GSA Data Repository 2017001

Conodonts in Silurian hypersaline environments: Specialized and unexpectedly diverse

Jarochowska et al.

Item DR1

TABLE DR1

Sample	Beds	Lithology	Sample weight [kg]	*Ozarkodina confluens*	*Ozarkodina bohemica*	*Ozarkodina roopaensis*	*Ozarkodina soegina*	*Ozarkodina wimani*	*Ozarkodina* spp.	*Wurmiella excavata*	*Oulodus excavatus*	*Oulodus siluricus*	*Ctenognathodus* sp. S	*Ctenognathodus jeppssoni*	*Ctenognathodus murchisoni*	*Ctenognathodus* spp.	Unidentified
EJ-So-5	Soeginina	Laminated mudstone with regular layers of vugs after gypsum? crystals	3.125	42						4		9					
EJ-So-4	Soeginina	Oncoidal floatstone	1.35	29	1	15	2?		2	3	9	1?				8	5
EJ-So-3	Soeginina	Oncoidal floatstone with gastropods and leperditids	2.23	21		11	1	1	1		10					11	3
EJ-So-2	Anikaitse	Floatstone with large (up to 15 cm) chaetetids	4.245	11	6						19		72				23
EJ-So-1	Vesiku	Stromatolite with desiccation cracks and vugs after evaporites	2.26		24				3				2	1?	1	28	11

Item DR2 - Methods

Field data

The Soeginina section (Fig. 1; 58°17’20.22’’ N, 21°50’30.05’’ E) was sampled for production of slabs, thin sections, and extraction of conodonts. Conodonts were extracted using 7% buffered acetic acid according to the method of Jeppsson et al. (1999). The fraction between 63 µm and 2 mm was retained after sieving. Quantitative data on newly recovered conodonts is given in Supplementary Material S1 and summarized together with previous data from Viira and Einasto (2003) in Figure 1. Illustrated material is hosted at Tallinn University of Technology (GIT-) and Univ. of Erlangen-Nuremberg (EJ-).

References

References used in the compilation of Homerian-Gorstian conodont occurrences with environmental data are listed below. Only studies explicitly reporting the full taxonomic composition were included. Approximately only half of available publications on Homerian-Gorstian conodonts could be included as the remainder lacked sufficient information on sampled lithology, environment, positions of the samples, or focused on individual taxa and not entire assemblages. The compilation includes assemblages from Laurentia, Baltica, Avalonia, and peri-Gondwanan terranes. Peritidal assemblages were recorded from Baltica (Estonia, Lithuania, Ukraine) and Laurentia (the US).

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Diversity analysis

All analyses were performed in R Sortware 3.2.4 (R Core Team, 2016). Occurrences with uncertain identifications (aff., cf., ?) have been removed. Each sample (collection) has been originally assigned to an environment in the Paleobiology Database (PBDB), based on either direct statement in the original publication or on associated literature (e.g. where the author of the conodont paper referred the reader to another paper for details of regional geology). We recoded these environments to unify redundant classes such as "offshore ramp" and "offshore shelf". This resulted in distinguishing seven successive environments along the onshore-offshore gradient.

Beta diversity was additionally calculated as multivariate dispersion (distance from the centroid of samples within each habitat) using betadisper() function of (version 2.3-4, Oksanen et al., 2016).

Because the number of collections varies substantially between environments, we standardized our data by drawing randomly and without replacement 24 samples (the minimum number of samples per habitat) from each environment. This subsampling procedure was repeated 1000 times to obtain mean values and standard errors for all measured statistics.

Subsampled dataset was used to calculate multiplicative diversity partitioning and turnover between environments using Jaccard dissimilarity (e.g. Legendre and Legendre, 1998 and references therein). An alternative approach accounts for the spatial turnover and the nestedness components of beta diversity (Baselga, 2010). This was calculated using the betapart package of Baselga and Orme (2012) using Jaccard dissimilarity. The results are shown in Appendix S3.

Ordination analysis

We used a restricted dataset with assemblages containing more than one species. The metaNMDS (Nonmetric Multidimensional Scaling with Stable Solution from Random Starts, Axis Scaling and Species Scores) procedure implemented in the vegan package for R software (version 2.3-4, Oksanen et al., 2016). Distances between assemblages in the final version (Fig. 3) were calculated using Bray-Curtis dissimilarity, but similar results were obtained using Jaccard dissimilarity. Very small dissimilarities were handled by adding a small value. The use of metaNMDS procedure results in centering the dataset so that the origin lies at the average of both axes and rotation with the principal component analysis. Multivariate variation among samples was thus maximized along the first ordination axis, which consequently corresponds to the strongest gradient in the assemblage composition. Axes are scaled in half-change, i.e. one unit means halving of community similarity from replicate similarity. As a result Fig. 3 can be directly interpreted in terms of distance between samples and axes are meaningful (reflect a composition gradient, which in this case corresponds to the peritidal-offshore transect).

References cited in the appendix

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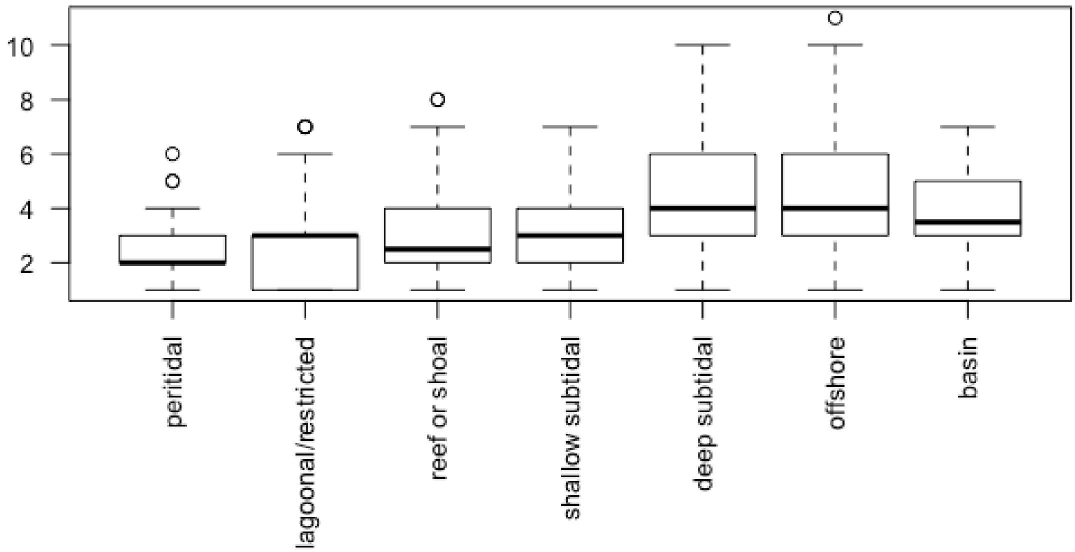
Item DR3 - Results

Number of occurrences per environment

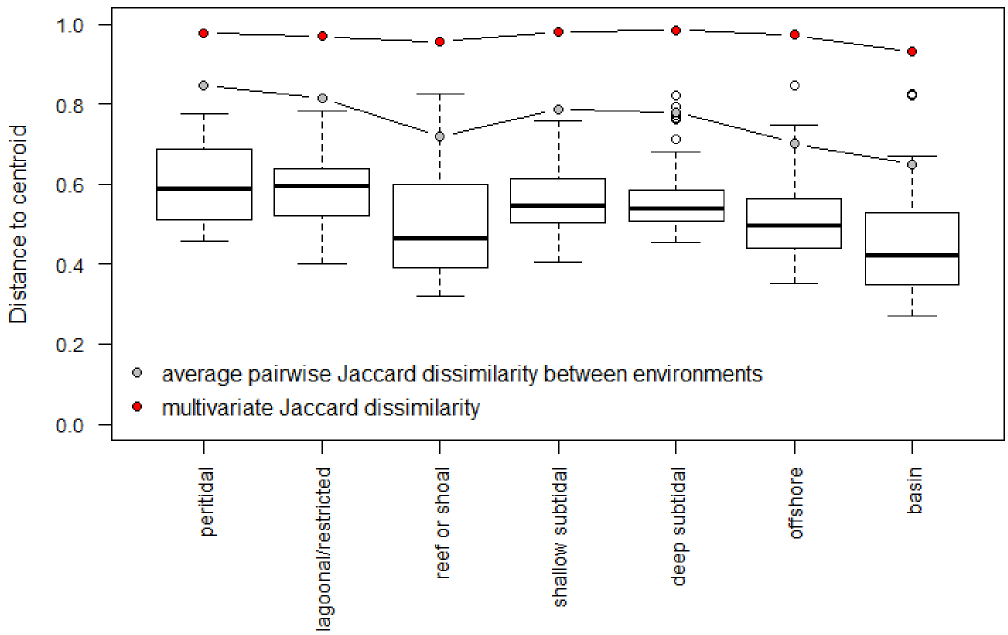
peritidal	lagoonal/restricted	reef or shoal	shallow subtidal	deep subtidal	offshore	basin
49	37	32	76	99	59	24

Sample-level raw (α) diversity per environment

Vertical axis shows the number of species. Boxes show the inter-quartile range, the thick line – the mean, whiskers – the total range, and dots – outliers.



Beta diversity (Jaccard dissimilarity) as pairwise average and as multivariate dispersion



ANOVA for beta diversity:

	Df	Sum of squares	Mean square	F value	P (>F)
Groups	6	0.5885	0.098083	9.1846	**2.207e-09**
Residuals	369	3.9406	0.010679		

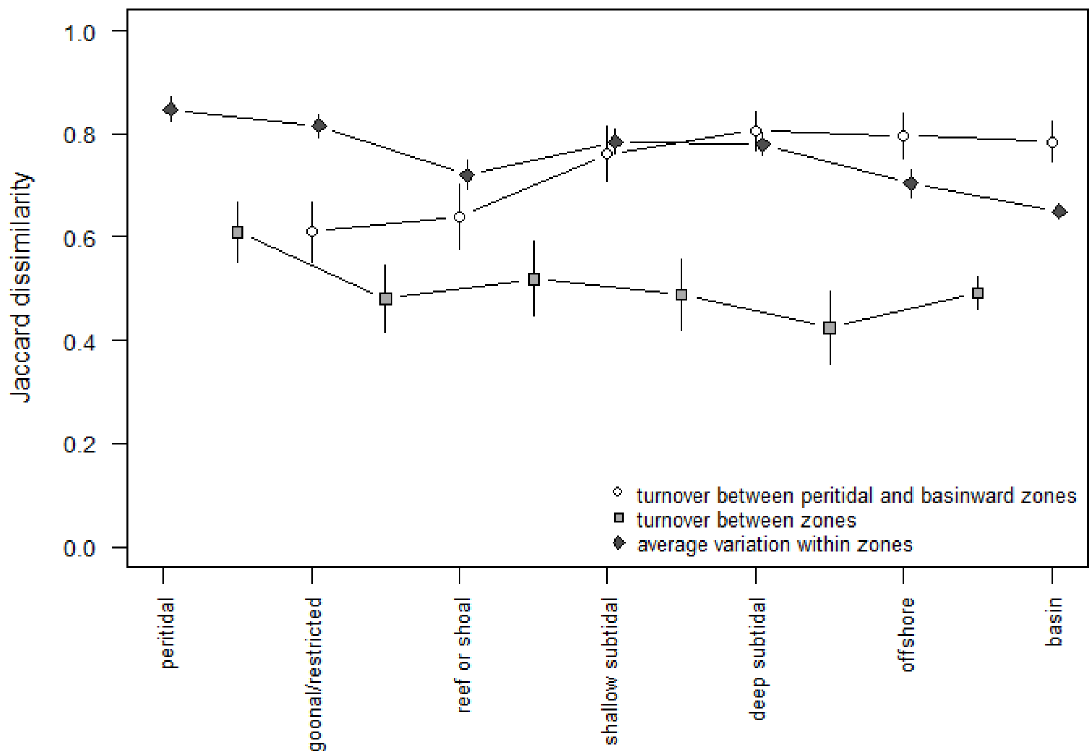
Tukey's correction for multiple comparisons

	Difference	Lower CI	Upper CI	Adjusted p value
lagoonal/restricted-peritidal	-0.0229	-0.0896	0.0439	0.9502
reef or shoal-peritidal	-0.0943	-0.1640	-0.0247	**0.0014**
shallow subtidal-peritidal	-0.0416	-0.0978	0.0145	0.2987
deep subtidal-peritidal	-0.0486	-0.1021	0.0049	0.1028
offshore-peritidal	-0.0977	-0.1569	-0.0385	**0.0000**
basin-peritidal	-0.1525	-0.2288	-0.0762	**0.0000**
reef or shoal-lagoonal/restricted	-0.0715	-0.1454	0.0025	0.0659
shallow subtidal-lagoonal/restricted	-0.0188	-0.0802	0.0427	0.9716
deep subtidal-lagoonal/restricted	-0.0258	-0.0848	0.0333	0.8548
offshore-lagoonal/restricted	-0.0749	-0.1391	-0.0106	**0.0109**
basin-lagoonal/restricted	-0.1296	-0.2099	-0.0493	**0.0001**
shallow subtidal-reef or shoal	0.0527	-0.0119	0.1173	0.1931
deep subtidal-reef or shoal	0.0457	-0.0166	0.1080	0.3116
offshore-reef or shoal	-0.0034	-0.0707	0.0639	1.0000
basin-reef or shoal	-0.0582	-0.1409	0.0246	0.3641
deep subtidal-shallow subtidal	-0.0070	-0.0537	0.0397	0.9994
offshore-shallow subtidal	-0.0561	-0.1093	-0.0029	**0.0309**
basin-shallow subtidal	-0.1109	-0.1826	-0.0391	**0.0001**
offshore-deep subtidal	-0.0491	-0.0995	0.0013	**0.0616**
basin-deep subtidal	-0.1039	-0.1736	-0.0342	**0.0003**
basin-offshore	-0.0548	-0.1289	0.0194	0.3041

Resampled diversity

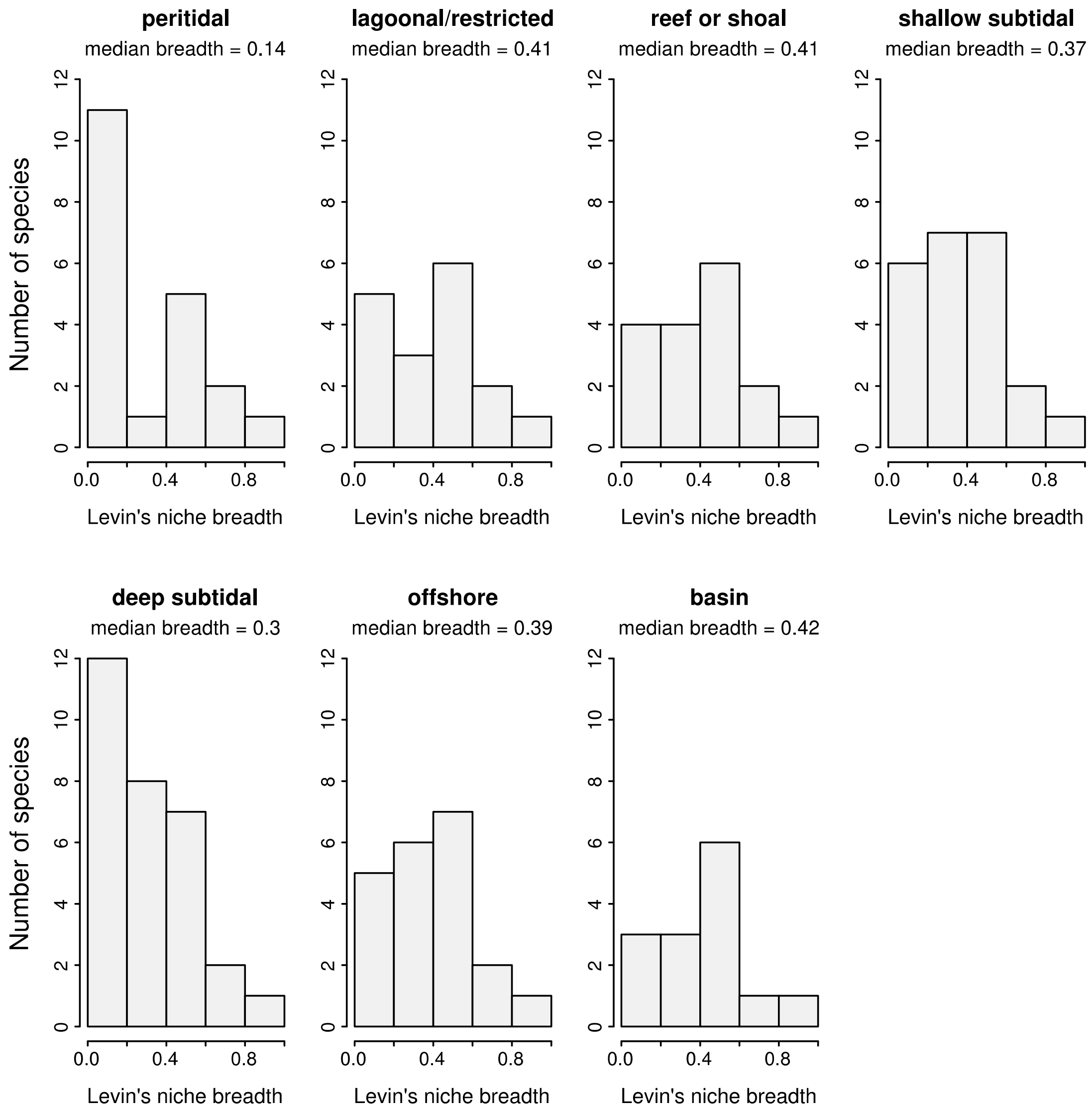
	Alpha	Beta	Gamma
peritidal	2.5	6.6	16.5
lagoonal/restricted	2.8	5.5	15.5
reef or shoal	3.3	4.6	15.1
shallow subtidal	3.1	5.1	16.1
deep subtidal	4.4	5.2	22.7
offshore	4.7	3.8	17.5
basin	3.8	3.7	14.0

Pairwise turnover between environments



Distribution of niche breadth within each environment

Niche breadth is expressed as a unitless value ranging from 0 to 1. It weights the range along the onshore-offshore gradient by frequency of samples in each environment and the relative frequency of the species in this environment. For two species occurring in the same number of environments, it will be lower (narrower niche) for the one which is mostly concentrated in one of them, and higher (wider niche) for the one which is uniformly distributed across all these environments.



Distribution of conodonts with different environmental ranges per environment

The plots show relative proportions of stenotopic and eurytopic taxa in each zone. E.g. in the peritidal zone the distribution is strongly bimodal: strict specialists occupying only one environment and eurytopic species occurring in all seven environments are the two most common groups.