CONSERVATION GENETICS OF THE ENDANGERED SAN CLEMENTE LOGGERHEAD SHRIKE
(LANIUS LUDOVICIÀNUS MEARNSI)

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ABSTRACT.- The San Clemente Loggerhead Shrike (Lanius ludovicianus mearnsi) is a critically endangered island endemic, with a current population of fewer than 50 individuals. We describe results from an ongoing population genetic study designed to obtain information relevant to the conservation of this subspecies. We developed non-invasive genotyping methods based on single flank feathers plucked from live birds during routine handling. The genetic markers used were mitochondrial DNA sequences and hypervariable nuclear microsatellite loci. Using a combination of these markers we can show that (i) there is substantial genetic differentiation between the San Clemente Loggerhead Shrike and the two other coastal southern Californian subspecies (L. l. gambeli and L. l. anthonyi), (ii) levels of genetic variation are low in the San Clemente Loggerhead Shrike population, but there is not a high level of inbreeding, (iii) individuals of mainland subspecies L. l. gambeli visit San Clemente Island, but do not stay to breed, and (iv) the current captive population of San Clemente Loggerhead Shrike is a reasonable genetic representation of the wild population. These results demonstrate how genetic studies of avian populations can make significant practical contributions to conservation. The methods and genetic markers developed in this study should be applicable to other shrike species.


The San Clemente Loggerhead Shrike (SCLS), Lanius ludovicianus mearnsi, is endemic to San Clemente Island (SCI), one of the larger (145 km²) Channel Islands which lies 80 km off the coast of southern California. Of the 10 or so subspecies of Loggerhead Shrikes, mearnsi is the most morphologically distinct (Miller 1931). It is known that the SCLS population was abundant in the past, but there is much uncertainty over the actual historical population size; various recent estimates were 150-300 individuals. The population has crashed during this century and by the mid-1980s there were only 5-10 breeding pairs left on the island (Scott and Morrison 1990). The causes of the decline are unknown but are thought to be largely due to habitat destruction by introduced goats and pigs (Sus scrofa), and increased predation at nests by a variety of native and introduced species, including cats (Felis catus), rats (Rattus), Channel Island foxes (Urocyon littoralis) and Common Ravens (Corvus corax). In 1989 a multifaceted recovery program was initiated by the U.S. Navy, which has administered San Clemente Island since the 1930s (for further information on various aspects of the recovery program see papers by Burr et al., Winchell et al., Everett et al. and Harvey et al. in this volume). One component of this program was captive propagation of SCLS for augmentation of the wild population.


In the present study the major objectives were (1) to assess the degree of genetic distinctiveness of the SCLS, (2) to compare the level of genetic variation remaining in SCLS population with that in large and apparently stable conspecific populations on the mainland, (3) to determine the current population structure (or system of mating) and especially whether inbreeding is occurring in the wild population, (4) to identify genetically important individuals and provide data of direct relevance to the captive breeding program, and finally (5) to provide a permanent database for use in future monitoring of the population.

The traditional problem of avian genetic studies...
tissue acquisition has been solved. The recent development of the polymerase chain reaction (PCR) permits genotyping studies to be performed on samples containing minute amounts of DNA, and/or highly degraded DNA. This allowed us to use samples obtained non-invasively (single plucked feathers), which is an important consideration in studies of endangered populations (Woodruff 1993, Morin et al. 1994).

MATERIALS AND METHODS

Feathers were provided by field workers who caught wild birds in Channing or Bal-Chatri traps, and were also obtained from museum specimens. A few whole carcasses were also available from individuals in the captive breeding program that died from natural causes. The following samples have been studied to date (see Fig. 1 for Californian localities): L. I. mearnsi: 60 individuals from SCI; L. I. gambeli: 20 individuals from Perris, southern California mainland and 19 individuals from San Diego, southern California mainland; L. I. anthonyi: 9 individuals from Santa Rosa Island and Santa Cruz Island, northern California Channel Islands; L. i. excubitorides: 9 individuals from Santa Rosa Island and Santa Cruz Island, northern California Channel Islands; L. i. excubitorides: 9 individuals from Saskatchewan province, Canada (about 2500 km NE of other sampling localities). DNA extraction, PCR amplification, and sequencing methods are given in Mundy et al. (1996).

RESULTS AND DISCUSSION

Variation in 400 base pairs of mtDNA sequence was low, and defined four haplotypes (sequence variants or genotypes) in 90 individuals (haplotypes A-D). Despite the low variability, there was strong differentiation between different subspecies. The predominant haplotype in SCLS was haplotype A, the predominant haplotype in L. I. gambeli from the adjacent mainland was haplotype C, and all individuals of L. I. anthonyi from the northern Channel islands were of haplotype B. Variation at seven polymorphic microsatellite loci also revealed strong differentiation between SCLS and L. I. gambeli. Five out of the seven loci showed large length polymorphism frequency differences between the island and each of the two mainland populations. Although no single genetic marker examined is unique to SCLS, the SCLS population is genetically distinct from other Loggerhead Shrike populations examined to date. The genetic evidence thus suggests that the morphological

Fig. 1. The range and sampling localities of the three subspecies of Loggerhead Shrike in coastal southern California (Lanius ludovicianus mearnsi, anthonyi, and gambeli).
Distinctiveness of this island endemic may be at least partly due to a separate evolutionary history, and supports conservation efforts for this population. Two measures of genetic variation were assessed using the microsatellite data: the number of alleles per locus (A) and the expected heterozygosity (H). Both of these measures were lower in SCLS than in the two populations of L. l. gambeli from the adjacent mainland. The number of alleles was lower in SCLS than the mainland populations at six of the seven loci, the most dramatic example being a locus which was monomorphic in SCLS but which was polymorphic with five alleles present in both mainland populations. Expected heterozygosity (as defined in Nei, 1987) in SCLS was around 60% of that in mainland populations when averaged across all loci. The low genetic variation in SCLS can be at least partly attributed to a low effective population size (Ne) throughout this century as a result of the population decline. Continued monitoring of genetic variation in SCLS will permit more accurate estimates of Ne, an important parameter for predicting the population's fate.

Potential evidence for inbreeding in SCLS (genotype frequencies different from panmictic expectations) was found at only one of seven microsatellite loci. Inbreeding between close relatives is a cause for concern in small, isolated populations, as it is known from theory and captive studies that inbreeding in species in which outbreeding is the norm can be detrimental (Ralls et al. 1988, Templeton and Read 1994). A combination of mtDNA and microsatellite data strongly suggest that some birds caught on San Clemente Island are in fact individuals of mainland L. l. gambeli that are temporary island visitors. Out of six birds caught on SCI which had the predominant mitochondrial haplotype of the mainland (haplotype C), three were trapped in winter in the northern half of the island, where no shrikes have bred in the last decade, and these were the only shrikes trapped in these areas; these birds were banded and were not sighted during the subsequent breeding season. Microsatellite analysis on four of the six birds revealed that each bird contained several alleles that were not present in the remainder of the population on SCI, but were present in mainland populations. These birds are probably temporary visitors from the mainland that do not stay to breed; they include one bird caught as a fledgling in July. The ability to detect temporary immigrants genetically is useful for the captive breeding program. Wild birds brought into the captive breeding program in 1995 were genotyped to verify that they were part of the resident population of SCLS. Microsatellite genotyping of individuals in the captive breeding program shows that the current captive population retains 12 of 14 alleles that are present in the wild population of SCLS and so should contain most of the genetic variation present in the wild population. Future assaying of the genetic variation of captive birds would be useful to monitor the extent of genetic drift in the captive population, and such information could be used to determine when it may be useful to bring in new birds from the wild population to counter its effects.

Further potential applications of these methods include (1) the use of microsatellites for paternity analysis in wild birds to establish fitness correlates of territory attributes, age, etc., and (2) the examination of about 20 old museum specimens collected early this century to try to determine the level of genetic variation before the population crash occurred.

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LITERATURE CITED


