

## LINKING LANDSCAPE DATA WITH POPULATION VIABILITY ANALYSIS FOR EVALUATING TRANSLOCATION AS A CONSERVATION STRATEGY FOR GREATER RHEA (*RHEA AMERICANA*) IN CENTRAL ARGENTINA

Gisela Bazzano<sup>1,2</sup>, Paola F. Giordano<sup>†</sup>, Joaquín L. Navarro<sup>1</sup>, & Mónica B. Martella<sup>1</sup>

<sup>1</sup>Instituto de Diversidad y Ecología Animal (IDEA-CONICET-UNC) and Centro de Zoología Aplicada (CZA), Universidad Nacional de Córdoba, Vélez Sarsfield 299, CP (5000) Córdoba, Argentina.

<sup>2</sup>Current address: Cátedra de Ecología, Facultad de Ciencias Exactas, Físicas y Naturales, Universidad Nacional de Córdoba, Vélez Sarsfield 299, CP (5000) Córdoba, Argentina.  
*E-mail:* gbazzano@efn.uncor.edu

**Resumen.** – Relacionando datos de paisaje a un análisis de viabilidad poblacional para evaluar la translocación como estrategia de conservación para el ñandú (*Rhea americana*) en el centro de Argentina. – Desarrollamos un análisis de viabilidad poblacional (PVA) para ñandúes silvestres (*Rhea americana*) en el centro de Argentina, relacionando datos poblacionales a un modelo metapoblacional no estructurado, con el fin de evaluar la efectividad de la translocación de ñandúes como una herramienta de manejo en paisajes agrícolas. Simulamos la expansión del área cultivada por un periodo de 10 años y bajo dos escenarios de simulación, con translocación de individuos (movimiento artificial de individuos entre poblaciones) y sin translocación. Registramos: la abundancia de ñandúes, el número de poblaciones en el tiempo, el tamaño mínimo poblacional y la probabilidad de que la población caiga por debajo del umbral de 30 individuos. Comparamos los resultados con datos colectados a campo en la misma área de estudio. Al final del periodo de simulación, el hábitat apropiado para los ñandúes se fragmentó y redujo en un 84%. Observamos una disminución en el tamaño poblacional en ambos escenarios; sin embargo, la probabilidad de extinción fue un 85% más alta en el modelo sin translocación de individuos. Este resultado fue respaldado por la abundancia de ñandúes registrada a campo, la cual se acercó más a la predicha por el modelo con translocación, que a la correspondiente sin translocación. En consecuencia, la translocación podría ser usada como una eficiente herramienta de conservación para esta especie.

**Abstract.** – We developed a population viability analysis (PVA) for wild Greater Rheas (*Rhea americana*) in central Argentina, linking spatial data to a non-structured metapopulation model, to evaluate the effectiveness of rhea translocations as a conservation management tool in agricultural landscapes. We simulated the expansion of the agricultural area for a 10-year period and recorded abundance, number of populations over time, expected minimum population size and the likelihood of the metapopulation to fall below the threshold of 30 individuals, under two simulation scenarios: “with translocation” (artificial movement of individuals between populations) and “without translocation.” We compared the results with field population data collected from the same study area. At the end of the simulation period, the habitat suitable for Greater Rheas was fragmented and reduced by 84%. We observed a decrease in population size in both scenarios, but the extinction probability was 85% higher in the “without translocation” model. This result was supported by the observed abundance of Rheas in the field, which was closer to

values predicted in the “with translocation” than those in the “without translocation” scenarios. Therefore, translocation might be used as an efficient conservation tool for this species. Accepted 30 April 2014.

**Key words:** Greater Rhea, *Rhea americana*, agro-ecosystem, conservation, populations, population viability analysis model, translocation.

## INTRODUCTION

The Greater Rhea (*Rhea americana*) is a bird species endemic to South America that inhabits mainly grassland ecosystems, one of the most human-modified and least protected biomes in the world (Bilenco & Miñarro 2004, Demaría *et al.* 2008). In Argentina, the original landscape structure of the pampas grasslands has undergone rapid changes due to intensified and specialized agricultural practices (Díaz-Zorita *et al.* 2002). These processes have been accelerated in the 2000s due to an increase in grain production (mainly soybean) at the expense of traditional cattle grazing, leading to the reduction and fragmentation of natural and implanted grasslands (Baldi *et al.* 2006).

Wild Greater Rhea populations have drastically declined in many areas of their historical geographic distribution, mainly due to habitat loss, illegal hunting and excessive egg harvesting (Martella & Navarro 2006). Consequently, the species has been categorized as near-threatened by the International Union for Conservation of Nature (IUCN 2014), which indicates that wild populations may face a high risk of extinction in the near future.

At present, most of the wild Greater Rhea populations inhabit agricultural landscapes. Recent studies have shown that although the suitable habitat for the species has been reduced and fragmented, their populations occur at low densities (Bazzano 2010, Giordano *et al.* 2010). Probably these populations persist because of dispersal of individuals among them, leading to the maintenance of

metapopulation dynamics (Giordano *et al.* 2010).

Population viability analysis (PVA), which relate demographic parameters to habitat quality, are a useful tool to predict the future of a population, particularly when it is assumed that habitat quality will change over time (Larson *et al.* 2004, Bonnot *et al.* 2013). PVA models provide a measure of the risk or the probability that a population may achieve a given threshold (e.g., extinction threshold) in the future and under certain conditions (Beissinger & Westphal 1998, Morris & Doak 2002), which can be useful to compare different management scenarios (Brook *et al.* 2000, Morris & Doak 2002, Dalerum *et al.* 2008, Unger *et al.* 2013).

Among management alternatives for restoration and conservation of threatened animal species, translocation could be considered (Fischer & Lindenmayer 2000). Translocation, defined as the “human-mediated movement of living organisms from one area, with release in another” by the IUCN (2013), can be used to increase the range of a species, augment the numbers in a critical population, or establish new populations and hence avoid the risk of extinction through local catastrophes (Rout *et al.* 2007). Preliminary studies involving translocation of Greater Rheas with the aim of restoring wild populations have been conducted in the last years, and results obtained so far are optimistic (Bellis *et al.* 2004a, Navarro & Martella 2008).

Given the vulnerable situation of wild Greater Rheas in agro-ecosystems of central Argentina and the persistent agricultural

expansion in the region, there is an urgent need to identify possible tendencies of these populations and to evaluate the effectiveness of rhea translocations as a management strategy for the conservation of this species in agricultural landscapes. Here we analyzed wild Greater Rhea population viability by linking spatial data directly to a non-structured meta-population model and compared the results with field data of the species collected from the same study area.

## MATERIALS AND METHODS

**Study area.** We conducted the study in an agro-ecosystem (ca. 4006 km<sup>2</sup>) located in southwestern Córdoba province (33°24'59.92"S; 65°5'0.67"W), the subregion known as Inland Pampa, in the Argentine pampas region (Fig. 1). The climate is temperate, with a mean temperature of 33°C in summer and 1.6°C in winter (Gorgas & Tassile 2002), and average annual rainfall of approximately 900 mm (Díaz-Zorita *et al.* 2002). The area is characterized by flat to gently rolling dunes. The vegetation, originally composed of grasslands and forests, is currently dominated by crops (*Zea mays*, *Triticum aestivum*, *Glycine max*, and *Arachis hypogaea*) and pastures (*Medicago sativa*, *Eragrostis* sp., *Agropyron* sp., and *Bromus* sp.) (Díaz-Zorita *et al.* 2002).

**PVA model.** We simulated agricultural expansion as a 3.78% annual rate of increase of area covered by crops (Bilanca & Miñarro 2004, INDEC 2004), for a 10-year period (2004–2014) on the basis of a large-scale spatially explicit model developed for Greater Rhea in the same agro-ecosystem (Giordano *et al.* 2010). This model generated the map of suitable habitat patch structure for Greater Rhea in the area in 2004 (initial situation, Fig. 2a) and was used to produce two other maps to simulate the progressive replacement of the areas classified as grassland and pastures with

crops for the years 2008 (situation two) and 2014 (situation three). We generated the maps using the geographic information system ENVI 4.0 (ENVI 2003) and randomly simulated the replacement of grasslands and pastures with crops.

We introduced these new maps (situations two and three) into RAMAS GIS (Akçakaya 2005) and linked them with the spatial model of Greater Rhea developed by Giordano *et al.* (2010). We combined this spatial information with demographic parameters to obtain the population viability model. We estimated and incorporated the following demographic parameters: (1) *Initial abundance*, which was estimated by multiplying Greater Rhea density in 2004 (Giordano *et al.* 2008) by the size of each suitable habitat patch, regardless of animal sex or age (unstructured model); (2) *Carrying capacity (K)* of each suitable habitat patch, defined at 0.6 ind./km<sup>2</sup>, was estimated by multiplying the average density plus its standard error by patch size, following the criterion of Perkins *et al.* (2008). Thus, as habitat loss increases, carrying capacity decreases; and (3) *Dispersal*, defined as a function of distance between patches and mean and maximum distances traversed by Greater Rheas in this environment. These distances were estimated as 4.18 and 9.3 km, respectively, by Bazzano (2010) from radiotelemetry monitoring of captive-bred Greater Rheas released in the area. Thus, dispersal rate is a negative exponential function of distance. We used a ceiling-type density dependence, which affected all vital rates and populations. The PVA model incorporated two types of stochasticity: environmental fluctuations and demographic variability, whereas it did not include catastrophic events.

We simulated two scenarios with 1000 replicates each, using RAMAS GIS (Akçakaya 2005). For each scenario, we simulated abundance of Greater Rheas over time, average number of populations, the probability of the

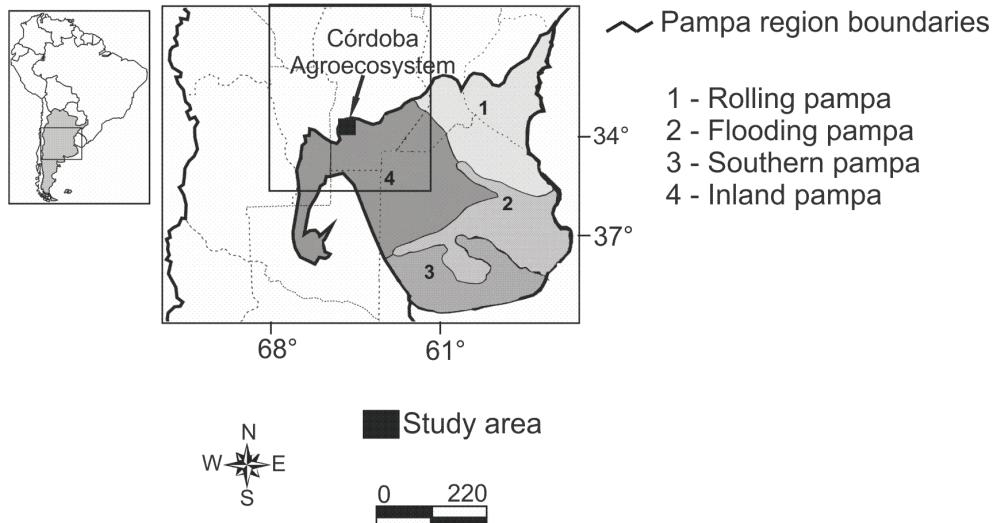


FIG. 1. Location of the study area in the Inland Pampa, within the Argentine pampas region. Figure taken from Giordano *et al.* (2010).

metapopulation to fall below the threshold of 30 individuals (Pullin 2002), and the expected minimum population size (the mean of the smallest population size recorded in each iteration of a PVA; McCarthy & Thompson 2001).

Firstly, we simulated the “without translocation” scenario, which did not include any management conservation action. Then, considering that results obtained under this scenario showed an important population decline, we simulated a second (“with translocation”) scenario, which involved the artificial movement of individuals from large populations to reinforce smaller populations, or to generate new ones within the study area. Under the assumption that translocation may reduce extinction risk (Akçakaya 2005), we applied this management tool in 2006 and 2010, the years when the “without translocation” scenario showed a marked decrease in abundance of Greater Rheas (Fig. 3a). The number of translocations simulated was 19 in 2005 and 17 in 2009, with a number of indi-

viduals translocated ranging between 1 and 37. In both years, the total number of translocated individuals did not exceed 45% of the abundances of the source populations.

*Model validation.* Within the study area, we selected two 80-km<sup>2</sup> survey sites, 40 km apart (s1: 33.82°S, 64.61°W and s2: 33.69°S, 64.92°W) as replicates, in which we counted the number of adult Rheas. From 2006–2008 and in 2010, we conducted 12 sample surveys (between one and five per year) at each site during the reproductive (September–January) and non-reproductive seasons (March–August) of the species, using line transects of variable width (Buckland *et al.* 1993, Greenwood 1996). We travelled transects of 35 km by vehicle (speed 10–20 km/h), recording the perpendicular distance between the observed individual/s and the transect line. We analyzed the collected data using Distance Sampling v. 5.0 software (Thomas *et al.* 2010) to estimate adult Greater Rhea density at each survey site and on each sampling date and,

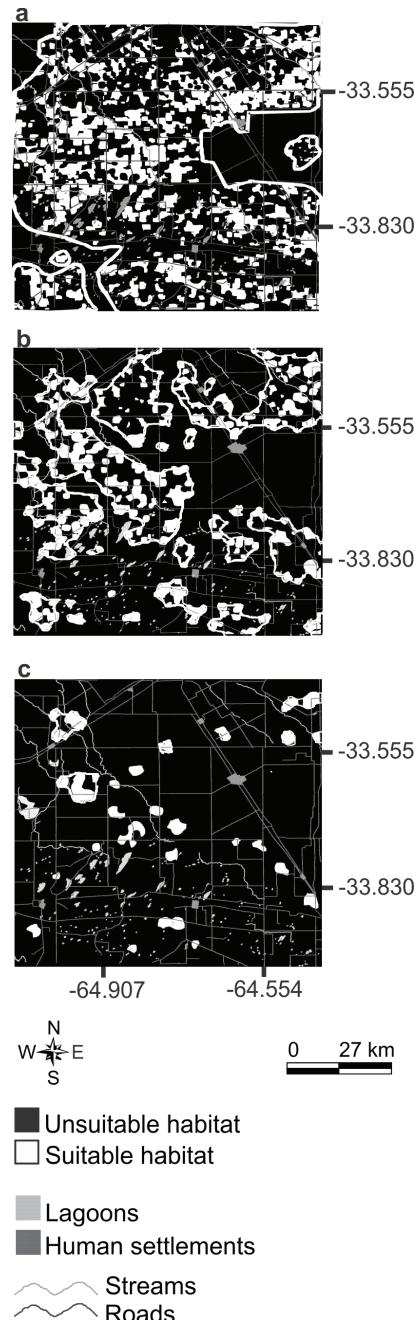


FIG. 2. Structure of habitat patches suitable for Greater Rhea in an agro-ecosystem of central Argentina: (a) initial situation (year 2004, Giordano *et al.* 2010); and situations resulting from a simulation scenario of agricultural expansion in 2008 (b) and 2014 (c).

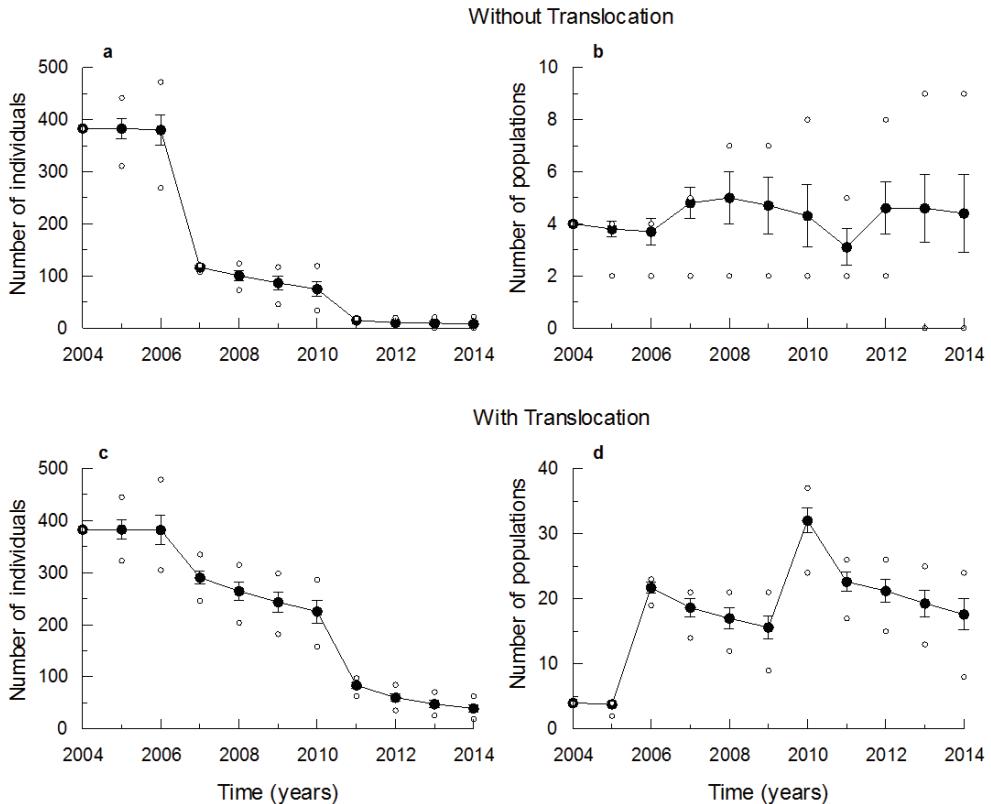


FIG. 3. Forecast of Greater Rhea mean abundance and number of populations ( $\pm$  SD) in an agro-ecosystem of central Argentina, as a function of time and under “without translocation” (a–b) and “with translocation” (c–d) scenarios. White circles represent extreme values.

based on those results, the average annual density for each study site.

To compare the population abundances predicted by the model with those observed in the field, we extrapolated the latter to the whole suitable habitat estimated by the model for the respective year. We assumed that the surveyed sites were a representative sample of the study area because they exhibited similar vegetation characteristics, land-use, and management (GB pers. observ.).

We performed a permutation test (Manly 1998) to assess whether population abundance values obtained from simulations with and without translocations differed from field

estimates. For this purpose, we used the average abundances and the 95 percentile confidence intervals of the data generated by the simulations *per* year. Accordingly, when the observed population abundances fell within the simulated confidence interval we concluded that they did not differ significantly ( $P > 0.05$ ) from those obtained by simulations (Manly 1998).

## RESULTS

Throughout the simulation period, the agro-ecosystem underwent changes in the number and size of suitable habitat patches with

respect to the initial situation (2004). In 2008, the landscape was composed of 21 patches (Fig. 2b), ranging between 1.9 and 115.7 km<sup>2</sup> in size. The distances between patches ranged from 4 to 65 km. At the end of the simulation period (2014), patch size was further reduced, ranging from 1.75 to 22.89 km<sup>2</sup>. In that year, the amount estimated of suitable habitat for Greater Rhea declined by 84% (from 1129 to 176.33 km<sup>2</sup>) and was fragmented into 26 patches of smaller size (Fig. 2c). Thus, the largest patch in 2014 represented only 13% of the total suitable area and the distances between patches ranged between 6 and 74 km.

As a consequence of the decrease in average patch size and the increase in number of fragments and distances between suitable patches, the simulation showed a decrease in population size since 2006 under both scenarios (Figs 3a, c). However, in the “without translocation” scenario the decrease was more abrupt than in the “with translocation” one; hence, in the former scenario, the average Greater Rhea abundance fell by 98% at the end of the simulation period (Figs 3a, c).

In the “without translocation” scenario, we observed a low (between three and five) average number of populations at the end of the simulation period (Fig. 3b), which would be the result of the high isolation between them; indeed, in most cases the distance between patches was greater than the maximum (9.3 km) travelled by Greater Rheas in this agro-ecosystem (Bazzano 2010). Consequently, the expected minimum population size was only of 7.2 individuals and from the seventh year of simulation, the probability of populations falling below 30 individuals was 100%. By contrast, in the “with translocation” scenario, the average number of populations observed was between four and 32 (Fig. 3d). The greater number of populations resulting at the end of this simulation scenario was due to a combined effect of the establishment of

new populations via translocation and dispersal of individuals between populations. The expected minimum population size was 38.4 individuals, and the risk of populations falling below 30 individuals was only 15% at the end of the simulation period.

In general, observed abundances were more similar to those predicted by the “with translocation” scenario than to those of the “without translocation” scenario. In 2006, the observed abundance was significantly lower than that resulting from both scenarios ( $P < 0.05$ ). In 2007, 2008, and 2010, the observed abundances did not differ significantly from those predicted by the “with translocation” scenario (in both years,  $P > 0.05$ ), but they were higher than those estimated for the “without translocation” scenario (in both years,  $P < 0.05$ ) (Fig. 4).

## DISCUSSION

The present results show that, should the rate of agricultural expansion recorded in central Argentina since the 2000s continue, the suitable habitat for Rheas might be fragmented into smaller patches and become drastically reduced. Consequently, the abundance of individuals would be reduced by 90 (0.22 ind./km<sup>2</sup>) to 98% (0.044 ind./km<sup>2</sup>), threatening the viability of rhea populations occurring in agro-ecosystems. Indeed, the loss of grasslands and pastures entails the loss of optimal habitat for feeding, reproduction and survival of the species (Martella *et al.* 1996, Bellis *et al.* 2004). At the same time, habitat reduction and fragmentation could further isolate the remaining populations, reducing dispersal of individuals and genetic exchange. This situation involves a high extinction risk, particularly because Greater Rhea is a species with low levels of genetic diversity (Alonso Roldán *et al.* 2009).

During the first four years of simulation, habitat fragmentation process was greater

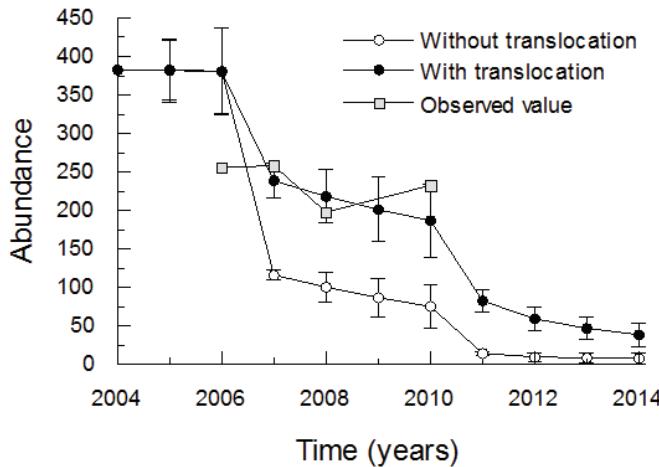


FIG.4. Abundances of Greater Rhea obtained by simulation using PVA model, under “with translocation” and “without translocation” scenarios ( $\pm$  95 percentile confidence interval of simulated data) and those actually observed in the field over time, in an agro-ecosystem of central Argentina.

than in subsequent years. The four suitable patches that existed in the habitat in 2004 were divided into 21 in 2008 and 26 in 2014. The increase of the agricultural land area at the expense of grasslands and pastures was simulated at a constant rate over time; for this reason, as the area covered by these vegetation types is reduced, so is habitat fragmentation.

At the end of the simulation period, translocation of individuals reduced the metapopulation extinction risk by 85% and the expected minimum population size increased by 81%. In addition, the abundances of rheas observed in the field were similar to those obtained under the “with translocation” scenario and greater than those of the “without translocation” scenario. This result suggests that Greater Rhea are able to disperse and that the crop matrix might not be completely hostile for the species, as assumed in the model; indeed, these birds might use this permeable matrix to disperse and obtain resources, thus mitigating fragmentation effects. Hence, the suitable habitat patches

may be larger or closer to one another than those identified by the model, and therefore abundance *per* patch would be higher, as recorded in the field. Accordingly, Alonso Roldán *et al.* (2009) did not find signs of differentiated genetic structure in Greater Rhea populations inhabiting the agro-ecosystem of central Argentina. Furthermore, recent studies indicate that glucocorticoid levels (indicators of stress) did not differ between Greater Rhea inhabiting environments modified for agricultural purposes and those occurring in low-disturbance grasslands (Lèche *et al.* in press), nor did reproductive rates differ significantly between populations occurring in those environments (Bazzano 2010). The matrix quality would be crucial in determining their abundance in fragmented habitats, because the Greater Rhea is a flightless bird; this assumption is consistent with findings reported for other vertebrate species (Prugh *et al.* 2008, Franklin & Lindenmayer 2009, Perfecto & Vandermeer 2010, Driscoll *et al.* 2013). Hence, translocation of Greater Rhea might be used as a management strategy for

the conservation of the species in agro-ecosystems of central Argentina. This management recommendation might turn out to be naive, considering that the agro-ecosystem is a highly modified environment and this would be the main negative factor affecting Greater Rhea populations. The main threat posed on them would be poaching and egg gathering, two activities that become more frequent with habitat fragmentation. Therefore, success of Greater Rhea translocations as a management tool would largely depend on the effective prevention of illegal uses of the species and suitable management of grassland and pasture remnants in the region.

The results of the present study warn us about the negative effect of grasslands loss on population abundance of wild Greater Rhea inhabiting agro-ecosystems of central Argentina and, at the same time, show the ability of this species to cope with human-induced disturbances, reproduce and disperse in agricultural environments. Hence, conservation of the Greater Rhea could be accomplished by implementing management practices that, on the one hand, increase population abundance through translocations of individuals and, on the other hand, maintain or improve the suitability of the matrix. The latter might be achieved by implanting pastures, such as *Medicago sativa*, because it is the preferred food item of this species and is compatible with cattle production (Martella *et al.* 1996), and grasslands, which provide refuge and nesting sites (Bazzano *et al.* 2002, Bellis *et al.* 2004). These types of actions might improve availability of resources (food, refuge, etc.) for the species throughout the year, facilitating dispersal of individuals. Translocations might be used as a management strategy for the rescue of individuals; however, more extensive studies are needed to evaluate the impact of this tool on population abundance of wild Greater Rheas in the long term.

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