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Molecular evidence for hybridisation between the two living species of South American ratites: potential conservation implications

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Abstract

In a private wildlife research facility and rhea farm of Argentina, artificially incubated eggs of putative hybrid origin between the Greater Rhea (*Rhea americana*) and the Lesser Rhea (*Rhea pennata*) hatched and gave birth to healthy chicks. Molecular genotyping by the analysis of mitochondrial Cytochrome b (Cyt b) and nuclear Chromo-Helicase DNA binding (CHD1) gene sequences confirmed the hybrid origin of these chicks which were molecularly sexed as females. The possibility of hybridisation argues for careful management of captive populations of these species, especially if individuals are to be released in the wild for conservation purposes.

Introduction

Ratites (order Struthioniformes) are large flightless birds represented by kiwis, emus, cassowaries, ostriches and rheas (Folch 1992). Among this order, rheas are endemic of South America and are represented by two living species: the common or greater rhea (*Rhea americana*) and Darwin's or lesser rhea (*Rhea pennata* formerly *Pterocnemia pennata*). Five and three sub-species are recognized within the geographical range of *R. americana* and *R. pennata*, respectively. Among these, the Andean endemic puna rhea (*R. p. tarapacensis/garleppi*) may merit consideration as a full species which is critically endangered since its population is thought to comprise only several hundred individuals at the most (Folch 1992). Both greater and lesser rheas have seen their populations declining dramatically in the recent past as the result of combined effects of high hunting pressure and habitat loss induced by the conversion of plains into farmland and pastures (Bellis et al. 2004). As a consequence, both species are classified as Near Threatened (NT) in the 2006 IUCN Red List (BirdLife International 2004).

In natural populations of both rhea species, the tasks of incubation and chick-rearing are left exclusively to the male, after all females from its harem have laid their eggs in a previously prepared nest (Folch 1992). Some orphan eggs laid outside active nests, long thought to be unfertile, have been shown to produce viable chicks after artificial incubation (Navarro et al. 1998). This property has led to the conservation strategy of using captive reared yearlings for reintroduction in declining natural populations (Bellis et al. 1999). Indeed, both species of rheas are commonly bred in South American farms and zoos. In captivity, some eggs are routinely collected and artificially incubated to increase successful reproduction. After hatching in the incubator, the chicks are brought together with the offspring produced by natural incubation and are reared naturally by males. In the first days after the laying, eggs from greater rheas are yellow colored whereas lesser rheas lay greenish eggs, and thus can be easily distinguished. Consequently, greater and lesser rheas are often bred in the same enclosures.

A private wildlife research facility (Estación de Incubación y Cría de Aves Silvestres - EICAS) in Mendoza (Argentina) maintains about 30 greater rheas together with a single female lesser rhea. Surprisingly, in October 1999, six green lesser rhea-like eggs were found in the enclosure. These eggs were artificially incubated, and two of them hatched 40 days later giving birth to healthy chicks (Figure 1A). Given the absence of male lesser rheas in the ratite farm, these chicks were suspected to represent viable hybrids of the lesser rhea female and one of the greater rhea males. Hybridisation is actually common in birds as Grant & Grant (1992) estimated that 9.2% of bird species hybridise either in nature or in captivity. However, the authors did not mention this possibility between species of the rhea family (Rheidae). The only mention of such a

possibility was briefly noted by Folch (1992: plate 2).

To test for hybridisation, we studied the two putative hybrid chicks by DNA sequencing of two widely used molecular markers: the nuclear Chromo-Helicase DNA binding (CHD1) (Miyaki et al. 2001) and the mitochondrial Cytochrome b (Cyt b) genes (Lee et al. 1997). Potential conservation implications of hybridisation between these near threatened species are discussed in the context of reintroduction plans from captive animals.

Methods

Complete genomic DNA was extracted from blood samples of two putative hybrids (H332 and H055) and a greater rhea *R. americana* (Ram) from the farm, and from muscle tissue of an unrelated lesser rhea *R. pennata* (Rpe) using standard procedures (Sambrook et al. 1989). Because standard molecular sexing protocols based on the study of the CHD genes do not work in ratites which have undifferentiated sex chromosomes (Griffiths et al. 1998; Ellegren 2000), we used the test especially designed by Huynen et al. (2002). The sex-specific sequence (kW1) was PCR amplified in the two putative hybrids using primers w1' (forward): 5'-ACCAGCCTTTAAACAAGCTATTAA-3' and k7' (reverse): 5'-TCTCTTTTGTTTTAGACACCCT-3' slightly modified from the ones defined in the original publication to specifically target rhea sequences (Huynen et al. 2002). A region of the CHD1 nuclear gene, encompassing approximately equal parts of a complete intron and portions of its flanking exons (García-Moreno & Mindell 2000) was also amplified with the universal sexing primers P8 and P2 (Griffiths et al. 1998) for the two putative hybrids, the greater rhea, and the lesser rhea. Finally, a 337 base pair (bp) fragment of the mitochondrial Cyt b gene from the two putative hybrids was directly

PCR amplified using the primers L2 (forward): 5'-TACCATGAGGACAAATATC-3' and H10 (reverse): 5'-CTGGGGTGTAGTTCTCTGGGTC-3'. PCR products for CHD1 and Cyt b genes were purified from 1% agarose gels using Amicon Ultrafree-DA columns (Millipore), and directly sequenced with PCR primers on both strands using automatic sequencing (Big Dye Terminator cycle kit) on an ABI 310 (PE Applied Biosystems). Sequences were manually aligned with the ED editor of the MUST package (Philippe 1993). The CHD1 gene was 319 bp long for all four individuals analyzed and no gaps needed to be introduced in the alignment. Sequences have been deposited in the EMBL data bank under Accession Numbers AJ430514 to AJ430519.

Results and Discussion

The two putative hybrids were molecularly sexed as females by the presence of the female specific 150 bp fragment of the kW1 region in the two PCR amplifications (Figure 1B). Alignment of the mitochondrial Cyt b sequences from the two putative hybrids with previously published sequences of *R. americana* and *R. pennata* has shown a perfect identity with *R. pennata* (Figure 2). Results from this maternally inherited gene confirmed that the artificially incubated lesser rhea-like eggs, giving birth to the putative hybrids, were laid by the lesser rhea female of the breeding facility. No lesser rhea males were kept on the farm and accidental mating with a wild living male was highly unlikely, as the facility is located in a semi-urban area of Mendoza free of wild rhea populations. This result thus strengthened the possibility that the chicks arose from hybridisation with a captive greater rhea male. Definitive confirmation of this suspicion came from the comparison of CHD1 gene sequences (Figure 3). Only three variable sites on the 319 sequenced sites of the CHD1 alignment were detected, of which two were diagnostic for

the hybrids (positions 104 and 109). These variable sites were all situated within the intronic region of the gene. When looking at these sites in chromatograms of the hybrids, we observed two exactly superimposed fluorochrome peaks corresponding to the nucleotides found in the parental species *R. americana* and *R. pennata* (Figure 3). As CHD1 appeared as non sex-linked in ratites with an autosomal mode of inheritance (Ellegren 2000), these sites indicated that the chicks possessed the two parental alleles: one likely inherited from the lesser rhea female and the other from one of the greater rhea males. The third variable site between the two parental sequences (position 149) was not diagnostic since hybrids unambiguously possessed an Adenine like their lesser rhea mother whereas a Guanine was found in the putative greater rhea father sequence. This observation suggests that the greater rhea male we randomly sampled in the farm is not actually the father of the hybrids. However, our results provide clear molecular evidence that hybridisation in captivity between the two living species of South American ratites led to viable first generation hybrids (F1 hybrids).

As expected, the hybrids showed mixed morphological characters from both maternal and paternal inheritance. Shortly after hatching, the hybrid chicks had greyish brown feathers, resembling offspring of greater rheas. A white line at the tip of the feathers could be observed at one year, which made the chicks look more similar to lesser rheas. Approximately two years after hatching, the hybrids showed a steel grey plumage that reaches the tarsus. The head is rounded as in lesser rheas, whereas the beak is long and flattened as in greater rheas (Figure 1C). The hybrids are slightly larger in size than greater rheas of the same age. Very unfortunately, we have been unable to collect any data on the age at which the described hybrids may reach sexual maturity, since they were sold after two years by the owner of the farm for commercial purposes.

Therefore, we cannot make any prediction about their potential fertility.

As demonstrated by the occurrence of occasional hybridisation, *Rhea americana* and *Rhea pennata* seem to be phylogenetically closely related species. At the molecular level, we observed only three differences on 319 nucleotides in the CHD1 gene (0.9 % divergence) and 23 differences on 337 nucleotides in the mitochondrial Cyt b gene (6.8 % divergence). Our results confirm that the genus-level taxonomic distinction introduced with the long use of the name *Pterocnemia pennata* Gray 1870 for the lesser rhea might not be justified. This gives credit to the recent taxonomic revision coming back to *Rhea pennata* as originally proposed by d'Orbigny in 1834. It also provides a good example of the trend for taxonomical splitting observed in birds where species have tended to be placed into separate genera at a lower level of genetic divergence than is often true for other vertebrates (Johns & Avise 1998).

The fact that hybridisation can occur in captivity points out that the differentiation between the two species is not complete and raises questions about the possibility of its occurrence in natural populations. The two species have a parapatric distribution range with a sympatric zone North of Patagonia in Argentina (Folch 1992) suggesting that hybridisation could potentially occur in this area. However, it is clear that captive living conditions are far from the natural ones. In the wild, it is likely that a number of pre-zygotic barriers, which are relaxed in captivity, prevent hybridisation between the two species. In particular, the complex courtship behaviour displayed by both species of rheas (Folch 1992) constitutes an ethological barrier to hybridisation. Continuing habitat fragmentation, reduction of population sizes by illegal hunting and isolation of subpopulations of both species could, however, increase the encounters between greater and lesser rheas (Bellis et al. 1999; Bouzat 2001). It can not be excluded that wild rheas

would hybridise with individuals of the other species if conspecifics are rare or absent during the mating season.

Numerous rhea populations are managed by man in farms and zoos and our results argue for a careful management of captive breeding populations in order to avoid hybridisation between greater and lesser rheas. In private husbandries and zoos, the two species must therefore be strictly separated and meaningful captive breeding programs should be followed to conserve the integrity of both species. This latter point is of primary importance in cases where captive bred animals are thought to be released in the wild for reintroduction or population increase purposes (Bellis et al. 1999; Allendorf et al. 2001).

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Figure legends

Figure 1. A. Putative hybrid egg hatching after 40 days of artificial incubation. Note the greenish colour of the shell, characteristic of *Rhea pennata* eggs. B. Molecular sexing of the two putative hybrids. The two PCR amplifications of the kW1 region in the two putative hybrid samples revealed the characteristic fragments of 350 bp and 150 bp identifying the two individuals as females. C. Juvenile female *Rhea pennata* x *Rhea americana* hybrids. Note the presence of mixed characters such as the grey plumage characteristic of *R. americana* and the rounded head typical of *R. pennata*.

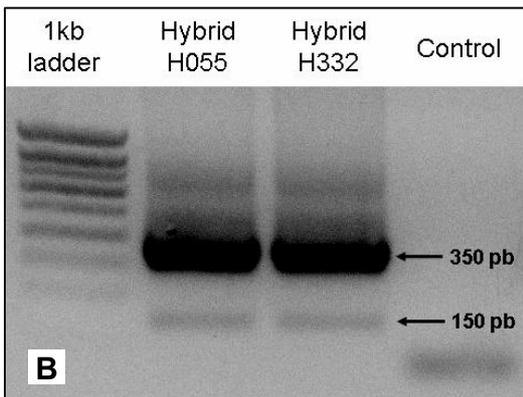
Figure 2. Alignment of the 24 variable sites over 337 base pairs from the mitochondrial Cytochrome b gene obtained from the two hybrids compared with previously published sequences (accession numbers in brackets) for *Rhea americana* (Ram) and *Rhea pennata*

(Rpe). Dots (.) indicate identity with the first nucleotide sequence and numbers refer to the position in the complete Cytochrome b sequence.

Figure 3. Chromatograms showing the hybrid diagnostic region of the CHD1 gene.

Hybrids possess the two parental alleles in their genomes resulting in perfectly superimposed peaks on the chromatograms at the sites where the *Rhea americana* and *Rhea pennata* nucleotide sequences differ. Y (for pYrimidine) and R (for puRine) are the ambiguity codes for Cytosine/Thymine (C/T) and Adenine/Guanine (A/G), respectively.

colour figure
[Click here to download colour figure: Delsuc-rhea-fig1-rev.ppt](#)

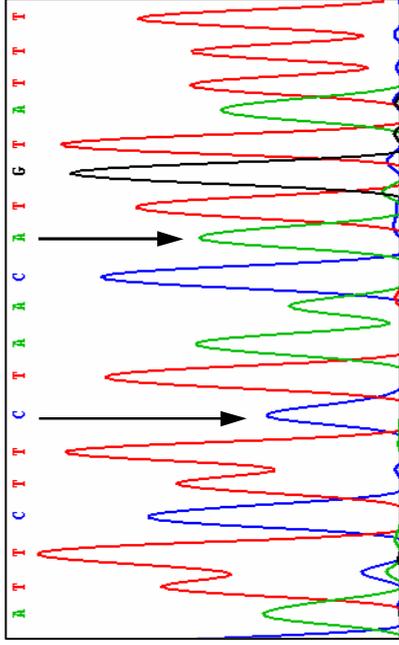


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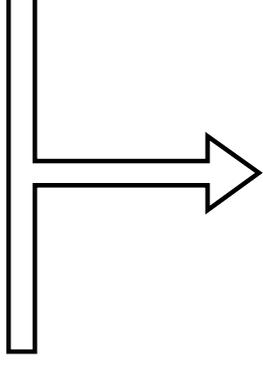
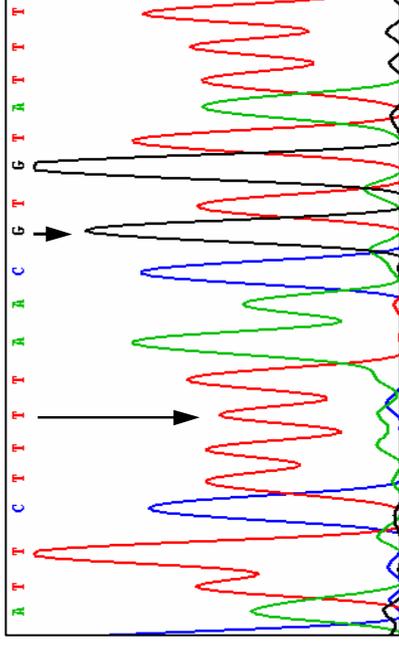
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2 2 3 4 8 9 9 0 2 3 4 8 1 2 4 9 9 9 1 1 2 3 4 5
0 9 8 8 1 2 5 4 2 1 6 5 5 8 8 6 7 9 1 7 3 2 4 1
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Ram (AF090339) A A T C T A T G T C G T G T T A C A T G A C C C
Ram (Y16884)   . . . T . . . . . . . . . . . . . . . . . .
Ppe (AF338709) C G C . C G C A C T A C A C C G T C C A G T T T
Ppe (U76054)  C G C . C G C A C T A C A C C G T C C A G T T T
Hybrid H332   C G C . C G C A C T A C A C C G T C C A G T T T
Hybrid H055   C G C . C G C A C T A C A C C G T C C A G T T T
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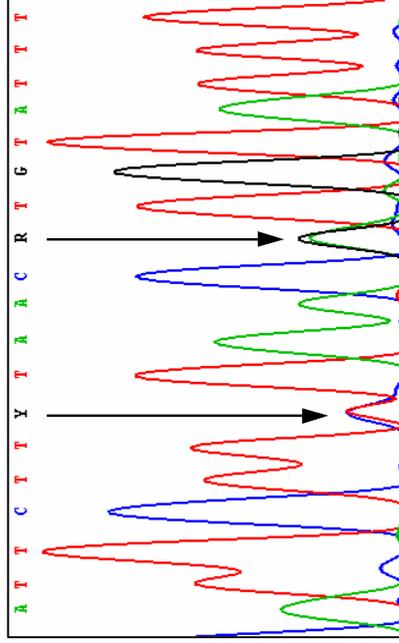
Male *Rhea americana*



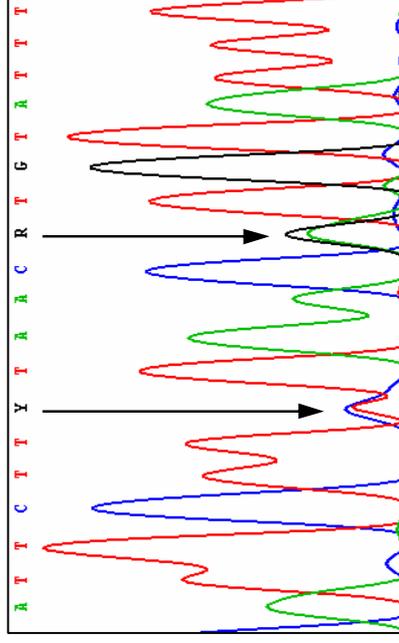
Female *Pterocnemia pennata*



Female hybrids *Rhea americana* X *Pterocnemia pennata*



H332



H055