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Hox genes are major transcriptional regulators that play roles in fate specification of regional identity along the antero-posterior axis. Seminal functional studies in insect and crustacean taxa have supported a role for Hox genes in the evolution of tagmatic boundaries. In arachnids, functional data on Hox homologs remain limited, though a previous work has linked *Antennapedia-1* (*Antp-1*) with the establishment of the prosomal-opisthosomal boundary. In that work, only the morphology of the RNAi embryos was reported; the functionality of the ectopic legs of the pedicel remains unknown. Here, we focused on the potential for the first opisthosomal segment of spiders (the vestigial pedicel) to form a pair of fully functional appendages. To induce ectopic legs, we replicated an experiment wherein we silenced *Antp-1* using maternal RNA interference and thus generated 10-legged spiders. To assess innervation and internal morphology during embryogenesis, we deployed fluorescent immunohistochemical staining to mark tropomyosin (a muscle marker) and acetylated tubulin (a neural marker). To assess proper morphogenesis of the appendages, we assayed for the incidence of proper podomere boundaries and sensory organs at the postembryo stage. Finally, to assess the motility of the ectopic appendage, we observed the use of the fifth leg pair in first instar stages. Our data show that the ectopic leg pair induced by *Antp-1* knockdown is functional in a subset of phenotypes.

Keywords: morphogenesis, genetic basis, *Parasteatoda tepidariorum*
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Nuevo género de tarántulas endémico de Perú (Araneae: Mygalomorphae: Theraphosidae)

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La familia Theraphosidae comprende a las arañas más grandes del mundo conocidas y engloba unos 149 géneros y 987 especies presentes en regiones tropicales y subtropicales de todos los continentes a excepción de la Antártida. La subfamilia Theraphosinae es exclusivamente Neotropical caracterizada por la presencia de setas urticantes como mecanismo de defensa. A partir de la examinación de material proveniente de la colección del MUSM de Lima, Perú, fue posible el reconocimiento de especímenes con setas urticantes de tipo III que compartían la forma del bulbo y quillas del émbolo como así también la forma general de la espermatecas de las hembras. En base al estudio detallado de su morfología junto con el análisis filogenético molecular involucrando tres genes, se propone un nuevo género de Theraphosidae presente exclusivamente en Perú. El nuevo

género se recuperó como monofilético y grupo hermano del género *Hapalotremus* a partir de la evidencia molecular. El *Gen. n.* comprende tarántulas de tamaño mediano y se diferencia de los restantes conocidos (excepto *Catanduba*, *Cyriocosmus* y *Kochiana*) en la presencia de setas urticantes de tipo III localizadas en un parche abdominal dorsal en combinación con cuatro quillas en el bulbo: prolateral superior, inferior, apical y subapical; y espermatecas compuestas por dos receptáculos seminales divergentes. Además, difiere de los géneros mencionados anteriormente y de *Hapalotremus* (grupo hermano) por la presencia de setas espiniformes en la cara ventral de las maxilas, forma del bulbo copulador en los machos y forma de las espermatecas en hembras. El *Gen. n.* propuesto contiene 7 nuevas especies, de las cuales cinco se conocen de machos y hembras, y dos de ellas solo de hembras. Las especies se distribuyen en la región Andina del centro de Perú, en los departamentos de Junín, Huancavelica y Ayacucho en altitudes entre los 3836 y 4689 metros sobre el nivel del mar y con temperaturas por debajo de los 0°C. Estas arañas habitan debajo de piedras u ocasionalmente pueden ocupar cuevas abandonadas.

Palabras clave: Theraphosinae, taxonomía, nuevas especies, sudamérica
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Molecular phylogeny of the tropical wandering spiders (Ctenidae) and the evolution of the eye conformation in the RTA clade

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Tropical wandering spiders (Ctenidae) are a diverse family within the order Araneae, reaching their greatest richness in the tropics. Their large size and predominant abundance in most tropical forests suggest that ctenids play an important role in tropical ecosystems as top generalist predators of invertebrates and small vertebrates. Traditionally, Ctenidae is diagnosed based on the presence of eight eyes arranged in three rows (2-4-2), bringing together a great diversity of morphotypes specialized in different habitats -e.g., litter, low vegetation, arboreal and aquatic-. Although to date morphological and molecular phylogenies have included few representatives of Ctenidae, these hypotheses suggest that the characteristic ocular pattern of the ctenidae has evolved independently in other families of the RTA clade. This study presents a molecular phylogeny of Ctenidae, including for the first time representatives of all subfamilies (Acantheinae, Cteninae, Acanthocteninae and Calocteninae). The molecular phylogeny was estimated using five nuclear (H3, 28S, 18S, Actin and ITS-2) and four mitochondrial (NADH, COI, 12S, 16S) markers for a total of 9,030 base pairs. This matrix was composed of 90 ctenid species and a total of 130 terminals, including representatives of other families of the RTA clade as outgroups. Phylogenetic analyses of maximum likelihood, parsimony, and Bayesian inference were carried out using the TNT, IQTREE and BEAST programs, respectively. Furthermore, the evolution of ocular conformation in the RTA clade was studied using maximum likelihood methods with the *APE* and *Phytools* R packages. The monophyly of Ctenidae was recovered with low support in the