

books.google.com Biology of the sauropod dinosaurs: understanding the life of giants Oliver Wings, András Borbély, Thomas Breuer, Andreas Christian, Marcus Clauss, Maïtena Dumont, Gordon Dzemski, Regina Fechner, Bergita Ganse, Rainer Goessling, Eva Maria Griebeler, Hanns-Christian Gunga, Oliver Hampe, Wolf-Dieter Heinrich, Bianca Hohn, Jürgen Hummel, Anke Kaysser-Pyzalla, Aleksander Kostka, Heinrich Mallison, Julia Mannhardt, Pascal De Micheli, Nadine Pajor, Steven F Perry, Holger Preuschoft, Oliver WM Rauhut, Katrin Reis, Alexander Stahn, Koen Stein, Stefan Stoinski, Tim Suthau, Thomas Tütken, David M Unwin, Jan Werner, Ulrich Witzel Indiana University Press, 2011 Sauropods, those huge plant-eating dinosaurs, possessed bodies that seem to defy every natural law. What were these creatures like as living animals and how could they reach such uniquely gigantic sizes? A dedicated group of researchers in Germany in disciplines ranging from engineering and materials science to animal nutrition and paleontology went in search of the answers to these questions. Biology of the Sauropod Dinosaurs reports on the latest results from this seemingly disparate group of research fields and integrates them into a coherent theory regarding sauropod gigantism. Covering nutrition, physiology, growth, and skeletal structure and body plans, this volume presents the most up-to-date knowledge about the biology of these enormous dinosaurs. Voir sur books.google.com Cité 97 fois

Autres articles Les 3 versions First rebbachisaurid dinosaur (Sauropoda, Diplodocoidea) from the early Cretaceous of Spain: palaeobiogeographical implications Xabier Pereda Suberbiola, Fidel Torcida, Luis Angel Izquierdo, Pedro Huerta, Diego Montero, Gustavo Perez Bulletin de la Société géologique de France 174 (5), 471–479, 2003 Première découverte d'un dinosaure rebbachisauride (Sauropoda, Diplodocoidea) dans le Crétacé inférieur d'Espagne : implications paléobiogéographiques, Des restes fossiles d'un sauropode provenant du Crétacé inférieur (Barremien supérieur–Aptien inférieur) de Salas de los Infantes (Burgos, Espagne) sont décrits. Le matériel, qui comporte plusieurs vertèbres caudales, des chevrons, une paire d'ischions et un fémur, pourrait appartenir à un seul individu de taille moyenne. D'après la hauteur de l'arc neural et la largeur de l'épine neurale des vertèbres caudales antérieures, le spécimen est rapporté aux Diplodocoidea. De plus, il montre des affinités avec les Rebbachisauridae, un clade basal de diplodocoïdes. La forme des vertèbres caudales antérieures et de l'ischion du sauropode de Burgos est similaire à celle de 'Rebbachisaurus' tessonei de l'Albien–Cénoomanien d'Amérique du Sud. Néanmoins, il existe des différences par rapport à celui-ci, de sorte que le sauropode de Burgos est rapporté provisoirement à un Rebbachisauridae indéterminé. Les rebbachisaurides sont connus dans l'Aptien–Cénoomanien des continents gondwaniens (Afrique et Amérique du Sud), même si du matériel provenant du Coniacien–Santonien d'Argentine et de l'Hauterivien–Barremien de Croatie leur a été rapporté. Le diplodocoïde de Burgos semble être un des plus anciens représentants des Rebbachisauridae. Cette découverte appuie l'hypothèse de déjà soutenue d'une connexion terrestre entre l'Europe et l'Afrique à travers la Téthys durant le Crétacé inférieur. Voir sur pubs.geoscienceworld.org Cité 91 fois

Autres articles Les 4 versions Detecting dinosaur DNA S Blair Hedges, Mary H Schweitzer Science 268 (5214), 1191–1192, 1995 The fact that DNA sequence can be obtained from fossil organisms has opened new windows of opportunity for research in organismal and molecular evolution (1). Among these is the possibility of obtaining genetic information from major

groups of organisms now extinct. Recently, SR Woodward et al. sequenced DNA from a portion of the mitochondrial cytochrome b gene from Cretaceous bone fragments apparently from a dinosaur that lived 80 million years ago (2). However, the likely source of those DNA sequences appears to be human contamination. In addition to experimental controls, a major line of evidence normally used to support a finding concerning ancient DNA is the phylogenetic relationship of the putative ancient sequence to those from the closest living relatives of the fossil organism (1). In the case of a possible dinosaur sequence, there is strong evidence from morphology that birds represent the closest living organisms to dinosaurs, and morphological and molecular evidence indicate that crocodilians are the closest living relatives of birds (3–4). Also, the fossil record indicates that, after splitting with mammals, at least 100 million years of evolution occurred on the lineage leading to dinosaurs and birds before the latter groups diverged (3). Therefore, a putative dinosaur sequence would be expected to cluster with birds and crocodilians in a phylogenetic analysis of amniotes. Woodward et al. (2) do not present an evolutionary tree, but discuss their sequences in terms of percent sequence difference, noting that these cytochrome b sequences differed from all others in the databases. We also performed a BLAST search using the majority rule consensus sequence [figure 6 in (2)] and obtained matches to 130 cytochrome b sequences of vertebrates (5). As reported by Woodward et al. (2), the consensus sequence differs by about 30% (26% to 52%) from those vertebrate sequences in the databases. However, 87 of the most similar sequences (closest matches) are mammals, including all nine eutherian orders represented, whereas birds, amphibians, and fish comprise nearly all of the remaining sequences and have the lowest similarity to the consensus sequence. Among the mammal sequences, the closest matches are to whales (99/133= 74% similarity). However, among the nucleotide sites showing similarity to the human sequence (93/133= 69%), four are rare variants in the other 129 vertebrate sequences (6). A phylogenetic analysis (7) with all tetrapod sequences obtained from the BLAST search joins the putative dinosaur DNA sequence (2) with human (Fig. 1). Although statistical support for most nodes in the tree is low as a result of the short length of this region (133 base pairs), bootstrap support for this cluster (91%) is relatively high. Furthermore, a consensus sequence of the nine bone sequences which maximizes similarity to human (118/133= 88% similarity) clusters with the human sequence at a statistically significant bootstrap P value of 100%. Consensus sequences with similarity maximized to each of the other taxa yield considerably lower (0 to 46%) probabilities for clustering with the taxon to which similarity was maximized (8). Despite meticulous care, contamination of polymerase chain reaction (PCR) experiments with foreign DNA, often of human origin, is an ever-present aspect of ancient DNA research because of the sensitivity of the methodology and rarity of the target molecules (1). The suggestion by Woodward et al. (2) that variation among the nine sequences (seven from the same bone fragment) is a result of damaged template may be correct. However, our results suggest that the DNA template was

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