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

P. Gaubert^{a,*}, M. Papeş^b, A.T. Peterson^b

^aEstación Biológica de Doñana (CSIC), Departamento de Biología Aplicada, Avda. María Luisa s/n Pabellón del Perú, 41013 Sevilla, Spain

^bNatural History Museum and Biodiversity Research Center, The University of Kansas, Lawrence, KS 66045, USA

ARTICLE INFO

Article history:

Received 1 September 2005

Received in revised form

21 November 2005

Accepted 15 December 2005

Available online 7 February 2006

Keywords:

Genetta cristata

Natural history collections

Ecological niche modeling

Species boundaries

Central African rainforest

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 (Viegais et al., 2000; Wheeler et al., 2004; Suarez and Tsutsui, 2004). Representative for mammal museum collections is MaNIS, a system which

* Corresponding author. Present address: Institut de Recherche pour le Développement, UR 136 "Aires Protégées", Centre IRD – 5, rue du Carbone, 45072 Orléans, France. Tel.: +33 2 38 49 95 63; fax: +33 2 38 49 95 47.

E-mail address: gaubert@orleans.ird.fr (P. Gaubert).
0006-3207/\$ - see front matter Published by Elsevier Ltd.
doi:10.1016/j.biocon.2005.12.006

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 Wither-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 north-eastern 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	<i>G. cristata</i>	<i>G. servalina</i>	<i>G. victoriae</i>
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.

and Misonne, 1964; Times Atlas of the World, 1987; Atlas Mondial Encarta, 1998; Alexandria Digital Library Gazetteer Server, 2004; Global Gazetteer, 2005). When available, we also took into account information directly associated with specimens and collections, field notes and curators' knowledge of collections.

2.2. Ecological niche modeling

Putative hybrids and specimens falling outside the known ranges were removed before analysis, resulting in a final dataset of 310 localities (46 *G. cristata*, 203 *G. servalina*, 61 *G. victoriae*). The method used to generate ENMs was the Genetic Algorithm for Rule-Set Prediction (GARP; Boston and Stockwell, 1994). GARP is a machine-learning method that builds ENMs based on non-random associations between known occurrence points for species and sets of raster GIS coverages describing ecological landscapes. Occurrence data are used by GARP as follows: half of the data points are set aside for an independent test of model quality ("extrinsic test data"), and half are used in model development ("training data"). Resampling from known presences and from areas from which the species is not known produces two data sets, each of 1250 points, in model development (Stockwell and Peters, 1999).

The algorithm uses an iterative process of developing and modifying rules randomly based on four inferential tools (logistic regression, atomic rules, bioclimatic rules, negated range rules). Specially defined operators analogous to chromosomal evolution (e.g., crossover, mutation) modify initial rules, so rules "evolve" towards higher overall fitness (i.e., higher predictive accuracy). Rule quality is tested against training data to maximize both significance and predictive accuracy, and a size-limited set of best rules is retained (Stockwell and Noble, 1992). The resulting rule set can be used to query environmental data layers to identify a potential geographic distribution. Expected correct values if model and test points were randomly associated were calculated as (proportional area in the study area predicted present \times number of extrinsic test data points). A chi-square approach (1 df) can then be used to test significance of positive departures from random expectations. In all analyses we used GARP version 1.1.3, available for download (<http://www.lifemapper.org/desktopgarp/>).

GARP, which produces binary predictions, is susceptible to two types of prediction error: areas actually presenting inappropriate conditions might be included in model predictions (commission error) or areas actually habitable might be excluded from predictions (omission error) (Fielding and Bell, 1997). Although our measurements of omission error are pure error (failure to predict independent test presence points), commission error can be real (i.e., areas presenting ecological conditions not within species' ecological niches are included) or apparent (i.e., areas not known to hold the species because of nondetection, or owing to historical or dispersal constraints; Peterson et al., 1999; Peterson, 2003). To filter out poor models based on multiple replicates, we followed recent best-practices recommendations (Anderson et al., 2003): we developed 100 replicate GARP models for each species, retaining models with <10% omission error, and then eliminated models falling outside of the central 50% of the distribution

of commission error. The 10 model predictions retained were then summed in ArcView 3.2. (ArcGIS 9.0. 1999–2004, ESRI) to produce a final, graded prediction for each species.

To characterize the ecological requirements of taxa, we combined final ENM predicted distributions with the original environmental layers to produce a composite data set summarizing all environmental combinations across the study area. Exporting a random subsample of 5% (necessary owing to limitations in software) of these combinations permitted visualization of the distribution of each species with respect to mean annual temperature, mean annual precipitation, and elevation. The result of this procedure is a simplified view of the multidimensional ecological niches reconstructed in GARP.

2.3. Geographic information

The present-day ecological landscape was summarized in terms of six climatic and four topographic digital raster GIS maps. We used climatic layers developed by the Intergovernmental Panel on Climate Change (New et al., 1999) representing annual means for 1961–1990 of precipitation, mean annual temperature, annual mean minimum monthly temperature, annual mean maximum monthly temperature, vapor pressure, and number of wet days. The topographic datasets representing aspect, elevation, slope, and compound topographic index were obtained from US Geological Survey' EROS Data Center database (<http://edc.usgs.gov/>). All data sets were resampled to 0.1° resolution for analysis.

The general distributional hypothesis produced for each species after ENM analyses was analyzed with respect to current land use and protected areas across central Africa. We used a year 2000 land-cover map of Africa, produced as part of the Global Land Cover mapping effort led by Global Vegetation Monitoring Unit (Bartholomé et al., 2002). This map is derived from satellite data collected with the VEGETATION instrument on the SPOT-4 satellite (1 km spatial resolution) classifying land cover types into 27 categories. We also aggregated the nine categories pertaining to forest habitats [closed evergreen lowland forest, degraded evergreen lowland forest, montane evergreen forest, submontane forest, swamp forest, mangrove, mosaic forest/croplands, mosaic forest/savanna, and closed deciduous forest (Miombo)] to create a generalized forest versus non-forest map.

Given temporal discords between occurrence data available for species and landscape information, land use information could not be included directly in model development, and had to be applied as a latter step to refine the hypothesized distribution of the species (Soberón and Peterson, 2005). Forested areas were used to refine the climate-based ENM results: we retained in final distributional hypotheses only those pixels overlapping areas predicted by ≥ 1 of the 10 best-subsets GARP models. Although these results are likely to represent slight overestimates of actual ranges, they were used to analyze the conservation status of the three genets based on the IUCN database of world reserves (UNEP-WCMC, 2002). We ignored reserves that are not yet decreed, as well as those for which no IUCN category was assigned. We then calculated proportions of species' distributions falling under some degree of protection.

3. Results

The four diagnostic morphological characters (Table 1) allowed us to correct taxonomic attributions for 14 heretofore misidentified specimens of *G. cristata* and 14 *G. servalina* (~23% and ~3% of specimens examined, respectively). We identified four specimens as putative hybrids exhibiting mosaics of character states between *G. cristata* and *G. servalina*: three from south-central Cameroon (AMNH 170378: Bafia; AMNH 87238: Efulan; MRAC 77032M0080: Dja region) and one from northwestern Gabon (AMNH 119899: Como Estuary area; Fig. 1 and electronic supplement material 1). Pure phenotypes of both species were found at each of these localities except for the Dja region (*G. servalina* only). The hybrids occurred in a zone of sympatry between *G. cristata* and *G. servalina* that appears to cover southern and central Cameroon, northwestern Gabon, and parts of the Congo (Etoumbi).

Based on these identifications, *G. cristata* is seen to range >500 km south of the Sanaga River to the rainforests of southern Cameroon, Gabon, and northern Congo, and ~180 km west (BMNH 39.687, between Oni and Epe) from the type locality of *Genetta bini* (junior synonym of *G. cristata*; Gaubert, 2003a) (Fig. 1). Our observations also expanded the known distribution of *G. servalina* to include several localities north of the Sanaga River (sympatry with *G. cristata*); the southernmost limits of the species' range reached: (1) southwestern Congo, thus forming a continuum between localities in Gabon and DRC, and (2) south-central and southeastern DRC, south to Lumumbashi, at the Zambian border (latitude >11°S). New localities were identified from southern Tanzania (Kondoa) to the coastal rainforest of the country (from Mikindani to Manderu and Usambara), confirming the existence of a population in this region (Kingdon, 1977). Most *G. victoriae* specimens reflected the known range of the species (i.e., northern and eastern DRC, right bank of Congo River), indicating broad sympatry with *G. servalina* (Fig. 1). However, we found three localities on the left bank of Congo River, with a southernmost point at latitude >7°S (Kakanga; other points: Mukulu and Iku-tu). The specimen from Cameroon attributed to *G. victoriae* in Depierre and Vivien (1992) corresponds to *G. cristata*.

On the basis of known occurrence distributions, *G. servalina* had the broadest elevational spectrum (range 0 to ~3200 m; 876 ± 675 m [mean \pm SD]; $n = 373$), whereas *G. cristata* was restricted to lower elevations (range 0 to ~1000 m; 254 ± 233 m; $n = 48$). *G. victoriae* occurred at intermediate elevations, from 400 to ~2000 m (769 ± 366 m; $n = 82$). The three genets overlapped elevationally in areas of sympatry. Data noted on specimen labels revealed *G. cristata* collections from rainforest, disturbed secondary rainforest, and urban areas ($n = 8$), whereas *G. servalina* was collected in swamp forest, submontane rainforest, coral rag with dense thicket (Zanzibar Isl.), and plantations ($n = 7$). No such data were available for *G. victoriae*.

The ENMs on which we based all subsequent analyses performed significantly better than random models for each species (all $P < 0.5 \times 10^{-9}$). *G. cristata* was predicted to have the most restricted present-day range. It was predicted to be present in mangroves and lowland rainforest of southern Nigeria, coastal lowland and montane rainforest in Cameroon and Equatorial Guinea, and a broad area of rainforest in Gabon. A potentially suitable area was also predicted in swamp forest

in eastern Congo and western DRC, on both sides of the Congo River (Fig. 1).

G. servalina was predicted to have the broadest potential distribution (Fig. 1). The whole rainforest zone (Upper and Lower Guinean Blocks, Congo Basin) was predicted to be within the potential distribution of this species, as were degraded lowland rainforest (northern Cameroon, Central African Republic, DRC, Uganda, and Kenya) and deciduous forest and woodlands (Tanzania). Mangroves (Mozambique, Nigeria) and deciduous forest and woodlands of southern Africa (Angola, Zambia, Mozambique) were also predicted as potentially suitable areas.

Among the potentially habitable areas predicted for *G. victoriae* was the known ecological range of the species, i.e. lowland, submontane, and montane rainforests of northeastern DRC and Uganda (Fig. 1). Other potentially suitable regions were predicted in: (1) lowland rainforest in Cameroon, southwestern Central African Republic, northern Gabon, and northwestern Congo (plus a small area of swamp forest between Congo and DRC); (2) deciduous forest and woodlands in southern DRC and Angola; and (3) patches of deciduous forest and woodland in Tanzania, northern Zambia, and Uganda.

Despite favourable ecological conditions, the absence of *G. cristata* and *G. victoriae* specimens east and west of the Congo-Oubangui rivers, respectively, might reflect: (1) low dispersal abilities and/or (2) the role of geographical barrier played by the riverine axis in this region.

Whereas the potential distribution of *G. servalina* overlapped with *G. cristata* and *G. victoriae*, the latter two showed clear niche differentiation from each other (Fig. 2). In addition, *G. cristata* appeared to focus in a particular subset of the ecological spectrum of *G. servalina*, namely high mean temperature and precipitation, and low elevation.

Three of four putative hybrids between *G. cristata* and *G. servalina* were in areas predicted most suitable for *G. servalina*. Specimen collection localities of *G. servalina* and *G. victoriae* from outside known ranges were in all cases included within the predictions, in spite of having been excluded from model development (see Section 2; Fig. 1), reinforcing the hypothesis that the species' geographic ranges are broader than previously appreciated. However, for *G. cristata*, almost half of the extralimital specimens fell outside its modeled range (northern Gabon, southeastern Cameroon and northwestern Congo), suggesting that ecological variables – at least, those considered in this study – may not act as the most stringent factors on the crested servaline genet's distribution.

Present-day predicted distributions were reduced by 30% (*G. cristata*), 61% (*G. servalina*), and 44% (*G. victoriae*) when overlaid with the forest cover map (Fig. 3). These reduced distributions, compared with IUCN-listed reserves in the region showed that only 6.1%, 5.8%, and 4.7% of predicted distributions of *G. victoriae*, *G. servalina*, and *G. cristata* are included in existing protected areas, respectively.

4. Discussion

4.1. Species boundaries and re-assessed geographic distributions

Previous attempts to distinguish *G. cristata* and *G. servalina* were based on two coat characters: a continuous mid-dorsal

line, and presence of a nuchal crest (Sanborn, 1940; Rosevear, 1974; characters 1 and 2 in Table 1). Given relatively high variability of coat pattern in genets, these traits have not pro-

vided convincing evidence for some authors to accept species status for *G. cristata* (e.g., Sanborn, 1940; Coetzee, 1971–1977; Honacki et al., 1982; Wozencraft, 1993). Following

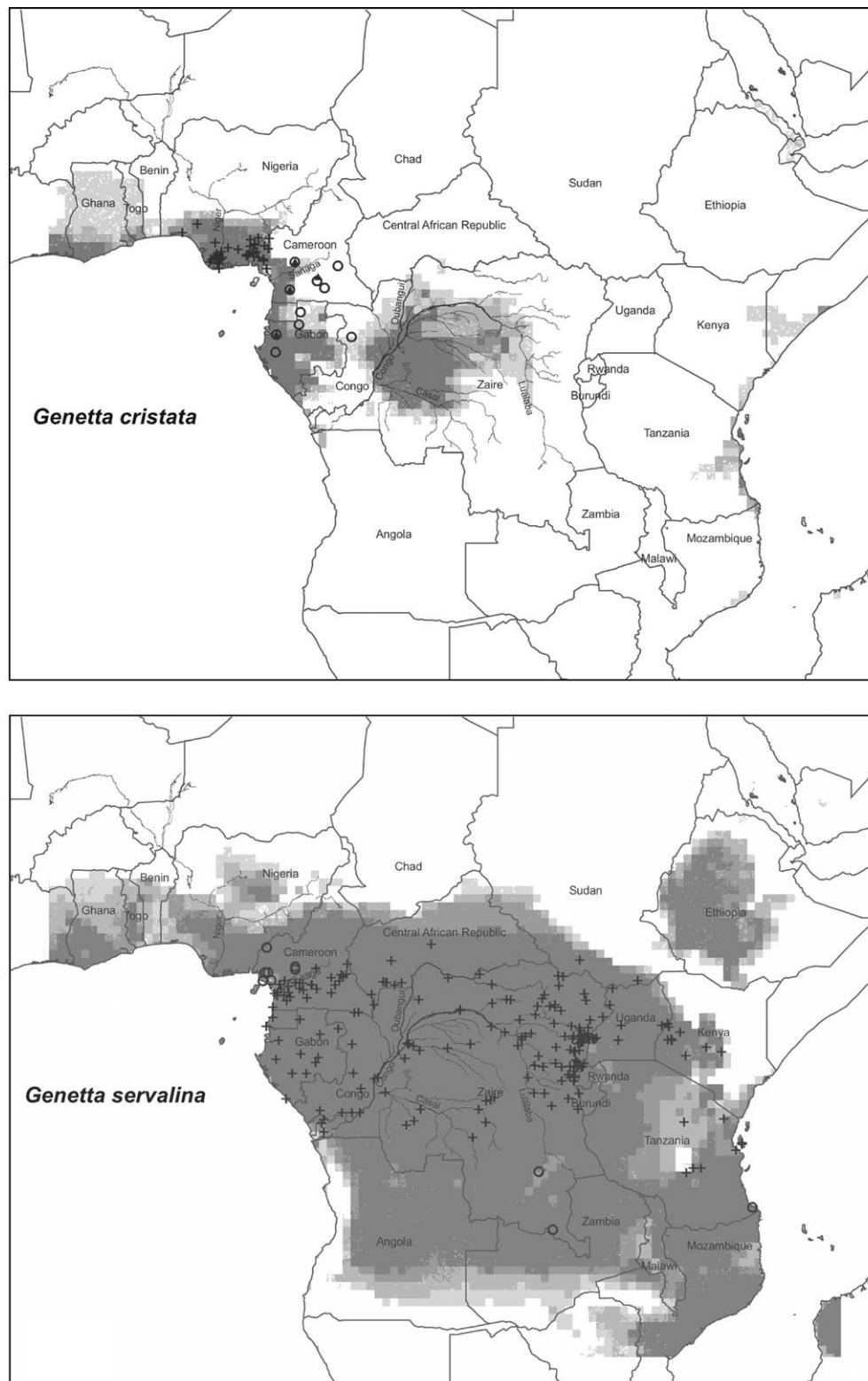


Fig. 1 – Predicted geographic distributions of *Genetta cristata*, *G. servalina*, and *G. victoriae*; dark colors indicate greater agreement between replicate models; black crosses indicate occurrence localities for each species; black circles indicate extralimital specimens, and black triangles indicate putative *G. cristata* × *G. servalina* hybrids (figured in map of *G. cristata*). The latter two symbols indicate localities not included in the GARP analysis.

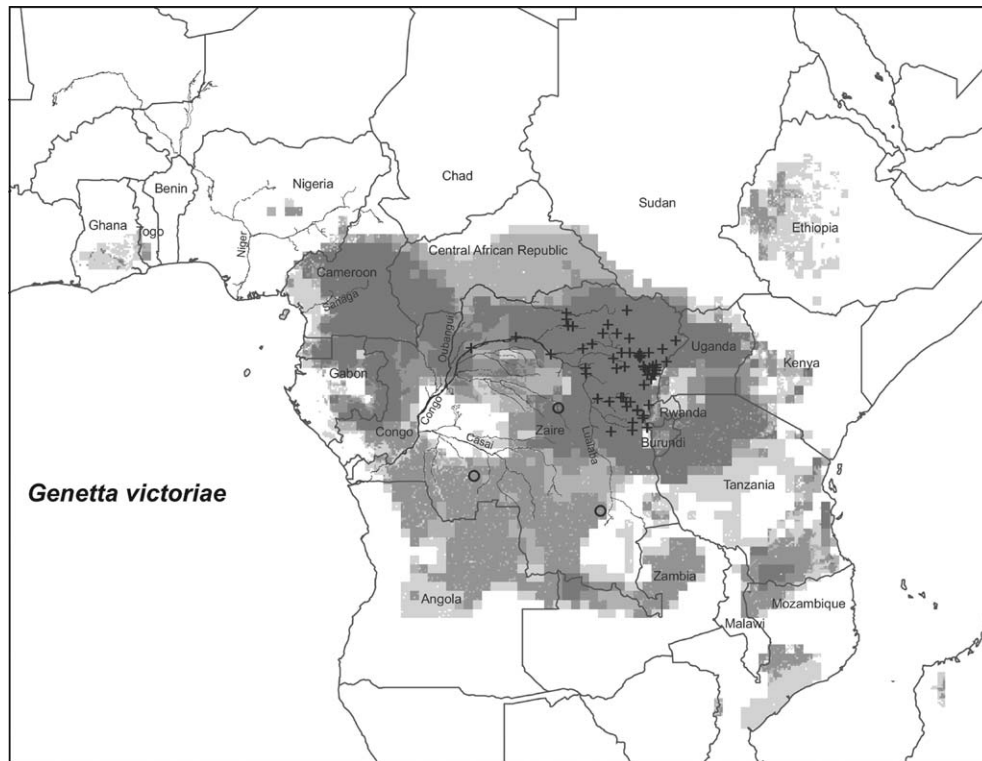


Fig. 1 – continued

Gaubert (2003a) and Gaubert et al. (2004, 2005a), we here added two diagnostic traits (width of bright rings relative to dark rings = 50–75%, and ratio of interorbital constriction to frontal width = 1.00 ± 0.12 ; Table 1) that allowed, in combination with the mid-dorsal line and nuchal crest, unambiguous identification of *G. cristata*.

The clear distinction between the two genets that we observed confirms molecular phylogenetic results suggesting species status of *G. cristata* (Gaubert et al., 2004). Although *G. servalina* specimens from Cameroon and Gabon (*G. s. servalina*) are larger and tend to have longer hairs than those from central and East Africa (Crawford-Cabral, 1970), they did not present a clinal continuum with *G. cristata*. The paler ground color of the dorsal pelage that distinguishes *G. cristata* from *G. servalina* (Sanborn, 1940; Heard and Van Rompaey, 1990; Powell and Van Rompaey, 1998) was less not helpful because of frequent polymorphism.

Here, for the first time, we suggest hybridization between *G. cristata* and *G. servalina*. The putative hybrids all were from a zone of sympatry between the two species (central Cameroon, northwestern Gabon, Congo); morphological polymorphism was absent from specimens from outside this zone. Although “ghost” hybrids (i.e., hybrids not detectable morphologically; Gaubert et al., 2005b) may bias our estimates of levels of hybridization in the region, the limited number of putative hybrids detected (4), together with presence of pure morphotypes of both putative parental species in most (three of four) of the hybrid localities argue again for species status for *G. cristata*.

Our results showed that compiling data from a broad suite of natural history museum collections can greatly increase

knowledge of ranges and habitats of poorly known species (O’Connell et al., 2004). Review of “sleeping” specimens (i.e., unpublished collections), combined with taxonomic expertise, led to significant range expansions, showed that roles of supposed geographic “barriers” (e.g., Sanaga and Congo rivers) needs to be reassessed, and provided new data on habitat use (e.g., Gaubert et al., 2002b; Gaubert, 2003b).

The range of *G. cristata* was expanded >500 km south and 180 km west from what was previously known (Powell and Van Rompaey, 1998). All new *G. cristata* localities were in lowland and submontane (<650 m) rainforests (Cameroon, Gabon, Congo; Fig. 1), which confirms the habitat specificity of the species (Powell and Van Rompaey, 1998; Angelici et al., 1999).

Conversely, *G. servalina* had the broadest distributional and ecological ranges within the tropical zone, extending from the Atlantic to the Indian coasts (Fig. 1). The new *G. servalina* localities in Cameroon (north of the Sanaga River) suggest a zone of sympatry and hybridization with *G. cristata* in lowland rainforest. In addition, the northern and eastern parts of the species’ range, including the new data obtained in this study, clearly evidence tolerance for degraded forest habitats (Central African Republic, Sudan, Uganda, Kenya). This species was also recorded from swamp forest in central Africa, open deciduous shrubland in Congo, submontane/montane rainforest in DRC and Uganda, and deciduous forest in southern DRC, with a wide elevational range (0–3200 m). Our results thus evidenced a broader habitat tolerance for *G. servalina* relative to other species, as already suggested by Goldman and Winther-Hansen (2003). The new localities we found in southern and coastal Tanzania showed that better screening of museum collections would have provided substantial

evidence for the species' presence in this region (Kingdon, 1977) well before rediscovery by De Luca and Mpunga (2002, 2005). Its reassessed distribution reaching coastal Tanzania

argues for natural presence on Zanzibar Island (Van Rompaey and Colyn, 1998), which was likely isolated from the continent during Pleistocene sea level changes (Schlüter, 1997). Our data

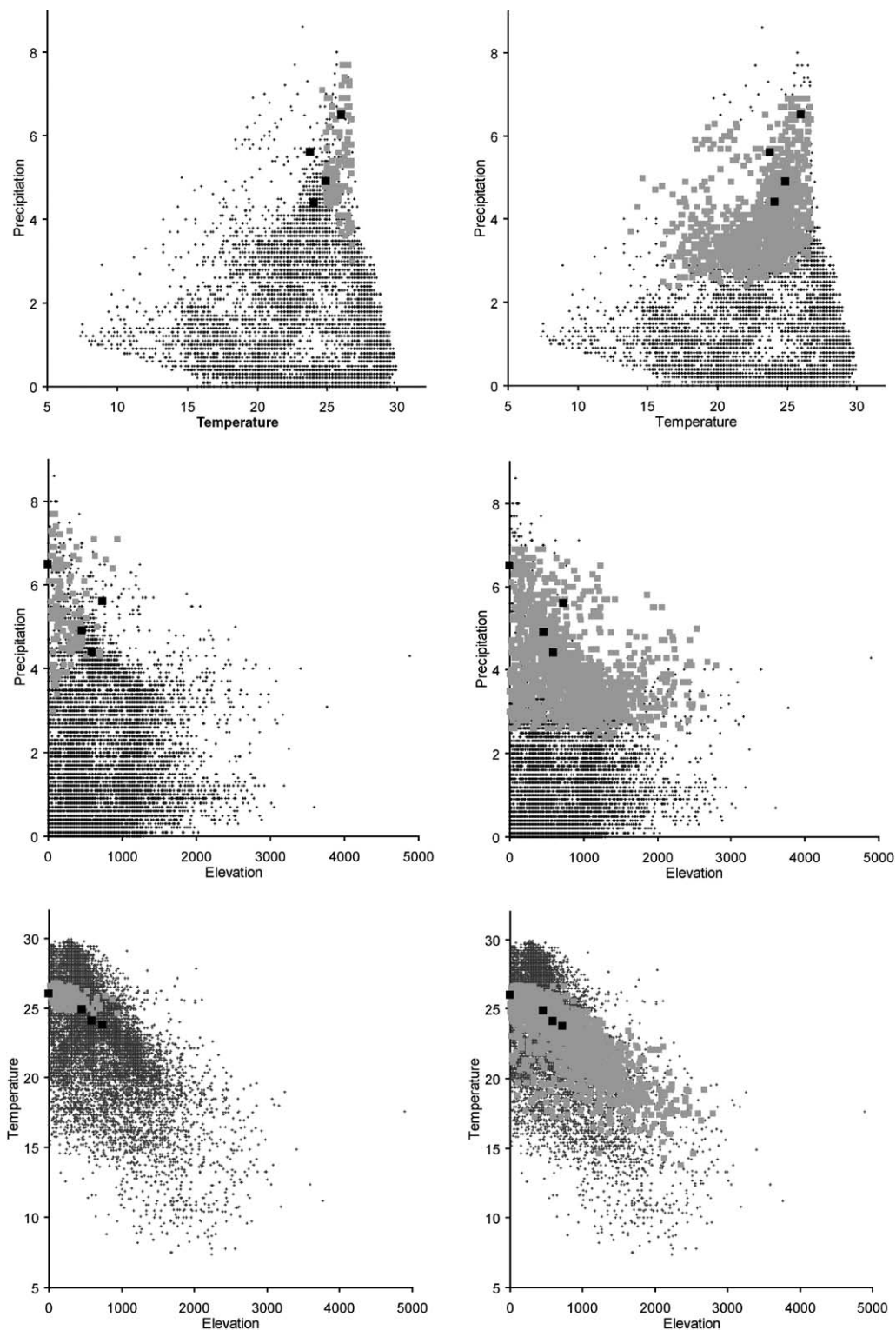


Fig. 2 – Visualization of ecological niches using three ecological variables (mean annual temperature (°C), mean annual precipitation (mm/day), and elevation (m)) for *G. cristata* (left), *G. servalina* (right), and *G. victoriae* (next page). Gray squares represent random subsamples of the ecological space occupied by the three genets; black dots show the total distribution of the ecological variables over the geographic area considered. Black squares indicate the position of the putative *G. cristata* × *G. servalina* hybrids.

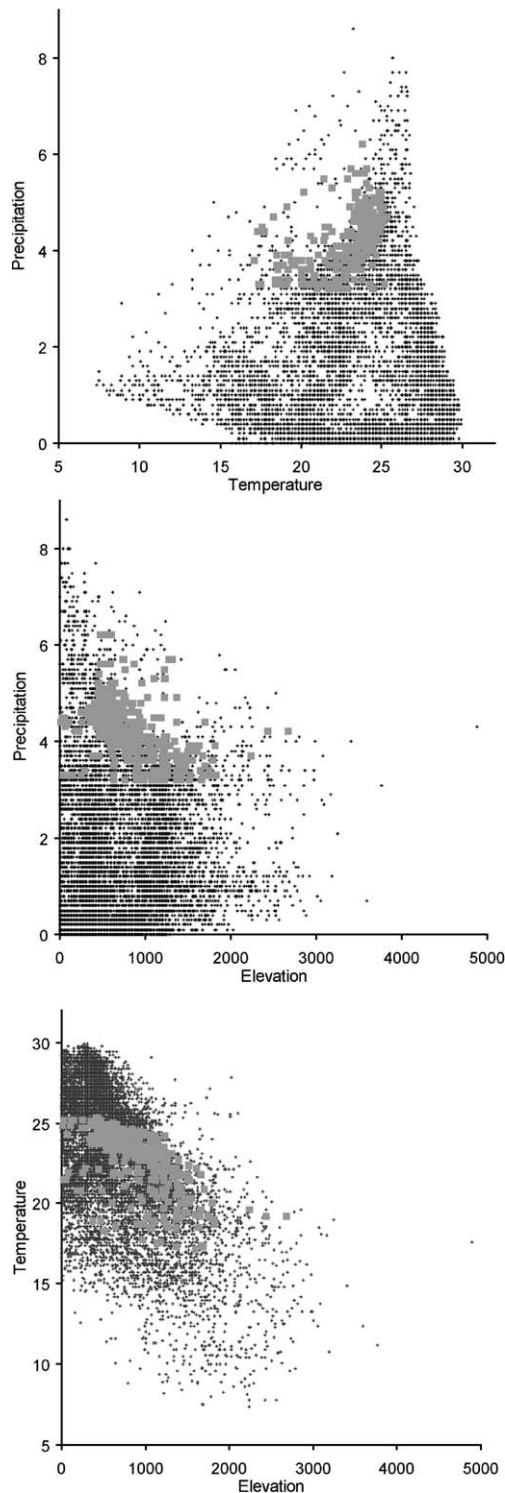


Fig. 2 – continued

also indicate the species' presence in areas now dramatically affected by agriculture (central Kenya and Tanzania); although this species can be found on borders of plantations (P. Gaubert, pers. obs.), further research is necessary to assess its tolerance to disturbed habitats.

Data for *G. victoriae* largely reflected the known range and habitats of the species: swamp forest and lowland-to-montane rainforests on the right bank of the Congo River, DRC

(Fig. 1; Schreiber et al., 1989), and western Uganda (Bere, 1962; Kingdon, 1977). However, our results expanded its range ~500 km south, on the left bank of the Congo River, including two specimens collected from deciduous forest (Kakanga and Mukulu, southern DRC), suggesting a new habitat type for the species.

4.2. Ecological characterization and conservation implications

ENMs successfully recovered the new “extralimital” records that we identified for *G. servalina* and *G. victoriae*, confirming these localities as ecologically “sensible” for the species. Conversely, almost all of the eastern extralimital records of *G. cristata* fell outside its modeled ecological and geographic range, within an ecological regime more typical of *G. servalina*. This finding suggests that: (1) environmental variables other than those considered in our analyses shape the species' distribution, or (2) the hybrid zone in Cameroon and Gabon is broader than expected from the few morphological mosaic specimens that we detected, with *cristata*-like hybrids occupying a *servalina*-like ecological niche.

Modeling ecological niches for the three species showed that almost all known occurrences are geographically connected by suitable ecological conditions (Fig. 1), suggesting relatively continuous, potential distributional areas. This result is particularly important given the scarcity of information about these species in many regions of Africa, leading to hypotheses of geographical isolates or patchy distributions in *G. servalina* and *G. victoriae*, respectively (Kingdon, 1977; Schreiber et al., 1989; Van Rompaey and Colyn, 1998). We suspect that these apparent gaps result from the elusive lifestyle of the genets, difficult access to their habitats, and geographic biases in collecting activities.

As concerns *G. cristata*, the ecological connection between localities from Nigeria-Cameroon and Gabon suggests that suitable conditions are likely to provide continuity with the new southern localities identified in our study, a continuum that could have been easily missed given difficulties in distinguishing *G. cristata* from *G. servalina* (also present in this region). ENM provided, in this case, a useful framework for representing areas where surveys should be concentrated to obtain a better assessment of the distribution and ecology of a poorly known species (Anderson et al., 2002b; Wiley et al., 2003).

When forested habitats were overlaid with potential present-day distributions of species, several otherwise suitable areas were outside of current forest cover, including southern Nigeria for *G. cristata*, southern DRC for *G. victoriae*, and the northern and eastern parts of the range of *G. servalina*. Forest degradation and fragmentation thus appear to be factors potentially important in survival of the genets, although the degree to which these losses are absolute remains to be evaluated. As such, further surveys will be necessary to assess whether the recent, numerous *G. cristata* records from disturbed habitats in southeastern Nigeria are indicative of successful adaptation to human perturbation (Angelici et al., 1999), or simply represent the lag time of persistence in populations that may eventually disappear. *G. victoriae* also appears to be dependent on forest cover; southern DRC

specimens collected in the 1950s may represent a population at risk given high deforestation rates in deciduous forests; again, surveys should be planned in the region to evaluate the species' status. *G. servalina*, because of its broader ecological niche, may show more flexibility towards disturbed and

open habitats, and greater connectivity between disparate populations (notably with the recently rediscovered Tanzanian populations).

That only 4–6% of the predicted distributions of the three genets are covered by protected areas reinforces the idea that

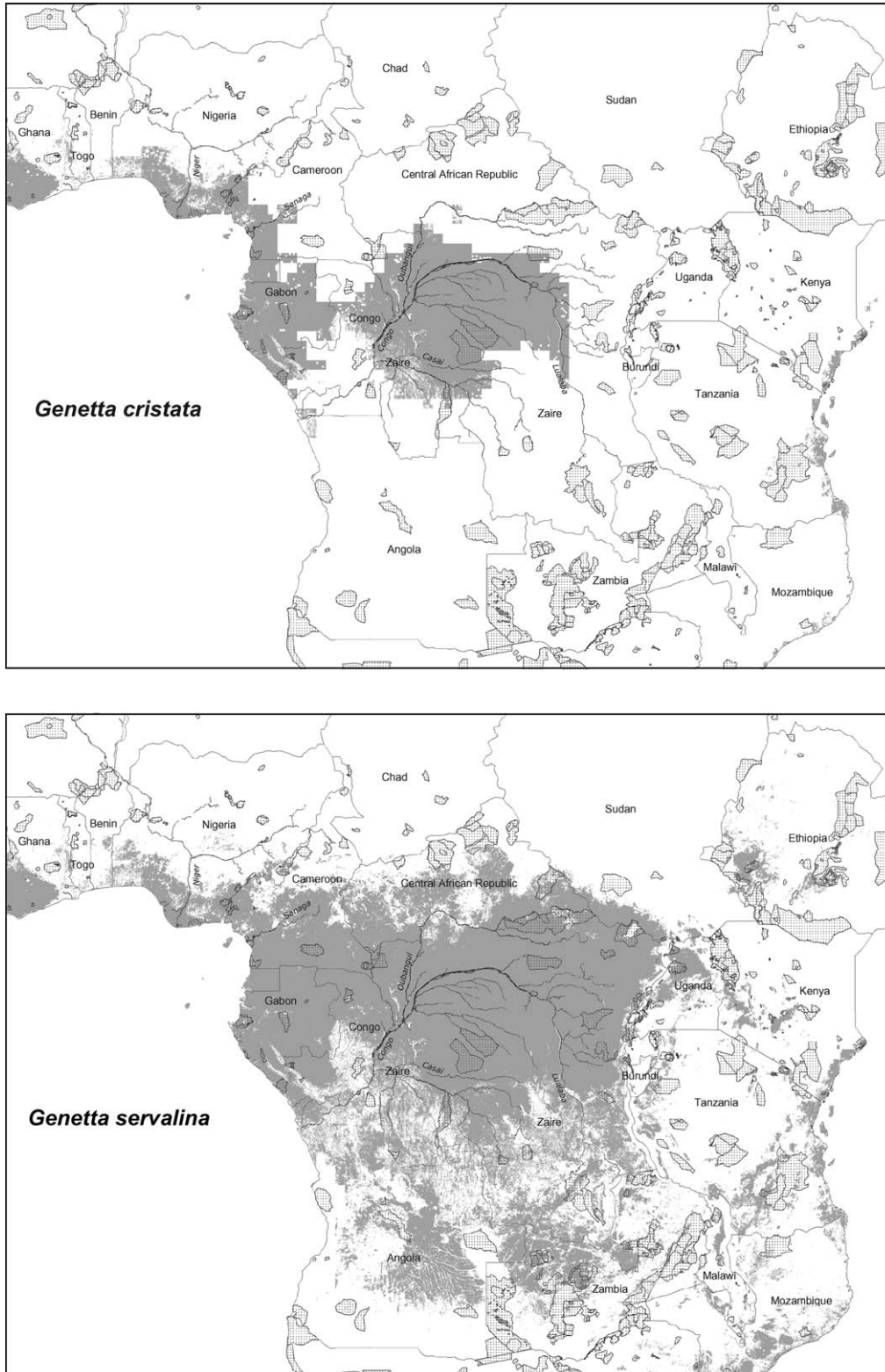


Fig. 3 – Present-day potential geographic distributions of *G. cristata*, *G. servalina*, and *G. victoriae* compared with the forest cover map; IUCN reserves are shown as stippled polygons.

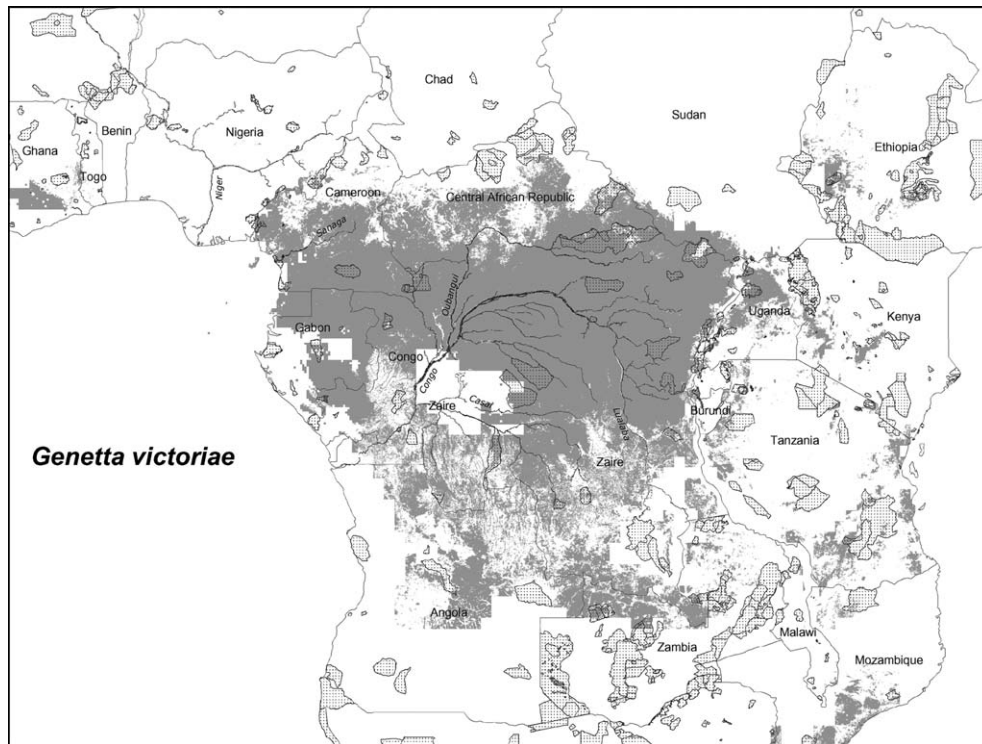


Fig. 3 – continued

field studies are urgently needed to characterize the distributions and ecology of these species better (Schreiber et al., 1989). *G. cristata* and *G. victoriae* are likely to be the most sensitive to forest perturbation because of their restricted ecological potential.

Our investigations combining taxonomic and ecological studies indicate considerable specificity of *G. cristata* relative to *G. servalina* in morphology, geographic distribution, and ecological niche. *G. cristata* should be considered as a distinct species and, as such, should be the subject of appropriate conservation attention.

5. Conclusions

The results of this study demonstrate that the combination of taxonomic investigations and ENM can provide useful insights into biodiversity conservation, shedding new light on species' boundaries by integrating several key suites of information (McNeely, 2002). Our results also exemplify the crucial role of natural history museum collections in improvement of knowledge on the distribution, ecology, evolutionary history, and conservation of poorly known species (Shaffer et al., 1998; Suarez and Tsutsui, 2004). This value is particularly emphasized when analyses that allow for management of spatial sampling bias inherent in museum specimens (Reddy and Davalos, 2003) are employed (Anderson et al., 2002a; Reutter et al., 2003). ENM and related techniques offer a means to derive the greatest benefit from each specimen existing in collections; the information in these collections can guide future field studies to maximize their benefits. In our case, ENM suggested potential connectivity between diverse and supposedly isolated populations where distribu-

tions of the three genet species should be re-assessed urgently. It also showed that a diversified spectrum of habitats should be taken into account in conservation action for these species.

Acknowledgements

P.G. is grateful to the following people and institutions for having given access to their collections and resources: Paula Jenkins and Daphne Hills (Natural History Museum, London, UK); Chris Smeenk (National Museum of Natural History, Leiden, Holland); Wim Van Neer and Wim Wendelen (Musée Royal d'Afrique Centrale, Tervuren, Belgium); Georges Lenglet and Georges Coulon (Institut Royal des Sciences Naturelles de Belgique, Brussels, Belgium); Robert Asher, Manfred Ade, and Irene Thomas (Museum für Naturkunde, Humboldt University, Berlin, Germany); Rainer Hutterer (Zoologisches Forschungsinstitut und Museum Alexander Koenig, Bonn, Germany); Jacques Cuisin and Alain Bens (Muséum National d'Histoire Naturelle, Paris, France); Lawrence Heaney and William Stanley (Field Museum of Natural History, Chicago, USA); and Jean Spence (American Museum of Natural History, New York, USA). The work of P.G. in London, Chicago and New York was supported by a Sys-Resource Grant (IHP Programme), a Travel Grant and a Collection Study Grant, respectively. P.G. thanks Harry Van Rompaey, Francesco M. Angelici and Marc Colyn for their contribution in the compilation of exhaustive distribution data sets for the central African genets. Financial support to M.P. and A.T.P. was provided by a contract from the US Department of Defense. We are grateful to two anonymous reviewers for having significantly improved the quality of the early draft of the manuscript.

Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at [doi:10.1016/j.biocon.2005.12.006](https://doi.org/10.1016/j.biocon.2005.12.006).

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