

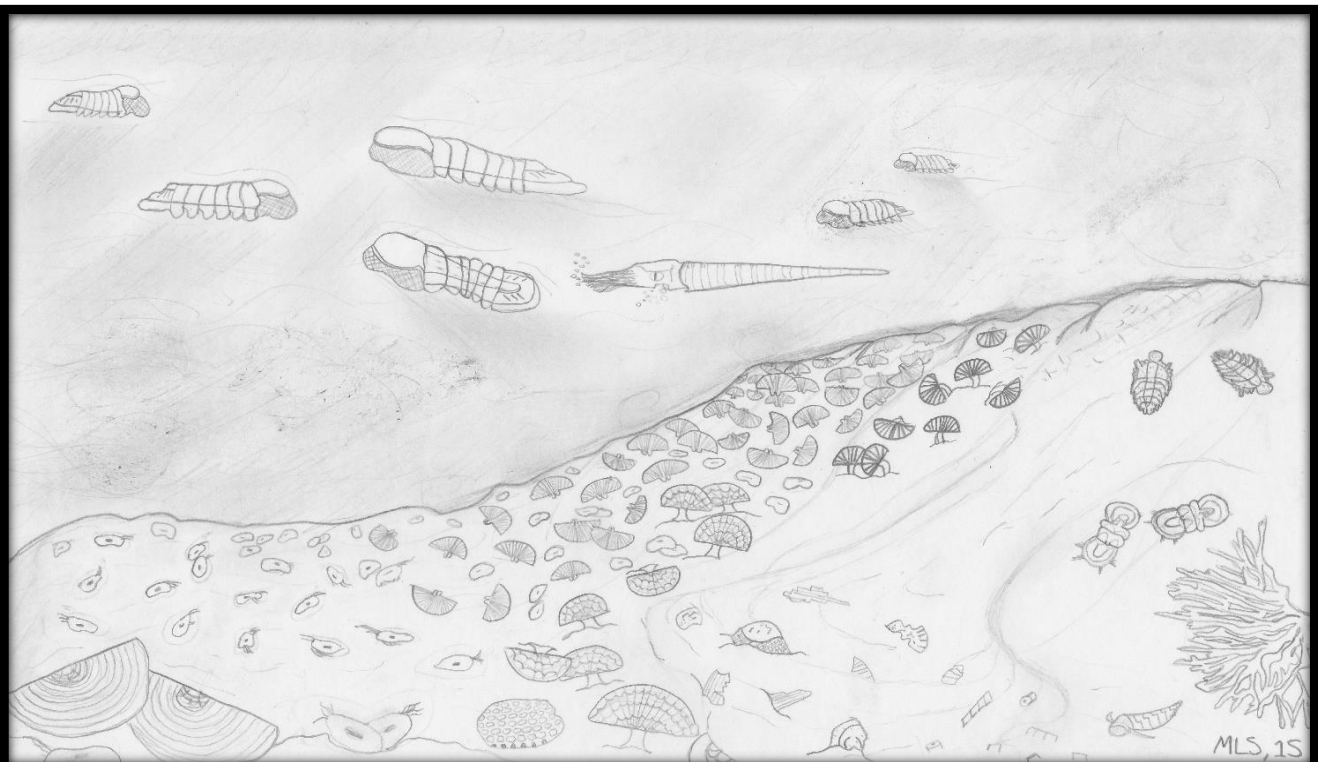


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THE COMPOSITION AND SIGNIFICANCE OF A DEEP-WATER FAUNA OF FOSSIL SHELLS FROM THE ORDOVICIAN PERIOD

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Front cover illustration

A detailed sketch of an imaginary scene of the ancient Oriel Brook environment during the late Katian Stage of the Upper Ordovician Period, (not to scale).

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Abstract: Organisms living on the deepest part of the continental shelf during the Ordovician Period included an association of shelled animals, brachiopods, termed the *Foliomena* fauna. This fauna persisted for some 15 million years before disappearing during the end Ordovician mass extinction event around 446 million years ago. A sparse *Foliomena* fauna from the upper Ordovician at Oriel Brook in eastern Ireland was described over thirty years ago. More recent collecting includes many more brachiopods. These fossils are identified to provide a fuller census of the species present and enable statistical comparison with late Ordovician brachiopod faunas from around the world. Four genera: a lingulate brachiopod, *Dedzetina*, *Cyclospira* and *Foliomena* itself are documented for the first time from Oriel Brook. The relative water depths inhabited by many *Foliomena* faunas are well known and so the statistical determination of which other faunas the Irish samples are closest to provides an indication where on the deep shelf the Irish fauna lived. Assessment of relative depths and palaeogeographic significance is achieved through the analysis of brachiopods and trilobites occurring in the same samples in comparison with *Foliomena* faunas of the late Katian elsewhere in the world. This provides an indication that the Oriel Brook fauna lies in the mid-deep end of the relative water depth spectrum, (BA5-6) and also correlates with similar faunas of the Iapetus region.

Key words: Ordovician, brachiopods, *Foliomena* fauna, late Katian, relative water depth spectrum, Iapetus region

1. Introduction

The organisms that lived on the deepest part of the continental shelf during the Ordovician Period included an association of brachiopods, shelled organisms belonging to what is known as the *Foliomena* fauna (Zhan *et al.* 2014). This fauna persisted for some 15 million years before disappearing during the end Ordovician mass extinction event around 446 million years ago. A sparse brachiopod fauna from the upper Katian stage of the upper Ordovician in eastern Ireland was described over thirty years ago, (Harper & Mitchell 1982) and considered to have similarities to the *Foliomena* fauna. More recent collecting (Owen & Romano 2011) has revealed a much more abundant brachiopod fauna. This has been investigated to provide a fuller census of the species present and, by statistical comparison with coeval brachiopod faunas from around the world, an indication of the likely position on the deep shelf in which the fauna lived.

1.1. *The Late Ordovician World*

The Ordovician was a geological period in the Earth's history, between 485.4 ± 1.9 - 443.8 ± 1.5 million years ago. This present study focuses particularly on the Katian stage of the Upper Ordovician, 453.0 ± 0.7 - 445.2 ± 1.4 million years ago, (Cohen *et al.* 2013; updated by The International Commission on Stratigraphy). It was a time when the land was barren and life was still largely confined to the oceans. The Ordovician witnessed many great changes to the history of life which are still relevant to research, as in today's rapidly changing world, climate change and its

impacts on biodiversity are hot topics. The Great Ordovician Biodiversification Event (GOBE), was one of most vital periods of change seen in marine organisms in the planet's history, which saw the diversity of marine animals increase threefold in just 25 million years (Webby *et al.* 2004; Harper 2006, cited in Servais *et al.* 2009). The greatest diversity peak of the GOBE, occurred in the late Katian (Webby, 2000; Webby *et al.*, 2004, cited in Zhan *et al.* 2014). This was the time, in which the Oriel Brook brachiopod fauna lived. However, this explosion in biodiversity came to an abrupt end at the end Ordovician mass extinction event, around 446 million years ago. This is thought to be caused by the southern supercontinent of Gondwana becoming glaciated (Brenchley 1990 cited in Harper & Owen 1996). This would have affected the climate, ocean chemistry and also lead to a reduction in global sea level, killing off many marine organisms, (BBC Nature 2014).

Brachiopods and trilobites are two main groups of animals that dominated the upper Ordovician seas (Harper & Owen 1996). They also radiated and diversified into numerous forms throughout this period. One such group of trilobites, that was particularly focused on in the present study was the cyclopygids, known for their large eyes. These pelagic (swimming) trilobites lived at different depths within the water column, so their diversity increases with increasing water depth as the dead animals fell to sea bed. With data collected from the brachiopods, both brachiopods and trilobites are important as they can be used in determining "palaeobathymetry", which is a measurement of ancient relative water depth.

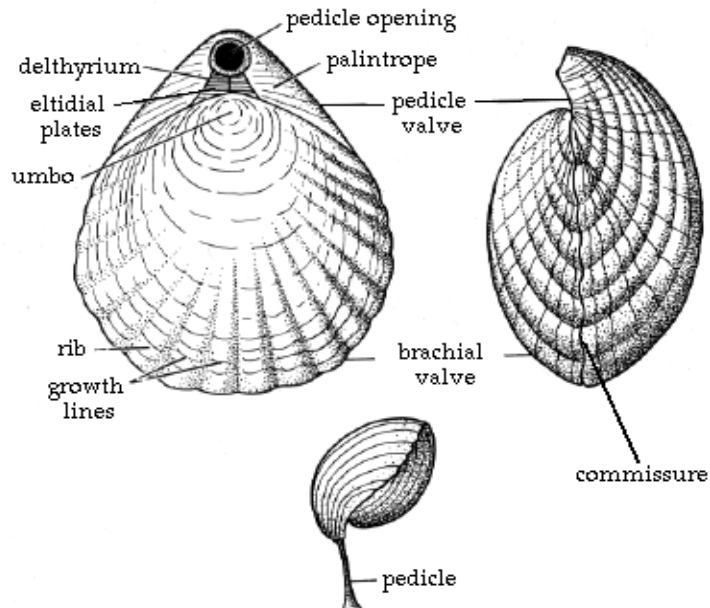


FIG. 1. General morphology of a brachiopod Clarkson (1986) cited in Wells Jr (1998).

In the Ordovician, the position of the Earth's continents was very different from those of today. The period saw the separation of the continents at their furthest (Servais *et al.* 2009). Some of today's continents came together to form large landmasses, whereas others were scattered throughout the oceans. This in turn resulted in different faunas living on different continents (Servais *et al.* 2009). For example, the Chinese region is placed far from the Iapetus region to the east during the late Katian, and so was inhabited by a different *Foliomena* fauna (Fig. 2).

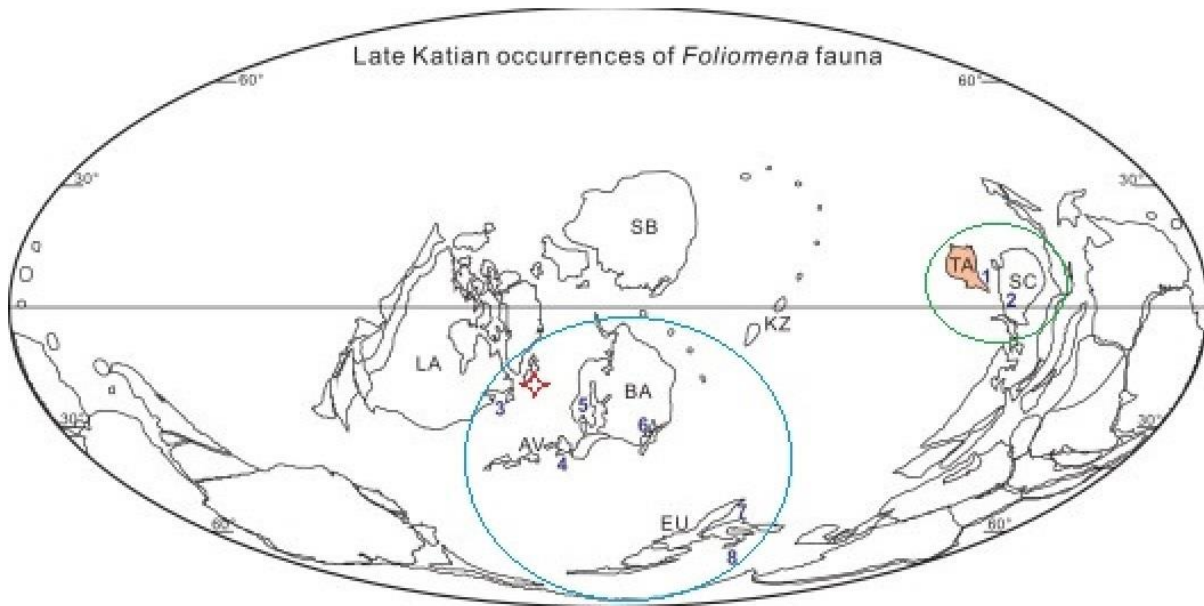


FIG. 2. Late Katian palaeogeography and spread of *Foliomena* faunas (adapted from base map of Boucot *et al.*, (2009), modified in Zhan *et al.* (2014)). Different regions circled; Iapetus (blue) and Chinese (green). Position of Oriel Brook (red star). 1: Kuruktag, northeastern Tarim (present orientation); 2: border region of Zhejiang and Jiangxi provinces, eastern South China; 3: Maine, Northeast USA; 4: central and northern Wales; 5: southern Sweden; 6: southern Poland; 7: Bohemia, Czech Republic; 8: Sardinia, Italy. Landmasses highlighted include; LA: Laurentia; AV: Avalonia; SB: Siberia; BA: Baltica; EU: Mediterranean margins of Gondwana (southern Europe); KZ: Kazakhstan; TA: Tarim; SC: South China.

The fragmentary landmasses that one day would become today's continents were also separated by long-gone oceans in the Ordovician. Scotland and the north of Ireland for example, were separated from England, Wales and the south of Ireland by an ancient ocean, known as the "Iapetus" which was once comparable to the size of the present day Atlantic. Contained within these oceans were microcontinents and even smaller pieces of the earth's crust called terranes. One such terrane, was the Irish Grangegeeth Terrane (Owen & Romano 2011), which lay close to what is now the northern part of Ireland on the margins of the continent of Laurentia, which was largely composed of present day North America and Greenland. Present on this terrane was a deep, muddy seabed in which the ancient Oriel Brook brachiopod

fauna lived. It would take over 400 million years for the continents to come to their present positions. Today, and the fossil brachiopods are exposed in mudstones along Oriel Brook, on the Grangegeeth terrane (Harper & Mitchell 1982), which is part of eastern Ireland (Fig. 3).

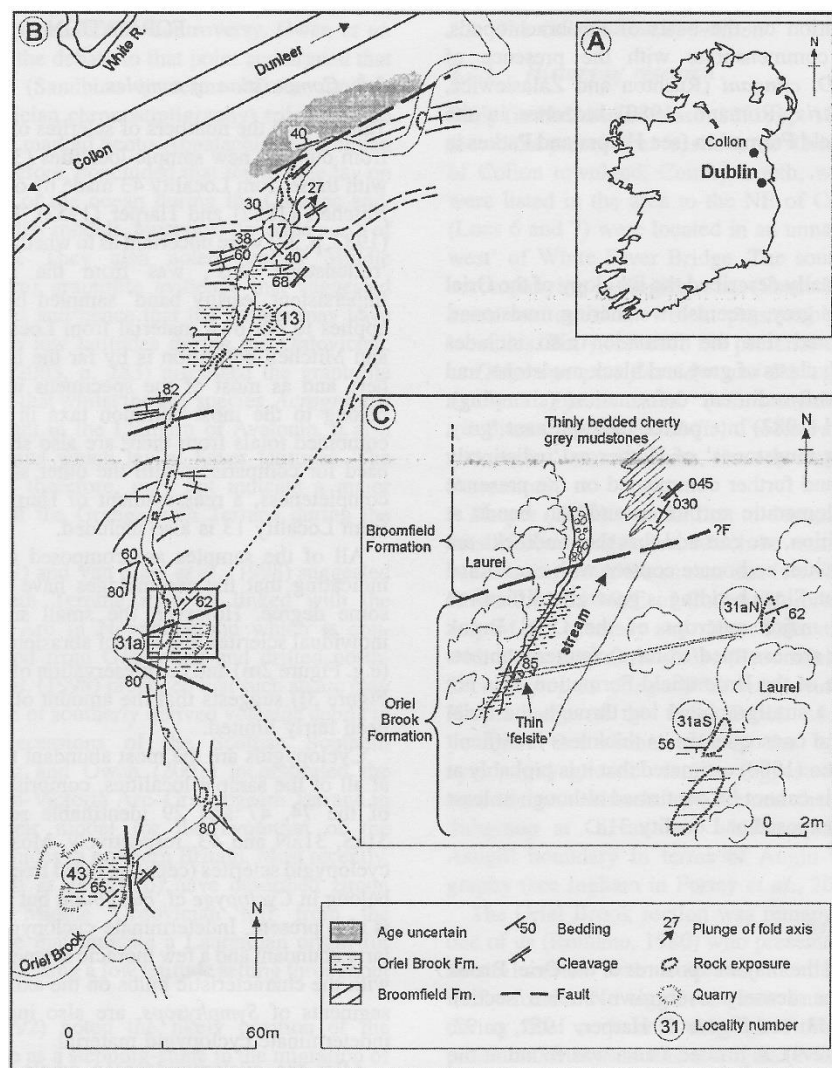


FIG. 3. Map of Oriel Brook (Owen & Romano 2011). **(a)** Collon village highlighted on a map of Ireland. **(b)** Geological map of Oriel Brook section, 2.75km from Collon (modified from Romano, 1980, figure 9). **(c)** Field sketch of Oriel Brook fossil localities.

Fossils found at Oriel Brook occur in the Oriel Brook Formation (Harper & Mitchell 1982). They include; brachiopods and bivalves (animals with the body housed in two shells), ostracods (shelled crustaceans), trilobites (segmented arthropods), nautiloids (squid-like animals), hyoliths (animals with cone-shaped shells) and bryozoans (colonial invertebrates) (Harper & Mitchell 1982; Wikipedia 2015). In the late Katian, this community of organisms lived on an underwater slope in which volcanism was present nearby (Harper & Mitchell 1982).



FIG. 4. Sketch of an imaginary scene of Oriel Brook during the late Katian, featuring organisms discussed above, (not to scale).

Of the fossils examined from Oriel Brook, many consist of shelly fragments, which suggest that some have been washed in from elsewhere and perhaps downslope. This could be interpreted as being deposited in a deep water environment.

In Owen & Romano (2011), this was confirmed as a low latitude shelf or slope facing an ocean. Specimens examined in the present study were all small, a few millimetres in size with some being weathered or partially weathered. In Owen & Romano (2011), they were also interpreted as delicate samples, as they were found in mudstones that were decalcified. Many specimens include brachiopods, trilobites and ostracods.



FIG. 5. Photograph (Owen & Romano 2011) of well-preserved fossils from Oriel Brook, which include; part of the headshield of trilobite *Phillipsinella* (right) and the brachiopod *Cyclospira* (left).

This report will investigate the following question:

Where was the Oriel Brook brachiopod fauna situated in the relative water depth spectrum and does it show the strongest similarity to the *Foliomena* faunas in the Iapetus region?

2. Materials and Methods

The fossil material collected from Oriel Brook and examined in this report can be divided into three sets of samples:

- The J.C. Harper Collection, collected in the late 1940's, cited in (Owen & Romano 2011).
- Material collected by D.A.T. Harper and W.I. Mitchell (Harper & Mitchell 1982).
- Material collected by Owen and Romano, (Owen & Romano 2011).

These fossils were sampled from numbered localities; 31aN, 31aS, 43, 13 and 17 (Owen & Romano 2011) (See Fig. 3).

The collected material from all these localities was examined in detail for brachiopod fossils, in doing so the material was also reorganised into appropriate groupings of samples with and without brachiopods, for their eventual transfer to the National Museum of Ireland collections.

Having undertaken some brachiopod familiarisation exercises, notes were carefully taken, documenting the field number of each sample and the number of rock fragments present, in decreasing order of size. Each piece of rock was then thoroughly examined using a binocular microscope and a brief description made. Sketches of well-preserved fossils were made in order to enable identification of each fossil brachiopod to a particular genus if at all possible.



FIG. 6. Photograph taken during the Oriel Brook fossil examination.

The process in identifying a fossil brachiopod to a particular genus began with comparing the specimen to photographs of identified brachiopods from Oriel Brook itself, which originated from Harper & Mitchell (1982). For further comparison and to reinforce any suspicions, the specimen was also compared to higher quality photographs from Sheehan (1973) and also compared to images of brachiopods from Girvan, Scotland from the three part monograph by D.A.T. Harper (1984, 1989, 2006), as with other *Foliomena* fauna papers (Zhan & Jin 2005; Zhan *et al.* 2014; Neuman 1994; Liang *et al.* 2014; Candela 2011; Villas *et al.* 2002; Cocks & Rong 1988; Rong *et al.* 1999). The final brachiopod identifications were then confirmed with the supervisor, the palaeontologist Dr Alan Owen.

In total, 384 individual rock fragments (ranging from over 15cm to smaller than 5mm) were examined. The brachiopod data collected from this examination of the Oriel Brook specimens such as the different genera present and their abundance is then used in further analysis.

2.1. Data compilation and analysis

Microsoft Excel 2010 was used to compile the data collected from Oriel Brook. First, the abundance data (see Appendix A) of each genus of brachiopod found in each locality was compiled onto a spreadsheet format. This allowed the data to be expressed as pie charts, showing the relative percentages of each genus per locality.

Excel was also used to construct a presence/absence matrix, (see Appendix B) where the number one represents that a particular genus is or might be present and zeroes represent that a particular genus is absent. Here, the presence and absence data of particular brachiopods from Oriel Brook was included with the presence and absence data of other late Katian Foliomena faunas.

This data matrix was then copied into PAST [PALaeontological STatistics] (<http://folk.uio.no/ohammer/past/>). This is a computer package used for a large number of numerical techniques and has become a standard tool for analyses in Palaeontology.

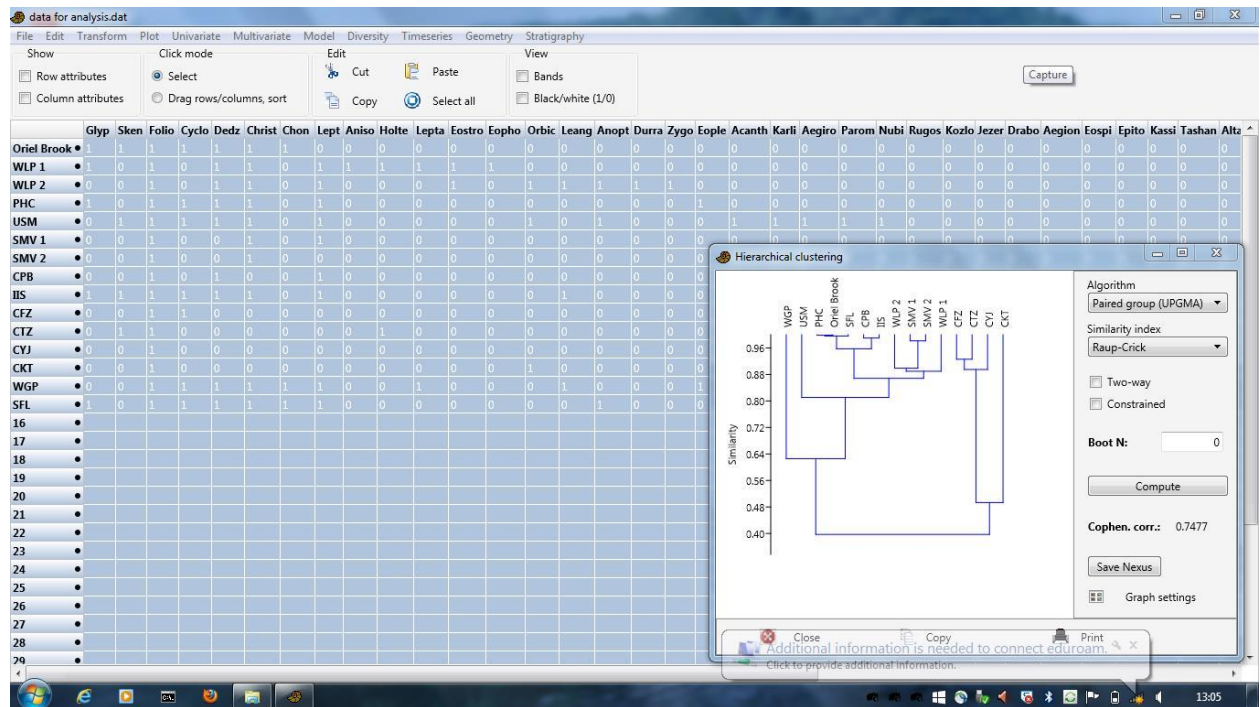


FIG. 7. Screen-print of the presence/absence analysis using PAST and produced dendrogram (bottom right).

Different forms of numerical analysis were considered in the present study. Cluster analysis and seriation were two forms used from PAST, as they both display data in a specific way that was required for a clear analysis.

A cluster analysis is a statistical method, which compares pairs of samples, and groups them in terms of greatest similarity. This is displayed on a tree-like diagram called a dendrogram.

Seriation is a numerical technique which compares samples by “shuffling” the samples and genera in the data matrix to get the best possible fit, of presences along a diagonal. If ordering along the diagonal is strong, then the sequence order of localities may indicate their original sequence along an environmental gradient.

3. Results

3.1. Faunal list

The composition of the Oriel Brook brachiopod fauna is shown in the table (Fig. 8), pie charts (Fig. 9) and in the photographed specimens (by Les Hill), (Fig. 10) below:

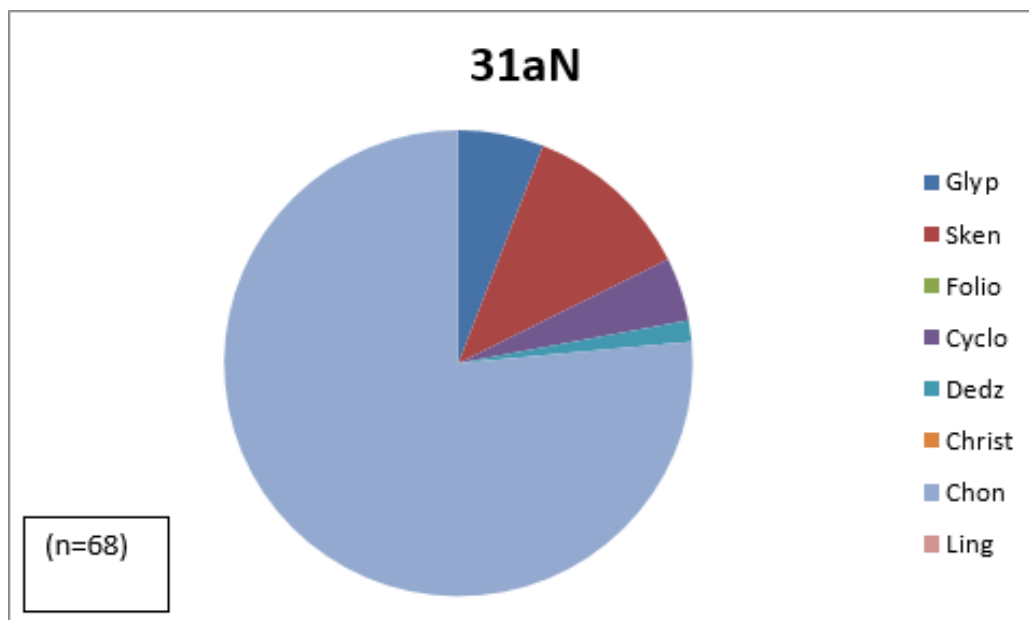
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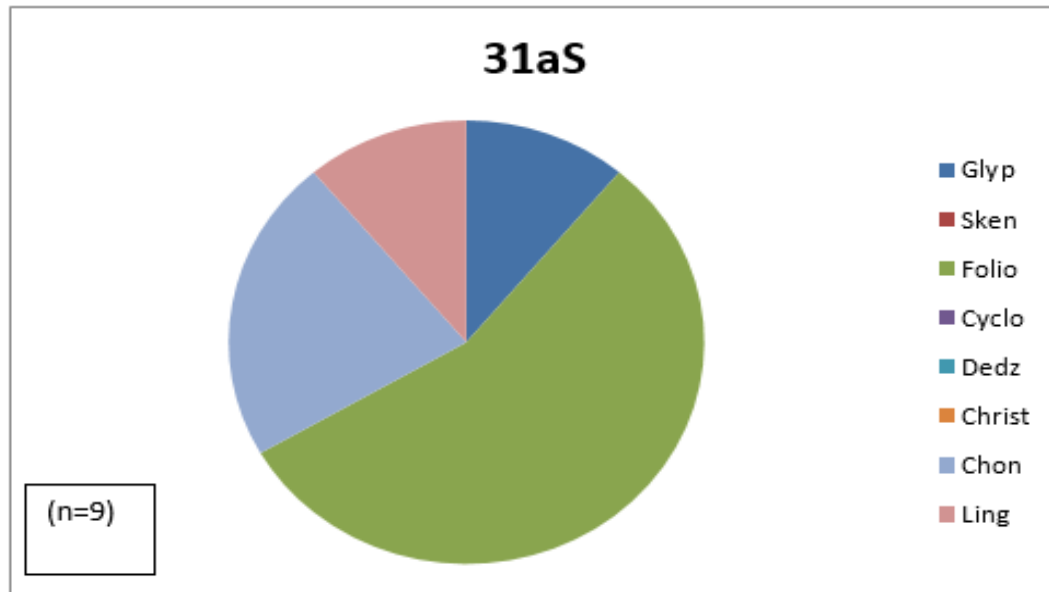
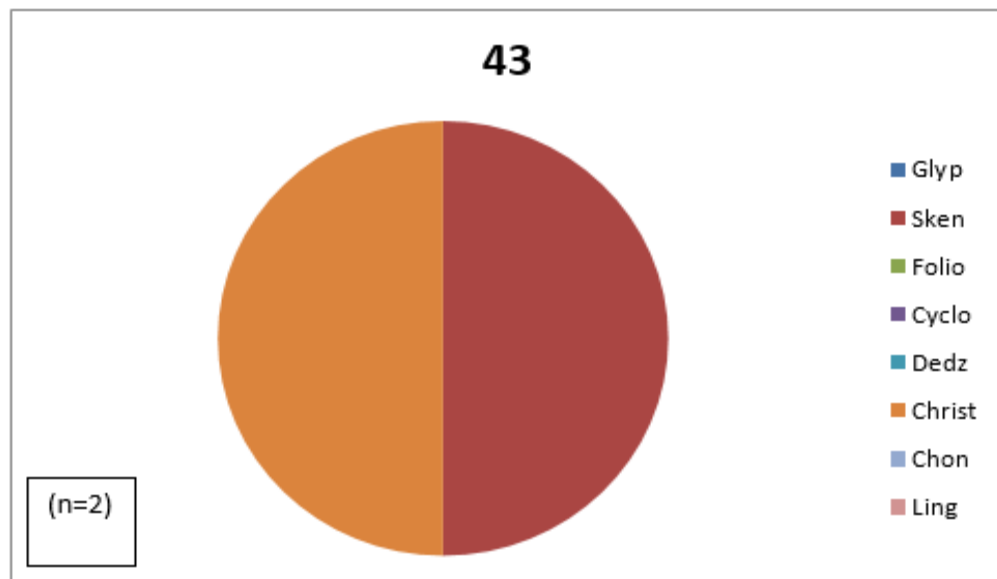
Glyp	<i>Glyptorthis</i>
Sken	<i>Skenidioides</i>
Folio	<i>Foliomena</i>
Cyclo	<i>Cyclospira</i>
Dedz	<i>Dedzetina</i>
Christ	<i>Christiania</i>
Chon	<i>Chonetoidea</i>
Ling	Lingulate brachiopod

Genera	Localities								
	31aN		31aS			43		Total	
	No.	%	No.	%	No.	%	No.	%	
Glyp	4	5.88	1	11.11	0	0	5	6.33	
Sken	8	11.76	0	0	1	50	9	11.39	
Folio	0	0	5	55.55	0	0	5	6.33	
Cyclo	3	4.41	0	0	0	0	3	3.8	
Dedz	1	1.47	0	0	0	0	1	1.27	
Christ	0	0	0	0	1	50	1	1.27	
Chon	52	76.47	2	22.22	0	0	54	68.35	
Ling	0	0	1	11.11	0	0	1	1.27	

FIG. 8. Table showing the number and percentage of each brachiopod genus from each locality then totalled.

(a)



(b)**(c)**

(d)

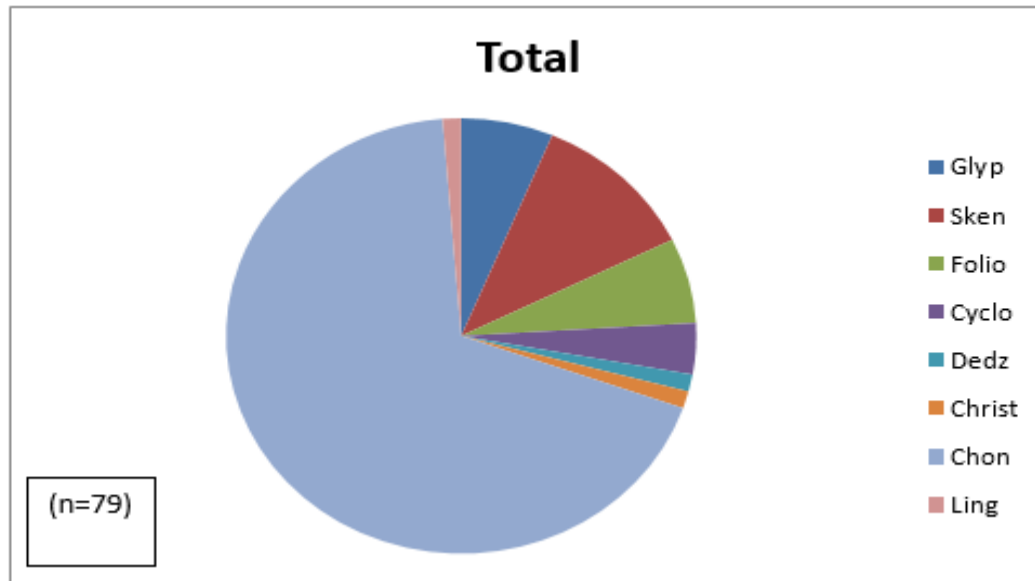


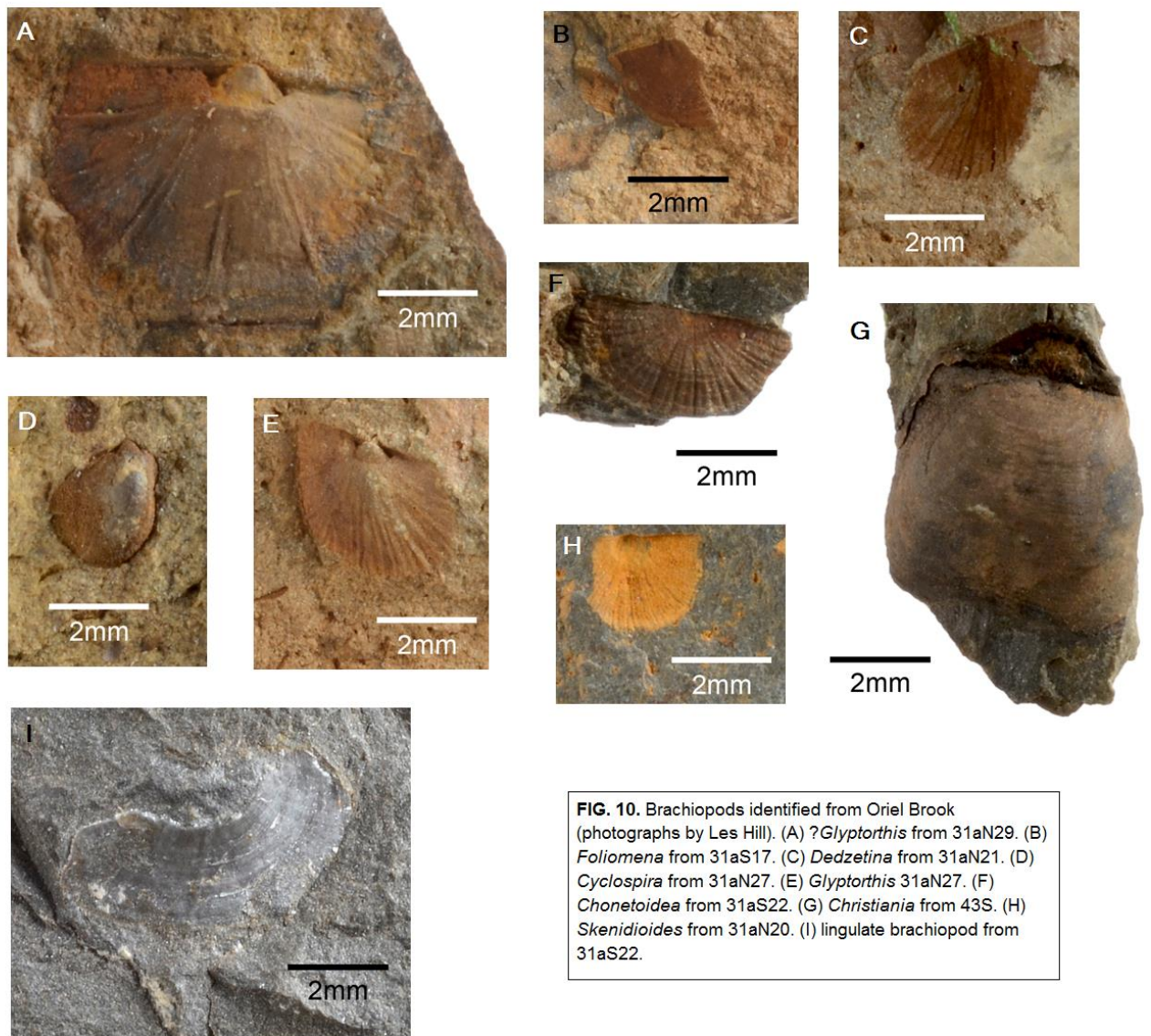
FIG. 9. Pie charts showing the percentage of each brachiopod genera found in each locality; **(a)** locality 31aN; **(b)** locality 31aS; **(c)** locality 43; **(d)** and from Oriel Brook in total, (n - number of specimens).

The results show that *Chonetidea* is by far the most abundant genus found from the Oriel Brook material investigated, totalling at 68.35% of all brachiopod specimens found. However, there are subtle differences between the localities. For example, *Skenidioides* is the second most abundant brachiopod found at 31aN at 11.76%, but is absent from 31aS. Also shown in the pie charts, 31aN had a sample size of 68 compared to the sample sizes of 9 for 31aS and 2 for 43. This might show that further sampling from 31aS and 43 is needed to obtain a clearer census of the different genera found at each locality.

Also, from initial observations of the Oriel Brook samples, in general, samples taken from 31aN were dominated by fossil brachiopods, particularly *Chonetoidea* whereas samples from 31aS were rich in fossil ostracods and contain all the *Foliomena*

specimens. This could indicate that subtle environmental differences might have existed between 31aN and 31aS.

Of the brachiopods featuring on the faunal list, four genera are previously undocumented from Oriel Brook: a lingulate brachiopod, *Foliomena*, *Dedzetina* and *Cyclospira*. The lingulate brachiopod differs from the rest of the brachiopods found as it has a calcium phosphate shell, while the others have a shell made from calcium carbonate.



4. Analysis

4.1. *Palaeogeographical Setting*

Zhan *et al.* (2014) undertook an analysis in order to group together similar late Katian Foliomena faunas. This cluster analysis used the Raup-Crick algorithm on PAST. The cluster analysis was recreated by accessing the faunal data from an older paper by Zhan & Jin (2005), but this time including the Oriel Brook data. The Zhan *et al.* (2014) and Zhan & Jin (2005) papers, used the same localities but used different abbreviations to identify each of the sample sites. The following table pairs each abbreviation used to its counterpart (Fig. 11).

Locality	Abbreviations of associations or communities in Zhan <i>et al.</i> (2014) and in the present study	Equivalent abbreviations in Zhan & Jin (2005)
Afon Penfhos, Llyn Peninsula, North Wales	WLP 1	AP
Crugan Lane, Llyn Peninsula, North Wales	WLP 2	CL
Holy Cross Mountain, Southeast Poland	PHC	HC
Northeastern Maine, USA	USM	MN
Västergötland, Sweden (Jonstorp Formation)	SMV 1	SW
Västergötland, Sweden (Ulunda Mudstone)	SMV 2	VG
Prague, Czech Republic	CPB	PR
Sardinia, Italy	IIS	SD
Fengzu, Zhejiang Province, eastern China	CFZ	FZ
Tanshi, Zhejiang Province, eastern China	CTZ	TS
Xiazhen, Jiangxi Province, eastern China	CYJ	XZ
Northeastern Tarim, Xinjiang, northwest China	CKT	not included
Garth District, Powys, central Wales	WGP	not included
Scania, Sweden	SFL	SC

FIG. 11. Abbreviations table showing the abbreviations used in Zhan *et al.* (2014) and in the present study against their equivalent used in Zhan & Jin (2005).

The cluster analysis in the present study was then compared with the original in Zhan *et al.* (2014), to see any similarities or differences. The cluster analysis exhibited a very similar pattern to the published one, with both grouping the Chinese faunas together on a separate branch. Oriel Brook was clustered next to the fauna from Scania, (Southern Sweden) and paired directly with Holy Cross Mountain, (Southeast Poland), hence showing that Oriel Brook is nearly identical to these faunas. Oriel Brook was also clustered close to the Prague, (Czech Republic) and Sardinia, (Italy) samples, suggesting they share very similar faunas. A major difference between the present cluster analysis and that of Zhan *et al.* (2014) is that the latter grouped the North-eastern Maine (USA) fauna between the Polish/Southern Swedish and Czech Republic/Italian faunas. However, in the present cluster analysis, the introduction of Oriel Brook has caused North-eastern Maine to branch off to the side. This shows that the Oriel Brook fauna has a closer affinity to the Polish/Southern Swedish and Czech Republic/Italian faunas than the fauna from North-eastern Maine.

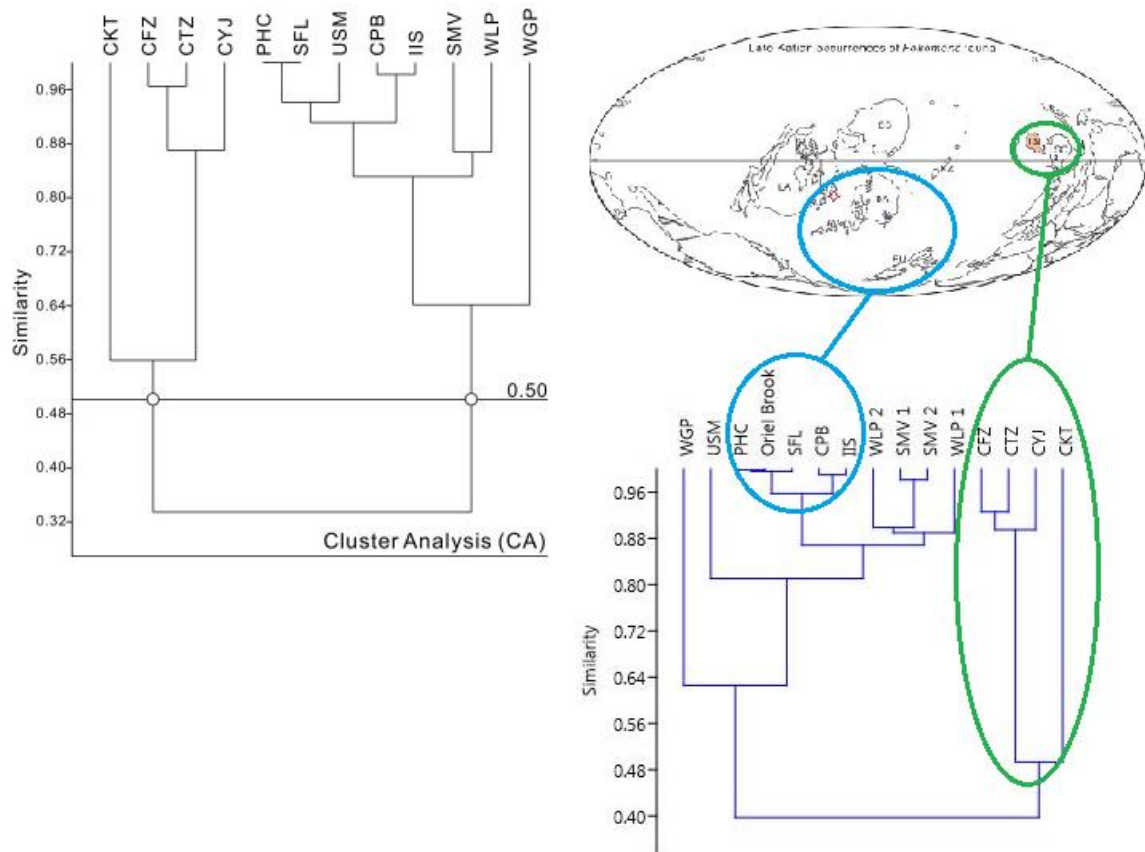


FIG. 12. Comparison between the cluster analysis in the present study (right) and the one in Zhan *et al.* (2014) (left). lapetus branch is matched with lapetus region (blue) and Chinese branch is matched with Chinese region (green). (Globe adapted from base map of Boucot *et al.*, (2009), modified in Zhan *et al.* (2014)).

The discussed localities, including Oriel Brook were close together around the area of the ancient lapetus Ocean on palaeogeographic reconstructions of the globe during the late Katian. As supported by the cluster analysis, the brachiopod faunas that inhabited this lapetus region are dissimilar to brachiopod faunas that are found in the Chinese region (See Figs. 2 & 12).

4.2. Relative Water Depth

The presence data were then used to find out where the Oriel Brook fauna lies on the relative water depth spectrum. Zhan & Jin (2005) undertook a numerical analysis of most of the then known *Foliomena* faunas. This cluster analysis used a different algorithm from that in Zhen *et al.* (2014), called Ward's method. The cluster analysis was recreated in the present study, but also including most of the late Katian data investigated by Zhen *et al.* (2014). This produced a dendrogram, which was compared with that in Zhan & Jin (2005) (see Fig. 13). Both cluster analyses grouped the Polish, Southern Swedish and Italian faunas that are close to Oriel Brook, with others in a particular cluster, labelled 'Cluster B' in the Zhan and Jin cluster analysis. This was also interpreted as 'Group B' in the Principal Component Analysis (PCA) used in Zhan & Jin (2005), which plotted the listed faunas along a gradient in terms of relative geological age and relative depth of the faunas.

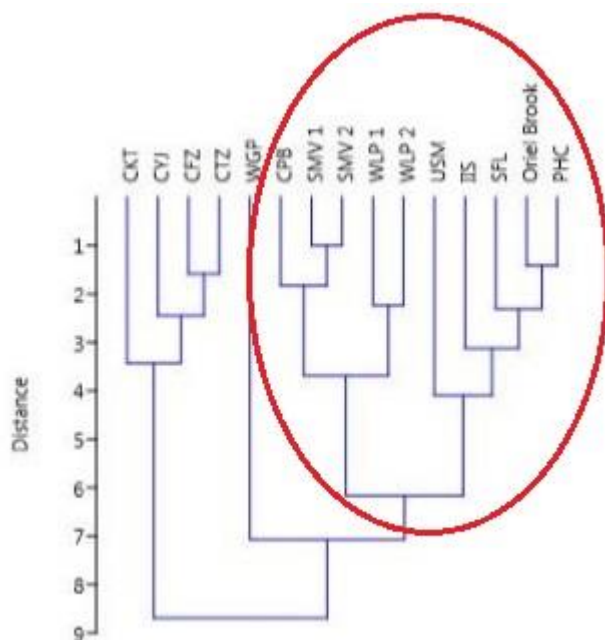


FIG. 13. Dendrogram produced in the current study using Ward's method. Localities, including Oriel Brook are present within red circle, interpreted as 'Cluster B' from Zhan & Jin (2005).

All the particular faunas listed above were plotted in Group B, which reflects the deeper end of the water depth spectrum (Zhan & Jin 2005). The Sardinia fauna, for example was thought of as living at a water depth of 200 metres or more (Villas *et al.* 2002). This suggests that the Oriel Brook brachiopod fauna lived at a similar depth. It is also long been considered that the Polish and Southern Swedish faunas lived in deep water, being a so called Benthic Assemblage (BA) 5-6 fauna, (Sheehan 1973; Harper 1980, 1984; Cocks & Rong 1988; also Rong *et al.* 1994, 1999 cited in Zhan & Jin 2005). The BA5-6 range is towards the deepest end of the benthic (living on the sea floor) assemblages, and is most likely the depth in which the Oriel Brook fauna lived.

Further evidence supporting that the Oriel Brook fauna was a deep water fauna comes from comparison with the associated trilobite faunas. Two seriations were performed, one involving trilobites and the other involving brachiopods. The trilobite seriation was constrained, which fixed the sequence of localities, along a depth gradient, which was based on a much bigger data matrix published by Owen & Bruton (2012). The brachiopod seriation was unconstrained, which allowed the sequence of localities to be changed during the seriation. Both seriations show an increasing water depth trend from left to right based on the number of cyclopygid trilobite genera also increasing from left to right. The seriations place Oriel Brook around the middle of the diagonal, which would position it in the mid-deep relative water depth spectrum.

	SMV 2	SFL	WLP 2	Oriel Brook	IIS	PHC	USM	CPB
Cyclopyge	■	■	■	■	■	■	■	■
Microparia		■	■			■	■	■
Symphyso				■	■	■	■	■
Degamella								■

FIG. 14. Comparison between trilobite (left) and brachiopod (right) seriations (Oriel Brook highlighted in red).

	SMV 2	SFL	WLP 2	Oriel Brook	PHC	CPB	IIS	USM
Rugos	■							
Dole		■						
Hetero		■						
Chon		■		■				
Durra			■					
Eostro			■					
Zygo			■					
Christ	■	■	■	■	■		■	■
Anopt		■	■					■
Glyp		■		■	■		■	
Folio	■	■	■	■	■	■	■	■
Kozlo		■				■	■	
Dedz		■	■	■	■	■	■	■
Eople					■			
Leang			■				■	
Lept		■	■		■	■	■	■
Cyclo		■		■	■		■	■
Orbic			■					■
Sken				■			■	■
Drabo							■	
Aegion							■	
Jezer							■	
Acanth								■
Aegiro								■
Nubi								■
Karli								■
Parom								■

5. Conclusions

According to the findings in this study, the Oriel Brook brachiopod fauna lay in the deeper end of the relative water depth spectrum, placing it in BA5-6 (Benthic Assemblage) which was obtained from the cluster analysis using Ward's method. This is supported more accurately in both seriations, which place this brachiopod fauna mid to deep in the relative water spectrum. In relation to their palaeogeographical setting, the Raup-Crick cluster analysis shows that the Oriel Brook fauna was most comparable to the Polish and Southern Swedish faunas with a strong correlation existing with other localities that lay within the Iapetus region, rather than with the Chinese region. This evidence now confirms that the Oriel Brook brachiopod fauna is a deep water fauna, like most *Foliomena* faunas and shares the closest similarity to these faunas that inhabited the Iapetus region of the globe during the late Katian.

5.1 Future work

Research that can be continued in this area, may include;

- The analysis of more brachiopod faunas. This can be achieved through recreating a large cluster analysis, like performed by Zhan & Jin (2005) with all *Foliomena* faunas presently known to date included.

- More sample collecting from Oriel Brook. This could include further collecting from Oriel Brook or from nearby outcrops of the Oriel Brook Formation. This might be particularly useful for localities 31aS and 43, as a larger sample of brachiopods is needed to obtain more accurate presence/absence results.
- Re-examination of museum specimens. A re-examination of material already in Ireland, could possibly yield more brachiopod fossils. This could then lead to increasing faunal list numbers and diversity of the different genera that inhabited Oriel Brook. Performing a Rarefaction analysis would also be useful here, which compares the various taxa present in samples of multiple sizes, (Hammer *et al.* 2001). This will show how thorough sampling at Oriel Brook has been and if it is worthwhile returning to further collect more samples.

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Appendix

	31aN	31aS	43		Total
Glyp	4	1	0		5
Sken	8	0	1		9
Folio	0	5	0		5
Cyclo	3	0	0		3
Dedz	1	0	0		1
Christ	0	0	1		1
Chon	52	2	0		54
Ling	0	1	0		1

Appendix A- Abundance data

	Oriel Broc	WLP 1	WLP 2	PHC	USM	SMV 1	SMV 2	CPB	IIS
Glyp	1	1	0	1	0	0	0	0	1
Sken	1	0	0	0	1	0	0	0	1
Folio	1	1	1	1	1	1	1	1	1
Cyclo	1	0	0	1	1	0	0	0	1
Dedz	1	1	1	1	1	0	0	1	1
Christ	1	1	1	1	1	1	1	0	1
Chon	1	0	0	0	0	0	0	0	0
Lept	0	1	1	1	1	1	0	1	1
Aniso	0	1	0	0	0	0	0	0	0
Holte	0	1	0	0	0	0	0	0	0
Lepta	0	1	0	0	0	0	0	0	0
Eostro	0	1	1	0	0	0	0	0	0
Eopho	0	1	0	0	0	0	0	0	0
Orbic	0	0	1	0	1	0	0	0	0
Leang	0	0	1	0	0	0	0	0	1
Anopt	0	0	1	0	1	0	0	0	0
Durra	0	0	1	0	0	0	0	0	0
Zygo	0	0	1	0	0	0	0	0	0
Eople	0	0	0	1	0	0	0	0	0
Acanth	0	0	0	0	1	0	0	0	0

Appendix B- Presence/absence matrix