THERYA, 2023, Vol. 14 (2): 201-206 DOI: 10.12933/therya-23-3864 ISSN 2007-3364

Letter to the Editor:

# Response to Valenzuela-Galvan *et al*. 2023: It is not necessary to "create" a new species for the sake of conservation: the case of the Cozumel's coati

Although we acknowledge the conservation efforts of McFadden *et al.* (2008), we suggest caution in suggesting the existence of a new species without providing sufficient evidence. Recall the work of Zachos (2016), and Zachos *et al.* (2013a, b), which stated that species are such fundamental units that they should not be introduced carelessly and that descriptions and splitting of species based on simple morphometric differences (even significant ones) or phylogenetic relationships derived from limited molecular datasets (for instance, only one or few mtDNA genes) should be strongly discouraged. They may serve to support conclusions derived from larger and more complete datasets, but are not enough on their own. The case of the Cozumel's coati (*Nasua nelsoni*, *Nasua narica nelsoni*, or a special population of *Nasua narica*) is an emblematic example in which multiple authors have considered a taxon to be a full species without providing strong justification.

From our perspective, there are two relevant points to consider in clarifying the issue of whether or not Cozumel's coati is a full species: the null hypothesis we presented and which definition of species should be used. The null hypothesis is that the Cozumel coati and the coati living in the nearby continental México (Campeche, Quintana Roo, Yucatán) are the same species (Cozumel island is separated from the Mexican mainland by 18 km). In Jaramillo and Ruiz-García (2022), we discuss the analysis of a complete mitogenome of a road specimen sampled on Cozumel Island. The specimen was a male with developed testicles, but its overall size was smaller than the coatis we had observed on the Yucatán Peninsula. Based on analysis, the specimen's mitogenome was not significantly different from the mitogenomes of specimens of *N. narica* sampled in the Yucatán Peninsula. In other words, we couldn't reject the null hypothesis and concluded that Cozumel's coati is not a different species from the Yucatán and Quintana Roo mainland coati. Authors claiming that this island coati is a different species, must reject the null hypothesis and demonstrate that the alternative hypothesis —that there are two different species— is more acceptable. However, based on the paper by McFadden *et al.* (2008) and others, there is insufficient evidence to reject the null hypothesis. Next, we discuss the shortcomings of the paper authored by these authors.

1. Valenzuela-Galvan *et al.* (2023) wrote "*Merriam (1901) described the Cozumel dwarf coati* (Nasua nelsoni) *as a distinct species, based on the minute size of Cozumel coatis in comparison to those from the mainland.*" and "*In* McFadden *et al.* (2008) *we start by considering* N. nelsoni *as a distinct species based on Merriam (1901).*" These quotes confirm that the study by Valenzuela-Galvan *et al.* (2023) was initially based on the typological species concept similar to studies conducted by many zoologists during the 19th century as well as the beginning of the 20th century. Because the quote specifically mentions Merriam (1901), we need to determine the criteria Merriam used in distinguishing different species. We find the answer in Merriam (1918). In this study, Merriam distinguished 86 different bear species just in North America. He based these "species" by noting minimal differences in the pelage and skulls of the sample that he analyzed. Today, the majority of these 86 bear taxa are forgotten. As Osgood (1943) claimed, Merriam ordered his findings and labeled them without any effort to interpret them. These zoologists ignored the within phenotypic and genetic variability which naturally occurred within a species, especially if a species has a wide geographical distribution. This mentality was eventually overcome with the arrival of synthetic neo-Darwinism (Dobzhansky 1937, 1970; Mayr 1942, 1963, 1970; Simpson 1944, 1953). Nevertheless, many biologists, including molecular ones, maintain a typological view of biological processes.

There are many examples of island dwarfism in mammals that are not representative of different species (anagenesis or phyletic evolution). For example, the extinct Japanese wolf (*Canis lupus*) and the extinct Balis's tiger (*Panthera tigris balica*) were significantly smaller than their continental counterparts. Mitochondrial DNA analysis showed that the Japanese wolf was indifferentiable from North American wolf lineages (Ishiguro *et al.* 2010; Matsumara *et al.* 2014). Similarly, mtDNA evidence indicates that the Balis's tiger is indifferentiable from the Sumatra tiger (*Panthera tigris sondaica*; Kitchener *et al.* 2017). There are other examples too, such as the goats (*Capra hircus*) introduced into the Juan Fernández archipelago during the 16th and 18th centuries by conquerors and pirates. These goats are half of the size of the goats from which they were derived (Muñoz-Pedreros *et al.* 2003). Recently, Ruiz-García *et al.* (2022) showed that the agouti from the Roatán Island (*Dasyprocta ruatanica;* Honduras), also considered a different species by its size, is molecularly indifferentiable from the Centro-American agouti, *Dasyprocta punctata*. Indeed, both forms of agoutis can breed without problem (Ruiz-García, unpublished observations). It has been shown that artificial, natural, and sexual selection can drastically change the mor-

© 2023 Asociación Mexicana de Mastozoología, www.mastozoologiamexicana.org

phology of different organisms without speciation in a just a small number of generations (the foxes of Belyaev, Dugatkin 2018; *Podarcis sicula*, Herrel *et al.* 2008; or *Poecilia reticulata*, Endler 1980, 1983, 1986; Reznick *et al.* 1997). Additionally, the average height of people within indigenous populations of different Southeast Asian islands (Andaman, Luzon, Panay, and Mindanao islands) is considerably less than that of humans from the Asian continent (Stock 2013; Endicott *et al.* 2003; Deng *et al.* 2022; Zhang *et al.* 2022). However, no one, considers each one of these insular dwarf human populations as different species. Thus, insular dwarfism in mammals is not a sufficient requirement to differentiate a species as is the case of the Cozumel's coati.

2. McFadden *et al.* (2008) claimed the Cozumel's coati as a full species, but they did not demonstrate this affirmation (*i. e.*, they never defined a possible species concept). None of the analyses they carried out showed the Cozumel's coati as a full species (This holds true whether we use the Biological Species Concept, BSC, Mayr 1942, 1963, 2004; or different variants of the Phylogenetic Species Concept, PSC: PSC1, Cracraft 1989, Wheeler and Nixon 1990;PSC2, De Queiroz and Donoghue 1988; PSC3, Baum and Donoghue 1995; Shaw 1998).

McFadden *et al.* (2008) analyzed mt control region data and calculated genetic heterogeneity statistics comparing the Cozumel's coati and the coati found in the Yucatán Peninsula. None of the statistical values they presented were less than 0.05; in other words, the statistical results were not significant ($F_{ST} = 0.166$, $p = 0.061$; $F_{ST} = 0.089$, $p = 0.050$). Therefore, the results presented by McFadden *et al.* (2008) are insufficient to suggest that there is a new species. Additionally, McFadden *et al.* (2008) stated that a global AMOVA supported a significant difference between the Cozumel coati population and other Mexican mainland coati populations. Yet again, statistical evidence did not support a clear difference ($F_{ST} = 0.108$, $p = 0.050$). The genetic distance that they obtained between the Cozumel's coati and the Yucatán counterpart was 0.51 %. Kartavtsev (2011) analyzed sequences of mt *COI* from 20,731 vertebrate and invertebrate animal species and obtained 0.89 % ± 0.16 % for populations within species, 3.78 % ± 1.18 % for subspecies or semispecies, and 11.06 % ± 0.53 % for species within a genus. Bradley and Baker (2001) claimed, for mt *Cytb*, that values less than 2 % would equal intra-specific variation, values between 2 % and 11 % would merit additional study, and values greater than 11 % would be indicative of specific recognition. Avise (1994) determined 5 to 7 % of differences at the mt control region for different species and around 2 % for subspecies in mammals. Thus, the genetic distance between the Cozumel's coati and the Yucatan's coati is at most typical of intra-specific variation. Additionally, McFadden *et al.* (2008) estimated the average temporal split between the Cozumel coati population and the populations of coati from Yucatán peninsula and Belize, respectively. They yielded a temporal value of 6,300 years ago (ya) with the population of Yucatán and around 12,000 ya with the population of Belize. Even, with the most rapid mutation rates, these temporal splits should be around 1,300 ya and 2,400 ya, respectively, which agree well with Decker (1991), Glaston (1994), and Zeveloff (2003) that the coati was introduced when Mayas colonized Cozumel Island around 2,500 years ago. In fact, the bones of Cozumel's coati found in excavations in the island were dated to the Mayan Classic Period (*ca.* 1,300 to 1,700 years bp; Hamblin 1984). In that period, the Cozumel's coati was widespread. Archaeological excavations have found them to be located at several sites on the island with a high number of coati remains found at each site (Hamblin 1984). However, we don't have information about older skeletal remains of this coati. Thus, it is possible that humans introduced this coati taxon in historical times.

Based on text and statistical data in McFadden *et al.* (2008) and McFadden (2004) there is no compelling evidence of a new species. For example, McFadden *et al.* (2008) wrote "*…it is difficult to make conclusions about this population's haplotype diversity or species level uniqueness…*", and, "*…our analyses suggest that the Cozumel taxa are most closely related to their Yucatan and Belize conspecifics…*", and "*…we believe small sample size and low level of population differentiation are responsible for the insignificant Fst value.*" Additionally, McFadden (2004) analyzed sequences of a nuclear gene (*CHRNA1*) which were indifferentiable for Yucatán and Cozumel coatis. Despite of this, the authors considered that the Cozumel's coati was a full species for conservation considerations. Again, based on the presented data and statistical analysis there is insufficient information to reject the aforementioned null hypothesis.

3. Nigenda-Morales *et al.* (2019) carried out a very interesting research project on *N. narica*. They included nine specimens of coatis sampled on Cozumel island. All of the analyses that they carried out (Phylogenetic tree based on maximum likelihood and Bayesian inference of 2,201 base pairs of concatenated mt sequences from three genes, *Cytb, NADH5*, and *16S rRNA*; timetree showing divergence times among the 21 mtDNA haplotypes that they found within *N. narica;* median-joining network with these 21 haplotypes of *N. narica*; genetic clustering [Structure] and neighbor-joining tree based on DA distance based on genotypes of 11 microsatellite loci in 85 specimens) showed the same results. The Cozumel's coati specimens formed a group together with the specimens from Yucatán, Belize, and part of Guatemala. This group is clearly differentiated from the groups of coatis from Morelos, Jalisco, and Arizona-New Mexico, which are all well differentiated from each them. It is interesting to note that if we follow the reasoning of Valenzuela-Galvan *et al.* 2023 these other *N. narica* clusters should be named as full new species of coatis. The rebuttal letter by Valenzuela-Galvan *et al.* 2023 cited Nigenda-Morales *et al.* (2019) and quoted several sentences: "*Nonetheless, the number of samples from Cozumel was low (eight samples) and seven of the samples were from pet or captive raised animals that may have been derived from the mainland*

*and transported to the island. Therefore, we suggest caution in interpreting our results regarding the genetic status of the coati samples from Cozumel. Given the uncertainty about the taxonomic status of the coati population on Cozumel, a more extensive analysis, including more samples and additional loci, will be required to reach any conclusions that could affect the conservation efforts of this population".* However, Valenzuela-Galvan *et al.* (2023) curiously forgot to comment on the following paragraph in the work of Nigenda-Morales *et al.* (2019): "*We did not find significant evidence indicating coatis from Cozumel Island represent a distinct lineage and therefore a different subspecies* (N. n. nelsoni) *from those on the Yucatan peninsula* (N. n. yucatanica*; table A.4, A.9; figure 1B, 3, 6). These results are largely consistent with the findings of* McFadden *et al.* (2008) *based on mtDNA control region sequence data that coatis on Cozumel Island may have colonized the island during the Late Pleistocene or Holocene (possibly through human-mediated dispersal)".* Therefore, Nigenda-Morales *et al.* (2019) also did not reject the null hypothesis that was mentioned earlier. It is always possible that the two specimens of McFadden (2004) and McFadden *et al.* (2008), the nine specimens of Nigenda-Morales *et al.* (2019), and the specimen of Jaramillo and Ruiz-García (2022), although sampled in the Cozumel island, do not represent the "true" Cozumel's coati because all of them may have been derived from the mainland and transported to the island, but the likelihood of that happening would have been extremely low.

4. When we wrote the article of Jaramillo and Ruiz-García (2022), we ignored the existence of the work of Flores-Manzanero *et al.* (2022). Flores-Manzanero *et al.* (2022) analyzed samples from 46 individuals of the Cozumel's coati (that were captured alive on site) and performed an analysis of mt *Cytb* and nuclear microsatellites. The authors obtained two main results. By using the Structure Program applied to microsatellite data, the authors demonstrated that the Cozumel's coati population was differentiated from the populations in Jalisco and Morelos (figure 2b). However, this result was not new. Nigenda-Morales *et al.* (2019) had already communicated this result to the scientific community. Curiously, the analysis by Flores-Manzanero *et al.* (2022) did not include coati specimens from Quintana Roo, Yucatán, and Campeche, which were genetically similar to the Cozumel's coati (Nigenda-Morales *et al.* 2019; Jaramillo and Ruiz-García 2022). Obviously, if they had introduced specimens from these nearby Mexican mainland areas, the differentiation of the Cozumel's coati would have been less conspicuous (conservation prejudice). On the other hand, multiple populations of the same species can significantly diverge for a set of microsatellites but this does not mean that they are different species. For instance, populations of pink river dolphins (*Inia geoffrensis*) from two Colombian rivers (Putumayo and Caquetá) and from different Peruvian rivers are significantly different based on microsatellite data (Ruiz-García 2010; Ruiz-García *et al.* 2018). Similarly, different populations of the Andean cat (*Leopardus jacobita*) from Perú, Bolivia, and Argentina are considered significantly different based on seven microsatellites (Cossíos *et al.* 2012; Ruiz-García *et al.* 2013a). Additionally, different populations of ocelots (*Leopardus pardalis*) throughout South American are significantly different at 10 microsatellites (Ruiz-García *et al.* 2013b). The last example we mention here from a very long list of examples is humans. Indigene human populations in South America are significantly different for 15 microsatellites (Demarchi 2009). Does this mean that they are different species because they have significant differences for nuclear microsatellites? The answer is no. In reference to the mt*Cytb*, Flores-Manzanero *et al.* (2022) showed a phylogenetic tree in figure 3. The authors found that the specimens from Jalisco and Morelos conformed well differentiated clades from the clade of the Cozumel's coati. Again, the scientific community had already been informed about this finding three years earlier (Nigenda-Morales *et al.* 2019). Within the Cozumel's coati clade, Flores-Manzanero *et al.* (2022) found three sub-clades. One of them included a few specimens from Quintana Roo that the authors included in their analysis. Therefore, no reciprocal monophyly exists between the Cozumel's coati and the coatis from the nearby Mexican mainland. Additionally, if Flores-Manzanero *et al.* (2022) had enclosed more specimens from Quintana Roo, Yucatán, or Campeche, surely more specimens of these Mexican mainland areas would have been clustered with the Cozumel's coati group. In other words, similar to McFadden (2004), McFadden *et al.* (2008), Nigenda-Morales *et al.* (2019), and Jaramillo and Ruiz-García (2022), Flores-Manzanero *et al.* (2022), did not reject the null hypothesis that *N. narica* and the Cozumel's coati are different species. In fact, Flores-Manzanero *et al.* (2022) indicated that they knew it was not a full species when they wrote "*These results support that, at least following the precautionary principle, the Cozumel dwarf coati should be considered and managed as a Significant Evolutionary Unit (sensu Moritz, 1994)".* Notwithstanding, the Cozumel's coati does not fit the definition of an ESU (sensu Moritz 1994). An ESU should be reciprocally monophyletic for mtDNA and this is not the case with the Cozumel's coati. The Cozumel's coati is, more likely, an example of a management unit (MU). Moritz (1994) originally defined an MU as a population that showed significant differences in allele frequencies at nuclear or mtDNA loci. This can show that their population dynamics depend more on local birth and death rates than on immigration (demographical independence; Bentzen 1998).

There are many definitions of a species besides those previously cited (BSC, PSC1, PSC2, PSC3) such as the Genotypic Cluster Species Concept (GCSC; Mallet 1995), Recognition Species Concept (RSC; Paterson 1985; Lambert *et al.* 1987), Cohesion Species Concept (CSC; Templeton 1989), etc. The Cozumel's coati does not meet most of these definitions. But, the most universally accepted concept is the BSC, in part because it is the one we apply to our own species. We agree with the explanation about concepts offered by Mayr (2004): "*it is very important to understand what the* *word concept means when combined with the word species. It implies the meaning of the species in nature. A population, or group of populations, is a species, according to BSC, if it configures a reproductive community and does not reproduce with members of similar communities. BSC, as defined, plays a concrete role in nature and differs in this respect from all those other so-called concepts of species that are nothing but instructions, based on human judgment, about how to delimit specific taxons."* Clearly, the Cozumel's coati is not "above" the BSC. It would not be surprising that the authors who support the Cozumel's coati as a full species, have some doubts about their suggestion. Why? The *N. narica* from the Mexican mainland is known to have been brought over to Cozumel (historically as pets), and it is suspected that they may have interbred with the island coati (Gomper, and others). There are no reproductive isolation barriers between the Cozumel's coati and the nearby Mexican mainland coati. In other words, the Cozumel's coati is the same species of coati that is found in the Mexican mainland.

Nevertheless, conservation biological prejudice exists (see McFadden 2004): "*Depending on how strictly one interprets the biological species definition (O'Brien and Mayr 1991), the island taxa of* N. nelsoni *could thus be classified as the same species as the mainland taxa of* N. narica. *If the criterion of reproductive isolation is generally applied, the taxa of dwarf carnivores may go unrecognized as evolutionarily differentiated populations and thus separate conservation units."* But it is not necessary to define new species to conserve "special" populations such as the Cozumel's coati (even biological conservation can be endangered by partition of a species in different supposed species; see Zachos *et al.* 2013b). For example, the US Endangered Species Act (ESA) of the United States has been a major stimulus to develop criteria for identifying intraspecific population units for biological conservation. The ESA provides full legal protection for subspecies and for Distinct Population Segments (DPSs) of vertebrate species, as if they were full species.

In conclusion, we agree with Valenzuela-Galvan *et al.* 2023 that the Cozumel's coati should be actively and urgently protected by Mexican institutions, but we urge caution in accepting the existence of a new species unless statistical analysis (p value less than 0.05) rejects the null hypothesis (*i. e.*, no difference).

Manuel Ruiz-García[1]*, Maria Fernanda Jaramillo[1], and Joseph Mark Shostell[2]

[1]Laboratorio de Genética de Poblaciones Molecular-Biología Evolutiva, Departamento de Biología, Facultad de Ciencias, Pontifcia Universidad Javeriana, Cra 7A, No. 43-82, Bogotá, DC, Colombia. Email: ocmafe@hotmail.com (MFJ), mruizgar@yahoo.es (MR-G).

[2]Math, Science and Technology Department, University of Minnesota Crookston, 2900 University Ave, Crookston, MN 56716, USA. Email: joseph.shostell@gmail.com (JMS).

*Corresponding author: https://orcid.org/0000-0003-2820-2950

## Literature cited

Avise, J. C. 1994. Molecular Markers, Natural History, and Evolution. Chapman and Hall, New York.

Bradley, R. D., and R. J. Baker. 2001. A test of the genetic species concept: cytochrome-b sequences and mammals. Journal of Mammalogy 82:960–973.

Baum, D. A., and M. J. Donoghue. 1995. Choosing among alternative phylogenetic species concepts. Systematic Botanic 20:560-573.

Bentzen, P. 1998. Seeking evidence of local stock structure using molecular genetic methods. Pp 244-266, *in* The implications of localized fisheery stocks (Hunt von Herbing, I., I. Kornfield, M. Tupper, and I. Wilson, eds). New York: Regional Agricultural Engineering Service. New York, U.S.A.

Cossíos, E. D., *et al.* 2012. Between high-altitude islands and high-altitude corridors. The population structure of the Andean cat (*Leopardus jacobita*). Endangered Species Research 16:283-294.

Cracraft, J. 1989. Speciation and its ontology: The empirical consequences of alternative species concepts for understanding patterns and process of differentiation. Pp. 28-59, *in* Speciation and its consequences (Otte, D., and J. A. Endler, eds.). Sinauer Associates. Sunderland, U.S.A.

Decker, D. M. 1991. Systematics of the coatis, genus *Nasua* (Mammalia: Procyonidae). Proceedings of the Biological Society of Washington 104:370-386.

Demarchi, D. A. 2009. Microsatélites, distancias genéticas y estructura de poblaciones nativas sudamericanas. Revista Argentina de Antropología Biológica 11:73-88.

Deng, L., *et al.* 2022. Genetic Connections and Convergent Evolution of Tropical Indigenous Peoples in Asia. Molecular Biology and Evolution 39:1-33.

De Queiroz, K. and M. J. Donoghue. 1988. Phylogenetic systematics and the species problem. Cladistics 4:317–338.

Dobzhansky, T. 1937. Genetics and origin of species. Columbia University Press. New York, U.S.A.

Dobzhansky, T. 1970. Genetics of the evolutionary process. Columbia University Press. New York, U.S.A.

Dugatkin, L. A. 2018. The silver fox domestication experiment. Evolution: Education and Outreach 11: 16-20.

Endicott, P. *et al.* 2003. The genetic origins of the Andaman Islanders. American Journal of Human Genetics 72: 178–184.

Endler, J. A. 1980. Natural selection on color patterns in *Poecilia reticulata*. Evolution 34:76-91.

Endler, J. A. 1983. Natural and sexual selection on color patterns in poeciliid fishes. Environmental Biology of Fishes 9:173-190.

Endler, J. A. 1986. Natural selection in the wild. Princeton University Press. Princenton, USA.

Flores-Manzanero, A., *et al.* 2022. Conservation genetics of two critically endangered island dwarf carnivores. Conservation Genetics 23:35-49.

Glatston, A. R. (compiler). 1994. Status survey and conservation action plan for Procyonids and Ailurids. The ed Panda, Olingos, Coatis, Raccoons, and their Relatives. IUCN. Gland, Switzerland.

Hamblin, N. L. 1984. Animal use by the Cozumel Maya. University of Arizona Press. Tucson, U.S.A.

Herrell, A., *et al*. 2008. Rapid large-scale evolutionary divergence in morphology and performance associated with explotation of a different dietary resource. Proceedings of the National Academy of Sciences 105:4792-4795.

Ishiguro N., Y. Inoshim, and N. Shigehara. 2010. Mitochondrial DNA analysis of the Japanese wolf (*Canis lupus hodophilax* Temminck, 1839) and comparison with representative wolf and domestic dog haplotypes. Zoological Science 26:765–770

Jaramillo, M. F., and M. Ruiz-García. 2022. Evidence of the genetic and spatial structure of *Nasua narica* in Central America and northern South America from mitogenomic analysis. Therya 13:205-224.

Kartavtsev, Y. 2011. Divergence at *Cyt-b* and *Co-1* mtDNA genes on different taxonomic levels and genetics of speciation in animals. Mitochondrial DNA 22:55–65.

Kitchener, A. C., *et al*. 2017. A revised taxonomy of the Felidae. The final report of the Cat Classication Task Force of the IUCN/SSC Cat Specialist Group. Cat News Special Issue 11. Bern, Switzerland.

Lambert, D. M., B. Michaux, and C. S. White. 1987. Are species self-defining? Systematic Zoology 36:196-205.

Mallet, J. 2005. A species definition for the modern synthesis. Trends in Ecology and Evolution 10:294-299.

Matsumura, S., Y. Inoshima, and N. Ishiguro. 2014. Reconstructing the colonization history of lost wolf lineages by the analysis of the mitochondrial genome. Molecular Phylogenetics and Evolution 80:105–112.

Mayr, E. 1942. Systematics and the origin of species. Columbia University Press. New York, U.S.A.

Mayr, E. 1963. Animal Species and Evolution. Harvard University Press. Cambridge, U.S.A.

Mayr, E. 1970. Populations, Species and Evolution. Harvard University Press. Cambridge, U.S.A.

Mayr, E. 2004. What makes biology unique? Considerations on the autonomy of a scientific discipline. The Press Syndicate of the University of Cambridge. Cambridge, U.S.A.

McFadden, K. W. 2004. The Ecology, Evolution and Natural History of the Endangered Carnivores of Cozumel Island, Mexico. PhD Thesis. Columbia University. New York, U.S.A

McFadden, K. W., *et al*. 2008. Evolutionary history of the critically endangered Cozumel dwarf carnivores inferred from mitochondrial DNA analyses. Journal of Zoology 276:176-186.

Merriam, C. H. 1901. Six new mammals from Cozumel Island, Yucatan. Proceedings of the Biological Society of Washington 14:99-104.

Merriam, C. H. 1918. Review of the grizzly and big brown bears of North America (genus *Ursus*) with descrption of a new genus *Vetularctos*. North America Fauna 41:1-137.

Moritz, C. 1994. Defining 'evolutionarily significant units' for conservation. Trends in Ecology and Evolution 9:373-375.

Muñoz-Pedreros, A., *et al*. Control integrado de plagas del Archipielago de Juan Fernandez, Chile. Informe técnico para el Proyecto CONAF/Holanda. Centro de Estudios Agrarios y Ambientales CEA. Valdivia, Chile.

Nigenda-Morales, S. F., *et al*. 2019. Phylogeographic and diversification patterns of the white-nosed coati (*Nasua narica*): Evidence for south-to-north colonization of North America. Molecular Phylogenetics and Evolution 131:149-163.

O'Brien, S. J., and E. Mayr. 1991. Bureaucratic mischief: recognizing endangered species and subspecies. Science 251:1187-1188.

Osgood, W. H. 1943. Clinton Hart Merriam 1855-1942. Journal of Mammalogy 24:421.

Paterson, H. E. H. 1985. The recognition concept of species. Pp. 21-29, *in* Species and speciation (Vrba, E. S., ed.). Transvaal Museum Monograph No 4. Pretoria, Sudafrica.

Reznick, D. N., *et al*. 1997. Evaluation of the rate of evolution in natural populations of guppies (*Poecilia reticulata*). Science 275:1934-1937.

Ruiz-García, M. 2010. Changes in the demographic trends of pink river dolphins (*Inia*) at the micro-geographical level in Peruvian and Bolivian rivers and within the upper Amazon: microsatellites and mtDNA analyses and insights into *Inia*'s origin. Pp. 161-192, *in* Biology, Evolution, and Conservation of River Dolphins within South America and Asia. (Ruiz-García, M., and J. M. Shostell, eds.). Nova Science Publishers Inc. New York, U.S.A.

Ruiz-García, M., *et al*. 2022. Mitogenomic phylogenetics and population genetics of several taxa of agouties (*Dasyprocta* sp., Dasyproctidae, Rodentia): molecular nonexistence of some claimed endemic taxa. Mammal Research 67:367-397.

Ruiz-García, M., *et al*. 2013a. Population genetics and spatial structure in two Andean cats (the Pampas cat, *Leopardus pajeros*, and the Andean cat, *L. jacobita*) by means of nuclear and mitochondrial markers and some notes on skull biometrics. Pp. 187-244, *in* Molecular population genetics. Evolutionary biology and biological conservation of Neotropical carnivores (Ruiz-García, M., and J. M. Shostell, eds.). Nova Science Publishers Inc. New York, U.S.A.

Ruiz-García, M., C. Corrales, and M. Pinedo-Castro. 2013b. Craniometric and microsatellite differentiation among putative ocelot subspecies (*Leopardus pardalis*) throughout Latin America. Pp. 289-332, *in* Molecular population genetics. ,Evolutionary biology and biological conservation of Neotropical carnivores (Ruiz-García, M., and J. M. Shostell, eds). Nova Science Publishers Inc. New York, U.S.A.

Ruiz-García, M., *et al*. 2018. Biodiversity in the Amazon: origin hypotheses, intrinsic capacity of species colonization, and comparative phylogeography of river otters (*Lontra longicaudis* and *Pteronura brasiliensis*, Mustelidae, Carnivora) and pink river dolphin (*Inia* sp., Iniidae, Cetacea). Journal of Mammalian Evolution 25:213–240.

Shaw, K. L. 1998. Species and the diversity of natural groups. Pp. 44-56, *in* Endless Forms: Species and Speciation (Howard, D. J., and S. J. Berlocher, eds.). Oxford University Press. Oxford, U.K..

Simpson, G. G. 1944. Tempo and mode in evolution. Columbia University Press. New York, U.S.A.

Simpson, G. G. 1953. The major features of evolution. Columbia University Press. New York, U.S.A.

Stock, J. T. 2013. The skeletal phenotype of "negritos" from the Andaman Islands and Philippines relative to global variation among hunter-gatherers. Human Biology 85:67-94.

Templeton, A. R. 1989. The meaning of species and speciation: a genetic perspective. Pp. 3-27, *in* Speciation and its consequence (Otte, D., and J. A. Endler, eds.). Sinauer Associates. Sunderland, U.S.A.

Valenzuela-Galván, D., *et al.* 2023. A single sample is not enough to claim systematic conclusions, much less for taxa of conservation concern: comments on Jaramillo and Ruiz-García (2022). Therya 14:197-199.

Wheeler, Q. D., and K. C. Nixon. 1990. Another way of looking at the species problem: A reply to de Queiroz and Donoghue. Cladistics 6:77-81.

Zachos, F. E. 2016. Tree thinking and species delimitation: Guidelines for taxonomy and phylogenetic terminology. Mammalian Biology 81:185-188.

Zachos, F. E., *et al.* 2013a. Species inflation and taxonomic artefacts—A critical comment on recent trends in mammalian classification. Mammalian Biology 78:1-6.

Zachos, F. E., *et al.* 2013b. Species splitting puts conservation at risk. Nature 494:35.

Zhang, X., *et al.* 2022. The distinct morphological phenotypes of Southeast Asian aborigines are shaped by novel mechanisms for adaptation to tropical rainforests. National Science Review 9:nwab072.

Zeveloff, S. I. 2003. A review of the taxonomic and conservation statuses of the island raccoons. Small Carnivore Conservation 29:10–12.