



Molecular phylogenetics of the white-lipped peccary (*Tayassu pecari*) did not confirm morphological subspecies in northwestern South America

M. Ruiz-García¹, M. Pinedo-Castro¹, K. Luengas-Villamil¹, C. Vergara^{1,2}, J.A. Rodríguez³ and J.M. Shostell⁴

¹Laboratorio de Genética de Poblaciones-Biología Evolutiva, Unidad de Genética, Departamento de Biología, Facultad de Ciencias, Pontificia Universidad Javeriana, Bogotá, DC, Colombia

²Instituto de Innovación en Biotecnología e Industria, Unidad de Biotecnología Médica, Santo Domingo, Republica Dominicana

³Instituto de Investigación de la Orinoquia Colombiana, Facultad de Ciencias Básicas e Ingenierías, Universidad de Los Llanos, Unillanos, Sede Barcelona, Colombia

⁴Biology Department, Penn State University-Fayette, Uniontown, PA, USA

Corresponding author: M. Ruiz-García

E-mail: mruiz@javeriana.edu.co / mruizgar@yahoo.es

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ABSTRACT. We sequenced the mitochondrial DNA (mtDNA) control region of 59 peccaries (44 white-lipped peccaries, *Tayassu pecari*, and 15 collared peccaries, *Pecari tajacu*). We also genotyped 3 DNA microsatellites from 78 white-lipped peccaries representing the 4 putative morphological subspecies (i.e., *spiradens*, *aequatoris*, *pecari*, and *albirostris*) present in northwestern South America (i.e., Colombia, Ecuador, Peru, and Bolivia). Our results showed:

1) the estimated diversity of the mtDNA control region in the *T. pecari* population was extremely high, whereas the average genetic diversity for the microsatellites was medium to high and similar to that observed in European pig breeds; 2) there was no significant genetic heterogeneity among the quoted putative morphological subspecies at the mitochondrial marker, but we did detect significant (although relatively small) genetic heterogeneity using microsatellites, indicating that *T. pecari albirostris* is a uniquely differentiated group; and 3) the phylogenetic mtDNA trees showed that haplotypes were intermixed independent of their “a priori” subspecies classification. In addition, the microsatellite assignment analyses yielded low percentages of well-classified individuals when the analysis considered the geographic morphology of the subspecies. Thus, the molecular results do not support the putative morphological subspecies of *T. pecari* in northwestern South America. Finally, our results did not detect clear historical demographic changes using the mtDNA control region sequences. These genetic results are discussed in the context of the ecological and social characteristics of *T. pecari*.

Key words: *Tayassu pecari*; Mitochondrial sequences; Microsatellites; Genetic heterogeneity; Demographic changes