

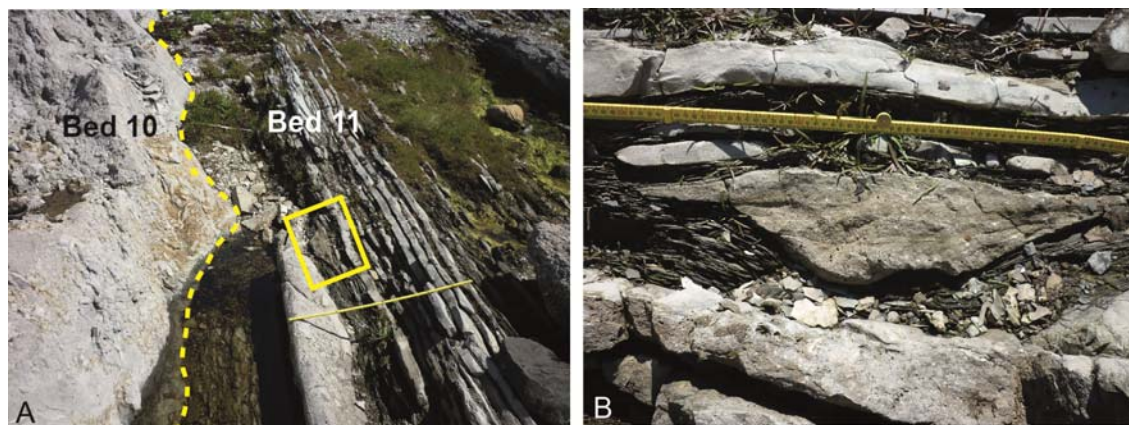
Paleoecologic and paleoceanographic interpretation of $\delta^{18}\text{O}$ variability in Lower Ordovician conodont species.

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DR1. Geologic setting

The Cow Head Group represents proximal slope deposition on the western, Laurentian, margin of the Iapetus Ocean at a low southern hemisphere equatorial paleolatitude. Conodonts analysed come from lowermost Bed 11 (unit 2) of the Factory Cove Member (Shallow Bay Formation, Cow Head Group) (Floian, Lower Ordovician), western Newfoundland. The sample was collected on the Cow Head peninsula at 49.9147° N, 57.8310° W. Bed 11 is ~20 m thick and consists of shales, ribbon limestones and dolostones, with channelized grainstone lenses deposited as gravity flows with minimal thermal overprint through burial (James and Stevens, 1986). The conodonts utilised in the study are from an 8.5 kg grainstone sample (Figure DR1) and have very good to excellent preservation with no evidence of recrystallization or element dissolution when examined with optical or electron microscopy. The elements have a color alteration index (CAI) of 1 indicating a maximum burial temperature of 80 °C (Epstein et al., 1977). A diverse fauna is present, including well-preserved fused clusters of conodont oral apparatuses, and is equivalent to sample CH17 of Stouge and Bagnoli (1988).

Fig. DR1. Field photographs of sample horizon on the Cow Head peninsula. A. Yellow box approximate position of Fig. DR1B in lowermost Bed 11. B. Close up of channelized grainstone from which sample for this study was taken.



DR2. Methods

Sample processing followed the protocols of Wheeley et al. (2012) for SIMS analyses of conodont elements. For rock dissolution the sample was broken into small (3-5 cm diameter blocks) and suspended in 10% acetic acid solutions buffered with calcium carbonate and spent acid buffered to maintain acid solutions above pH 3.5 and avoid risk of corroding conodont elements, using the methodology of e.g. Jeppsson (1999) and Griffin et al. (2015). Samples were washed and sieved

regularly, and recovered insoluble residues were dried in a warm oven. Conodonts were picked directly from these residues without use of any heavy liquid separation. Only the most pristine, complete, and largest conodont elements recovered were selected for isotopic analysis. For SIMS analyses at the University of Edinburgh, UK, NERC Ion Microprobe Facility, conodonts were mounted in resin blocks, polished, gold coated. Conodonts were referenced to a Durango apatite standard independently determined by conventional gas isotope ratio mass spectrometry ($\delta^{18}\text{O} = 8.7\text{‰} \pm 0.3\text{‰}$, $n = 24$; Wheeley et al., 2012) that was interspersed with samples to monitor instrumental drift. Five to ten spot analyses of Durango were made before and after every set of conodont analyses. The mean standard deviation on each day's Durango analyses was $\pm 0.1\text{--}0.3\text{‰}$ (S2, GSA Data Repository¹). Results are reported relative to V-SMOW. To test for histologic $\delta^{18}\text{O}$ variability, analyzed conodonts were inspected with microscopy to determine whether analyses had taken place primarily in a single tissue type, a mix of histologies, or potentially included mineral deposits from basal cavity fillings. For consistency, we targeted the same type of conodont element (position in apparatus) for each species. Only in *Bergstroemognathus extensus* did we analyse two types of element (M and S elements). The values for the two types of elements representing this species (all histologies) are very similar – M-elements with $\delta^{18}\text{O}$ values of 15.8–17.1‰ (mean 16.6‰) and S-elements with $\delta^{18}\text{O}$ values of 15.9–16.8‰ (mean 16.3‰), therefore the species mean that we use (16.4‰) is representative.

DR3. Conodont $\delta^{18}\text{O}$ data for each element analyzed.

Specimens are housed in the Lapworth Museum of Geology, University of Birmingham (BIRUG numbers in Table DR3).

Table DR3. Conodont $\delta^{18}\text{O}$ from analyzed specimens where WM = white matter, H = hyaline crown, BC = basal cavity filling, B = both (white matter and hyaline). Type of element analysed (position in multielement apparatus) given as S, M or as morphologic descriptor. Statistical calculations for each conodont element for the species listed are shown on the last row for that individual as for all histologies and white matter only. Overall taxon values are shown in bold at the bottom of each species section. For reference, the taxonomy of the conodonts follows the description of the Cow Head fauna by Stouge and Bagnoli (1988).

<i>Tropodus sweeti</i> (S elements)				All histologies		White matter only	
BIRUG	Tissue	Analyses	VSMOW	Mean	StDev	Mean	StDev
BU5290	WM	1	16.1	16.6	0.3	16.5	0.4
	WM	2	17.0				
	WM	3	16.3				
	WM	4	16.1				
	WM	5	16.9				
	B	6	16.7				
	B	7	16.8				
	BC	8	16.7				
	BC	9	16.8				
	BC	10	16.8				

BU5291	WM	1	16.4				
	WM	2	16.3				
	WM	3	14.6				
	WM	4	15.6				
	WM	5	15.7				
	WM	6	15.7				
	WM	7	17.2				
	WM	8	16.1				
	WM	9	16.2				
	WM	10	16.5	16.0	0.7	16.0	0.7
Taxon values				16.3	0.6	16.2	0.6

***Bergstroemognathus
extensus***

(M & S elements)

BIRUG	Tissue	Analyses	VSMOW	All histologies		White matter only	
				Mean	StDev	Mean	StDev
BU5292 (M)	H	1	15.6				
	H	2	15.4				
	H	3	15.8				
	H	4	15.8				
	H	5	15.5				
	H	6	15.8				
	H	7	16.3				
	H	8	16.1				
	H	9	15.5	15.8	0.3	n/a	n/a
BU5293 (M)	H	1	16.9				
	H	2	16.4				
	H	3	16.9				
	H	4	16.9				
	H	5	16.7				
	H	6	16.9				
	H	7	16.3				
	H	8	16.9				
	H	9	16.6				
	H	10	15.6	16.6	0.4	n/a	n/a
BU5294 (M)	WM	1	16.1				
	WM	2	16.3				
	H	3	16.5				
	H	4	17.3				
	H	5	17.7				
	H	6	17.8				
	H	7	17.1				
	H	8	16.9				
	H	9	17.2				
	H	10	18.0	17.1	0.7	16.2	0.2
BU5295 (M)	H	1	17.3				
	H	2	17.3				
	H	3	17.1				

	H	4	17.4				
	H	5	17.8				
	H	6	16.8				
	H	7	16.6				
	H	8	16.5				
	H	9	16.0				
	H	10	15.3	16.8	0.8	n/a	n/a
BU5296 (S)	H	1	16.6				
	H	2	16.4				
	H	3	16.6				
	H	4	16.7				
	H	5	16.4				
	H	6	17.2				
	H	7	17.0				
	H	8	17.1				
	H	9	17.0				
	H	10	17.2	16.8	0.3	n/a	n/a
BU5297 (S)	H	1	16.8				
	H	2	16.8				
	H	3	16.8				
	H	4	16.6				
	H	5	16.5				
	H	6	16.0				
	H	7	16.5				
	H	8	16.6				
	H	9	16.3				
	H	10	16.1	16.5	0.3	n/a	n/a
BU5298 (S)	BC	1	15.9				
	H	2	16.0				
	WM	3	15.9				
	H	4	15.7				
	H	5	15.3				
	H	6	16.1				
	H	7	16.2				
	H	8	16.4				
	H	9	16.0				
	H	10	16.1	16.0	0.3	n/a	n/a
BU5299 (S)	H	1	16.2				
	H	2	16.0				
	H	3	15.8				
	H	4	15.6				
	H	5	15.2				
	WM	6	15.2				
	H	7	15.5				
	H	8	16.1				
	H	9	16.3				
	H	10	16.7	15.9	0.5	n/a	n/a
Taxon values				16.4	0.5	15.9	0.5

Periodon***flabellum*****(S elements)**

BIRUG	Tissue	Analyses	VSMOW	All histologies		White matter only	
				Mean	StDev	Mean	StDev
BU5300	WM	1	16.0				
	WM	2	15.4				
	H	3	15.5				
	B	4	16.0				
	H	5	15.4				
	H	6	15.7				
	H	7	16.0				
	B	8	14.7				
	WM	9	16.1				
	WM	10	15.9	15.7	0.4	16	0
BU5301	WM	1	16.3				
	WM	2	15.8				
	WM	3	15.8				
	WM	4	16.0				
	WM	5	15.8				
	WM	6	15.8				
	WM	7	15.7				
	WM	8	15.8				
	WM	9	15.2				
	WM	10	16.4	15.8	0.3	15.8	0.3
Taxon values				15.8	0.4	15.8	0.3

Protopanderodus gracilis**(S elements)**

BIRUG	Tissue	Analyses	VSMOW	All histologies		White matter only	
				Mean	StDev	Mean	StDev
BU5302	WM	1	16.0				
	WM	2	15.1				
	WM	3	15.0				
	WM	4	15.5				
	WM	5	15.5				
	WM	6	15.0				
	WM	7	16.4				
	WM	8	16.2				
	WM	9	17.4				
	WM	10	17.3	15.9	0.9	15.9	0.9
BU5303	BC	1	16.5				
	WM	2	16.9				
	WM	3	16.3				
	WM	4	16.5				
	H	5	16.0				
	H	6	15.2				
	WM	7	15.5				
	WM	8	15.1				

	WM	9	15.1				
	WM	10	15.2	15.8	0.7	15.8	0.7
BU5304	BC	1	15.9				
	WM	2	15.1				
	WM	3	15.4				
	B	4	15.3				
	WM	5	15.0				
	WM	6	14.8				
	WM	7	15.3				
	WM	8	15.1				
	BC	9	15.5	15.3	0.3	15.1	0.2
Taxon values				15.7	0.7	15.7	0.8

***Oistodus* aff. *O.*
*lanceolatus***

(S elements)

BIRUG	Tissue	Analyses	VSMOW	All histologies		White matter only	
				Mean	StDev	Mean	StDev
BU5305	WM	1	14.9				
	WM	2	15.2				
	WM	3	16.1				
	WM	4	15.8				
	WM	5	15.6				
	WM	6	15.4				
	H	7	16.1				
	H	8	15.7				
	WM	9	15.3				
	WM	10	15.1	15.5	0.4	15.4	0.4
BU5306	H	1	13.9				
	B	2	14.7				
	B	3	14.5				
	H	4	14.0				
	H	5	13.5				
	B	6	14.9				
	B	7	14.2				
	H	8	14.5				
	H	9	14.6				
	BC	10	14.4	14.3	0.4	n/a	n/a
BU5307	B	1	14.7				
	WM	2	15.2				
	WM	3	15.3				
	WM	4	15.1				
	WM	5	14.8				
	WM	6	14.8				
	WM	7	15.0				
	WM	8	15.1				
	WM	9	15.1				
	B	10	15.2	15.0	0.2	15.0	0.2
Taxon values				15.0	0.6	15.2	0.4

Cornuodus longibasis**(S elements)**

BIRUG	Tissue	Analyses	VSMOW	All histologies		White matter only	
				Mean	StDev	Mean	StDev
BU5308	WM	1	15.3				
	WM	2	14.8				
	WM	3	14.2				
	WM	4	14.8				
	WM	5	14.6				
	WM	6	14.1				
	WM	7	14.8				
	WM	8	14.7				
	WM	9	14.6				
	WM	10	15.6	14.8	0.4	14.8	0.4
BU5309	BC	1	16.4				
	BC	2	16.4				
	BC	3	15.8				
	BC	4	16.3				
	BC	5	16.4				
	BC	6	16.1				
	WM	7	16.1				
	WM	8	15.6				
	WM	9	16.0				
	WM	10	15.7	16.1	0.3	15.8	0.3
BU5310	WM	1	15.0				
	WM	2	14.4				
	WM	3	15.4				
	WM	4	16.0				
	WM	5	15.0				
	WM	6	16.1				
	WM	7	14.6				
	WM	8	15.6				
	WM	9	14.4				
	WM	10	14.1	15.1	0.7	15.1	0.7
Taxon values				15.3	0.7	15.1	0.6

Oepikodus evae**(P elements)**

BIRUG	Tissue	Analyses	VSMOW	All histologies		White matter only	
				Mean	StDev	Mean	StDev
BU5311	WM	1	15.1				
	WM	2	14.9				
	WM	3	15.8				
	WM	4	15.3				
	WM	5	15.3				
	WM	6	16.3				
	WM	7	15.6				
	WM	8	15.4				
	WM	9	16.4				
	WM	10	16.1	15.6	0.5	15.6	0.5

BU5312	WM	1	15.2				
	WM	2	14.6				
	WM	3	15.2				
	WM	4	15.9				
	WM	5	15.2	15.2	0.5	15.2	0.5
BU5313	WM	1	13.8				
	WM	2	14.3				
	WM	3	14.4				
	WM	4	15.4				
	WM	5	14.7				
	WM	6	15.3				
	WM	7	15.1				
	WM	8	15.1				
	WM	9	14.9				
	WM	10	15.1				
	WM	11	14.5				
	WM	12	14.5	14.8	0.5	14.8	0.5
BU5314	WM	1	16.0				
	WM	2	15.4				
	WM	3	15.9				
	WM	4	14.5				
	WM	5	15.1				
	WM	6	14.3				
	WM	7	14.6				
	WM	8	15.6				
	WM	9	15.5				
	WM	10	14.8	15.2	0.6	15.2	0.6
BU5315	WM	1	14.5				
	WM	2	14.3				
	WM	3	14.1				
	WM	4	13.4				
	WM	5	13.4				
	WM	6	13.6				
	WM	7	14.4				
	WM	8	14.7				
	WM	9	14.2				
	WM	10	14.3	14.1	0.4	14.1	0.4
Taxon values				14.9	0.7	14.9	0.7

Paroistodus proteus

(M elements)

BIRUG	Tissue	Analyses	VSMOW	All histologies		White matter only	
				Mean	StDev	Mean	StDev
BU5316	WM	1	14.9				
	WM	2	14.6				
	WM	3	14.6				
	H	4	14.5				
	H	5	15.1				
	H	6	14.6				

	WM	7	13.6				
	WM	8	14.3				
	WM	9	13.8				
	WM	10	14.6	14.5	0.5	14.3	0.5
BU5317	WM	1	14.9				
	WM	2	15.0				
	H	3	15.3				
	B	4	14.8				
	WM	5	13.7				
	WM	6	14.1				
	H	7	14.4				
	H	8	15.0	14.6	0.5	14.4	0.6
BU5318	B	1	15.5				
	B	2	15.3				
	B	3	15.5				
	B	4	14.0				
	B	5	15.2				
	B	6	15.5				
	WM	7	15.4				
	WM	8	15.5				
	B	9	15.8				
	B	10	15.3	15.3	0.5	15.4	0.1
Taxon values				14.8	0.6	14.5	0.6

***Drepanodus
planus*
(Arcuatiform
elements)**

BIRUG	Tissue	Analyses	VSMOW	All histologies		White matter only	
				Mean	StDev	Mean	StDev
BU5319	WM	1	14.5				
	WM	2	15.0				
	WM	3	14.6				
	WM	4	14.4				
	WM	5	13.8				
	WM	6	14.5				
	WM	7	14.7				
	WM	8	13.8				
	WM	9	12.5				
	WM	10	14.3	14.2	0.7	14.2	0.7
BU5320	BC	1	15.6				
	BC	2	16.0				
	BC	3	15.7				
	BC	4	16.3				
	BC	5	15.4				
	WM	6	14.1				
	WM	7	14.1				
	WM	8	14.3				
	WM	9	14.5				
	WM	10	13.9	15.0	0.9	14.2	0.2

BU5321	WM	1	15.0				
	WM	2	14.1				
	WM	3	15.3				
	WM	4	15.8				
	WM	5	15.9	15.2	0.7	15.2	0.7
Taxon values				14.7	0.9	14.4	0.8

77 **DR4. Durango apatite standard**

78

79 **Table DR4. Order in which conodont samples were analysed with respect to**
 80 **Durango**

81

Date	Specimen	Mean	StDev	n	Range
12/12/2011	Durango	8.9	0.2	10	0.7
	BU5313	14.8	0.48	12	1.6
	Durango	8.6	0.2	5	0.5
	BU5314	15.2	0.60	10	1.7
	Durango	8.5	0.1	5	0.2
	BU5315	14.1	0.45	10	1.3
	Durango	8.6	0.2	5	0.4
	BU5319	14.2	0.7	10	2.6
	BU5320	15.0	0.9	10	0.6
	Durango	8.7	0.1	5	0.4
	BU5305	15.5	0.40	10	1.2
	BU5321	15.2	0.7	5	1.8
	Durango	8.8	0.1	5	0.4
		Mean	StDev		
Day					
Durango		8.7	0.2		
Date	Specimen	Mean	StDev	n	Range
15/12/2011	Durango	8.6	0.1	5	0.3
	BU5297	16.5	0.28	10	0.8
	Durango	8.7	0.1	5	0.2
	BU5298	16.0	0.29	10	1.1
	BU5299	15.9	0.48	10	1.4
	Durango	8.8	0.2	5	0.5
		Mean	StDev		
Day					
Durango		8.7	0.1		
Date	Specimen	Mean	StDev	n	Range
16/12/2011	Durango	8.7	0.2	10	0.6
	BU5316	14.5	0.46	10	1.5
	BU5317	14.6	0.52	8	1.5
	BU5318	15.3	0.48	10	1.8
	Durango	8.8	0.2	5	0.4
	BU5306	14.3	0.42	10	1.4
	BU5307	15.0	0.20	10	0.7
	Durango	8.7	0.2	5	0.2
		Mean	StDev		
Day					
Durango		8.7	0.2		

Date	Specimen	Mean	StDev	n	Range
8/13/12	Durango	8.4	0.2	10	0.6
	BU5292	15.8	0.3	9	0.9
	Durango	9.0	0.3	5	0.7
	BU5293	16.6	0.4	10	1.3
	Durango	8.8	0.4	5	0.9
	BU5294	17.1	0.7	10	1.9
	Durango	9.7	0.3	5	0.7
	BU5295	16.8	0.8	10	2.5
	Durango	7.8	0.2	5	0.4

		Mean	StDev
Day			
Durango		8.7	0.3

Date	Specimen	Mean	StDev	n	Range
08/14/12	Durango	8.7	0.2	10	0.5
	BU5302	15.9	0.9	10	2.4
	Durango	9.8	0.1	5	0.3
	BU5303	15.8	0.68	10	1.8
	Durango	8.8	0.2	5	0.4
	BU5304	15.3	0.33	9	1.1
	Durango	8.3	0.1	5	0.2
	BU5290	16.6	0.3	10	0.9
	Durango	8.7	0.7	5	1.0
	BU5291	16.0	0.7	10	2.6
	Durango	8.7	0.3	5	0.9

		Mean	StDev
Day			
Durango		8.8	0.3

Date	Specimen	Mean	StDev	n	Range
08/15/12	Durango	8.7	0.2	10	0.6
	BU5308	14.8	0.4	10	1.5
	Durango	8.7	0.3	5	0.7
	BU5309	16.1	0.3	10	0.8
	Durango	8.7	0.3	5	0.9
	Durango	8.5	0	4	0.2
	BU5310	15.1	0.7	10	2.0
	Durango	8.8	0.2	5	0.4
	BU5300	15.7	0.4	10	1.4
	Durango	9	0.2	5	0.4
	BU5301	15.8	0.3	10	1.1
	Durango	8.5	0.2	5	0.5

		Mean	StDev
Day			
Durango		8.7	0.2

Date	Specimen	Mean	StDev	n	Range
08/16/12	Durango	8.7	0.1	4	0.3
	BU5311	15.6	0.51	10	1.5
	Durango	8.8	0.2	4	0.3
	BU5296	16.8	0.32	10	0.8
	Durango	8.7	0.2	4	0.3
	BU5312	15.2	0.46	5	1.3
	Durango	8.7	0.3	3	0.6
		Mean	StDev		
Day					
Durango		8.7	0.2		

DR5. Statistical model fitting

Measurements of $\delta^{18}\text{O}$ differed systematically among tissue types (Fig. DR5A), and the distribution of tissue types sampled differs among taxa (Fig. S5B). White matter samples occur in all taxa (Fig. DR5B), and so these were used for statistical analysis to avoid a histological bias. Visual comparison of the white matter samples (Fig. DR5C) with the whole dataset (Fig. DR5D) shows that a similar gradient is present in both, although the rank ordering of taxa is slightly different.

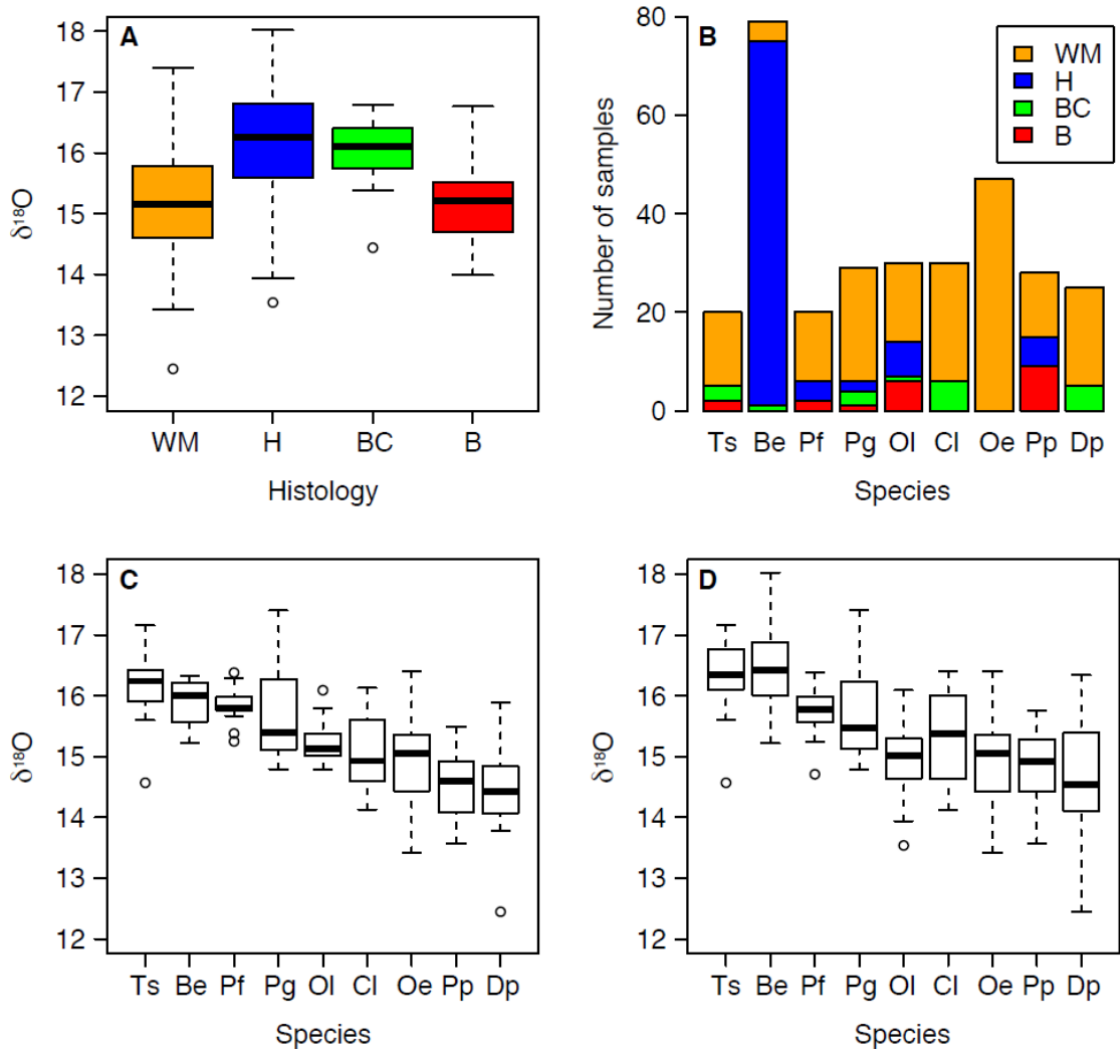


Figure DR5. A) Boxplots showing the distribution of $\delta^{18}\text{O}$ values grouped by histology. WM = white matter, H = hyaline crown, BC = basal cavity filling, B = both (white matter and hyaline). B) Bar chart showing number of samples of each histological type within each species. Ts = *Tropodus sweeti*, Be = *Bergstroemognathus extensus*, Pf = *Periodon flabellum*, Pg = *Protopanderodus gracilis*, Ol = *Oistodus* aff. *O. lanceolatus*, Cl = *Cornuodus longibasis*, Oe = *Oepikodus evae*, Pp = *Paroistodus proteus*, Dp = *Drepanodus planus*. C) Boxplot of $\delta^{18}\text{O}$ values grouped by species for white matter samples only. D) Boxplot of $\delta^{18}\text{O}$ values grouped by species for all samples.

Statistical model fitting was carried out following procedures outlined in Zuur et al. (2009). While the aim was to test for statistically significant differences among taxon $\delta^{18}\text{O}$ means, the data contain features that could violate the assumptions of a standard ANOVA, specifically samples taken from a number of elements within each taxon (violating the assumption of independence) and differing variances among the samples from each element (violating the assumption of homogeneity). Therefore, the optimum model structure was determined by fitting a series of models of increasing complexity:

- 1) a linear model with no variance covariate or random factors, corresponding to a simple ANOVA,
- 2) a generalised least squares model with element as a variance covariate,
- 3) a linear mixed model with element as a random factor,
- 4) a linear mixed model with element as a variance covariate and as a random factor.

Model selection using Akaike's 'An Information Criterion' (AIC), which incorporates both model fit and model complexity, showed that models 3 and 4 (the mixed effect models) had considerably lower AIC values than models 1 and 2 (Table DR5.1). While model 3 had the lowest AIC, model 4 performed better in residuals diagnostic plots, and was a significantly better fit according to a likelihood ratio test ($\text{LR} = 45.24$, $p = 0.008$). Model 4 was therefore selected as the preferred model structure for hypothesis testing, although we note that both models have very similar fits and numerical outputs (Table DR5.2).

Carrying out the same procedure on the entire dataset led to very similar results, with a clear preference for model 4 using both AIC (Table DR5.1) and graphical validation, and the presence of a gradient in $\delta^{18}\text{O}$ means where the isotopically lightest taxa are statistically significantly different from the isotopically heaviest taxon.

Table DR5.1. Model fit and significance for the four candidate models, both on the white matter samples only, and all samples. All models support a statistically significant difference in $\delta^{18}\text{O}$ values among taxa.

Model	White matter only		All samples	
	AIC	<i>p</i> (species)	AIC	<i>p</i> (species)
M1. Linear model	377.9	<0.0001	664.3	<0.0001
M2. Linear model with variance structure	377.7	<0.0001	658.4	<0.0001
M3. Linear mixed model	346.3	0.0157	570.6	0.0002
M4. Linear mixed model with variance structure	351.0	0.0144	561.2	0.0002

Table DR5.2. Model outputs for models 3 and 4, fitted to white matter samples only. Taxa that are statistically significantly different from *Tropodus sweeti*, the isotopically heaviest taxon and the model intercept, are shown in bold.

a) M3: Linear mixed model					
	Value	Standard error	Degrees of freedom	<i>t</i> value	<i>p</i> value
<i>T. sweeti</i> (intercept)	16.245864	0.3469934	150	46.81894	0
<i>B. extensus</i>	-0.406783	0.5146909	17	-0.79034	0.4402
<i>Pe. flabellum</i>	-0.406551	0.4939631	17	-0.82304	0.4219
<i>Pr. gracilus</i>	-0.616964	0.4467001	17	-1.38116	0.1851
<i>Oi. aff. Oi. lanceolatus</i>	-1.012739	0.4873744	17	-2.07795	0.0532
<i>C. longibasis</i>	-1.059305	0.4476626	17	-2.3663	0.0301
<i>Oe. evae</i>	-1.279738	0.4082039	17	-3.13505	0.006
<i>Pa. proteus</i>	-1.583351	0.4620562	17	-3.42675	0.0032
<i>D. planus</i>	-1.732334	0.4498484	17	-3.85093	0.0013
b) M4: Linear mixed model with variance structure					
	Value	Standard error	Degrees of freedom	<i>t</i> value	<i>p</i> value
<i>T. sweeti</i> (intercept)	16.263553	0.3606806	150	45.09129	0
<i>B. extensus</i>	-0.333596	0.4740283	17	-0.70375	0.4911
<i>Pe. flabellum</i>	-0.424605	0.4979054	17	-0.85278	0.4056
<i>Pr. gracilus</i>	-0.693977	0.4685801	17	-1.48102	0.1569
<i>Oi. aff. Oi. lanceolatus</i>	-1.036767	0.4951162	17	-2.09399	0.0516
<i>C. longibasis</i>	-1.034238	0.460422	17	-2.24628	0.0383
<i>Oe. evae</i>	-1.300498	0.4236269	17	-3.06991	0.0069
<i>Pa. proteus</i>	-1.483409	0.4645052	17	-3.19352	0.0053
<i>D. planus</i>	-1.803788	0.4698171	17	-3.83934	0.0013

Table DR5.3. Fitted means and CIs for M4. Note that 95% confidence intervals here are greater than that cited in the text for the raw data because M4 takes into account the grouping structure in the data (i.e. measurements within specimens within taxa) when calculating the standard errors that generates larger uncertainties and therefore larger confidence intervals.

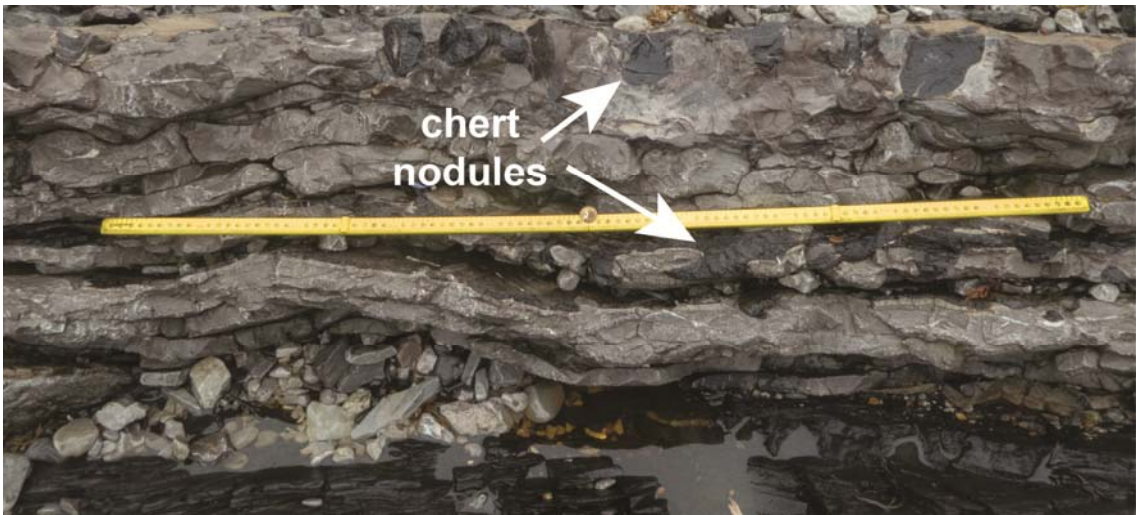
	Fitted mean	Upper95CI	Lower95CI
<i>T. sweeti</i> (intercept)	16.26	16.97	15.56
<i>B. extensus</i>	15.93	16.86	15.00
<i>Pe. flabellum</i>	15.84	16.81	14.86
<i>Pr. gracilus</i>	15.57	16.49	14.65
<i>Oi. aff. Oi.</i> <i>lanceolatus</i>	15.23	16.20	14.26
<i>C. longibasis</i>	15.23	16.13	14.33
<i>Oe. evae</i>	14.96	15.79	14.13
<i>Pa. proteus</i>	14.78	15.69	13.87
<i>D. planus</i>	14.46	15.38	13.54

DR6. Field photographs

Fig. DR6.1. Field photograph of phosphatic nodule development in lowermost Bed 11, Factory Cove Member (Shallow Bay Formation, Cow Head Group), Cow Head Peninsula, western Newfoundland, Canada, which are supportive of a cool-water upwelling regime.



Fig. DR6.2. Early diagenetic chert nodules in lower Bed 11, Factory Cove Member (Shallow Bay Formation, Cow Head Group), Cow Head Peninsula, western Newfoundland, Canada.



Supplementary references

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