cytochrome *b* (*cyt-b*) gene. This gene was selected because it has been broadly surveyed in many avian taxa and has proven useful in conservation studies (Heidrich and Wink, 1994, Heidrich et al., 1995, König and Wink, 1995, Johns and Avise 1998). Phylogeographic variation was examined in samples from Arizona ( $n = 14$ ), Mexico ( $n = 63$ ), and Texas ( $n = 18$ ) and FEPO samples from Argentina were used as an outside reference group. As mentioned above, König et al. (1999) recently suggested the Argentine population was a unique species (*G. ridgwayi*).

Tissue and blood serum were collected from FEPOs in Kenedy and Willacy counties, Texas, Pima and Pinal counties, Arizona, and Sonora, Mexico. In Arizona and Texas, information obtained from concurrent banding studies conducted from 1994–1999 was used to reduce any bias resulting from comparisons of full and half siblings. In Sonora, sample sites were established >50 km apart to reduce the probability of examining related individuals derived from the same female lineage. To identify individuals a USFWS aluminum leg band was placed on all FEPOs captured. In addition to samples collected in the field, museum preparators provided tissue samples from FEPOs in Chiapas ( $n = 7$ ), Michoacan ( $n = 8$ ), Nayarit ( $n = 1$ ), Oaxaca ( $n = 13$ ), Sinaloa ( $n = 1$ ), Sonora (9), Tabasco ( $n = 10$ ), Tamaulipas ( $n = 4$ ), Veracruz ( $n = 11$ ), and Yucatan ( $n = 2$ ), Mexico. Sequences from FEPOs in South America that were used as an outgroup were provided by Professor M. Wink of Heidelberg, Germany, and geographic location of these samples are referenced in Heidrich et al. (1995) and König and Wink (1995).

DNA extractions were performed with a commercial kit (DNeasy, Qiagen®). Target gene regions were amplified by polymerase chain reaction (PCR) (Saiki et al., 1988, Hillis et al., 1989). *Cyt-b* sequences obtained from GenBank for Elf Owl (*Micrathene whitneyi*, #MWU89170), Northern Saw-whet Owl (*Aegolius acadicus*, #AAU89172) and Long-eared Owl (*Asio flammeus*, #AFU89171) were used to design and subsequently synthesize primers F1822

(5' > CCCAACATCCGAAARTCTCAC <3') and R1823 (5' > GGATGCTAGTTGGCCGATRAT <3') for initial PCR amplification and sequencing. Sequences obtained using these original primers allowed design and synthesis of additional internal species specific primers that were used to amplify and sequence >1,000 base pairs (bp) of *cyt-b* for comparative analysis. All PCR fragments were sequenced for both strands with the use of a Perkin Elmer® 377 automated sequencer.

Because a preliminary survey revealed low variation (2/240 bp) in the mtDNA control region (Proudfoot et al. unpub. data), which is suspected to be highly variable in birds (Baker and Marshall, 1997), we expanded the molecular study to include portions of *cyt-b*. Third position bases in *cyt-b* provide sequence variability equal to the control region (Zink and Blackwell, unpubl. data). Thus, we estimated sequence variability in *cyt-b*. Our final data set included 95 individuals, from Arizona, Texas, and Mexico. We compared 899 bp of *cyt-b* sequence obtained from FEPOs in Arizona, Texas, and Mexico to the same piece of *cyt-b* from FEPOs in Argentina. Argentine FEPOs' PCR and sequencing followed strategies similar to those outlined above and are described in detail in Heidrich et al. (1995).

MtDNA haplotypes were identified on the basis of sequence differences. Haplotype diversity within and between populations was assessed using both distance and maximum parsimony analysis available in PAUP 4.0.

## RESULTS

A total of 29 mtDNA haplotypes was observed among the samples sequenced, and these haplotypes showed differences from 1 to 11 base pairs each, resulting in haplotype divergences ranging from 0.1% to 1.0% (Table 1, Figure 1). Haplotype divergence was highest between Arizona and Texas populations, with little variation observed within populations. In comparison to Mexico, both Arizona (e.g., NW Tucson) and Texas have extremely low levels of average haplotype diversity (Table 2).

Phylogenetically, Arizona and Texas populations are unique, with no shared haplotypes (Figure 2). Populations from Sonora and Sinaloa, Mexico were distinct from remaining populations in Mexico and group closest to haplotypes in Arizona. Similarly, populations from Texas and Tamaulipas, Mexico, constitute a distinct group. FEPOs from Arizona differed by as much as 1.0% from FEPOs in Oaxaca, Mexico, and by as much as 0.7% from FEPOs in Texas.

## DISCUSSION

Patterns of mtDNA variation provide strong evidence of two genetically distinct units, one in Arizona, Sonora, and Sinaloa and the other in Texas and Tamaulipas, and regions of South-Central Mexico. These results are congruent with earlier taxonomic studies that recognized birds from these regions as distinct subspecies (van Rossem, 1937, Peters, 1940, Phillips, 1966, König et al., 1999). The separation of these two groups is probably the consequence of barriers to gene flow provided by the altitudinal Sierra Madre Occidental, because FEPO rarely occur above 1,300 m (Proudfoot and Johnson, 2000). Although Texas haplotypes fall within a large clade containing numerous haplotypes from Mexico, the Texas individuals form a distinct clade that clusters with birds from Tamaulipas. This pattern has two implications. First, the clustering of Texas haplotypes and low haplotypic diversity in Texas relative to Mexico suggests current genetic separation between these two areas. Second, Texas birds appear to be the result of a spreading out from earlier dispersal from a northern Mexico clade. Similarly, the low haplotypic diversity and distinct clade occurring in NW Tucson suggests current separation between populations in NW Tucson and populations in the Altar Valley, Sonora, and Sinaloa.

The lower haplotypic diversity in the Arizona and Texas populations is probably the result of founder events. The low levels of % divergence probably reflects recency of common ancestry. Other studies of owls have found similar situations. For example, Heidrich and Wink (1994) found no variation in a sample of *Strix woodfordii*, although their sample sizes were

small. In addition, no variation was found within a sample (4-7 birds/population) of *G. brasilianum* originating from Iguazu, the Salta or Cordoba region of Argentina (Konig et al., 1999). Many other birds have been surveyed for mtDNA variation within and among populations (Wink et al., 1993, 1996; Heidrich et al., 1995, Helberg et al., 1995, Wink, 1995, Wittmann et al., 1995), and this level of haplotype variation appears in many species that are not considered in peril. However, there is a distinct differences between the Arizona and Texas populations and, thus, suggestive genetic reason based on mtDNA sequence variation to advocate separate management for the FEPO populations in the United States. In addition, given the extreme similarities within the Arizona (i.e., samples from NW Tucson) and Texas populations, it is possible that the population as a whole underwent two bottlenecks sometime in the not-too-distant past and if other genetic markers, such as microsatellites, show low level genetic variation, concern could be warranted. Genetic data, however, play only one role in conservation policy and demographic data might indicate that the populations are currently in peril and require special management attention (Barrowclough, 1992).

Although a haplotypic separation exist between the FEPO populations of Arizona, Texas, and regions of South-Central Mexico, our data do not indicate genetic isolation between the distinct populations in the US and those immediately across the border in northwestern or northeastern Mexico. Obviously, obtaining more sequences may reveal additional haplotypes and differences among populations. However, our data suggest that such a division would be extremely "shallow" (Avice, 1994), indicative of a relatively recent split, if at all, between the populations. In addition, if geographic isolation of the Arizona and Texas populations from Mexican populations resulted from urban and agricultural expansion (Oberholser, 1974, Monson and Phillips, 1981), the span of isolation was approximately 75 years (an extremely short time span in population genetic terms). Other geographic surveys of owls (Heidrich and Wink, 1994, Heidrich et al., 1995, Konig et al., 1996), and many other birds, have revealed geographic subdivisions with similar molecular methods (Avice, 1994, Helbig et al., 1995, Wink, 1995,

Wittmann et al., 1995, Helbig et al., 1996, Wink et al., 1996). Thus, according to established genetic criteria (Moritz, 1994), mtDNA data reveal no evolutionary significant units for special conservation concern. Although there are relatively few examples of deep nuclear divisions without concomitant mtDNA separation (Zink, 1997), mtDNA restricts analysis to maternal lineages, hence, other genomic regions (e.g., microsatellites) should be studied to test this conclusion.

In addition to revealing a phylogeographic division between populations in Arizona and Texas, information obtained from this study (i.e., the 2.2 to 2.8% sequence divergence between study group and out group) supports Heidrich et al. (1995) and König et al.'s (1999) suggestion to treat the North American "population" as a distinct species (*G. ridgwayi*). There are few comparisons of conspecific sequence over such great geographic distances (Baker and Marshall, 1997) and further sampling is required to determine whether a distinct break exists and, if so, where the break occurs. Because of the genetic differences between North and South American FEPO populations, they may both merit separate management. However, given the relatively low sequence divergence between Argentine and US populations, local geographic structuring seems unlikely.

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Table 1. Absolute pairwise nucleotide distance between Ferruginous Pygmy-Owls in Arizona (AZ871, AZ876, AZ877), Texas (TX NBS20), and Mexico (geographic location after sample number), based on analysis of 899 bp of cytochrome *b* gene.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1 7 S. America	-																	
2 AZ871 NWT	25	-																
3 AZ876 AV	24	5	-															
4 AZ877 AV	23	2	3	-														
5 TX NBS20	22	5	6	3	-													
6 1TABASCO	23	4	5	2	1	-												
7 2SINALO	23	2	3	0	3	2	-											
8 3MICHOCAN	24	5	6	3	2	1	3	-										
9 5OAXACA	24	5	6	3	2	1	3	2	-									
10 11TAMAULIPAS	22	5	6	3	0	1	3	2	2	-								
11 12CHIAPAS	24	5	6	3	2	1	3	2	2	2	-							
12 16OAXACA	25	6	7	4	3	2	4	3	3	3	3	-						
13 18OAXACA	24	5	6	3	2	1	3	2	2	2	2	3	-					
14 20MICHOCAN	24	5	6	3	2	1	3	2	2	2	2	3	2	-				
15 22OAXACA	25	6	7	4	3	2	4	3	1	3	3	4	3	3	-			
16 27VERACRUZ	25	6	7	4	3	2	4	3	3	3	3	4	3	3	4	-		
17 31OAXACA	28	9	10	7	6	5	7	6	6	6	6	7	6	6	7	3	-	
18 33MICHOCAN	24	5	6	3	2	1	3	2	2	2	2	3	2	2	3	3	6	-
19 34TABASCO	24	5	6	3	2	1	3	2	2	2	2	3	2	2	3	3	6	2
20 35MICHOCAN	25	6	7	4	3	2	4	3	3	3	3	4	3	3	4	4	7	1
21 38MICHOCAN	24	5	6	3	4	3	3	4	4	4	4	5	4	4	5	5	8	2
22 40MICHOCAN	24	7	8	5	2	3	5	4	4	2	2	5	4	4	5	5	8	2
23 51VERACRUZ	24	5	6	3	2	1	3	2	2	2	2	3	2	2	3	3	6	2
24 56OAXACA	26	7	8	5	4	3	5	4	4	4	4	5	4	4	5	1	2	4
25 57TABASCO	24	5	6	3	2	1	3	2	2	2	2	3	2	2	3	3	6	2
26 58VERACRUZ	23	6	7	4	3	2	4	3	3	3	3	4	3	3	4	2	5	3
27 61YUCATAN	22	3	4	1	2	1	1	2	2	2	2	3	2	2	3	3	6	2
28 63YUCATAN	26	7	8	5	4	3	5	4	4	4	4	5	4	2	5	5	8	4
29 67TABASCO	24	5	6	3	2	1	3	2	2	2	2	3	2	2	3	3	6	2
30 68VERACRUZ	24	5	6	3	2	1	3	2	2	2	2	3	2	2	3	3	6	2
31 75SONORA	24	1	4	1	4	3	1	4	4	4	4	5	4	4	5	5	8	4
32 76SONORA	25	6	1	4	7	6	4	7	7	7	7	8	7	7	8	8	11	7

Absolute distance matrix (continued)

	19	20	21	22	23	24	25	26	27	28	29	30	31	32
19 34TABASCO	-													
20 35MICHOCAN	3	-												
21 38MICHOCAN	4	3	-											
22 40MICHOCAN	4	1	4	-										
23 51VERACRUZ	2	3	4	4	-									
24 56OAXACA	4	5	6	6	4	-								
25 57TABASCO	2	3	4	4	2	4	-							
26 58VERACRUZ	3	4	5	5	3	3	3	-						
27 61YUCATAN	2	3	2	4	2	4	2	3	-					
28 63YUCATAN	4	5	6	6	2	6	4	5	4	-				
29 67TABASCO	2	3	4	4	2	4	2	3	2	4	-			
30 68VERACRUZ	2	3	4	4	2	4	2	3	2	4	2	-		
31 75SONORA	4	5	4	6	4	6	4	5	2	6	4	4	-	
32 76SONORA	7	8	7	9	7	9	7	8	5	9	7	7	5	-

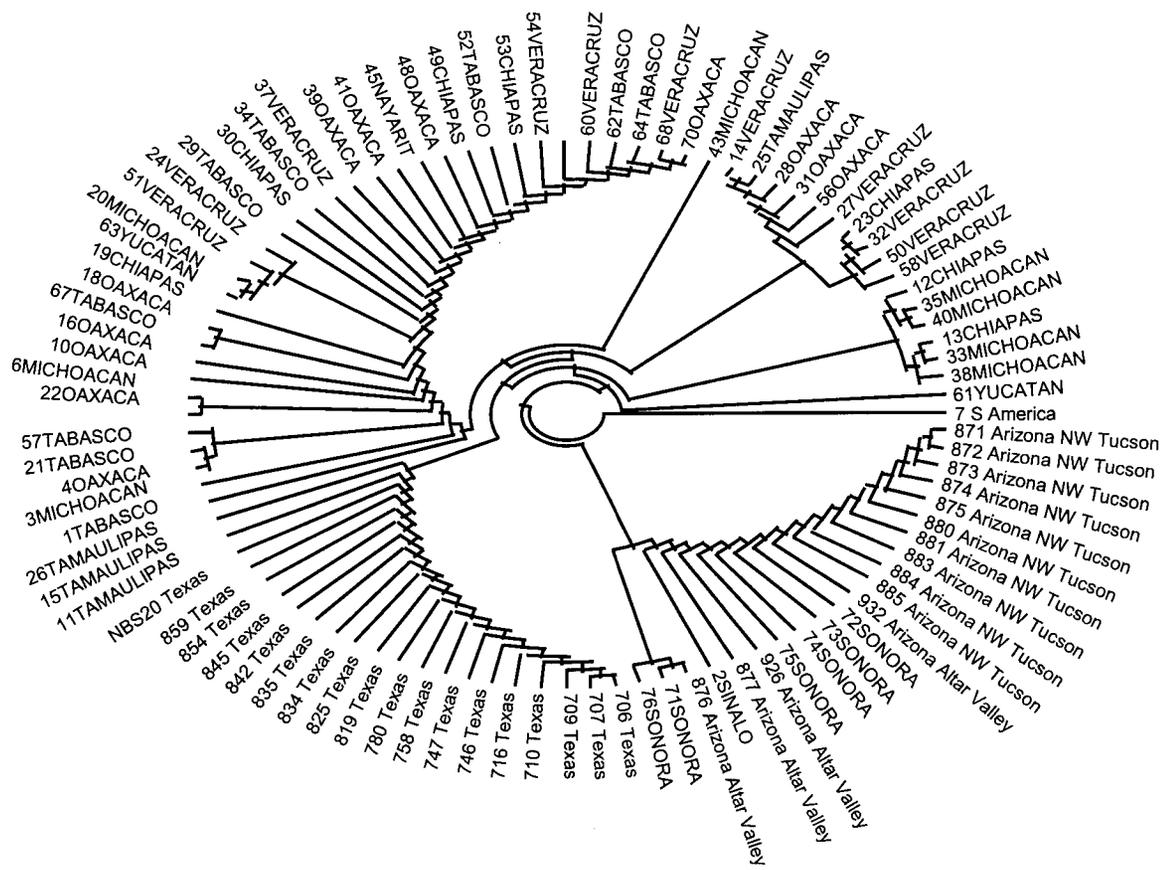


Figure 2. Genetic relationship between 95 Ferruginous Pygmy-Owls in Arizona, Texas, and Mexico, based on 899 bp of cytochrome *b* gene, using Neighbor-joining analysis, PAUP 4.0.

Table 2. Absolute pairwise nucleotide distance between Ferruginous Pygmy-Owls in Arizona (NWT = NW Tucson, AV = Altar Valley), Texas, and Mexico (geographic location after sample number), based on analysis of 899 bp of cytochrome *b* gene.

	7	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33
7 7 S America	-																
18 871 Arizona NWT	25	-															
19 872 Arizona NWT	25	0	-														
20 873 Arizona NWT	25	0	0	-													
21 874 Arizona NWT	25	0	0	0	-												
22 875 Arizona NWT	25	0	0	0	0	-											
23 876 Arizona AV	24	5	5	5	5	5	-										
24 926 Arizona AV	23	2	2	2	2	2	3	-									
25 877 Arizona AV	23	2	2	2	2	2	3	0	-								
26 880 Arizona NWT	25	0	0	0	0	0	5	2	2	-							
27 881 Arizona NWT	25	0	0	0	0	0	5	2	2	0	-						
28 883 Arizona NWT	25	0	0	0	0	0	5	2	2	0	0	-					
29 884 Arizona NWT	25	0	0	0	0	0	5	2	2	0	0	0	-				
30 885 Arizona NWT	25	0	0	0	0	0	5	2	2	0	0	0	0	-			
31 932 Arizona AV	25	0	0	0	0	0	5	2	2	0	0	0	0	0	-		
32 706 Texas	22	5	5	5	5	5	6	3	3	5	5	5	5	5	5	-	
33 707 Texas	22	5	5	5	5	5	6	3	3	5	5	5	5	5	5	0	-
34 709 Texas	22	5	5	5	5	5	6	3	3	5	5	5	5	5	5	0	0
35 710 Texas	22	5	5	5	5	5	6	3	3	5	5	5	5	5	5	0	0
36 716 Texas	22	5	5	5	5	5	6	3	3	5	5	5	5	5	5	0	0
37 746 Texas	22	5	5	5	5	5	6	3	3	5	5	5	5	5	5	0	0
38 747 Texas	22	5	5	5	5	5	6	3	3	5	5	5	5	5	5	0	0
39 758 Texas	22	5	5	5	5	5	6	3	3	5	5	5	5	5	5	0	0
40 780 Texas	22	5	5	5	5	5	6	3	3	5	5	5	5	5	5	0	0
41 819 Texas	22	5	5	5	5	5	6	3	3	5	5	5	5	5	5	0	0
42 825 Texas	22	5	5	5	5	5	6	3	3	5	5	5	5	5	5	0	0
43 834 Texas	22	5	5	5	5	5	6	3	3	5	5	5	5	5	5	0	0
44 835 Texas	22	5	5	5	5	5	6	3	3	5	5	5	5	5	5	0	0
45 842 Texas	22	5	5	5	5	5	6	3	3	5	5	5	5	5	5	0	0
46 845 Texas	22	5	5	5	5	5	6	3	3	5	5	5	5	5	5	0	0
47 854 Texas	22	5	5	5	5	5	6	3	3	5	5	5	5	5	5	0	0
48 859 Texas	22	5	5	5	5	5	6	3	3	5	5	5	5	5	5	0	0
49 NBS20 Texas	22	5	5	5	5	5	6	3	3	5	5	5	5	5	5	0	0
50 1TABASCO	23	4	4	4	4	4	5	2	2	4	4	4	4	4	4	1	1
51 2SINALO	23	2	2	2	2	2	3	0	0	2	2	2	2	2	2	3	3
52 3MICHOCAN	24	5	5	5	5	5	6	3	3	5	5	5	5	5	5	2	2
53 4OAXACA	24	5	5	5	5	5	6	3	3	5	5	5	5	5	5	2	2
54 5OAXACA	24	5	5	5	5	5	6	3	3	5	5	5	5	5	5	2	2
55 6MICHOCAN	23	4	4	4	4	4	5	2	2	4	4	4	4	4	4	1	1
56 10OAXACA	23	4	4	4	4	4	5	2	2	4	4	4	4	4	4	1	1
57 11TAMAULIPAS	22	5	5	5	5	5	6	3	3	5	5	5	5	5	5	0	0
58 12CHIAPAS	24	5	5	5	5	5	6	3	3	5	5	5	5	5	5	2	2
59 13CHIAPAS	24	5	5	5	5	5	6	3	3	5	5	5	5	5	5	2	2
60 14VERACRUZ	26	7	7	7	7	7	8	5	5	7	7	7	7	7	7	4	4
61 15TAMAULIPAS	22	5	5	5	5	5	6	3	3	5	5	5	5	5	5	0	0
62 16OAXACA	25	6	6	6	6	6	7	4	4	6	6	6	6	6	6	3	3
63 18OAXACA	24	5	5	5	5	5	6	3	3	5	5	5	5	5	5	2	2
64 19CHIAPAS	26	7	7	7	7	7	8	5	5	7	7	7	7	7	7	4	4
65 20MICHOCAN	24	5	5	5	5	5	6	3	3	5	5	5	5	5	5	2	2
66 21TABASCO	24	5	5	5	5	5	6	3	3	5	5	5	5	5	5	2	2
67 22OAXACA	25	6	6	6	6	6	7	4	4	6	6	6	6	6	6	3	3
68 23CHIAPAS	23	6	6	6	6	6	7	4	4	6	6	6	6	6	6	3	3
69 24VERACRUZ	23	4	4	4	4	4	5	2	2	4	4	4	4	4	4	1	1
70 25TAMAULIPAS	26	7	7	7	7	7	8	5	5	7	7	7	7	7	7	4	4
71 26TAMAULIPAS	22	5	5	5	5	5	6	3	3	5	5	5	5	5	5	0	0
72 27VERACRUZ	25	6	6	6	6	6	7	4	4	6	6	6	6	6	6	3	3

Table 2. (continued)

	7	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33
73 28OAXACA	26	7	7	7	7	7	8	5	5	7	7	7	7	7	7	4	4
74 29TABASCO	23	4	4	4	4	4	5	2	2	4	4	4	4	4	4	1	1
75 30CHIAPAS	23	4	4	4	4	4	5	2	2	4	4	4	4	4	4	1	1
76 31OAXACA	28	9	9	9	9	9	10	7	7	9	9	9	9	9	9	6	6
77 32VERACRUZ	23	6	6	6	6	6	7	4	4	6	6	6	6	6	6	3	3
78 33MICHOACAN	24	5	5	5	5	5	6	3	3	5	5	5	5	5	5	2	2
79 34TABASCO	24	5	5	5	5	5	6	3	3	5	5	5	5	5	5	2	2
80 35MICHOACAN	25	6	6	6	6	6	7	4	4	6	6	6	6	6	6	3	3
81 37VERACRUZ	23	4	4	4	4	4	5	2	2	4	4	4	4	4	4	1	1
82 38MICHOACAN	24	5	5	5	5	5	6	3	3	5	5	5	5	5	5	4	4
83 39OAXACA	23	4	4	4	4	4	5	2	2	4	4	4	4	4	4	1	1
84 40MICHOACAN	24	7	7	7	7	7	8	5	5	7	7	7	7	7	7	2	2
85 41OAXACA	23	4	4	4	4	4	5	2	2	4	4	4	4	4	4	1	1
86 43MICHOACAN	24	5	5	5	5	5	6	3	3	5	5	5	5	5	5	2	2
87 45NAYARIT	23	4	4	4	4	4	5	2	2	4	4	4	4	4	4	1	1
88 48OAXACA	23	4	4	4	4	4	5	2	2	4	4	4	4	4	4	1	1
89 49CHIAPAS	23	4	4	4	4	4	5	2	2	4	4	4	4	4	4	1	1
90 50VERACRUZ	23	6	6	6	6	6	7	4	4	6	6	6	6	6	6	3	3
91 51VERACRUZ	24	5	5	5	5	5	6	3	3	5	5	5	5	5	5	2	2
92 52TABASCO	23	4	4	4	4	4	5	2	2	4	4	4	4	4	4	1	1
93 53CHIAPAS	23	4	4	4	4	4	5	2	2	4	4	4	4	4	4	1	1
94 54VERACRUZ	23	4	4	4	4	4	5	2	2	4	4	4	4	4	4	1	1
95 56OAXACA	26	7	7	7	7	7	8	5	5	7	7	7	7	7	7	4	4
96 57TABASCO	24	5	5	5	5	5	6	3	3	5	5	5	5	5	5	2	2
97 58VERACRUZ	23	6	6	6	6	6	7	4	4	6	6	6	6	6	6	3	3
98 59TABASCO	23	4	4	4	4	4	5	2	2	4	4	4	4	4	4	1	1
99 60VERACRUZ	23	4	4	4	4	4	5	2	2	4	4	4	4	4	4	1	1
100 61YUCATAN	22	3	3	3	3	3	4	1	1	3	3	3	3	3	3	2	2
101 62TABASCO	23	4	4	4	4	4	5	2	2	4	4	4	4	4	4	1	1
102 63YUCATAN	26	7	7	7	7	7	8	5	5	7	7	7	7	7	7	4	4
103 64TABASCO	23	4	4	4	4	4	5	2	2	4	4	4	4	4	4	1	1
104 67TABASCO	24	5	5	5	5	5	6	3	3	5	5	5	5	5	5	2	2
105 68VERACRUZ	24	5	5	5	5	5	6	3	3	5	5	5	5	5	5	2	2
106 70OAXACA	23	4	4	4	4	4	5	2	2	4	4	4	4	4	4	1	1
107 71SONORA	24	5	5	5	5	5	0	3	3	5	5	5	5	5	5	6	6
108 72SONORA	25	0	0	0	0	0	5	2	2	0	0	0	0	0	0	5	5
109 73SONORA	24	1	1	1	1	1	4	1	1	1	1	1	1	1	1	4	4
110 74SONORA	24	1	1	1	1	1	4	1	1	1	1	1	1	1	1	4	4
111 75SONORA	24	1	1	1	1	1	4	1	1	1	1	1	1	1	1	4	4
112 76SONORA	25	6	6	6	6	6	1	4	4	6	6	6	6	6	6	7	7

Table 2. (continued)

	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50
34 709 Texas	-																
35 710 Texas	0	-															
36 716 Texas	0	0	-														
37 746 Texas	0	0	0	-													
38 747 Texas	0	0	0	0	-												
39 758 Texas	0	0	0	0	0	-											
40 780 Texas	0	0	0	0	0	0	-										
41 819 Texas	0	0	0	0	0	0	0	-									
42 825 Texas	0	0	0	0	0	0	0	0	-								
43 834 Texas	0	0	0	0	0	0	0	0	0	-							
44 835 Texas	0	0	0	0	0	0	0	0	0	0	-						
45 842 Texas	0	0	0	0	0	0	0	0	0	0	0	-					
46 845 Texas	0	0	0	0	0	0	0	0	0	0	0	0	-				
47 854 Texas	0	0	0	0	0	0	0	0	0	0	0	0	0	-			

Table 2. (continued)

	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50
48 859 Texas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	-	-
49 NBS20 Texas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	-	-
50 1TABASCO	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	-
51 2SINALO	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	2
52 3MICHOACAN	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1
53 4OAXACA	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1
54 5OAXACA	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1
55 6MICHOACAN	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0
56 10OAXACA	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0
57 11TAMAULIPAS	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
58 12CHIAPAS	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1
59 13CHIAPAS	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1
60 14VERACRUZ	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	3
61 15TAMAULIPAS	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
62 16OAXACA	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	2
63 18OAXACA	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1
64 19CHIAPAS	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	3
65 20MICHOACAN	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1
66 21TABASCO	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1
67 22OAXACA	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	2
68 23CHIAPAS	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	2
69 24VERACRUZ	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0
70 25TAMAULIPAS	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	3
71 26TAMAULIPAS	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
72 27VERACRUZ	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	2
73 28OAXACA	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	3
74 29TABASCO	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0
75 30CHIAPAS	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0
76 31OAXACA	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	5
77 32VERACRUZ	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	2
78 33MICHOACAN	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1
79 34TABASCO	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1
80 35MICHOACAN	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	2
81 37VERACRUZ	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0
82 38MICHOACAN	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	3
83 39OAXACA	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0
84 40MICHOACAN	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	3
85 41OAXACA	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0
86 43MICHOACAN	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1
87 45NAYARIT	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0
88 48OAXACA	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0
89 49CHIAPAS	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0
90 50VERACRUZ	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	2
91 51VERACRUZ	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1
92 52TABASCO	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0
93 53CHIAPAS	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0
94 54VERACRUZ	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0
95 56OAXACA	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	3
96 57TABASCO	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1
97 58VERACRUZ	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	2
98 59TABASCO	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0
99 60VERACRUZ	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0
100 61YUCATAN	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1
101 62TABASCO	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0
102 63YUCATAN	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	3
103 64TABASCO	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0
104 67TABASCO	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1
105 68VERACRUZ	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1
106 70OAXACA	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0
107 71SONORA	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	5

Table 2. (continued)

	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50
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108	72SONORA	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	4
109	73SONORA	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	3
110	74SONORA	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	3
111	75SONORA	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	3
112	76SONORA	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	6

Table 2. (continued)

	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	
51	2SINALO	-																
52	3MICHOACAN	3	-															
53	4OAXACA	3	2	-														
54	5OAXACA	3	2	2	-													
55	6MICHOACAN	2	1	1	1	-												
56	10OAXACA	2	1	1	1	0	-											
57	11TAMAULIPAS	3	2	2	2	1	1	-										
58	12CHIAPAS	3	2	2	2	1	1	2	-									
59	13CHIAPAS	3	2	2	2	1	1	2	2	-								
60	14VERACRUZ	5	4	4	4	3	3	4	4	4	-							
61	15TAMAULIPAS	3	2	2	2	1	1	0	2	2	4	-						
62	16OAXACA	4	3	3	3	2	2	3	3	3	5	3	-					
63	18OAXACA	3	2	2	2	1	1	2	2	2	4	2	3	-				
64	19CHIAPAS	5	4	4	4	3	3	4	4	4	6	4	5	4	-			
65	20MICHOACAN	3	2	2	2	1	1	2	2	2	4	2	3	2	2	-		
66	21TABASCO	3	2	0	2	1	1	2	2	2	4	2	3	2	4	2	-	
67	22OAXACA	4	3	3	1	2	2	3	3	3	5	3	4	3	5	3	3	-
68	23CHIAPAS	4	3	3	3	2	2	3	3	3	3	3	4	3	5	3	3	4
69	24VERACRUZ	2	1	1	1	0	0	1	1	1	3	1	2	1	3	1	1	2
70	25TAMAULIPAS	5	4	4	4	3	3	4	4	4	0	4	5	4	6	4	4	5
71	26TAMAULIPAS	3	2	2	2	1	1	0	2	2	4	0	3	2	4	2	2	3
72	27VERACRUZ	4	3	3	3	2	2	3	3	3	1	3	4	3	5	3	3	4
73	28OAXACA	5	4	4	4	3	3	4	4	4	0	4	5	4	6	4	4	5
74	29TABASCO	2	1	1	1	0	0	1	1	1	3	1	2	1	3	1	1	2
75	30CHIAPAS	2	1	1	1	0	0	1	1	1	3	1	2	1	3	1	1	2
76	31OAXACA	7	6	6	6	5	5	6	6	6	2	6	7	6	8	6	6	7
77	32VERACRUZ	4	3	3	3	2	2	3	3	3	3	3	4	3	5	3	3	4
78	33MICHOACAN	3	2	2	2	1	1	2	2	0	4	2	3	2	4	2	2	3
79	34TABASCO	3	2	2	2	1	1	2	2	2	4	2	3	2	4	2	2	3
80	35MICHOACAN	4	3	3	3	2	2	3	1	1	5	3	4	3	5	3	3	4
81	37VERACRUZ	2	1	1	1	0	0	1	1	1	3	1	2	1	3	1	1	2
82	38MICHOACAN	3	4	4	4	3	3	4	4	2	6	4	5	4	6	4	4	5
83	39OAXACA	2	1	1	1	0	0	1	1	1	3	1	2	1	3	1	1	2
84	40MICHOACAN	5	4	4	4	3	3	2	2	2	6	2	5	4	6	4	4	5
85	41OAXACA	2	1	1	1	0	0	1	1	1	3	1	2	1	3	1	1	2
86	43MICHOACAN	3	2	2	2	1	1	2	2	2	4	2	3	2	4	2	2	3
87	45NAYARIT	2	1	1	1	0	0	1	1	1	3	1	2	1	3	1	1	2
88	48OAXACA	2	1	1	1	0	0	1	1	1	3	1	2	1	3	1	1	2
89	49CHIAPAS	2	1	1	1	0	0	1	1	1	3	1	2	1	3	1	1	2
90	50VERACRUZ	4	3	3	3	2	2	3	3	3	3	3	4	3	5	3	3	4
91	51VERACRUZ	3	2	2	2	1	1	2	2	2	4	2	3	2	2	2	2	3
92	52TABASCO	2	1	1	1	0	0	1	1	1	3	1	2	1	3	1	1	2
93	53CHIAPAS	2	1	1	1	0	0	1	1	1	3	1	2	1	3	1	1	2
94	54VERACRUZ	2	1	1	1	0	0	1	1	1	3	1	2	1	3	1	1	2
95	56OAXACA	5	4	4	4	3	3	4	4	4	0	4	5	4	6	4	4	5
96	57TABASCO	3	2	0	2	1	1	2	2	2	4	2	3	2	4	2	0	3
97	58VERACRUZ	4	3	3	3	2	2	3	3	3	3	3	4	3	5	3	3	4
98	59TABASCO	2	1	1	1	0	0	1	1	1	3	1	2	1	3	1	1	2
99	60VERACRUZ	2	1	1	1	0	0	1	1	1	3	1	2	1	3	1	1	2
100	61YUCATAN	1	2	2	2	1	1	2	2	2	4	2	3	2	4	2	2	3
101	62TABASCO	2	1	1	1	0	0	1	1	1	3	1	2	1	3	1	1	2

Table 2. (continued)

	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	
102	63YUCATAN	5	4	4	4	3	3	4	4	4	6	4	5	4	0	2	4	5



86	43	MICHOACAN	1	-																
87	45	NAYARIT	0	1	-															
88	48	OAXACA	0	1	0	-														
89	49	CHIAPAS	0	1	0	0	-													
90	50	VERACRUZ	2	3	2	2	2	-												
91	51	VERACRUZ	1	2	1	1	1	3	-											
92	52	TABASCO	0	1	0	0	0	2	1	-										
93	53	CHIAPAS	0	1	0	0	0	2	1	0	0									
94	54	VERACRUZ	0	1	0	0	0	2	1	0	0	-								
95	56	OAXACA	3	4	3	3	3	3	4	3	3	3	-							
96	57	TABASCO	1	2	1	1	1	3	2	1	1	1	4	-						
97	58	VERACRUZ	2	3	2	2	2	0	3	2	2	2	3	3	-					
98	59	TABASCO	0	1	0	0	0	2	1	0	0	0	3	1	2	-				
99	60	VERACRUZ	0	1	0	0	0	2	1	0	0	0	3	1	2	0	-			
100	61	YUCATAN	1	2	1	1	1	3	2	1	1	1	4	2	3	0	1	-		
101	62	TABASCO	0	1	0	0	0	2	1	0	0	0	3	1	2	0	0	1	-	
102	63	YUCATAN	3	4	3	3	3	5	2	3	3	3	6	4	5	3	3	4	3	
103	64	TABASCO	0	1	0	0	0	2	1	0	0	0	3	1	2	0	0	1	0	
104	67	TABASCO	1	2	1	1	1	3	2	1	1	1	4	2	3	1	1	2	1	
105	68	VERACRUZ	1	2	1	1	1	3	2	1	1	1	4	2	3	1	1	2	1	
106	70	OAXACA	0	1	0	0	0	2	1	0	0	0	3	1	2	0	0	1	0	
107	71	SONORA	5	6	5	5	5	7	6	5	5	5	8	6	7	5	5	4	5	
108	72	SONORA	4	5	4	4	4	6	5	4	4	4	7	5	6	4	4	3	4	
109	73	SONORA	3	4	3	3	3	5	4	3	3	3	6	4	5	3	3	2	3	
110	74	SONORA	3	4	3	3	3	5	4	3	3	3	6	4	5	3	3	2	3	
111	75	SONORA	3	4	3	3	3	5	4	3	3	3	6	4	5	3	3	2	3	
112	76	SONORA	6	7	6	6	6	8	7	6	6	6	9	7	8	6	6	5	6	

Table 2. (continued)

	102	103	104	105	106	107	108	109	110	111	112		
102	63	YUCATAN	-										
103	64	TABASCO	3	-									
104	67	TABASCO	4	1	-								
105	68	VERACRUZ	4	1	2	-							
106	70	OAXACA	3	0	1	1	-						
107	71	SONORA	8	5	6	6	5	-					
108	72	SONORA	7	4	5	5	4	5	-				
109	73	SONORA	6	3	4	4	3	4	1	-			
110	74	SONORA	6	3	4	4	3	4	1	0	-		
111	75	SONORA	6	3	4	4	3	4	1	0	0	-	
112	76	SONORA	9	6	7	7	6	1	6	5	5	5	-