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## PHYLOGEOGRAPHY, HISTORICAL PATTERNS, AND CONSERVATION OF NATURAL AREAS

Ella Vázquez-Domínguez

### Abstract

Genetic diversity, a fundamental component of biodiversity, has been largely ignored up to this point in the creation of parks and protected areas. However, the theory is now available to confront this unexplored dimension of diversity given more advanced theoretical models, molecular technologies, and conceptual frameworks. The comparative analysis of phylogeography allows for evaluation of the geographic patterns of the genetic component of biodiversity, emphasizing the evolutionary differentiation and historical demography within and among populations. These advances make it possible to incorporate genetic diversity and evolutionary processes as goals in the assessment of conservation priorities.

### Introduction

From a biological perspective, there is a major deficiency in the ecological research that has been undertaken to date related to parks and protected areas. After identification of important sites or areas because of their high species richness, or high endemic values, it is now evident that more detailed ecological research is needed to maximize representation of different taxa, and to incorporate evolutionary processes as primary goals within natural protected areas. Accordingly, genetic diversity is now recognized as a fundamental component of biodiversity and the need for

its protection has been incorporated into conservation programs and policies (Humphries, Williams, and Vane-Wright 1995). However, little priority has been given to the direct estimation of genetic diversity, partly because of the absence of suitable data and an appropriate conceptual framework (Avisé 1992), but also because it has been erroneously assumed that by protecting diversity at or above the species level, the underlying genetic and evolutionary diversity will also be protected (Avisé 1989, Moritz et al. 1996).

Table 24.1. Comparison of the Terrestrial Ecosystem Diversity in Some Latin-American Countries (Dinerstein et al. 1995)

	Mexico	Brazil	Colombia	Chile	Argentina	Costa Rica
Kind of ecosystems	5	5	4	3	3	3
Kind of habitat	9	8	6	4	6	4
Ecoregions	51	34	29	12	19	8

### Mexico as a Megadiverse Country

Although Mexico is ranked fourteenth for its size among the countries of the world, it is fourth for its biological diversity and is defined as "megadiverse" (Mittermeier 1988). Such remarkably high diversity is a consequence of its dominant vegetation types, which can be subdivided in thirty to fifty subtypes, or ecoregions, depending on the classification used (Ramamoorthy et al. 1993). Among Latin-American countries, Mexico has the highest number of ecoregions (Dinerstein et al. 1995; table 24.1). At the species level, and only considering angiosperms, insects (butterflies), and vertebrates, Mexico has approximately 10 percent of the species described in the world, 1 percent of which are endemic (table 24.2). Marine biodiversity, however, is less well known as is the case worldwide, and many new species are described regularly (Vázquez-Domínguez et al. 1998). The nation's genetic diversity, only recently being directly evaluated, ranges from the genetic variability of many endemic or threatened species to, for example, genes of *Zea diploperennis*, the only wild relative of maize. Topography, together with climatic variability, have produced heterogeneous landscapes within every ecosystem, in which speciation and evolution have yielded an immense genetic and evolutionary variability.

Table 24.2. Number of Species and Endemic Species in Mexico, and Ranking of Mexico Among the 17 Most Megadiverse Countries

Group	# species in Mexico	# endemic species	# species globally	Megadiversity Rank	
				by group	by endemics
Mammals	450	140	4,629	5	3
Birds	1,050	125	9,040	12	6
Reptiles	717	368	6,458	2	2
Amphibians	284	169	4,222	4	6
Freshwater fishes	347		8,411		
Vertebrates <sup>a</sup>	2,501	802	10,680	6	3
Butterflies	2,237	200		6	7
Plants <sup>b</sup>	18-30,000	10-15,000	250,000	4	8

<sup>a</sup>without fish; <sup>b</sup>angiosperms, gymnosperms, ferns, and bryophytes (Data from Mittermeier et al. 1998)

### Toward Improved Understanding of Genetic Diversity

Species should not be visualized as monotypic entities, but rather as a series of populations that differ geographically, with a distinguishable genetic and historical structure. A great number of species studied in different environments, such as tropical forests, show a marked genetic divergence as well as structured populations (Moritz, J. Cunningham, and Schneider 1997, Patton et al. 1997, Moritz and Faith 1998, Schneider, M. Cunningham, and Moritz 1998), which are not evident from phenotypic comparisons (Vázquez-Domínguez et al. 2001). This suggests that the descriptions of biodiversity based on the distribution of vegetation types, number of species or number of endemic species, do not adequately represent the evolutionary diversity of the biota. Accordingly, we have started to better understand the temporal, spatial, and evolutionary processes that have shaped the present distribution of biodiversity; information that is essential to guarantee the long-term viability of natural systems.

The fragmentation of habitats, one of the main challenges for the conservation of natural resources, has two components: current anthropogenic alterations, and long-term natural processes. Habitats and ecosystems have experienced contractions and expansions in their distribution during geologic history such as glacial and interglacial periods (Flenley 1979). These changes can be appreciated through geographic

patterns of genetic variation, which would be congruent among different species that have been affected by similar means. Accordingly, since historical changes in the distribution of ecosystems are strong determinants of the current distribution of genetic diversity and of species, it is essential to consider the historical perspective in order to have a more complete knowledge about biodiversity (Nix 1991, Joseph, Moritz, and Huggall 1995).

Protection of genetic diversity should consider the amount of genetic diversity within and among populations, as well as the maintenance of historical patterns of independent evolution and of evolutionary potential among populations within species. Thus, the assessment of conservation priorities on a regional basis also depends on an understanding of the genetic uniqueness and genetic diversity of local populations. Common conservation approaches are likely to encompass the adaptive component of genetic diversity, but fail to recognize explicitly the genetic diversity accumulated through geographic isolation *per se*.

Genetic surveys of regional biotas have become a practical goal only recently with the development of rapid, molecular methods of genetic evaluation. The analysis of mitochondrial DNA (mtDNA) in animals is an effective tool in evolutionary biology (Hillis, Moritz, and Mable 1996), but also has a high potential for practical studies in conservation (Moritz 1994a, Moritz et al. 1996). Because it is homologous across animals, analysis on mtDNA variation permits objective, quantitative comparisons across independently evolving taxa and provides a particularly useful tool for regional biotic surveys; it is especially useful to detect frontiers between genetically different populations (Smith and Wayne 1996). Molecular studies can also reveal the phylogeny of alleles within species, allowing us to discern historical biogeographic and population processes which were inaccessible before (Avice 1994, Joseph, Moritz, and Huggall 1995, Moritz, J. Cunningham, and Schneider 1997). The information from mtDNA variability within species has two applications or advantages: to know (a) the phylogenetic interrelations among the DNA molecules themselves, and (b) the geographic distribution of the phylogenetic groups. Together, these two elements form part of the discipline of phylogeography. Phylogeography has helped prove that many species have a different phylogenetic history and are geographically structured (Avice et al. 1987, Joseph, Morris, and Huggall 1995). It is possible, through the comparative analysis of the phylogeography of codistributed

species, to know the geographic patterns of the genetic component of biodiversity; in turn, this can be used as an element to allocate conservation and management priorities (Avice 2000, Newton et al. 1999).

## History, Populations, and Conservation

A different conservation approach emphasizes historical and current isolation among populations. The study of the phylogenetic content of the mtDNA sequences is particularly valuable to evaluate the evolutionary differentiation and the historical demography within and among populations. This kind of study is useful to identify groups of populations that have been historically isolated and which together comprise the evolutionary diversity of a taxon; these groups allow us to define or delimit geographic regions in which multiple species have populations that are genetically unique (Evolutionary Significant Units, ESUs *sensu* Ryder 1986). Thus, these historically isolated populations are identified as those with phylogenetically distinct clusters of alleles; where multiple species are surveyed across the same sites, such information can be combined to identify areas where patterns of isolation coincide across multiple species (Crandall et al. 2000, Moritz 1994b).

Geographic areas also can be identified within which the populations of a high proportion of a species present in a region have been evolving independently from conspecific populations from other areas (Avice 1992). This allows different conservation priorities to be assigned to different areas, because each one would comprise an evolutionarily different or divergent community (Moritz, J. Cunningham, and Schneider 1997). Information obtained through these kinds of studies, for the design and conservation of natural areas, is important because combining information on the distribution of genetic variation and of species can be useful in prioritizing areas for protection and management. It is also useful in developing more sensitive criteria in the selection of future parks and protected areas (Crandall et al. 2000, Soberón, Rodríguez, and Vázquez-Domínguez 2000). High priority areas can be identified, although they might not have a collection of endemic species as it is usually acknowledged under conventional methods.

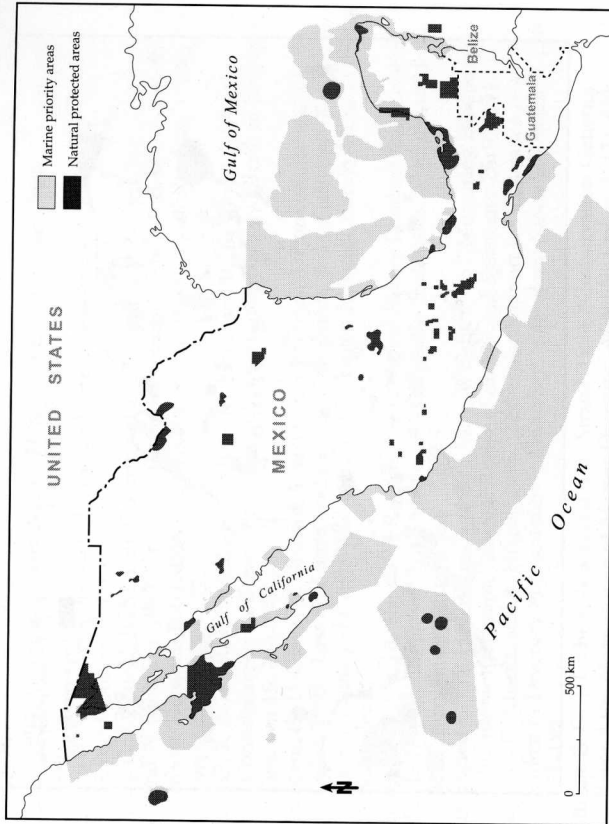
## Potential Applications

1. Endangered or vulnerable single species
  - a) Genetically divergent populations increasingly are being recognized as appropriate units for conservation, regardless of their taxonomic status. The ghost bat (*Macroderma gigas*) of Australia, a vulnerable species, requires warm and humid caves, so it has a naturally, patchy distribution. Genetic studies of four of the contracted populations of this species—as found in suitable caves or abandoned mine shafts—indicate that these represent effectively separate populations. Thus, it is clear that the extirpation of regional breeding populations will not be reversed by natural immigration within a time frame relevant to management. Also, each of the four populations represents a substantial fraction of the species' genetic diversity that should be protected (Moritz et al. 1996).
  - b) Successful translocations of individuals, the most plausible conservation strategy for some endangered species, depend upon precise knowledge of their genetic structure. The hairy-nosed wombat (*Lasiorhinus krefftii*) is one of the most endangered species of mammal in Australia, restricted to a single population of fewer than seventy individuals. For its recovery, the immediate actions are to protect and increase the size of this population through habitat management and future translocations to new sites. Genetic studies have provided fine-scale analysis of mating systems, information used as a guide for the managed movement of individuals and for future design of an appropriate translocation strategy (Moritz et al. 1996).

## 2. Parks and protected areas

- a) An exciting application of phylogeography is to define geographic regions within which multiple species have genetically unique populations or ESUs. This leads us from species to community genetics, testing for congruence of phylogeographic patterns among species, in order to define geographic regions within which a substantial proportion of species has had evolutionary histories separate from their respective conspecifics (Avice 1992, Crandall et al. 2000, Moritz 1994b). The significance of this is that regions with a high proportion of ESUs should be accorded high conservation priority. A study on the distribution of montane endemic bird species in Cameroon and Equatorial Guinea, in which morphologic data was combined with information on phylogeographic structure and endemism, permitted the identification of three biogeographical regions for their conservation and management (Smith et al. 2000).

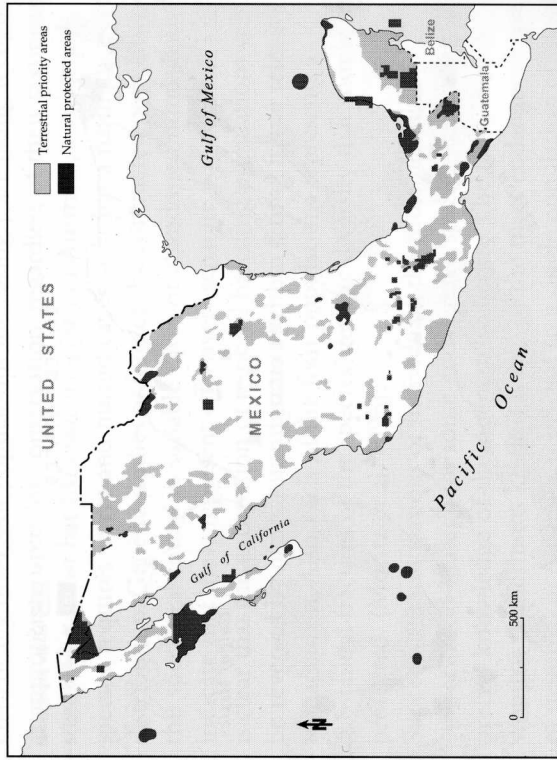
Figure 24.1 Marine priority and natural protected areas



b) Adaptive management of reserves requires information on population size and connectivity, both to assess their current status and to predict outcomes of specific management actions. Molecular phylogenies can provide insights into long-term population trends and patterns of gene flow, to be used as a basis for management of populations (Milligan, Leebens-Mack, and Strand 1994). This information also is valuable for a wide range of applications: such as the design and evaluation of potential or actual biological corridors adjoining natural vegetation fragments; the analysis of complementarity among conservation areas; or the description, on a regional or continental scale, of the geographic distribution of intraspecific biodiversity, which would serve as a basis to direct the conservation of biological diversity (Moritz and Faith 1998, Taberlet 1998).

In Mexico, seventy priority coastal and oceanic areas have been identified, delimited and characterized based either on their high biodiversity, the lack of information regarding biodiversity, or the diversity of their resource uses. This prioritization was done with the

**Figure 24.2 Terrestrial priority and natural protected areas in Mexico**



objective of developing a framework that would contribute to the planning, conservation and sustainable use of marine as well as terrestrial environments in the country (Arriaga et al. 1998; figs. 24.1 and 24.2). Together with more biological and ecological research, these areas will benefit from detailed genetic surveys, especially those where biologically important populations and species exist. Use of the different phylogeographic applications described here, in the design and delimitation of parks and protected areas within these priority marine areas, will allow for protection of the evolutionary diversity within them. Establishment of such areas would be valuable in their own right and could assist with the building of the Baja to Bering Sea Marine Conservation Initiative (see Jessen and Ban, this volume).

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## Retrospectives

# Protected Areas

and the

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