

No evidence of genetic variation in microsatellite and mitochondrial DNA markers among remaining populations of the Strange-tailed Tyrant *Alectrurus risora*, an endangered grassland species

ADRIAN S. DI GIACOMO, ALEJANDRO G. DI GIACOMO, RAFI KLIGER,
JUAN C. REBOREDA, RALPH TIEDEMANN and BETTINA MAHLER

Summary

The Strange-tailed Tyrant *Alectrurus risora* (Aves: Tyrannidae) is an endemic species of southern South American grasslands that suffered a 90% reduction of its original distribution due to habitat transformation. This has led the species to be classified as globally Vulnerable. By the beginning of the last century, populations were partially migratory and moved south during the breeding season. Currently, the main breeding population inhabits the Iberá wetlands in the province of Corrientes, north-east Argentina, where it is resident all year round. There are two remaining small populations in the province of Formosa, north-east Argentina, and in southern Paraguay, which are separated from the main population by the Parana-Paraguay River and its continuous riverine forest habitat. The populations of Corrientes and Formosa are separated by 300 km and the grasslands between populations are non-continuous due to habitat transformation. We used mtDNA sequences and eight microsatellite loci to test if there were evidences of genetic isolation between Argentinean populations. We found no evidence of genetic structure between populations ($\Phi_{ST} = 0.004$, $P = 0.32$; $F_{ST} = 0.01$, $P = 0.06$), which can be explained by either retained ancestral polymorphism or by dispersal between populations. We found no evidence for a recent demographic bottleneck in nuclear loci. Our results indicate that these populations could be managed as a single conservation unit on a regional scale. Conservation actions should be focused on preserving the remaining network of areas with natural grasslands to guarantee reproduction, dispersal and prevent further decline of populations.

Resumen

El Yetapa de Collar *Alectrurus risora* (Aves: Tyrannidae) es una especie endémica del cono sur de Sudamérica que ha sufrido una reducción del 90% de su distribución geográfica histórica debido a la transformación del hábitat. Esto condujo a que la especie sea clasificada como vulnerable a nivel global. A principios del siglo pasado, las poblaciones eran parcialmente migratorias migrando al sur durante la temporada reproductiva. Actualmente la principal población reproductiva habita en los Esteros del Iberá en la provincia de Corrientes, en el noreste de Argentina, donde es residente durante todo el año. Existen otras dos pequeñas poblaciones restantes en la provincia de Formosa, en el noreste de Argentina, y en el sur del Paraguay, que están separadas de la población principal por el río Paraná-Paraguay y los hábitats de selva ribereña continua. Las poblaciones de Corrientes y Formosa están separadas por 300 km y los pastizales entre ambas poblaciones no son continuos

debido a la fragmentación por los cambios recientes en el uso de la tierra. El objetivo de este trabajo fue estudiar la estructura genética entre ambas poblaciones utilizando secuencias de ADN mitocondrial y ocho microsatélites, con el fin de inferir patrones de aislamiento. No se encontraron evidencias de estructura genética entre las poblaciones de Argentina ($\Phi_{ST} = 0.004$, $P = 0.32$; $F_{ST} = 0.01$, $P = 0.06$), lo que puede explicarse ya sea por la retención de un polimorfismo ancestral o por la dispersión actual de los individuos entre ambas poblaciones. Tampoco se encontraron evidencias de un cuello de botella demográfico reciente. Estas poblaciones podrían ser manejadas como una única unidad de manejo a escala regional y las acciones de conservación deberían enfocarse en la conservación de una red de áreas con pastizales naturales que garanticen la reproducción, la dispersión y eviten así la disminución de las poblaciones actuales de la especie.

Introduction

Loss of suitable habitat and the subsequent fragmentation of populations are recognised as the major threat affecting birds (Owens and Bennett 2000, Fischer and Lindenmayer 2007, Hoffman et al. 2010, Rands et al. 2010). Among the variety of biological processes negatively affected by habitat fragmentation, one of the most important is the geographic structure of genetic diversity and the reduction in gene flow among populations (Höglund 2009, Frankham et al. 2010). Also, the small population sizes in remaining fragments may cause increased levels of inbreeding and a stronger effect of random genetic drift (Wade 2001). Both processes result in a loss of genetic variability within populations, which generally causes a reduction in individual fitness and population adaptability and ultimately may lead to local and global extinction (Gilpin and Soulé 1986, Hedrick and Kalinowski 2000, Höglund 2009).

Loss of gene flow because of reduced dispersal, and reduction in genetic diversity because of genetic drift, can re-distribute genetic variability among spatially structured populations over the course of only few generations (Harrison and Hastings 1996, Caizergues et al. 2003). Patterns of genetic variation can provide insights into dispersal patterns and population connectivity on scales that direct field measures of dispersal are unable to address (Koenig et al. 1996). Thus, genetic information, including data on population genetic structure, has become relevant in species conservation (Frankham 2010, Haig et al. 2011). Ryder (1986) introduced the concept of evolutionarily significant units (ESU) to account for genetic diversity below recognised taxonomic levels. Although ESU definitions might differ (Moritz 1994, Crandall et al. 2000, Kizirian and Donnelly 2004, Degner et al. 2007), genetic data always play a critical role for identifying evolutionary units for conservation purposes (for a review see Palsbøll et al. 2006). The protection of genetically distinct populations helps to maintain high levels of biodiversity minimising extinction risks (Waples 1991).

The Strange-tailed Tyrant *Alectrurus risora* belongs to the group of Tyrant flycatchers (Aves: Tyrannidae), which are endemic of the New World. Thirteen percent of the 429 species of this group (Fitzpatrick 2004) are threatened (10 'Endangered' and 19 'Vulnerable' species) or 'Near Threatened' (27 species) at global level (Birdlife International 2013a). Most of the tyrant flycatchers are typical forest inhabitants (Fitzpatrick 1980, 2004), although some of them have diversified towards open habitats occupying grasslands, steppes and wetlands along the Andes, Patagonia and Pampas in western and southern South America (Ohlson et al. 2008). Populations of endemic Neotropical grassland birds, including tyrant flycatchers, have declined dramatically over recent decades in these habitats where they now exist mostly in isolated fragments scattered in an agricultural matrix (BirdLife International 2008, Azpiroz et al. 2012).

The Strange-tailed Tyrant has suffered a large contraction reaching a 90% loss of its original range. This was associated with the conversion of natural grasslands to agriculture during the last century (Di Giacomo and Di Giacomo 2004). At present, it is classified as a globally 'Vulnerable' species (IUCN 2013) and further decline in range and number is expected because suitable

habitats are subject to extensive agricultural modification, intensification of livestock farming and afforestation (Collar *et al.* 1992, BirdLife International 2013b). Range contraction was accompanied by a change in migration behavior. While one century ago the species was partially migratory and reproduction also occurred in Central Argentina, at present all populations are resident and breed in grasslands of Northern Argentina and Paraguay (Di Giacomo and Di Giacomo 2004, Di Giacomo *et al.* 2011a). The current main breeding population inhabits Iberá wetlands in the province of Corrientes, north-east Argentina, while other small populations occur in the province of Formosa, north-east Argentina, and in southern Paraguay (Birdlife International 2013b; Figure 1). The Parana-Paraguay River and its continuous riverine forest habitat historically separate these small populations from the main one. With regard the Argentinean populations, they are separated by 300 km and the grasslands between them are non-continuous due to fragmentation by changes in land use. However, a comprehensive study that has been carried out on the Formosa population for the last 10 years showed that banded fledglings are rarely seen in the population in the following years, suggesting that young individuals might disperse from their natal area (Di Giacomo *et al.* 2011b).

The aim of this study was to analyse the genetic variability and the genetic structure of the main population and one isolated Argentinean population of the Strange-tailed Tyrant, using both mtDNA and microsatellite molecular markers. These markers differ in mutation rates and mode of inheritance and provide essential information about population history and demographics (Wayne and Morin 2004). Current conservation and management efforts are focused on preserving

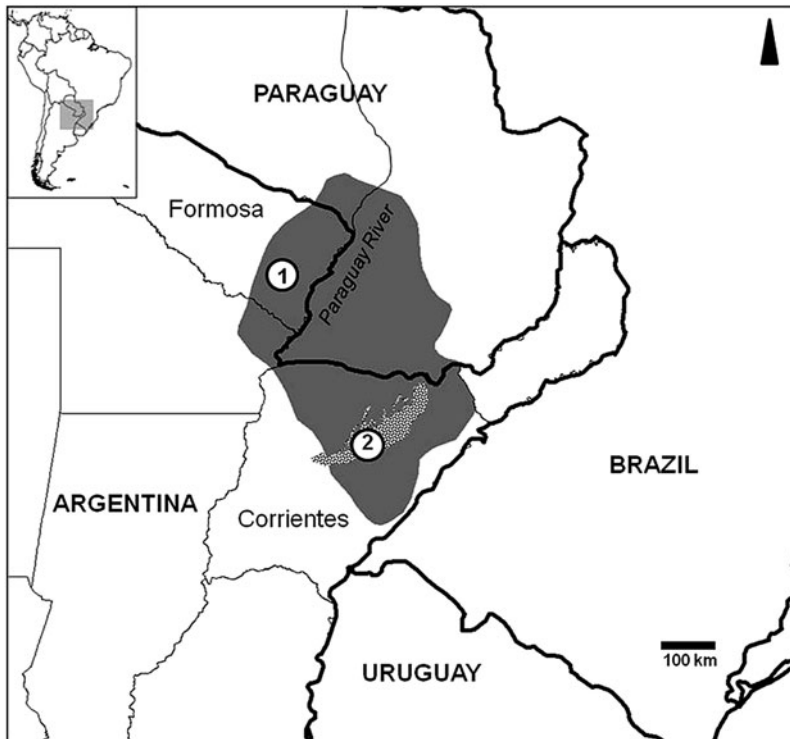


Figure 1. Map showing the present distribution of the Strange-tailed Tyrant (grey area) from Di Giacomo *et al.* (2011a). Numbers indicate the location of the two populations included in this study: 1) 'Reserva Ecológica El Bagual', Formosa Province, and 2) 'Reserva Natural del Iberá', Corrientes Province.

a high degree of biodiversity (Allendorf and Luikart 2007), which can be evaluated through ecological and/or genetic means (Schwartz *et al.* 2006, Pertoldi *et al.* 2007). Therefore, to determine how intraspecific genetic diversity is geographically partitioned in natural populations may help to identify which populations are genetically depleted or fragmented (Storfer 1999, Allendorf *et al.* 2008) and to identify the presence of evolutionarily significant units.

Materials and methods

Study site and sample collection

We mist-netted individuals between 2004 and 2011 during the reproductive (September–January) and non-reproductive (February–August) seasons at 'Reserva Ecológica El Bagual', Formosa Province, (26°10'S; 58°56'W), and 'Reserva Natural del Iberá', Corrientes Province (28°36'S; 57°49'W), Argentina (Figure 1). These populations are approximately 300 km apart. Before release, we took a small amount (15–30 µL) of blood through brachial vein puncture with a 31G needle. Blood was collected with an 80 µL heparinized capillary tube, immediately added to 0.5 mL of lysis buffer (100mM Tris pH 8, 10mM NaCl, 100mM EDTA, 2% SDS), and stored at room temperature until analysis. In total, we captured 68 adult individuals: 46 in Formosa and 22 in Corrientes.

Genetic analysis

We extracted DNA from blood samples with QIAGEN (Hilden, Germany) extraction kit and amplified a 700 bp fragment of mtDNA cytochrome *b* gene using the following primers: H15767 (Edwards *et al.* 1991) and Aris (ATGAAGGGATGTTCTACTGGTTG). We performed PCR amplifications in 10 µL reaction volumes using 50–100 ng DNA, 0.5 µM forward and reverse primers, 0.25 mM dNTPs, 2.5 mM MgCl₂, and 0.25 units Taq-Polymerase (Invitrogen), with annealing temperatures set at 56°C for 30 cycles. We amplified products on an Applied Biosystems Model 3130xl Genetic Analyzer using ABI Big Dye™ Terminator Chemistry.

For microsatellite loci, we performed PCR amplifications in 25 µL reaction volumes using 10–80 ng of DNA template, 136 nM forward and reverse primers, 0.2 mM dNTPs, 1.5 mM MgCl₂ and 0.5 units Taq-Polymerase (Q-BIOgene Taq Core Kit 10). We used 8 published primer pairs that have been successfully tested in our study species (Mahler *et al.* 2013). Although the number of polymorphic loci included in the analyses is moderate, previous studies have shown that diversity indices and the presence of a bottleneck can be confidently studied with this number of markers for a sample size like ours (Spencer *et al.* 2000, Pruett and Winker 2008). We used multiplex PCR reactions with fluorescent-labelled forward primers (fluorescent dyes were 6-FAM, VIC, NED, and PET) and non-labelled reverse primers. Reactions were cycled: 5 min at 94°C, then 30 s at 94°C, 60 s at the annealing temperature + 3°C, 45 s at 72°C, 3 times, then 30 s at 94°C, 60 s at the annealing temperature, 45 s at 72°C, 37 times, and finally 10 min at 72°C. Annealing temperatures for each pair of primers are detailed in Mahler *et al.* (2013).

Statistical analysis

We edited cytochrome *b* sequences with the software BioEdit v7.0 (Hall 1999), performed the alignment with CLUSTAL W (Thompson *et al.* 1994), and determined the number of haplotypes and their frequencies. We constructed a haplotype network using the Median-joining algorithm as implemented in Network v4.6.1.0 (Bandelt *et al.* 1999). Networks are better suited to depict intraspecific phylogenies than are tree algorithms because they allow for the coexistence of ancestral and descendant alleles in a sample, whereas trees treat all sequences as terminal taxa (Posada and Crandall 2001). We used Arlequin v3.11 (Excoffier *et al.* 2005) to calculate genetic diversity indices.

We analysed polymorphic loci with GeneMapper v3.7 (Applied Biosystems). We used MicroChecker v2.2.3 (Van Oosterhout *et al.* 2004) to assess the quality of polymorphic loci scoring, calculated observed and expected heterozygosity and allelic richness with GenALEx v6 (Peakall and Smouse 2006), and tested for Hardy–Weinberg disequilibrium and for departures from linkage equilibrium using a Markov chain method with Genepop v4.0 (Raymond and Rousset 1995a, Rousset 2008). We tested for differences in genetic variability parameters between populations with a Mann–Whitney test. We used the software Bottleneck v1.2.02 (Cornuet and Luikart 1997) to detect recent effective population size reductions as a consequence of habitat contraction. For this analysis we used 1,000 iterations and the infinite alleles model.

We analysed genetic structure between populations using Arlequin v3.11 and used AMOVA (Excoffier *et al.* 1992) and the Exact Test of Population Differentiation (Raymond and Rousset 1995b) to calculate Φ_{ST} analogous of Wright’s (1965) *F* statistics for mtDNA and F_{ST} for microsatellites. Significance levels were determined using permutation procedures as implemented in Arlequin. For microsatellites we also evaluated population structure using Bayesian cluster analysis with STRUCTURE 2.1 (Pritchard *et al.* 2000). We carried out Markov chain Monte Carlo simulations without prior information on the admixture model and using correlated allele frequencies. We assumed that the maximum number of populations (*K*) varied between one and four. We set the number of steps for burn in and simulations to 50,000 and 100,000, respectively, and performed three replications for each *K*.

Results

Mitochondrial DNA

We sequenced the cytochrome *b* fragment for 58 adult individuals, 42 belonging to the Formosa population and 16 to the Corrientes population. The remaining 10 individuals could not be sequenced due to amplification problems or poor chromatogram quality. The amplified fragment contained 12 variable sites that yielded 11 different haplotypes (Table 1). Haplotype sequences have been deposited in the EMBL, GenBank, under accession numbers KJ002490–KJ002500. One haplotype (H1) was very frequent, while the others were found at low frequencies and in most cases in only one individual (Table 1). The haplotype network showed a star-like fashion, with H1 occupying the central position and the remaining haplotypes diverging in only one site, except for H9 and H11 (Figure 2). Three haplotypes (H1, H5 and H6) were found in both populations, while the remaining were found in only one population (Figure 2). Haplotype number was similar for both populations (*n* = 7), but haplotype diversity was higher for the Corrientes population (*H* = 0.69 vs. *H* = 0.38).

Table 1. Variable sites and frequencies (with number of individuals) for eleven haplotypes (H1 – H11) determined for the 700 bp cytochrome *b* fragment sequenced for 58 Strange-tailed Tyrants.

	9	19	111	115	243	423	447	483	570	585	624	667	Frequency % (n)
H1	G	G	T	C	C	T	C	A	G	A	T	C	72.41 (42)
H2	-	-	-	-	-	-	-	-	-	-	C	-	1.72 (1)
H3	-	-	-	T	-	-	-	-	-	-	-	-	1.72 (1)
H4	-	-	-	-	-	-	-	-	-	C	-	-	1.72 (1)
H5	A	-	-	-	-	-	-	-	-	-	-	-	5.17 (3)
H6	-	-	-	-	-	-	-	G	-	-	-	-	5.17 (3)
H7	-	-	-	-	-	-	T	-	-	-	-	-	1.72 (1)
H8	-	-	-	-	T	-	-	-	-	-	-	-	5.17 (3)
H9	-	-	-	-	-	C	-	-	A	-	C	-	1.72 (1)
H10	-	A	-	-	-	-	-	-	-	-	-	-	1.72 (1)
H11	-	-	C	-	-	-	-	-	-	-	-	G	1.72 (1)

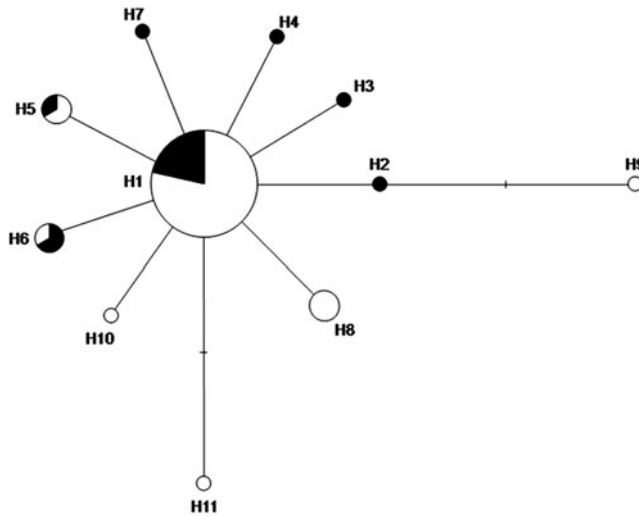


Figure 2. Network for eleven haplotypes belonging to a 700-bp fragment of the cytochrome *b* gene sequenced for 58 Strange-tailed Tyrants. The size of the circle represents haplotype frequency; colour distribution within the circle corresponds to the proportion of individuals carrying that haplotype found in each population (white: Formosa; black: Corrientes). Each segment represents one variable site.

AMOVA results showed that less than 1% of the variation is explained among populations and that there is no haplotype frequency difference between them ($\Phi_{ST} = 0.004$, $P = 0.32$). The exact test showed similar results ($P = 0.06$).

Microsatellites

We genotyped 68 individuals, 46 belonging to Formosa and 22 to Corrientes populations. Seven polymorphic loci were in Hardy–Weinberg equilibrium (Table 2), while one locus (SAP94) was significantly heterozygote deficient and not in Hardy–Weinberg equilibrium ($P < 0.001$). MicroChecker results and preliminary data on family groups indicate that locus SAP94 might have a high proportion of null alleles and was consequently eliminated from posterior analyses. Expected (Mann-Whitney $Z = 0.18$, $P = 0.85$) and observed (Mann-Whitney $Z = 0.23$, $P = 0.81$) heterozygosity, as well as allelic richness (Mann-Whitney $Z = 0.57$,

Table 2. Genetic diversity measured as number of alleles (A), expected heterozygosity (H_E), observed heterozygosity (H_O) and deviation from Hardy-Weinberg proportion (P_{HW}) for eight loci studied for two Strange-tailed Tyrant populations: Formosa ($n = 46$) and Corrientes ($n = 22$).

	Formosa				Corrientes			
	A	H_E	H_O	P_{HW}	A	H_E	H_O	P_{HW}
EMIZ1	3	0.362	0.435	0.422	3	0.241	0.273	0.908
SAP94	3	0.397	0.109	0.000	3	0.397	0.109	0.000
EMIZ27	6	0.553	0.457	0.043	6	0.645	0.682	0.780
SAP66	2	0.502	0.565	0.559	2	0.449	0.318	0.171
EMID46	3	0.200	0.217	1.000	2	0.210	0.238	0.536
SAP39	6	0.462	0.457	0.622	5	0.353	0.318	0.883
SAP108	2	0.436	0.413	0.742	2	0.496	0.636	0.184
SAP156	6	0.431	0.435	0.898	5	0.353	0.318	0.883

$P = 0.56$), did not differ between populations. Pairwise tests for linkage between the seven polymorphic loci revealed significant genotypic linkage disequilibrium between one set of paired loci (SAP₃₉-SAP₁₅₆).

AMOVA results showed that the percentage of variation explained among populations was 1.45 % and that population differentiation was not significant ($F_{ST} = 0.01$, $P = 0.06$). We found similar results with the exact test ($P = 0.19$). We did not find evidence for a recent demographic bottleneck in nuclear loci (Sign test: Formosa population, $P = 0.47$; Iberá population, $P = 0.56$; Global population, $P = 0.47$). Results did not change when excluding one of the paired loci (SAP₃₉ or SAP₁₅₆).

Bayesian clustering analysis showed the lowest likelihood for a population structure of $K = 2$ and the highest likelihood for a population structure of $K = 3$ (Table 3). The assignment of individuals to populations with $K = 3$ was not associated with sampling locations (Figure 3).

Discussion

Strange-tailed Tyrants, together with other species such as the Saffron-cowled Blackbird *Xanthopsar flavus*, Black-and-White Monjita *Xolmis dominicanus* and Pampas Meadowlark *Sturnella defilippii*, are good examples of threatened species inhabiting South American grasslands that have suffered a sharp decline in their populations during the last century due to extensive changes in land use (see Azpiroz *et al.* 2012). Historically, these species were widespread throughout southern South American grasslands but they have experienced local extinctions and fragmentation of their populations, which at present are small and isolated.

The effect of grassland fragmentation on genetic diversity in southern South America has been previously documented only for flightless Greater Rheas *Rhea americana* (Bouzart 2001). Our paper represents the first study on the genetic diversity of a globally threatened grassland passerine with documented extinctions at broad scale that could affect the maintenance of its adaptive evolutionary potential (Frankham *et al.* 2010).

The loss of natural grasslands has been very pronounced during the last century in southern South America (Azpiroz *et al.* 2012) and approximately 90% of the Strange-tailed Tyrant's habitat has disappeared (Di Giacomo and Di Giacomo 2004). The Strange-tailed Tyrant is currently confined to several areas or patches of natural grasslands containing a few resident populations in Argentina and Paraguay and total population size is estimated in 6,000–15,000 mature individuals (Birdlife International 2013b). Our genetic analysis of the main populations of the species in Argentina showed an absence of genetic differentiation between them and no evidence of a recent demographic bottleneck. These findings are not biased by a smaller sample size of the larger Iberá wetlands population, since sample size adjusts the minimum number necessary to represent population variability (Hale *et al.* 2012). The star-like pattern of the haplotype network might indicate a recent expansion of the species in evolutionary time (Bandelt *et al.* 1995) as has been recently reported for other grassland birds of southern South America (Campagna *et al.* 2012).

The lack of genetic structure between our study populations could be explained by the short time elapsed since these populations became isolated or by movements of individuals among populations. Genetic similarity might reflect retained ancestral polymorphism in both populations,

Table 3. Mean maximum likelihood values (\pm standard deviation) calculated with the software Structure 2.1 for different K .

K	Mean likelihood \pm SD
1	-742.8 \pm 0.26
2	-758.7 \pm 19.2
3	-727.2 \pm 10.0
4	-748.4 \pm 16.7

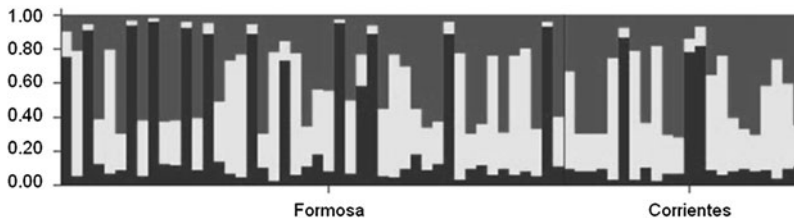


Figure 3. Bar plot of population assignment probabilities of individuals of Strange-tailed Tyrants for $K = 3$ estimated by STRUCTURE. Each individual is represented by a single vertical line divided into the three (light gray, dark gray and black) inferred clusters.

indicating that a bottlenecked population is absent or genetic processes acting on it are less pronounced than expected. The analysis of skin samples would allow analysing historical genetic variability and compare it to present-day samples. Museum skins include the larger part of the area of ancestral distribution (see Di Giacomo and Di Giacomo 2004 for historical records) thus representing geographical variability of the species' historical presence.

The time necessary to detect the genetic consequences of recent processes of fragmentation and loss of habitat in endangered birds can be of only a few generations. For example, a study of Cerrado dry forest fragmentation and its association with the genetic structure of Pfrimer's Parakeet *Pyrrhura pfrimeri* populations suggested a 35-year lag between deforestation and its effect on genetic structure (Miller et al. 2013). On the other hand, the species' ability to disperse might account for the genetic pattern. For example, populations of the Florida Grasshopper Sparrow *Ammodramus savannarum floridanus*, a threatened grassland passerine of North America that has suffered significant population decline due to habitat destruction and fragmentation during the last century, showed limited genetic structure, likely as a result of dispersal among populations (Mylecraine et al. 2008). On the contrary, the Sierra Madre Sparrow *Xenospiza baileyi*, another threatened grassland bird with current fragmented populations due to habitat loss in Mexico, showed significant genetic differentiation suggesting the species' inability to cross areas of unsuitable habitat (Oliveras de Ita et al. 2012).

The ability of the Strange-tailed Tyrant to fly long distances due to its historical migratory behavior is an indicator of its capacity to disperse among reproductive populations and thus generate gene flow between them. The lack of observation of fledglings in posterior breeding seasons, as well as the replacement of males, supports the idea of dispersal. Bayesian clustering confirmed the lack of genetic structure between both geographically distant populations, and showed the highest probability of individuals belonging to three populations. Assignment of individuals to these panmictic units was not associated to current geographical distribution; moreover, both areas showed a similar composition of individuals, i.e. individuals assigned to the three clusters (Figure 3). One possible explanation for this pattern is that individuals are assigned with higher probability to their source population corresponding to reproductive areas, of which the Paraguayan population would represent the third cluster.

Alternatively, assignment to three populations might reflect ancestral reproductive behavior. If individuals were phylopatric for reproductive areas, each of these three groups might be reflecting different areas to which individuals migrated during the reproductive season. Transformation of grasslands in the Southern and Northern part of the distribution of the species has led this species to change from migratory to resident approximately 50 years ago (Di Giacomo and Di Giacomo 2004). Thus, current populations are not migratory and remain only in areas where they were resident all year round in the past or were also occupied by wintering individuals from southward breeding populations. Consequently, individuals of the studied populations might be assigned with higher probability to ancestral reproductive areas and more generations have to go past to cause genetic homogenization.

Further studies conducted on museum skins and the Paraguayan population of Strange-tailed Tyrants may help to better understand how habitat fragmentation and recent changes in migratory behavior in this species are imprinted on the genetic pattern observed within and between populations.

Conservation implications

Populations that are genetically distinct may require separate management (*sensu* Moritz 1994), whereas source populations for reintroduction or translocation projects should be as genetically similar as possible to the historical population in an area (IUCN/SSC 2013). In absence of genetic differentiation, the populations of Strange-tailed Tyrants could be managed as a single management unit at a regional scale rather than as two separated management units. Fortunately, both populations are within protected natural reserves, where the number of individuals has not declined during the last 20 years (Di Giacomo 2005, Di Giacomo *et al.* 2011a). However, because of the transformation of natural grasslands to agriculture, conservation actions for this species should be first directed to the protection of breeding sites to provide a network of natural grassland areas that ensure the recruitment and further dispersal of individuals. Finally, considering that population increase and the dispersal of young individuals might allow the establishment of new reproductive populations that may even be founded through artificial translocation of individuals from other populations, the conservation of further areas with natural grasslands should be encouraged.

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ADRIAN S. DI GIACOMO, RAFI KLIGER, JUAN C. REBORDA, BETTINA MAHLER*
 Departamento de Ecología, Genética y Evolución, Facultad de Ciencias Exactas y Naturales,
 Universidad de Buenos Aires, Pabellón II Ciudad Universitaria, C1428EGA Buenos Aires,
 Argentina.

ALEJANDRO G. DI GIACOMO
 Departamento de Conservación, Aves Argentinas/Asociación Ornitológica del Plata, Matheu
 1246, C1249AAB, Buenos Aires, Argentina.

RALPH TIEDEMANN
 Unit of Evolutionary Biology/Systematic Zoology, Institute of Biochemistry and Biology,
 University of Potsdam, Potsdam-Golm, Germany.

* Author for correspondence; e-mail: bemahler@ege.fcen.uba.ar