

## **Biology Letters - Electronic Supplementary Material**

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### ***Atolchelys lepida*, a new side-necked turtle from the Early Cretaceous of Brazil and the age of crown Pleurodira**

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#### **INTRODUCTION: Location and geology**

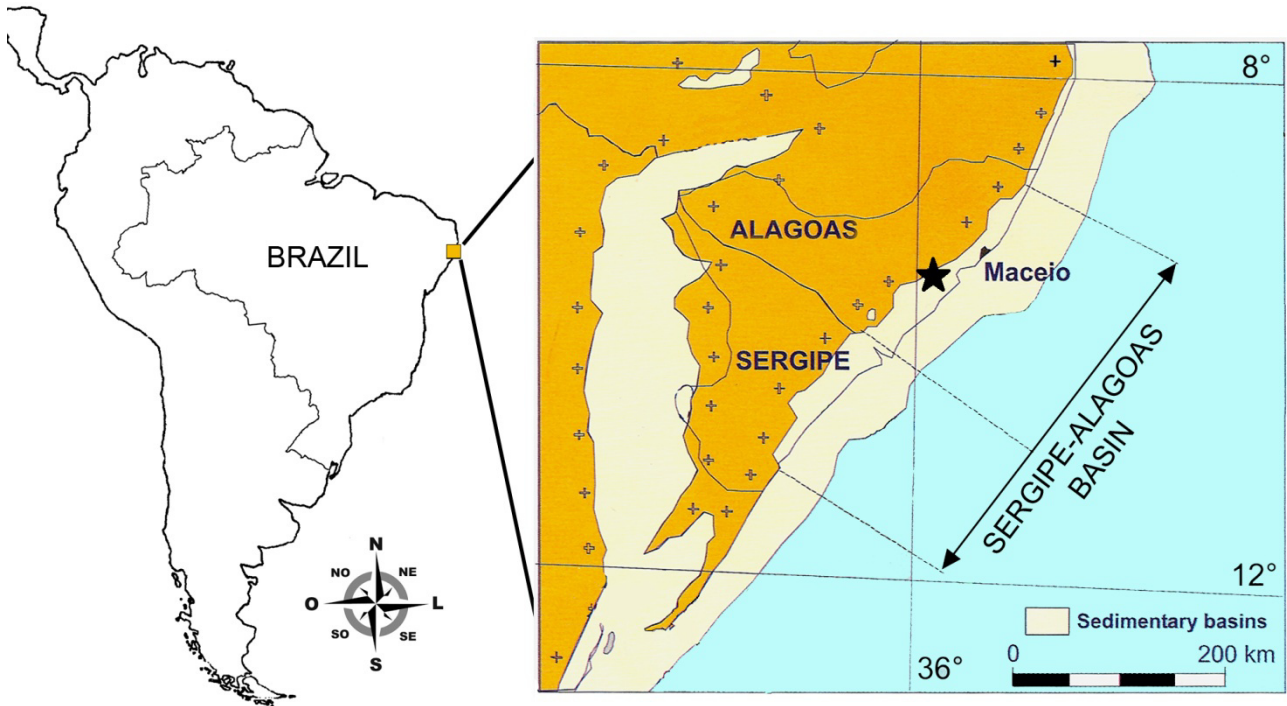
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*Atolchelys lepida* gen. et sp. nov. holotype UERJ.MC 2 were collected during field work on CIMPOR quarry (former “Atol quarry”) located 6.7 km WNW from the city of São Miguel dos Campos, Alagoas State, Northeastern Brazil by V. Gallo, R.C.C. Ramos, and L. Antonioli at January, 2009. The reference coordinate is 09°45’38” S / 36°09’22” W (Figure S1).

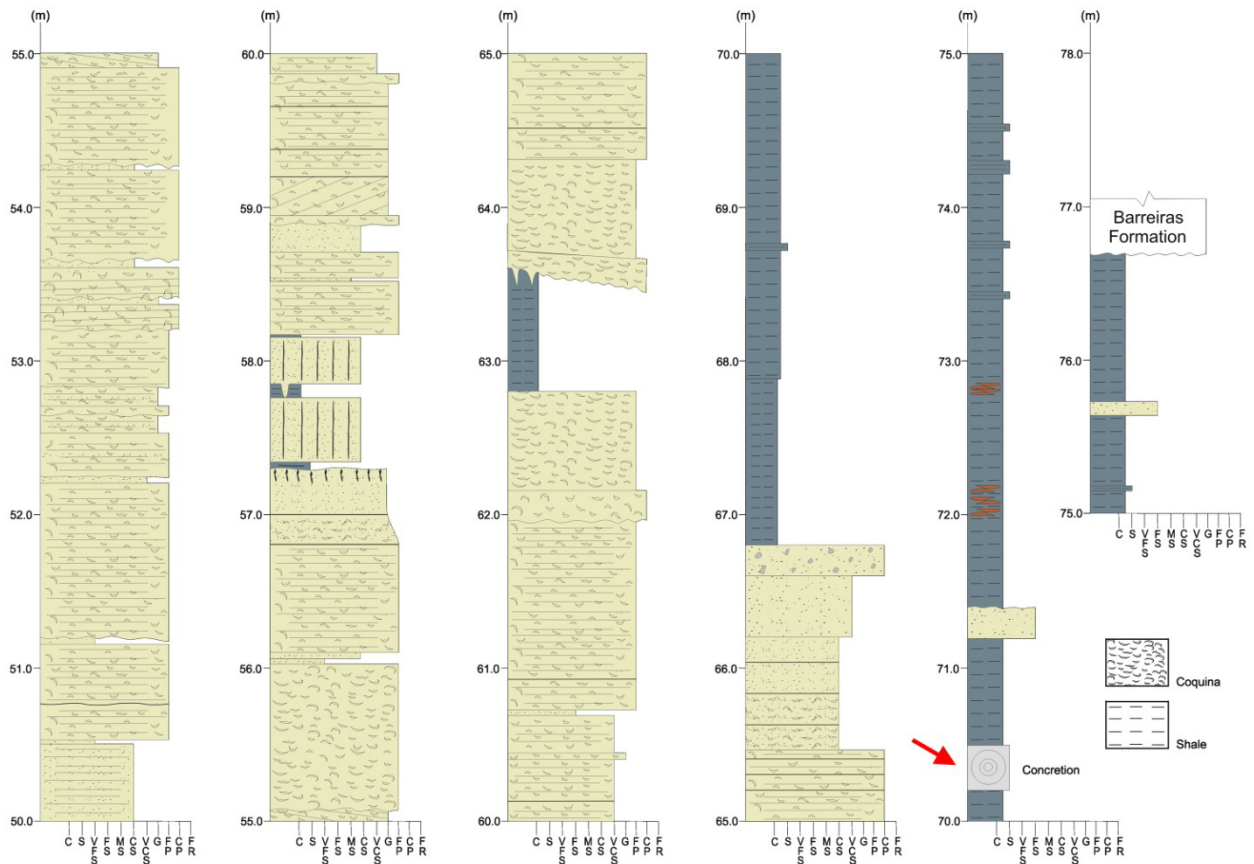
CIMPOR quarry are included in the Morro do Chaves Formation. This lithostratigraphic unit, associated to the rift stage of Sergipe-Alagoas Basin, is characterized by an intercalation of bioclastic calcarenites, calcirudites (coquinas) and shale beds, deposited in a lacustrine paleoenvironment, under seasonal conditions [1]. The studied fossil was found in a carbonate concretion collected at the upper part of the quarry in a thick pelitic interval, related to distal portions of a paleolake, under anoxic conditions.

The Morro do Chaves Formation has been dated as Upper Barremian-Lower Aptian [2]. More recently, Antonioli *et al.* [3], based on the associated occurrences of *Aequitiradites spinulosus*, *Transitoripollis crisopolensis*, and *Dicheiropollis etruscus*, recognized the palynozone *Dicheiropollis etruscus* in the studied stratigraphic section, which suggests a Late Barremian age (Lower Jiquiá local stage).

UERJ.MC 2 was collected in the upper part of the Morro do Chaves Formation, characterized by a pelitic succession with a few sandstone layers (Figure S2). The CIMPOR quarry is shown in Figure S3.



**Figure S1.** Map showing the position of CIMPOR quarry, type-locality of *Atolchelys lepida* gen. et sp. nov. (black star). Figure by L. Antonioli.



**Figure S2.** Final stratigraphic sequence (50 to 78m) of CIMPOR quarry, type-locality of *Atolchelys lepida* gen. et sp. nov. The red arrow indicates the position of UERJ.MC 2. Figure by R.C.C. Ramos.



**Figure S3.** Panoramic photograph of CIMPOR quarry. The red arrow indicates the position of UERJ.MC 2 in the site; the thin black line indicates the final stratigraphic sequence shown in Figure S2; North (N) South (S) orientation is given. Scale bar of 10 meters. Photo by: R.R.C. Ramos.

## **INTRODUCTION: Pleurodirans phylogeny and classification**

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Joyce *et al.* [4] proposed a rank-based taxon names following PhyloCode nomenclature (the crown group convention). However, Gaffney *et al.* (several references, but see [5,6]) keep using monophyletic groups' names following the rules of the ICZN ignoring [4]. As consequence, there is some confusion on side-necked turtle's nomenclature, given the current use of two different nomenclature systems. It is likely that most people will follow the crown group convention from now on. We are following "crown group convention", i.e.: PhyloCode nomenclature [4].

The turtles taxonomy discussion involves the definition of Pleurodira (i.e.: side-necked turtles) and, consequently, the age of it. Such debate regards, among other things, on the phylogenetic position of the European Upper Triassic *Proterochersis* [5,6,7,8,9,10,11].

The traditional ICZN nomenclature for the side-necked turtles [5,6,7,8] includes Platychelyidae and *Proterochersis* as side-necked turtles whereas the PhyloCode nomenclature of "Pleurodira" includes only the first [9,10,11,12] because *Proterochersis* is considered a stem Testudines. So, the apomorphic and nodal definitions of side-necked turtles lies on the debate about the phylogeny of basal turtles [9,10,11,12,13] and is not the objective of the present contribution to address this issue.

The ICZN Casichelydia Gaffney, 1975 equals to PhyloCode Testudines Linnaeus, 1758 (*sensu* [4]). The ICZN "Megapleurodira" clade (*sensu* [14]; i.e.: all pleurodirans, except *Proterochersis*) equals to PhyloCode "Pan-Pleurodira" (*sensu* [4]). The ICZN "Eupleurodira" clade (i.e.: all Megapleurodira except Platychelyidae) equals the PhyloCode "crown Pleurodira" (*sensu* [4]).

Sereno and ElShafie [15] proposed the most comprehensive and updated Phylogenetic definitions for crown groups of Pleurodira. However, the resulted phylogeny (see results) implies on the exclusion of Podocnemidoidea Cope, 1868 as defined in [15] because it would equals to Pelomedusoides Cope, 1868 (node 59 of Figure S4). We preferred the use of Pelomedusoides since it is a more common term in the literature.

## **MATERIAL AND METHODS**

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The phylogenetic analysis performed consisted on the inclusion of *Atolchelys lepida* gen. et sp. nov. as a 49th terminal in a data set of 175 parsimony informative characters based on most recent matrix published [5] with subsequent additions and modifications proposed [8,15,16]. *Araripemys* was scored as proposed by [15]. The tree was rooted using [5] outgroup "Synapsida/Diapsida" because the question about the placement of turtles among Amniota would not alter relationships within turtles as analyzed here. We performed all analysis using parsimony search algorithms in TNT version 1.1 [17].

The cladistic analyses were based on a maximum parsimony simultaneous analysis with *a posteriori* polarization of characters using the outgroup [18]. The complete matrix of 175x49 were analyzed via traditional heuristic search, with start trees based on a Wagner search followed by a tree bisection-reconnection (TBR) swapping algorithm with 100 replicates, holding 200 trees in each replicate, and zero random seeds. All characters were left unweighted and the multistate characters were treated as nonadditive (i.e.: Fitch optimization). We reached 24 most parsimonious trees of 437 steps (strict consensus tree in Figure S4).

Besides search strategy described above, we had performed other heuristic searches with more replicates, holding more trees, and changing the number of random seeds. Of course, we have changed the default memory parameter of TNT in order to maximize the number of trees stored in the memory. However, some of the search strategy maximizing the number of permutations exhausted memory limit and did not changed the results (Table S1).

To evaluate, at least partially, if our assumption about connectivity of multistate characters may influence the phylogenetic position of *Atolchelys lepida* gen. et sp. nov. we performed the original search considering all multistate characters as additive. We reached 120 most parsimonious trees of 511 steps. Although the relationships inside Bothremydidae is affected, the phylogenetic positing of *Atolchelys lepida* gen. et sp. nov. do not change.

Bremer (keeping in memory all suboptimal trees up to +5 steps) and bootstrap (1000 replications and cutoff below 50%) clade supports were also calculated using the same search mechanism. The results of Bremer and Bootstrap are in Figures S5 and S6, respectively.

To evaluate the presence of multiple islands disturbing the data, we performed New Technologies search algorithms, changing the number of random seeds to zero (TNT default is 1 random seed, which limits the search performance). By doing it, each new taxon added during tree search is put on several positions until the memory limit is reached. This provide more possible combinations and optimize the performance. First, we ran Ratchet + Tree fusing TNT defaults, resulting in six trees of 437 steps. After, we gradually increased the perturbation to up and down weighting probabilities to +/-6 and +/-10, reaching similar results (i.e.: equal strict consensus tree). Drift strategy (instead of Ratchet) + Tree fusing, using default parameters, also achieved same results of Ratchet + Tree fusing (Table S2). Such results were expected, since it is a relatively small matrix.

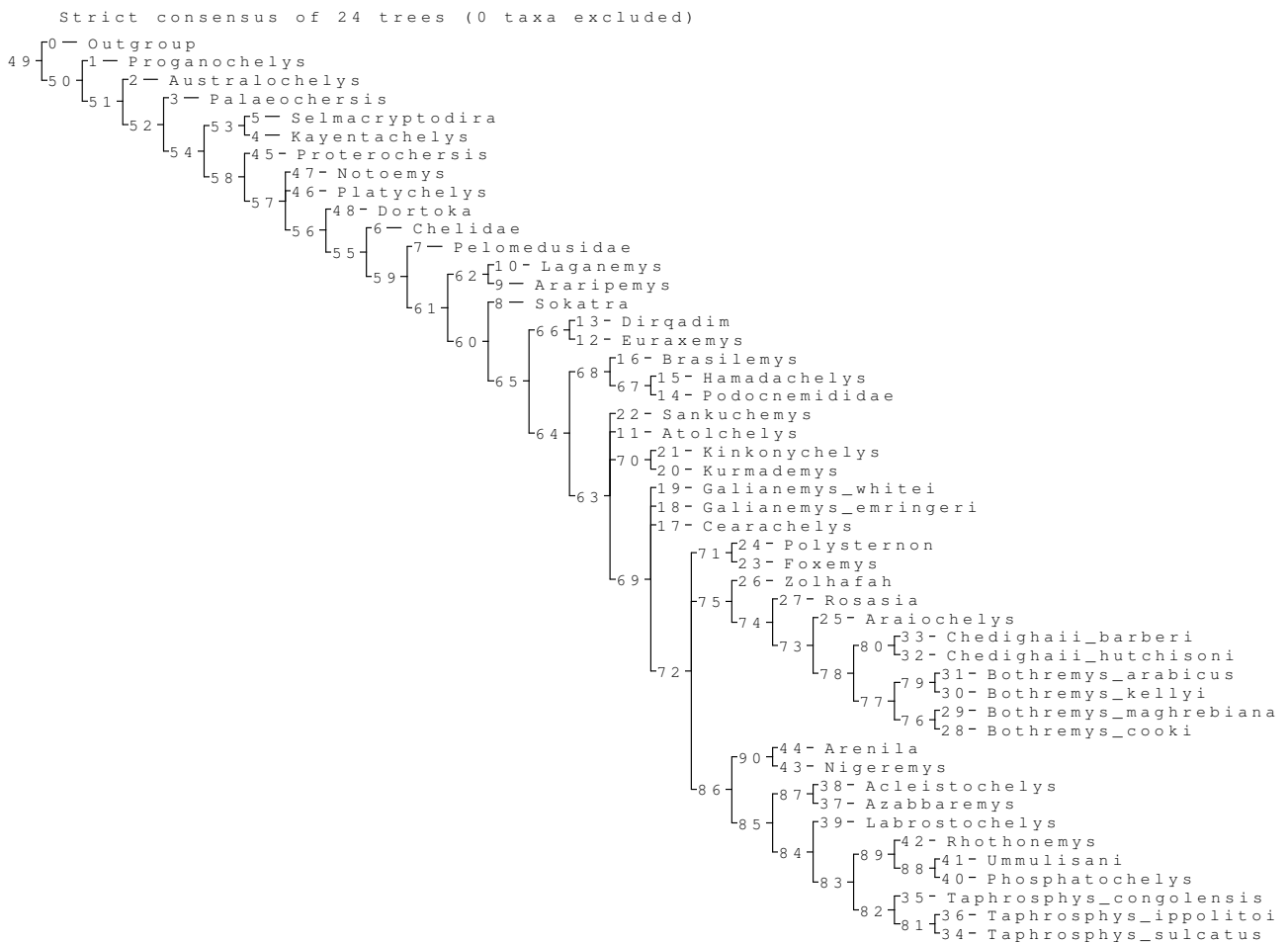
**Table S1.** Comparison of different traditional search mechanism performed in TNT.

Search	Original	2nd	3th	4th	5th	6th
<b>Algorithm</b>	TBR	TBR	TBR	TBR	TBR	TBR
<b>Number of replicas</b>	100	100	1000	1000	10000	10000
<b>Number of random seeds</b>	0	10	0	10	0	10
<b>Number of trees hold each time</b>	200	200	200	500	500	500
<b>Number of steps</b>	437	437	437	437	437	437
<b>Most parsimonious trees retained</b>	24	24	24	24	24	24
<b>Number of times hitting best score</b>	90 of 100	96 of 100	928 of 1000	927 of 1000	9216 of 10000	9234 of 10000
<b>Number of rearranges exanimated</b>	43.958.187	29.514.145	322.816.711	311.452.946	3.237.103.346	3.255.186.540
<b>Time consumed</b>	0:00:01	0:00:01	0:00:12	0:00:11	0:01:20	0:02:01

**Table S2.** Comparison of different New Technology search mechanism performed in TNT.

Search	Ratchet #1	Ratchet #2	Ratchet #3	Drift
<b>Up and down weighting probabilities</b>	+/- 4	+/- 6	+/- 10	---
<b>Number of random seeds</b>	0	0	0	0
<b>Best score (number of steps)</b>	437	437	437	437
<b>Most parsimonious trees retained</b>	6	5	6	7
<b>Number of rearranges exanimate</b>	4.622.122	4.588.509	4.698.450	4.751.518

**RESULTS: Resulted trees**



**Figure S4.** Strict consensus tree of 24 most parsimony trees of 437 steps (see Tables S1 and S2). Numbers in the nodes represent nodes to apomorphies mapping described below. Figure by P. S. R. Romano.





**Figure S6.** Bootstrap consensus tree of TBR original search. Numbers in the nodes represent Bootstrap % support (1000 replications). Nodes collapsed if Bootstrap below 50%. Figure by P. S. R. Romano.



## RESULTS: List of synapomorphies

All synapomorphies common to 24 most parsimonious trees. Node numbers refer to nodes in consensus, see Figure S4.

<b>Outgroup</b>	Char. 12: 0 --> 1	<b><i>Galianemys emringeri</i></b>	Char. 164: 1 --> 0
All trees:	Char. 13: 1 --> 2	Some trees:	
No autapomorphies	Char. 28: 0 --> 1	Char. 67: 0 --> 1	<b><i>Bothremys cooki</i></b>
	Char. 83: 0 --> 1	Char. 94: 0 --> 1	All trees:
<b><i>Proganochelys</i></b>	Char. 119: 1 --> 0		No autapomorphies
All trees:	Char. 140: 0 --> 1	<b><i>Galianemys whitei</i></b>	<b><i>Bothremys maghrebiana</i></b>
No autapomorphies		All trees:	All trees:
	<b><i>Atolchelys</i></b>	No autapomorphies	Char. 76: 0 --> 1
<b><i>Australochelys</i></b>	All trees:	<b><i>Kurmademys</i></b>	<b><i>Bothremys kellyi</i></b>
All trees:	Char. 18: 1 --> 0	All trees:	All trees:
Char. 41: 0 --> 1	Char. 29: 0 --> 1	No autapomorphies	Char. 73: 1 --> 5
	Char. 34: 0 --> 1	<b><i>Kinkonychelys</i></b>	<b><i>Bothremys arabicus</i></b>
<b><i>Palaeochersis</i></b>	Char. 105: 2 --> 4	All trees:	All trees:
All trees:	Some trees:	Char. 94: 1 --> 2	No autapomorphies:
No autapomorphies	Char. 10: 0 --> 1	Char. 59: 1 --> 0	<b><i>Chedighaii hutchisoni</i></b>
	Char. 30: 1 --> 0	Char. 83: 0 --> 1	All trees:
<b><i>Kayentachelys</i></b>	Char. 67: 0 --> 1	<b><i>Sankuchemys</i></b>	Char. 30: 2 --> 1
All trees:	Char. 68: 0 --> 1	All trees:	<b><i>Chedighaii barberi</i></b>
No autapomorphies	Char. 84: 1 --> 2	No autapomorphies	All trees:
	Char. 163: 0 --> 1	<b><i>Foxemys</i></b>	Char. 33: 2 --> 1
<b><i>Selmacryptodira</i></b>		All trees:	<b><i>Taphrosphys sulcatus</i></b>
All trees:	<b><i>Euraxemys</i></b>	Char. 41: 0 --> 1	All trees:
Char. 73: 0 --> 4	All trees:	Some trees:	Char. 86: 1 --> 0
Char. 74: 0 --> 1	No autapomorphies:	Char. 94: 0 --> 1	<b><i>Taphrosphys congolensis</i></b>
	<b><i>Dirqadim</i></b>	<b><i>Polysternon</i></b>	All trees:
<b>Chelidae</b>	All trees:	All trees:	No autapomorphies
All trees:	Char. 14: 1 --> 0	Char. 59: 0 --> 1	<b><i>Taphrosphys ippolitoi</i></b>
Char. 37: 0 --> 2	Char. 29: 0 --> 1	Char. 174: 1 --> 3	All trees:
Char. 172: 0 --> 1	Char. 76: 0 --> 1	Some trees:	No autapomorphies
Some trees:		Char. 153: 0 --> 1	<b><i>Azabbaremys</i></b>
Char. 149: 1 --> 0	<b>Podocnemididae</b>	Char. 163: 1 --> 0	All trees:
	All trees:	<b><i>Araiochelys</i></b>	Char. 29: 0 --> 1
<b>Pelomedusidae</b>	Char. 118: 0 --> 1	All trees:	Char. 30: 1 --> 0
All trees:	Char. 121: 0 --> 1	Char. 4: 1 --> 0	Char. 50: 3 --> 2
Char. 44: 1 --> 2	<b><i>Hamadachelys</i></b>	Char. 33: 2 --> 1	Some trees:
Char. 46: 0 --> 2	All trees:	Char. 76: 0 --> 1	Char. 23: 1 --> 0
Char. 75: 0 --> 1	No autapomorphies:	Char. 144: 2 --> 4	
Char. 83: 0 --> 1	<b><i>Brasilemys</i></b>	Char. 145: 2 --> 3	<b><i>Acleistochelys</i></b>
Char. 88: 0 --> 1	All trees:	Char. 166: 0 --> 1	All trees:
Char. 140: 0 --> 123	No autapomorphies:	Some trees:	Char. 22: 0 --> 1
	<b><i>Cearachelys</i></b>	Char. 117: 1 --> 0	Char. 34: 0 --> 1
<b><i>Sokratra</i></b>	All trees:	<b><i>Zolhafah</i></b>	
All trees:	Char. 26: 1 --> 0	All trees:	Char. 35: 0 --> 1
Char. 103: 0 --> 2	Char. 51: 1 --> 02	Char. 73: 4 --> 5	Char. 67: 0 --> 2
Some trees:	Some trees:	Some trees:	Char. 73: 1 --> 5
Char. 84: 0 --> 4	Char. 19: 0 --> 1	Char. 78: 1 --> 0	<b><i>Labrostochelys</i></b>
	Char. 52: 1 --> 0	<b><i>Rosasia</i></b>	All trees:
<b><i>Araripemys</i></b>	Char. 143: 0 --> 1	All trees:	Char. 5: 0 --> 1
All trees:	Char. 164: 1 --> 0	Char. 67: 0 --> 1	
Char. 10: 0 --> 1	Char. 174: 1 --> 4		
Char. 120: 0 --> 1			
Char. 147: 1 --> 0			
Char. 157: 2 --> 3			
Some trees:			
Char. 149: 1 --> 0			
<b><i>Laganemys</i></b>			
All trees:			

Char. 6: 0 --> 1	Char. 107: 0 --> 1	Char. 3: 0 --> 1	All trees:
Char. 29: 0 --> 1	Char. 108: 0 --> 1	Char. 13: 0 --> 1	Char. 12: 0 --> 1
Char. 30: 1 --> 2	Char. 110: 0 --> 1	Char. 14: 0 --> 1	Char. 55: 2 --> 1
Char. 39: 0 --> 2		Char. 112: 0 --> 1	Char. 85: 0 --> 1
Char. 48: 1 --> 0	<b>Node 52</b>	Char. 127: 2 --> 1	Char. 105: 2 --> 1
Char. 50: 3 --> 1	All trees:	Char. 137: 0 --> 1	Some trees:
Char. 74: 1 --> 0	Char. 61: 0 --> 1		Char. 84: 0 --> 2
<b>Phosphatochelys</b>	Char. 63: 0 --> 1	<b>Node 60</b>	<b>Node 67</b>
All trees:	Char. 104: 0 --> 1	All trees:	All trees:
Char. 15: 0 --> 1		Char. 93: 0 --> 1	Char. 12: 0 --> 1
<b>Ummulisani</b>	<b>Node 53</b>	Char. 98: 0 --> 1	Some trees:
All trees:	All trees:	Some trees:	Char. 81: 1 --> 2
Char. 5: 0 --> 1	Char. 7: 0 --> 1	Char. 35: 0 --> 1	
Char. 50: 3 --> 2	Char. 28: 0 --> 1		<b>Node 68</b>
Char. 79: 1 --> 0	Char. 71: 0 --> 1	<b>Node 61</b>	All trees:
	Char. 95: 0 --> 1	All trees:	Char. 140: 0 --> 1
		Char. 124: 0 --> 1	Some trees:
<b>Rhothonemys</b>	<b>Node 54</b>		Char. 35: 1 --> 0
All trees:	All trees:	<b>Node 62</b>	Char. 68: 0 --> 1
Char. 29: 0 --> 1	Char. 2: 0 --> 1	All trees:	
	Char. 31: 0 --> 1	Char. 29: 0 --> 1	<b>Node 69</b>
<b>Nigeremys</b>	Char. 50: 0 --> 3	Char. 39: 0 --> 3	All trees:
All trees:	Char. 80: 0 --> 1	Char. 49: 0 --> 1	Char. 28: 0 --> 1
No autapomorphies	Char. 82: 0 --> 1	Char. 76: 0 --> 1	Char. 55: 2 --> 0
	Char. 87: 0 --> 1	Char. 105: 2 --> 3	Char. 91: 0 --> 1
<b>Arenila</b>	Char. 97: 0 --> 1	Char. 128: 2 --> 0	Some trees:
All trees:	Char. 110: 1 --> 2	Char. 138: 1 --> 4	Char. 13: 1 --> 2
No autapomorphies	Char. 111: 0 --> 1	Char. 143: 0 --> 2	Char. 43: 1 --> 0
	Char. 129: 0 --> 1	Char. 152: 0 --> 1	Char. 59: 1 --> 0
<b>Proterochersis</b>	Char. 130: 0 --> 1	Char. 153: 0 --> 1	Char. 100: 0 --> 1
All trees:	Char. 139: 0 --> 2	Char. 158: 1 --> 0	Char. 105: 2 --> 1
Char. 139: 2 --> 1	Char. 150: 0 --> 2	Char. 171: 0 --> 2	
Char. 150: 2 --> 1	Char. 158: 0 --> 1	Char. 174: 1 --> 5	
Char. 171: 0 --> 1			<b>Node 70</b>
<b>Platyachelys</b>	<b>Node 55</b>	<b>Node 63</b>	All trees:
All trees:	All trees:	Some trees:	Char. 73: 4 --> 2
Char. 150: 2 --> 1	Char. 128: 1 --> 2	Char. 26: 0 --> 1	Char. 74: 1 --> 0
Char. 171: 0 --> 1	Char. 144: 0 --> 2	Char. 30: 0 --> 1	Some trees:
		Char. 33: 0 --> 1	Char. 54: 0 --> 1
<b>Notoemys</b>	<b>Node 56</b>	Char. 37: 0 --> 1	Char. 67: 0 --> 1
All trees:	All trees:	Char. 51: 02 --> 1	Char. 81: 1 --> 2
No autapomorphies	Char. 125: 0 --> 1	Char. 52: 0 --> 1	Char. 99: 0 --> 1
	Char. 138: 0 --> 1	Char. 75: 0 --> 1	
<b>Dortoka</b>	<b>Node 57</b>	Char. 78: 0 --> 1	<b>Node 71</b>
All trees:	All trees:	Char. 84: 0 --> 1	All trees:
Char. 142: 0 --> 1	Char. 147: 0 --> 1	Char. 94: 0 --> 1	Char. 67: 0 --> 2
Char. 147: 1 --> 2	Char. 159: 0 --> 1	Char. 101: 0 --> 1	Char. 138: 1 --> 2
Char. 169: 0 --> 2	Some trees:	Char. 113: 0 --> 1	Char. 172: 0 --> 1
	Char. 157: 0 --> 1	Char. 115: 0 --> 1	Some trees:
<b>Node 50</b>	Char. 161: 0 --> 1	Char. 117: 0 --> 1	Char. 52: 1 --> 0
All trees:	Char. 170: 0 --> 1		Char. 105: 1 --> 2
No synapomorphies		<b>Node 64</b>	Char. 165: 0 --> 1
	<b>Node 58</b>	All trees:	
<b>Node 51 :</b>	All trees:	Char. 58: 0 --> 1	<b>Node 72</b>
All trees:	Char. 131: 0 --> 1	Char. 86: 0 --> 1	All trees:
Char. 45: 0 --> 1	Char. 132: 0 --> 1	Char. 93: 1 --> 2	Char. 56: 0 --> 1
Char. 60: 0 --> 1	Char. 133: 0 --> 1	Char. 103: 0 --> 1	Char. 92: 0 --> 1
Char. 62: 0 --> 1	Char. 134: 0 --> 1	Char. 164: 0 --> 1	Char. 118: 0 --> 1
	Char. 153: 1 --> 0		Char. 119: 1 --> 0
Char. 64: 0 --> 1	Char. 167: 0 --> 1	<b>Node 65</b>	Char. 121: 0 --> 1
Char. 65: 0 --> 1	Char. 173: 0 --> 1	All trees:	Char. 140: 0 --> 2
Char. 66: 0 --> 1		Char. 74: 0 --> 1	Some trees:
Char. 79: 0 --> 1	<b>Node 59</b>	Some trees:	Char. 13: 2 --> 0
Char. 96: 0 --> 1	All trees:	Char. 13: 1 --> 0	Char. 23: 0 --> 1
	Char. 0: 0 --> 1	<b>Node 66</b>	Char. 99: 0 --> 1
			Char. 100: 1 --> 0
			Char. 120: 0 --> 1

Char. 163: 0 --> 1	<b>Node 78</b>	All trees:	Char. 103: 1 --> 2
<b>Node 73</b>	All trees:	Char. 32: 0 --> 1	Some trees:
All trees:	Char. 10: 0 --> 1	Char. 72: 0 --> 1	Char. 49: 1 --> 0
Char. 5: 0 --> 1	Char. 36: 0 --> 1	Char. 103: 2 --> 1	<b>Node 87</b>
Char. 6: 0 --> 1	Char. 102: 0 --> 1	Char. 105: 1 --> 2	All trees:
Char. 29: 0 --> 1	Char. 103: 1 --> 2	Some trees:	Char. 43: 0 --> 1
Char. 31: 1 --> 2	<b>Node 79</b>	Char. 23: 1 --> 0	Char. 46: 0 --> 1
Char. 73: 4 --> 1	All trees:	<b>Node 84</b>	<b>Node 88</b>
<b>Node 74</b>	Char. 30: 2 --> 1	All trees:	All trees:
All trees:	<b>Node 80</b>	Char. 12: 0 --> 2	Char. 9: 0 --> 1
Char. 30: 1 --> 2	All trees:	Char. 24: 0 --> 1	<b>Node 89</b>
<b>Node 75</b>	Char. 22: 1 --> 0	Char. 25: 0 --> 1	All trees:
All trees:	Char. 34: 1 --> 0	Char. 28: 1 --> 0	Char. 17: 0 --> 1
Char. 22: 0 --> 1	<b>Node 81</b>	Char. 53: 0 --> 1	Char. 36: 0 --> 1
Char. 34: 0 --> 1	All trees:	<b>Node 85</b>	Char. 39: 0 --> 3
<b>Node 76</b>	Char. 109: 0 --> 1	All trees:	<b>Node 90</b>
All trees:	<b>Node 82</b>	Char. 27: 1 --> 2	All trees:
Char. 40: 0 --> 1	All trees:	Char. 42: 0 --> 1	Char. 50: 3 --> 2
<b>Node 77</b>	Char. 73: 1 --> 5	Char. 73: 4 --> 1	Char. 59: 0 --> 2
All trees:	<b>Node 83</b>	<b>Node 86</b>	Char. 67: 0 --> 2
Char. 39: 0 --> 1		All trees:	Char. 105: 1 --> 4
		Char. 48: 0 --> 1	

## DISCUSSION: Biogeography

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A previous hypothesis [19, agreeing with 20] suggests that the Pelomedusoides-Chelidae split is consistent with a vicariance event that occurred during the Early Cretaceous: a basaltic magmatism responsible for the accumulation of the Serra Geral Formation (Southeastern Brazil), at 133 Ma. This event is associated to the node 55 of Figure S4.

The second vicariance event is the complete opening of the central Atlantic and the separation of Africa from South America. This event was associated to *Hamadachelys* (Cenomanian of Morocco) sister-group relationships with Podocnemididae, which the basal members are from the Turonian-Coniacian of Argentina and Maastrichtian of Brazil, respectively, *Portezueloemys* and *Bauruemys* (Figure S4, node 67) [19].

At the time of previously publication [19] *Dirqadim*, *Euraxemys*, and *Laganemys* were not described yet. Thus, two other sister-group relationships between northern African and northeastern Brazilian pelomedusoids species can be now associated with the complete opening of the central Atlantic and the separation of Africa from South America: the euraxemydids *Dirqadim* (Cenomanian of Morocco) + *Euraxemys* (Aptian-Albian of Brazil) (Figure S4, node 66) and the araripemydids *Laganemys* (Aptian-Albian of Niger) + *Araripemys* (Aptian-Albian of Brazil) (Figure S4, node 62).

So, the results of the presented analysis confirm and provide more robust evidence about the previous biogeography scenario.

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*Galianemys\_emringeri*

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*Galianemys\_whitei*

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*Kurmademys*

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*Kinkonychelys*

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*Sankuchemys*

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*Rosasia*

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*Bothremys\_cooki*

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*Bothremys\_maghrebiana*

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*Chedighaii\_hutchisoni*

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*Chedighaii\_barberi*

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*Taphrosphys\_sulcatus*

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*Taphrosphys\_ippolitoi*

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*Azabbaremys*

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*Acleistocheles*

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*Arenila*

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*Proterochersis*

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*Notoemys*

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*Dortoka*

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