

circumstances in every case will differ, and the particular scientific evidence available will determine whether a population is considered significant. Our DPS policy states that the consideration of significance may include, but is not limited to, the following: (1) Persistence of the discrete population segment in an ecological setting unusual or unique for the taxon; (2) evidence that loss of the discrete population segment would result in a significant gap in the range of the taxon; (3) evidence that the discrete population segment represents the only surviving natural occurrence of a taxon that may be more abundant elsewhere as an introduced population outside its historic range, or (4) evidence that the discrete population segment differs markedly from other populations of the species in its genetic characteristics.

If a population is determined to be both discrete and significant, it can be considered a DPS and its status as an endangered or threatened species then is evaluated, based on the ESA's definitions of those terms and on a review of the factors enumerated in ESA section 4(a). Only then, if the population's status warrants it, would a listing or reclassification be appropriate through the usual rulemaking procedures specified in the ESA.

#### Discreteness

As explained above, if a population meets either of two specified conditions, it may be considered discrete under our DPS policy. One of the conditions is specific to a population delimited by international governmental boundaries across which there are differences in control of exploitation, management of habitat, conservation status, or regulatory mechanisms. Because there was no clear way to delimit the Northern or the Florida Panhandle subpopulations by international boundaries, the Services have decided not to rely on this criterion to establish the discreteness of either of these two subpopulations.

The other condition under which a population can be determined to be discrete is if it is markedly separated from other populations of the same taxon as a consequence of physical, physiological, ecological, or behavioral factors. Quantitative measures of genetic or morphological discontinuity may provide evidence of this separation. With regard to this condition, we examined several lines of evidence to evaluate whether the Northern and Florida Panhandle nesting subpopulations of loggerhead sea turtles are discrete based on the DPS policy criteria. These lines of evidence include

information related to genetics (including maternally inherited mtDNA and biparentally inherited nuclear (nDNA)), physiological and ecological factors, foraging behavior as related to the distribution of loggerheads at areas other than nesting beaches, and morphometrics (measurement of the structure and form of organisms).

Genetic information comes from studies of the maternally inherited mtDNA genome, as well as from nDNA genetic markers (microsatellites) that are biparentally inherited. The results of the mtDNA and nDNA studies differ, as described below.

Non-coding regions of the mtDNA genome serve as maternally-inherited neutral markers that can be used to help evaluate population substructure. The TEWG (2000) concluded that studies of mtDNA support a stock structure of at least five different nesting assemblages of loggerhead sea turtles in the western North Atlantic (as described above), including the Northern and the Florida Panhandle nesting subpopulations that are the subject of the petitioned action. The tendency of females to return to their natal beaches to lay eggs restricts maternal gene flow. Results of mtDNA studies of sea turtles support the hypothesis of natal homing (Encalada *et al.*, 1996; Encalada *et al.*, 1998; Bass, 1999; Dutton *et al.*, 1999). Based on mtDNA analyses, Encalada *et al.* (1998) reported there is evidence of strong mtDNA (maternally inherited) differences between the identified nesting subpopulations, which they considered to be demographically independent.

A subsequent study by Francisco *et al.*, (2000) expanded the sites from which samples were taken for mtDNA analysis, and found the situation to be somewhat more complex. For instance, they reported a tentative conclusion that there is an additional, separate nesting assemblage associated with beaches in Volusia County, Florida which is within the area described as comprising the Northern subpopulation. They also reported that there were no statistically significant differences in the mtDNA analysis for some widely separated populations, including Amelia Island (in the Northern nesting assemblage) and Eglin Air Force Base (in the Florida Panhandle nesting assemblage).

Fine-scale mtDNA analysis from Florida rookeries indicates that separations of nesting assemblages generally begin to appear (from the standpoint of being detected through mtDNA analysis) between nesting beaches separated by more than 100 kilometers (km) (62 miles) of coastline that do not host nesting (Francisco *et al.*,

2000). Consistent with the results obtained from mtDNA analyses, data collected from females tagged on nesting beaches indicate high nesting site fidelity, with nest site relocations of distances greater than 100 km (62 miles) occurring only rarely (CMTTP, unpub. data; LeBuff, 1974, 1990; Ehrhart, 1979; Richardson, 1982; Bjorndal *et al.*, 1983). The typical distance between nest sites used by individual nesting females is 3 miles (5 km) or less (Schroeder *et al.*, in press).

Overall, the mtDNA information is consistent with natal homing, with nesting colonies separated by a few hundred kilometers appearing to represent isolated reproductive aggregates. The Northern subpopulation may be an exception to this pattern, however. Encalada *et al.* (1998) found that loggerheads from various beaches within the range of the Northern subpopulation from Amelia Island, in northeastern Florida, to North Carolina are indistinguishable based on mtDNA. However, they suggested the possibility of differentiation within the Northern nesting assemblage that has not yet been detected, concluding that the lack of mtDNA differentiation may be due to relatively recent colonization that has not allowed sufficient time to accumulate the genetic variation needed to detect any fine-scale population substructure. The subsequent analysis of samples from a larger number of areas and the resulting indication that the vicinity of Volusia County may have a separate nesting assemblage (Francisco *et al.*, 2000) suggests that the subpopulation may be further differentiated or that Volusia County may represent an area of overlap, including nesting females from both the Northern and South Florida subpopulations. With regard to the Florida Panhandle, Encalada *et al.* (1998) found insufficient genetic diversity to further differentiate the stock structure within the subpopulation. Thus, although partitioning within these nesting assemblages may exist, as appears to be indicated by the results of Francisco *et al.* (2000), we are unable to clearly discern it based on available information. Fine-structure analysis will benefit from additional data collection and analyses, and may well reveal that the identified subpopulations can be further divided.

In addition to studies based on maternally inherited mtDNA, other studies have used nuclear (nDNA) genetic markers (microsatellites) to examine fine-scale population structure. Since these nDNA markers are biparentally inherited, information on