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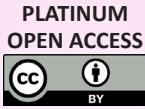
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NOTE

FILLING A GAP IN ANDEAN CAT *LEOPARDUS JACOBITA* (CORNALIA, 1865) (MAMMALIA: CARNIVORA: FELIDAE) DISTRIBUTION RANGE: NEW RECORD IN LA RIOJA PROVINCE, ARGENTINA

Cintia Gisele Tellaeche, María de las Mercedes Guerisoli, Constanza Napolitano,
Dante Luis Di Nucci & Juan Ignacio Reppucci

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Filling a gap in Andean Cat *Leopardus jacobita* (Cornalia, 1865) (Mammalia: Carnivora: Felidae) distribution range: new record in La Rioja province, Argentina

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The Andean Cat *Leopardus jacobita* is one of the least known felids in South America (AGA 2011; Hunter 2015). Its distribution is restricted to arid regions of the High Andes of Argentina, Bolivia, Chile, Peru and a portion of the Patagonian steppe in Argentina. It is classified as Endangered by the IUCN (Villalba et al. 2016). Main threats for this species, evaluated and categorized by the Andean Cat Alliance (2011), are habitat loss and degradation, opportunistic and traditional hunting and reduction of prey populations.

In 1998, all our understanding of Andean Cat was based on only 18 museum specimens. During the last

20 years, knowledge about the species has increased greatly. Andean Cat diet, distribution, habitat use, population density, activity patterns, genetic structure and some other aspects have been studied in several areas across its range. Many aspects of its ecology and biology, however, remain unknown (Walker et al. 2007; Napolitano et al. 2008; Lucherini et al. 2009; Reppucci et al. 2011). Basic knowledge on the distribution of the species has improved in the past few years because of new data. In 2006, a new record expanded the range 500km south, and four years later, another record expanded it another 150km south to a new ecoregion

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Figure 1. The reported Andean Cat record (red dot) and the currently identified evolutionarily significant units for Andean Cat (green areas). Adapted from Cossíos et al. (2012).

(Patagonian steppe) 80km east of the Andes (Sorli et al. 2006; Novaro et al. 2010). This last record at 650m updated the known elevation range for the Andean Cat, which was until then thought to be above 3,500m (Lucherini & Vidal 2003). We have gained a more complete understanding of Andean Cat distribution, but some questions remain unanswered. Particularly in Argentina, there is a large region in the province of La Rioja where no records have been found, and despite sampling efforts in the neighbouring province of San Juan, only one record was found; these provinces provide a large amount of suitable habitat for Andean Cats (Marino et al. 2011).

Genetic diversity across the currently known distribution has been studied. The Andean Cat populations have low genetic diversity, and two evolutionarily significant units (ESU) have been suggested for Argentina (Cossíos et al. 2012). The two ESU are separated by a large gap in the distribution range between 26°S and 35°S, which corresponds to the mentioned area with suitable habitat, but no records in La Rioja province. Genetic information was not obtained from the only sample collected in San Juan province.



Image 1. Pelt of the Andean Cat individual poached in Las Cuevas, La Rioja Province, Argentina.

Here we present the first Andean Cat record for La Rioja province in northwestern Argentina (Image 1), from a pelt found in General Felipe Varela Department in the west of La Rioja Province (Figure 1) in an area called Las Cuevas (29.22°S, 68.71°W) at an elevation of approximately 1,815m. The animal was poached in retaliation for alleged harm to domestic goats, and the pelt was kept as ornament in Villa Unión City. We collected a sample from the skin and conducted genetic analysis as described in Cossíos et al. (2012) to confirm that it was an Andean Cat. Using multi-locus genotype data, further analysis is currently ongoing to assign this specimen to a known genetic population and ESU, and to integrate this new data into the overall genetic structure analysis within known Andean Cat populations.

This record is particularly important because it fills an extensive gap in the distribution range of the species and will also provide relevant genetic information for a better understanding of the relationship between the two currently identified evolutionarily significant units.

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