Diversification patterns based on the largest morphological phylogenetic analysis of Pleurodira

Gabriel S. Ferreira*[1], Juliana Sterli[2], Mario Bronzati Filho[3,4], Max C. Langer[1].

(1) Laboratório de Paleontologia de Ribeirão Preto, Faculdade de Filosofia Ciências e Letras de Ribeirão Preto, Universidade de São Paulo, Ribeirão Preto, SP, Brazil. (2) CONICET - Museo Paleontológico Egidio Feruglio, Trelew, Chubut, Argentina. (3) Ludwig-Maximilians-Universität München, Munich, Germany. (4) Bayerische Staatssammlung für Paläontologie und Geologie, Munich, Germany.

* gsferreirabio@gmail.com

Background. Most studies on pleurodiran turtles are about the behavior and/or feeding habits analyzes, description of new taxa or specimens (both extinct and extant), or phylogenetic analyzes of one of its subclades with extant taxa: Chelidae, Pelomedusidae or Podocnemididae. With the exception of some molecular phylogenies, there are no phylogenetic analyses of extant and extinct representatives of Pleurodira including all of its lineages. A broader understanding of the evolutionary history of Pleurodira requires a phylogenetic hypothesis based on more extensive taxonomic and character samplings.

Methods. We constructed a taxon-character matrix including 227 morphological characters and 87 taxa from all the Pleurodira lineages, plus one stem Pan-Pleurodira, *Notoemys laticentralis*, and one stem-Testudinata, *Proganochelys quenstedti*, as outgroups. The resulting matrix was analyzed using parsimony, Tree Bisection and Reconnection (TBR) algorithms, with 5000 replicates, and a hold of 20. The obtained strict consensus tree was used as the basis of a diversification analysis using topology-based methods. A nested-growing tree approach was employed to create a corresponding tree for different intervals of the geological history of the group. Six distinct time bins were created for periods in which members of Pleurodira occur: Early Cretaceous, Late Cretaceous, Paleocene, Eocene, Miocene, and Recent.

Results. All main pleurodiran clades were recovered in the strict consensus tree, but with some changes in their relationship compared to previous analyses, e.g. the inclusiveness of both Pelomedusoides and Bothremydidae. The diversification analysis shows that, after the establishment of the two major lineages (i.e. Chelidae and Pelomedusoides) in the Early Cretaceous, these subgroups diversified in distinct rates along their evolutionary history. Two

main diversification shifts were identified: one at the early evolution of Podocnemoidea, during the Late Cretaceous, and another during the Miocene, deep nested in the Podocnemididae clade.

Discussion. The resulting strict consensus tree is the largest exclusive phylogenetic hypothesis for Pleurodira, including both extant and extinct taxa. Based on morphological data, it allows more inclusive inferences on the general morphological and diversification patterns of the group. The diversification pulses analysis suggests variation on the rates of diversification on the different pleurodiran clades. The first shift detected is related to the great radiation of Bothremydidae and Podocnemoidae in the Late Cretaceous; the second shift, detected in the Miocene, is related to a diversification within the Stereogenyina, a Podocnemididae clade. Ongoing analysis will determine which factors could enforce those different diversification rates in the evolution of Pleurodira.