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Molecular evidence for the hadrosaur *B. canadensis* as an outgroup to a clade containing the dinosaur *T. rex* and birds

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Abstract

Molecular analysis of collagen sequences from an 80 million year old hadrosaur *B. canadensis* and a 68 million year old dinosaur *T. rex* suggest strongly that *B. canadensis* is an outgroup to a clade containing *T. rex* and birds, fully consistent with the well-established phylogeny based on morphological analyses of fossils.

Molecular analysis of collagen sequences from an 80 million year old hadrosaur *B. canadensis* and a 68 million year old dinosaur *T. rex* suggest that the two dinosaurs belong to a clade to the exclusion of birds [1,2,3]. However, well-established morphological analyses of fossils show that *T. rex* is more closely related to birds than it is to the ornithischian hadrosaur *B. canadensis* [4]. The molecular analyses were based on the molecular clock paradigm, which is known to be contradicted by fossil sequences

[5,6]. It is therefore necessary to reevaluate the molecular data independent of the molecular clock paradigm.

Here, I analyzed all the collagen sequences reported for *B. canadensis* and *T. rex*.

There are a total of four peptides whose sequences are known in the two dinosaurs and extant chicken. But, only one of these is informative as the other three are identical among the three species. For this single informative 18 amino acid peptide (GLPGESGAVGPAGPPGSR), I compared its sequence from all extant species including birds, reptiles, amphibians, fishes, and mammals where the sequence information is available (Table 1). The data show that *T. rex* is identical to *G. gallus* whereas *B. canadensis* differs from *T. rex* and *G. gallus* at residue position 15. An Ile residue at this position is completely conserved in all extant species of mammals, birds, and reptiles. And yet, *B. canadensis* has a Pro at this position. From the Dayhoff's PAM (accepted point mutation) matrix [7], a change from Ile to Pro or vice versa is highly uncommon. Furthermore, not a single extant species from mammals, birds, reptiles, amphibians, and fishes (19 species analyzed) has a Pro at this position.

These molecular data therefore suggest strongly that *B. canadensis* is an outgroup to a clade containing *T. rex* and birds, fully consistent with the well-established phylogeny based on morphological analyses of fossils [4]. The unusual change from a conserved Ile to a Pro also show that *B. canadensis* is genetically more distant to the outgroup fish than extant birds and reptiles, confirming the previous observation that ancient fossil specimens of extinct species are more distant to a simpler outgroup than extant sister species [5,6]. Thus, fossil sequences consistently contradict the molecular clock paradigm and would inevitably lead to absurd conclusions if analyzed under the assumptions of that paradigm.

Reference:

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4. Pisani D, Yates AM, Langer MC, Benton MJ (2002) A genus-level supertree of the Dinosauria. *Proc Biol Sci* 269: 915-921.
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Table 1. Sequence alignment of a peptide from collagen alpha 2 type 1.

B. canadensis	GLPGESGAVGPAGPPGSR
T. rexI...
G. gallusI...
T. guttata	.P.....I...
S. camelus	.P.....I...
A. mississippiensisV..I...
A. carolinensis	.A.....S..I...
H. sapiens	.P.....A..T..I...
M. mulluta	.P.....A..T..I...
B. taurus	.P.....A..T..I...
M. americanum	.P..Q...A..T..I...
L. afiricana	.P..Q...A..T..I...
M. musculus	.T.....A..S..I...
R. norvegicus	.P.....A..S..I...
E. telfairi	.P..Q...A..T.SI...
M. domestica	.P.....T.SI...
X. levis	.T.....A..F..L.P.
X. tropicalis	.A.....A..L.AL.P.
R. catesbeiana	.A.....GA..H.PS...
D. rerio	.N..PA..A.AQ..I.A.
O. mykiss	.NS.PA.SA.SQ.AI.A.
P. olivaceus	.IN.VA..S.VQ.AV.A.