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Natural history collections and the conservation of poorly known taxa: Ecological niche modeling in central African rainforest genets (*Genetta* spp.)

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ABSTRACT

Natural history collections are crucial resources for conservation biology, particularly given the development of the ecological niche modeling (ENM) approach. We combined ENM with taxonomic investigations to address ecological, geographic, and phenotypic variation in the poorly known central African rainforest genets (*Genetta cristata*, *Genetta servalina*, *Genetta victoriae*) to provide new insights into their conservation status. Taxonomic identification was based on four discrete morphological characters. ENMs were developed using the Genetic Algorithm for Rule-Set Prediction (GARP), 10 environmental data layers and 310 georeferenced localities extracted from 667 museum specimens and 22 literature sources. Re-assessed taxonomic identifications allowed us to expand significantly the known range and ecological limits of the three genets. We suggested limited hybridization between *G. cristata* and *G. servalina*, in a zone of sympatry likely to cover central Cameroon, northwestern Gabon and Congo. ENM showed that almost all known occurrences were connected geographically by suitable ecological conditions, suggesting continuous potential distributions between supposedly isolated populations of the three genets. Our investigations indicated that *G. cristata* is distinct from *G. servalina* in morphology, geographic ranges and ecological niches, indicating species status for *G. cristata*, which, as such, should be the subject of appropriate conservation attention. Areas of predicted connectivity and actual zones of occurrence falling outside current forest cover should be surveyed to re-assess the status of the rainforest genets. Our study shows that combining ENM and taxonomic investigations can substantially improve data utilization from natural history collections, especially in the case of poorly known species.

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1. Introduction

Natural history museum collections and associated data have been recognized as crucial information resources for conservation in terms of distribution and geographic variation (Burgman et al., 1995; Shaffer et al., 1998; Ponder et al., 2001; McNeely, 2002; Golding and Timberlake, 2003; Wheeler et al., 2004). An important new impetus in this role is development of powerful software tools now available for managing, integrating, and analyzing such data (Vieglais et al., 2000; Wheeler et al., 2004; Suarez and Tsutsui, 2004). Representative for mammal museum collections is MaNIS, a system which

enhances the value of collections by facilitating open access to specimen information, and georeferencing of collecting localities (Stein and Wieczorek, 2004).

Among the new software tools that are being applied to questions of biodiversity are diverse methodologies for ecological niche modeling (ENM). Ecological niches may be defined, for the purposes of ENM, as the suite of environmental conditions that permits a species' survival without immigrational subsidy (Grinnell, 1917, 1924). ENM applications use known occurrences of species, in relation to digital thematic map coverages, to develop rule-sets that describe ecological niches of species (Soberón and Peterson, 2005), which in turn provide a predictive understanding of distributional and ecological phenomena for that species (Soberón and Peterson, 2004). These techniques have now been applied to diverse biodiversity studies, including simple distributional predictions (e.g., Anderson et al., 2002a; Reutter et al., 2003; Wiley et al., 2003; Chefaoui et al., 2005), predicting species' geographic potential as invasive species (Peterson, 2003), predicting the likely existence of unknown species (Raxworthy et al., 2003), and predicting species' potential distributions under different climatic conditions (Martínez-Meyer, 2002; Martínez-Meyer et al., 2004; Thomas et al., 2004). A methodology that has seen extensive application is the Genetic Algorithm for Rule-set Prediction (GARP; Stockwell and Noble, 1992; Stockwell and Peters, 1999), an evolutionary-computing application designed to produce predictive rule-sets even in highly dimensional, complex environmental spaces.

In spite of the exciting potential of the ENM approach for assessing the status and distribution of poorly known taxa, few explicit case studies are available in the literature. Here, we address ecological, geographic, and taxonomic variation in the endangered crested servaline genet *Genetta cristata* (Carnivora, Viverridae, Viverrinae); this genet has been problematic as to its taxonomic status (Gaubert, 2003a), and remains poorly known owing to its elusive mode of life in the Lower Guinean Block of the central African rainforest (Heard and Van Rompaey, 1990; Powell and Van Rompaey, 1998; Gaubert, 2003b). Although ranked as a species by the IUCN (2004), it "is considered by some authorities to be a subspecies of the servaline genet [...], and as such has probably not received the required conservation attention" (UNEP-WCMC, 2005).

As such, we also included in this study the more widespread servaline genet *G. servalina* (Gaubert et al., 2005a), sister-species to *G. cristata* (Gaubert et al., 2004), which may itself present conservation challenges; recent discoveries on Zanzibar Island (Van Rompaey and Colyn, 1998; Goldman and Winther-Hansen, 2003) and in the Eastern Arc Mountains of Tanzania (Kingdon, 1977; De Luca and Mpunga, 2002) suggest relict populations isolated from the central African core distribution of the species. We also include in our analyses the giant genet *G. victoriae*, endemic to the rainforest of northeastern Democratic Republic of Congo (DRC), because it has traditionally been included within the "servaline" group (Crawford-Cabral, 1981) and is itself in need of additional information regarding distribution and ecology (Schreiber et al., 1989). Our purpose is thus to combine ENM with taxonomic investigations to provide new insights into: (1) phenotypic, ecological, and geographic boundaries between *G. cristata* and *G. servalina*, (2) ecological distribution of the genets in the central African rainforest, and (3) the conservation status of the endangered *G. cristata*.

2. Materials and methods

2.1. Phenotypic variation and distributional data

We based our analyses on 667 specimens in 15 natural history museum collections (electronic supplementary material 1), including 80 *G. cristata*, 520 *G. servalina*, and 122 *G. victoriae*. Following previous works (Gaubert, 2003a; Gaubert et al., 2004, 2005a,b), we used four discrete morphological characters to distinguish between *G. cristata* and *G. servalina* (Table 1). Since juveniles can be difficult to identify correctly (Gaubert et al., 2002a, 2005b), only full adults were considered; among adults, we found no intraspecific variability in the four traits. We defined putative morphological hybrids as phenotypes possessing mosaics of character states of *G. cristata* and *G. servalina* (Allendorf et al., 2001; Gaubert et al., 2005b).

Following the diagnostic characters defined above, we supplemented specimen data with occurrences from 22 literature sources that provided unambiguous taxonomic identifications (electronic supplementary material 1). We assigned coordinates to localities based on diverse sources from published and electronic geographic atlases and gazetteers (Davis

Table 1 – Four discrete morphological characters used to discriminate between adult specimens of *G. cristata* and *G. servalina*

Characters	G. cristata	G. servalina	G. victoriae
Mid-dorsal line	Hairs relatively long (dorsal crest), giving a continuous aspect to the line	Hairs short (no dorsal crest) and mid-dorsal line discontinuous	Hairs relatively long (dorsal crest), giving a continuous aspect to the line
Nuchal crest (hairs with opposite direction to those of adjacent regions)	Present	Absent	Present
Width of bright rings relative to dark rings on the middle of the tail	50–75%	<20%	<20%
Ratio between inter-orbital constriction/frontal width (Gaubert, 2003a)	1.00 ± 0.12	>1.00 + 0.12	<1.00 − 0.12

Data for *G. victoriae* are also presented.