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Author for correspondence:
Russell D. C. Bicknell
e-mail: rdcbicknell@gmail.com

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Computational biomechanical analyses demonstrate similar shell-crushing abilities in modern and ancient arthropods

Russell D. C. Bicknell[1,2], Justin A. Ledogar[1,2,3], Stephen Wroe[1,2], Benjamin C. Gutzler[4], Winsor H. Watson III[4] and John R. Paterson[1]

[1]Palaeoscience Research Centre, School of Environmental and Rural Science, and [2]Function, Evolution and Anatomy Research Lab, School of Environmental and Rural Science, University of New England, Armidale, New South Wales 2351, Australia
[3]Department of Evolutionary Biology, Duke University, Durham, NC 27708, USA
[4]Department of Biological Sciences and School of Marine Science and Ocean Engineering, University of New Hampshire, Durham, NH 03824, USA

RDCB, 0000-0001-8541-9035; SW, 0000-0002-6365-5915

The biology of the American horseshoe crab, *Limulus polyphemus*, is well documented—including its dietary habits, particularly the ability to crush shell with gnathobasic walking appendages—but virtually nothing is known about the feeding biomechanics of this iconic arthropod. *Limulus polyphemus* is also considered the archetypal functional analogue of various extinct groups with serial gnathobasic appendages, including eurypterids, trilobites and other early arthropods, especially *Sidneyia inexpectans* from the mid-Cambrian (508 Myr) Burgess Shale of Canada. Exceptionally preserved specimens of *S. inexpectans* show evidence suggestive of durophagous (shell-crushing) tendencies—including thick gnathobasic spine cuticle and shelly gut contents—but the masticatory capabilities of this fossil species have yet to be compared with modern durophagous arthropods. Here, we use advanced computational techniques, specifically a unique application of 3D finite-element analysis (FEA), to model the feeding mechanics of *L. polyphemus* and *S. inexpectans*: the first such analyses of a modern horseshoe crab and a fossil arthropod. Results show that mechanical performance of the feeding appendages in both arthropods is remarkably similar, suggesting that *S. inexpectans* had similar shell-crushing capabilities to *L. polyphemus*. This biomechanical solution to processing shelly food therefore has a history extending over 500 Myr, arising soon after the first shell-bearing animals. Arrival of durophagous predators during the early phase of animal evolution undoubtedly fuelled the Cambrian 'arms race' that involved a rapid increase in diversity, disparity and abundance of biomineralized prey species.

1. Introduction

Modern predatory arthropods use a range of morphological structures to acquire and consume food [1]. Some of the oldest fossil arthropods display masticatory spines called gnathobases: tooth-like projections located on the proximal margins of cephalic and trunk appendages [2–5]. Gnathobases are common in various (typically predatory) arthropod clades throughout the Phanerozoic [2–12]. However, only one extant group has gnathobases developed on a series of appendages: the xiphosurids, true horseshoe crabs [1]. Within Xiphosurida is the iconic American horseshoe crab, *Limulus polyphemus*: a species that shreds soft prey and crushes shell (durophagy) using gnathobases on coxal segments of cephalothoracic appendages II–VI [13–15]. Adduction of opposing coxae in the transverse plane optimizes *L. polyphemus* appendages for crushing and shredding [1,16].

The *L. polyphemus* feeding apparatus is an ideal modern analogue for testing and quantifying ideas regarding feeding mechanics of extinct arthropods with gnathobase-bearing appendages, including eurypterids [6,17], trilobites [18] and disparate Cambrian taxa, such as the early Cambrian (*ca* 518 Ma) radiodontan *Amplectobelua symbrachiata* [3], and the mid-Cambrian (*ca* 508 Ma) euarthropod *Sidneyia inexpectans* [4,19,20]. *Sidneyia inexpectans* in particular, from the Burgess Shale of British Columbia, Canada [21], is often compared with *L. polyphemus*, due to their similar walking appendages [19,22–24]. Heavily sclerotized gnathobases on *S. inexpectans* appendages would have allowed it to crush shell, akin to *L. polyphemus* [4,19,22,24]. This is supported by the microstructural similarity of *L. polyphemus* and *S. inexpectans* gnathobases, and specimens of *S. inexpectans* with shelly gut contents [4,19,20,22]. However, just how effective *S. inexpectans* was at processing prey, particularly crushing shells, or how its mechanical performance might have compared with a modern analogue such as *L. polyphemus* [17], has never been tested. This is a central question regarding the feeding ecology of Cambrian arthropods. Addressing this question has important implications for understanding early animal evolution in the Cambrian, as the first durophages probably evolved at this time and helped escalate a major diversification of biomineralized prey species [20]. Here, we digitally reconstruct and simulate the feeding apparatus in *L. polyphemus* and *S. inexpectans*, and apply three-dimensional (3D) finite-element analysis to compare shapes of the two masticatory structures and test whether the shell-crushing tools of these two taxa, separated by 500 Myr, were functionally similar.

3D biomechanical modelling is a powerful tool that allows researchers to non-destructively predict mechanical performance in living and extinct animals. 3D FEA, specifically, can qualitatively and quantitatively predict how stresses and strains are distributed through biological features [25]. However, most FEA studies have considered vertebrate groups [26]. The limited arthropod FEA studies have mostly examined the performance of insect legs and wings [27–31], with rare studies showing the mechanical performance of mandibles and pincers [32–36]. The first 3D finite-element model (FEM) of a micro-computer tomography (micro-CT) scanned *L. polyphemus* coxa is presented to further develop arthropod-focused FEA research. Gnathobasic feeding is modelled and a strain contour map is produced. Distribution of von Mises microstrain and reaction force values at constrained gnathobases is calculated. A validation test involving comparison of bite reaction forces to FEM reaction forces using a live specimen is also presented.

Conducting FEA on extant groups allows strain patterns and magnitudes of modern analogues to be compared with extinct taxa [37–40]. FEA on extinct arthropods has never been conducted. Here we present the first application of 3D FEA to a well-known Cambrian gnathobase-bearing euarthropod: *Sidneyia inexpectans*. We conducted analyses using our three-dimensional reconstructions of the gnathobase-bearing segments of the walking appendages, the protopodite and coxa, of *S. inexpectans* and *L. polyphemus*, respectively. Here, we assume that *S. inexpectans* was one of the first Cambrian durophages and explore this assumption by qualitatively comparing the microstrain distributions and magnitudes of the *S. inexpectans* protopodite with the *L. polyphemus* coxa— the only appropriate modern analogue—and statistically analyse microstrain patterns of both taxa. Understanding the

biomechanics of the *S. inexpectans* protopodite and its bearing on durophagous feeding allows us to explore questions about how this iconic Cambrian animal potentially impacted the benthic community of an early complex marine ecosystem. For example, was *S. inexpectans* only capable of crushing small, thin-shelled prey, as the gut contents would suggest?

2. Methods

(a) *Limulus polyphemus* model and validation

A female *L. polyphemus* specimen from the Marine Biological Laboratory at Woods Hole, USA was used for the FEM. The specimen was submerged in 1% iodine-ethanol solution for 13 days and washed in 100% ethanol for 2 days prior to scanning (see methods in [15,41,42]); staining increased muscle density. Muscles used in mastication were made easier to identify in the micro-CT scan and allowed muscle cross-sectional area (MCSA) data of adductor muscles to be gathered. These data are a proxy for the muscle forces that inform the feeding simulation described below. The specimen was scanned using computed tomography (CT) in the micro-CT scanner (GE-Phoenix V|tome|xs micro-CT scanner with 240 kV 'Direct' tube) at the University of New England, New South Wales. Data were captured using DATOS acquisition software v. 2.2.1 (Phoenix, Wunstorf, Germany) and reconstruction software v. 2.2.1 RTM. The specimen was mounted on a rotating stage and imaged using optimized X-ray tube settings (150 kV, 200 µA, 200 ms integration time per projection). Projections (3600 in 360°) were captured using a 2000 × 2000 pixel 'virtual' (moving) detector array. Isotropic voxel side length was 92 µm. The GE constant rotation CT function was used to improve acquisition time and sample movement. Scan consisted of 1000 slices.

The scan was imported into MIMICS v. 20 (Materialise, Leuven, Belgium). The posterior-most pair of walking legs (cephalothoracic appendage set V), dorsal cephalothoracic cuticle above the appendages, muscles used in mastication (discussed below) and endosternite (internal structure to which mastication muscles attach) were segmented out using the MIMICS 'segmenting' tool. Cephalothoracic appendage set V was modelled because these appendages, coupled with the pushing legs (set VI), are the primary shell-crushing tools (as observed during the validation test). Notably, gnathobases on set V are also the most morphologically similar to *Sidneyia inexpectans* gnathobases [4]. Segmented exoskeletal components were converted to STL files in MIMICS 20 and imported into GEOMAGIC STUDIO (3D Systems, North Carolina, USA). Exoskeletal components were smoothed in GEOMAGIC STUDIO. Smoothed STL files were exported from GEOMAGIC STUDIO and a 3D PDF was generated using 3D REVIEWER (Adobe Systems), following Bicknell *et al.* [15] and Lautenschlager *et al.* [43]. Distinct elements were assigned different colours (figure 1c). 3D PDF is presented as a supplementary file (figure S1 [70]).

Limulus polyphemus muscles involved in food processing are attached to epidermal cells on the inside of the exoskeleton. A digital dissection of muscles within the stained specimen was used to calculate MCSA values for the FEM, as muscle divisions are clearer in micro-CT scans than in gross dissections [16,42,44]. Furthermore, delicate muscles are often disturbed or destroyed during gross dissection [44]. Destruction of these muscles would have decreased muscle weights and therefore underestimated muscle force for the FEM. Muscles included in this study are those that adduct the coxae. Wyse & Dwyer ([16], p. 574) noted that muscles 25, 27–29 and 38–40 (their numbers) are all variably involved in adduction, but '38 [anterior], 38 [posterior], 39, and 40 … serve as the main adductors'. As such, only muscles 38 (anterior and posterior parts), 39 and 40 were segmented and used (figure 1c). MCSA values (mm^2) from CT scans are collected by reviewing the segmented muscles and measuring the muscle's thickest area, perpendicular to the
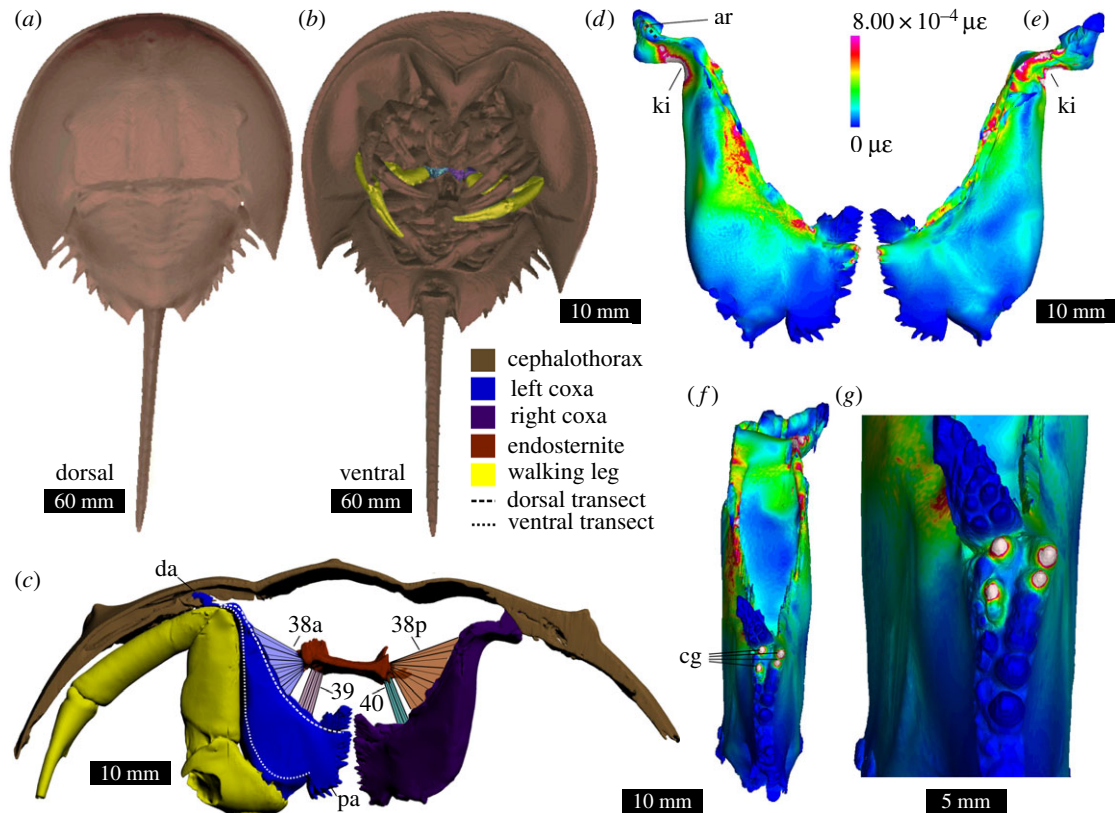
Figure 1. 3D reconstruction of *Limulus polyphemus* and von Misses (VM) microstrain maps. (*a,b*) 3D reconstruction of *L. polyphemus* specimen (Va.06) figured by Bicknell *et al*. [15], highlighting the position of the studied appendages (cephalothoracic appendage set V). Specimen is housed in the Natural History Museum of the University of New England (Armidale, New South Wales, Australia). (*a*) Va.06 in dorsal view. (*b*) Va.06 in ventral view. Colours correspond to coloured parts in (*c*). (*c*) Studied cephalothoracic section in anterior view. The 3D PDF is presented in figure S1 [70]. Muscles 38, 39 and 40 used in FEM are overlayed on reconstruction. Trajectories for dorsal and ventral transects are also shown (white dotted lines). (*d−g*) FEM VM microstrain maps of the left coxa. White regions exceed scale (8×10^{-4} με). (*d*) Anterior view; black dotted line shows axis of rotation. (*e*) Posterior view. (*f*) Sagittal view, showing constrained gnathobases that are first involved in processing. (*g*) Close up of gnathobases (ar, axis of rotation; cg, constrained gnathobases; da, distal area; ki, coxal kink; pa, proximal area).

long axis of muscle fibres [45,46]. Segmented muscles were imported into GEOMAGIC STUDIO and MCSA values were calculated using the 'Compute' tool. MCSA values were converted into maximum muscle force to inform the FEM using a conversion of 0.25 N mm^{-2} [47] (table S1 [70]). Coxa was solid-meshed in 3-MATIC v. 9.0 (Materialise, Leuven, Belgium). *Limulus polyphemus* coxa cuticle was modelled as a solid homogeneous structure. This will influence absolute stress/strain magnitudes, but results remain informative in purely comparative, shape-related contexts, as *Sidneyia inexpectans* was modelled similarly. The widely applied comparative FEA method that yields relative as opposed to absolute predictions was therefore used and the role of geometry in determining mechanical performance was explored [37,47–49]. The left *L. polyphemus* coxa model was imported as a Nastran (NAS) file into STRAND7 (Strand7 Pty Ltd, Sydney, Australia) FEA software [50]. The model was treated as isotropic with Young's modulus of 867 N mm^{-2} (for sclerotized cuticle [51]) and a Poisson ratio of 0.3 (for isometric cuticle [35]). Muscle origins were tessellated as plate elements onto the meshed surface and modelled as 3D membrane (thickness = 0.0001 mm). Forces for each muscle, directed toward their respective insertion sites, were then applied to plate elements using Boneload [50,52]. Muscle insertions were treated as single points and identified using the 'point coordinates' tool in GEOMAGIC STUDIO. The four largest, dorsally located gnathobases were constrained in all directions at the most apical node in STRAND7 (figure 1*d,e*). These gnathobases were constrained to accurately reflect the mechanics of *L. polyphemus* appendages during mastication (as observed in the validation test; discussed below); constraining all gnathobases would have produced an unrealistic loading scenario. The coxa

was constrained, but allowed to rotate about the coxal hinge. After FEM was solved, a colour-coded von Mises (VM) microstrain map was generated in STRAND7 and reaction force magnitudes at the constrained nodes on the gnathobases were output from STRAND7 in newtons.

The *L. polyphemus* validation test was conducted using a live female individual of similar size to the modelled specimen. This specimen, housed at the University of New Hampshire, was induced to process food using small (less than 1 cm) slices of lobster meat placed at the coxal bases. During processing, a FSR 402 force-sensitive resistor (Interlink Electronics, Westlake Village, CA) was placed between the posterior coxae and force measurements (in force-grams) recorded every 0.5 s. An Arduino-based data logging system, previously used to measure crab claw force (J. S. Goldstein 2017, personal communication), recorded the *L. polyphemus* bite force data. Force-gram measurements were converted into newtons to compare with FEM data. Shells were also fed to the individual to confirm it was capable of durophagy. Shells less than 1.5 cm long and less than 0.5 mm thick could be crushed by cephalothoracic appendages V and VI. We also noted that not all gnathobases are engaged in mastication at the same time: the most dorsally located spines perform initial processing.

(b) *Sidneyia inexpectans* model

A 3D reconstruction of the *S. inexpectans* thoracic appendage (exopod, endopod and protopodite) was made in ZBRUSH (Pixologic, Inc) (figure 2*c−e*). Micro-CT scanning of *S. inexpectans* was not possible as fossils are preserved as 2D carbon films on shale and the density difference between carbon and rock matrix is
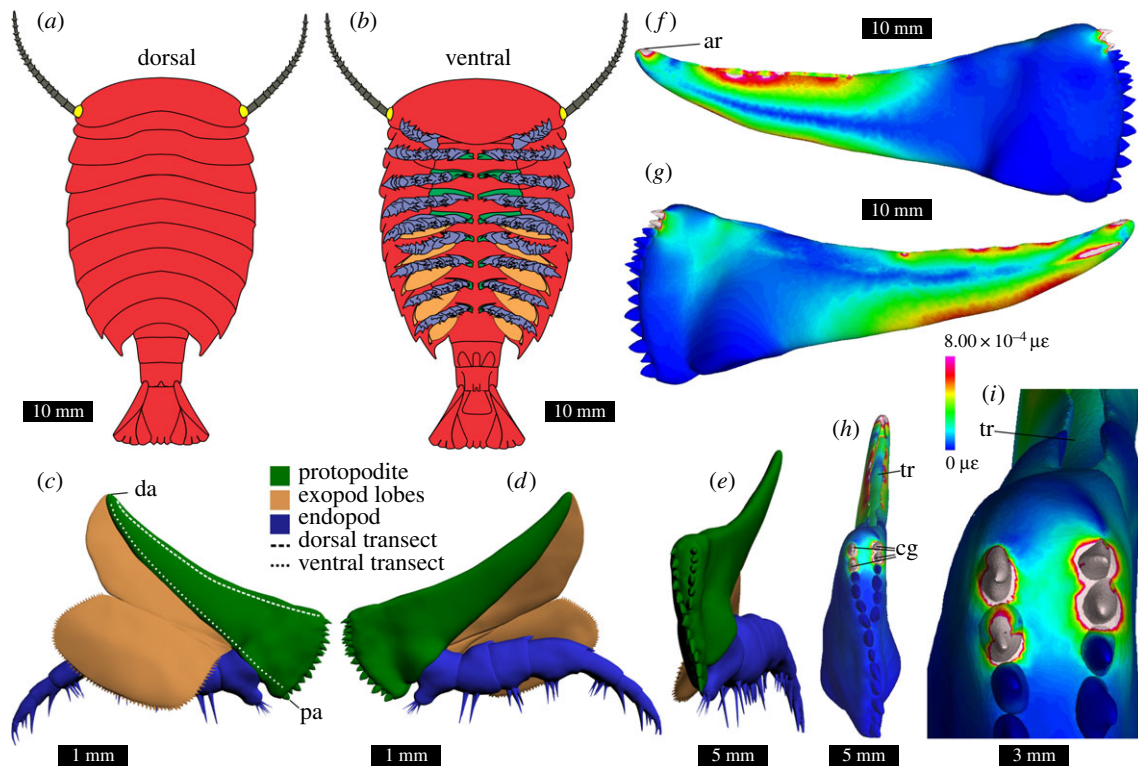
Figure 2. 2D and 3D reconstructions and VM microstrain maps of *Sidneyia inexpectans*. (*a,b*) Reconstruction of *S. inexpectans*, modified after Bruton [22]. (*a*) Dorsal view. (*b*) Ventral view; appendages are colour-coded to match 3D reconstructions (*c–e*). (*c–e*) Thoracic appendage showing only the major rami in various views, modified after Stein [24]. The 3D PDF is presented in figure S2 [70]. (*c*) Posterior view; trajectories for dorsal and ventral transects are shown (white dotted lines). (*d*) Anterior view. (*e*) Oblique view showing two rows of gnathobases. (*f–i*) FEM VM microstrain maps of the protopodite scaled to *Limulus polyphemus* volume. White regions exceed scale (8×10^{-4} $\mu\varepsilon$). (*f*) Posterior view. (*g*) Anterior view. (*h*) Sagittal view, showing the constrained gnathobases (chosen because of their relative positions on the *L. polyphemus* coxa). (*i*) Close up of the constrained gnathobases. Size scale of *S. inexpectans* reconstruction represents the actual size of fossil specimens. Size of *S. inexpectans* appendage (as indicated by scale bars in *c–i*) is scaled up to *L. polyphemus* model (ar, axis of rotation; cg, constrained gnathobases; da, distal area; pa, proximal area; tr, trough).

insufficient for scanning. Morphological details of the reconstruction (e.g. approximating relative dimensions of segments and spines) were based on published images of several thoracic appendage specimens of similar size, with some preserved at different orientations relative to the sediment laminations, allowing different perspectives to be considered [4,19,22,24]. As specimens are preserved in 2D, the third dimension—especially the 'inflation' of the protopodite—was extrapolated by comparing similar-sized *L. polyphemus* appendages, in addition to the relative dimensions of broadly comparable gnathobasic mandibles in modern copepod crustaceans [11]. Our reconstruction most closely resembles that illustrated by Stein ([24], fig. 9). However, two key differences are apparent, following recent observations by Bicknell *et al.* [4]. (1) The protopodite in our reconstruction has two rows of gnathobasic spines that 'v' into a single row towards the ventral section, as seen in both *L. polyphemus* and *Eurypterus tetragonophthalmus* [4,17,53]; Stein [24] reconstructed only one row of gnathobases. (2) Gnathobases in our reconstruction show a saw-toothed pattern with spines of alternating sizes, whereas Stein [24] showed a slight size gradation of spines along the gnathal edge. Thoracic appendage components were converted into .STL files in Zbrush and a 3D PDF was generated using 3D Reviewer. Distinct elements were assigned different colours and the 3D PDF is presented as a supplementary file (figure S2 [70]).

Boundary and loading conditions applied to *Sidneyia inexpectans* follow those applied to the *Limulus polyphemus* model to assess shape difference. First, the *S. inexpectans* model was scaled up to the same volume as the *L. polyphemus* coxa in GEOMAGIC STUDIO [36,54,55]. Scaling up was conducted as *S. inexpectans* has a maximum exoskeletal length of 13 cm [22], which is much smaller than *L. polyphemus* (*ca* 24 cm without

telson [56]); furthermore, extinct taxa should be scaled to the modern analogue (e.g. by scaling models to the same volume and loading parameters [55,57], or scaling muscle forces to the size of the fossil organism using a two-thirds power relationship [38]). A trough was constructed on the dorsal side of the protopodite for muscle origins (figure 2*h,i*). The muscle groups in *L. polyphemus* are assumed to be analogous to *S. inexpectans*, as muscles or scars are not preserved in the fossils. Size and locality (particularly origins and insertions) of muscles in *S. inexpectans* were estimated by comparing the morphology of the *L. polyphemus* coxa, particularly the trajectory and length of muscles 38, 39 and 40. The *L. polyphemus* muscle force magnitudes were used for *S. inexpectans*, as the models are of the same volume [52] (tables S1 and S2 [70]). Four dorsally located gnathobasic spines—considered to be functionally homologous to those in *L. polyphemus* (figure 1*g*), based on their relative positions and orientations on the coxa/protopodite of both taxa—were used to constrain the *S. inexpectans* model (figure 2*i*). This allowed a direct comparison with the *L. polyphemus* model. A colour-coded VM microstrain map was produced, but no reaction forces were calculated as the scaled model would have produced unrealistic reaction forces for a *S. inexpectans* individual that is considerably bigger than the largest known specimens of this species.

Brick elements were selected at equidistant points along the dorsal and ventral sides of the models (figures 1*c* and 2*c*) to assess changes in VM microstrain magnitudes and distributions between the two FE models. VM values at nodes were found by averaging microstrain of the six bricks around the nodes (following [58]). These values were analysed using a two-sample Anderson–Darling test. The non-parametric analysis assumes that a dataset is drawn from the same distribution as a second
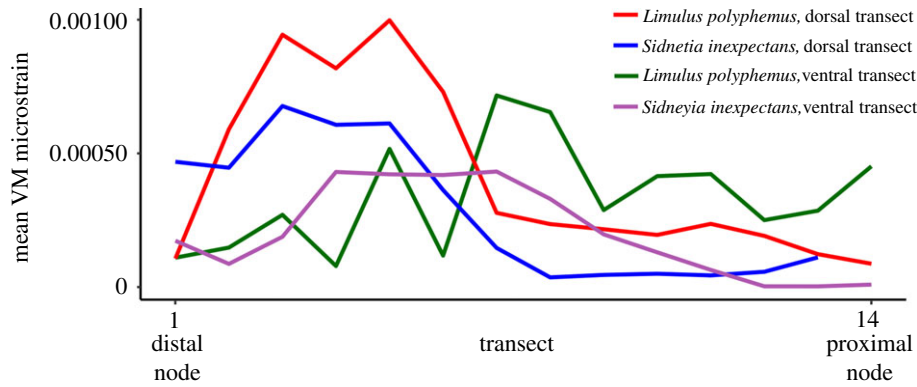
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Figure 3. Distribution of mean VM microstrain values along dorsal and ventral transects of the two models. Most proximal node on the *Sidneyia inexpectans* dorsal transect was not included because the node was close to a constrained gnathobase.

dataset [59] and can therefore be applied to the non-normal data and small sample sizes collected here [60]. The analysis tests the following hypotheses:

> H_0: The two datasets are from the same distribution. Here, the two transects are statistically similar and therefore the two features are functionally similar: both taxa were durophagous predators/scavengers that operated in a similar way.

> H_1: The two datasets are from different distributions. Here, the two transects are statistically different and therefore the two features are functionally different: *S. inexpectans* used its similar morphology in a functionally different way to *L. polyphemus*.

VM microstrain values along the dorsal transects were analysed separate to the VM microstrain values from the ventral transects. The most distal point of the *L. polyphemus* transect was omitted as 13 points were collected for the *S. inexpectans* dorsal transect. Analyses were run using 1000 simulations in an R environment using the *kSamples* [61] package.

3. Results

The magnitudes and distributions of VM microstrain in the *L. polyphemus* model are similar to those generated in the *S. inexpectans* model (compare figures $1d-g$ with $2f-i$). The *L. polyphemus* model displays high levels of VM microstrain along the dorsal portion of the coxa, with very high VM microstrain at the coxal kink, and generally lower VM microstrain along the ventral section (figure $1d-f$). The anterior–posterior (A-P) VM microstrain distribution is asymmetrical, with slightly higher VM microstrain on the anterior side of the coxa (figure $1d,e$). *Sidneyia inexpectans* experienced highest VM microstrain along the dorsal and ventral sides of the distal portion of the protopodite (figure $2f,g$). No areas of extreme VM microstrain were noted, other than at the constraints, which contrasts with the *L. polyphemus* model. The A-P VM microstrain distribution for *S. inexpectans* is also asymmetrical (figure $2f,g$).

Mean VM microstrain transects follow similar trends in both models, especially the dorsal transects, although there is considerable variation along the ventral transect for *L. polyphemus* (figure 3). For the distal sections of each transect, both models have higher VM microstrain along the dorsal transects and lower VM microstrain along the ventral transects. This reverses around the transect midpoints of both models, where the ventral transects have slightly higher VM microstrain than the dorsal transects in the proximal sections. The VM microstrain peaks at more dorso-distal sections

of the two models and decreases proximally from the areas of rotation. The ventral transects show that VM microstrain is generally higher in the proximal section of the *L. polyphemus* model, compared to the *S. inexpectans* model (figure 3). Constrained gnathobases are not considered, as the very high VM microstrain at these points is probably artefactual. The Anderson–Darling tests show that pairs of transects are from the same distributions (dorsal: $n = 13$, $p = 0.207$; ventral: $n = 14$, $p = 0.055$). We therefore fail to reject the null hypothesis in favour of the alternative for both datasets. Estimated reaction forces of the *L. polyphemus* FEM and validation force values are of the same order of magnitude. Validation values range between 0 and 3.5 N (with most values between 0.5 and 1 N), and FEM reaction forces range between 2.2 and 4.5 N (figure 4).

4. Discussion

FEA modelling demonstrates that the *S. inexpectans* protopodite was functionally similar to the *L. polyphemus* coxa. This is supported by the Anderson–Darling tests, which confirmed that transect pairs are from the same distribution. One obvious difference shown in the *L. polyphemus* model is the very high VM microstrain at the coxal kink—a feature that is lacking in the *S. inexpectans* protopodite. In addition, strain is more evenly distributed along the dorsal and ventral sections of the *S. inexpectans* protopodite compared to the *L. polyphemus* coxa. This might be expected due to the straighter and smooth dorso-ventral margins of the *S. inexpectans* protopodite. These results confirm our original assumption that *S. inexpectans* was a durophage with gnathobasic appendages that had a similar functional capability to those of *L. polyphemus*. However, the more widely distributed regions of VM microstrain, coupled with thicker gnathobases [4], suggests that *S. inexpectans* may have been a more effective shell crusher than *L. polyphemus*. Thick sclerotized cuticle observed in *S. inexpectans* gnathobases may have permitted them to absorb more force during processing without affecting nerve endings within the spines [4].

Heavily sclerotized shell-crushing features probably arose in the Cambrian as a means of capitalizing on the abundance of benthic biomineralized prey. Calcitic trilobites, in particular, are one of the most abundant groups in the Burgess Shale community [62,63]. Shelly gut contents show that *S. inexpectans* primarily consumed juvenile trilobites, and to a lesser extent small agnostid arthropods, plus calcitic
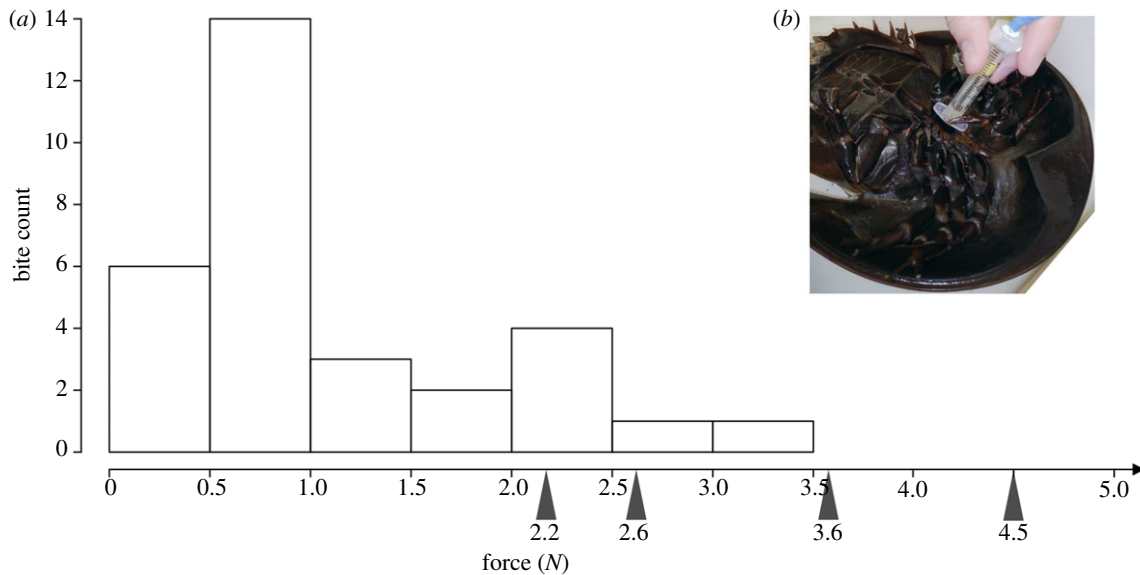
Figure 4. Distribution of bite force values from the *Limulus polyphemus* validation test, FEM reaction force values, and the device used to measure bite force. (*a*) Bite force and FEM reaction force data. The grey arrows are FEM values, each corresponding to a constrained gnathobase (figure 1*f*,*g*). (*b*) FSR 402 force-sensitive resistor (Interlink Electronics, Westlake Village, CA) placed between posterior coxae of the *L. polyphemus* specimen used for bite force test.

and phosphatic brachiopods [19]. This diet, and the lack of 'thick sclerotized or mineralized fragments' in the gut, suggests that *S. inexpectans* was perhaps limited to crushing only thin-shelled prey [19, p.215]. Yet, given the demonstrated biomechanical efficiency of the protopodite, its potential ability to crush thicker-shelled prey (such as adult trilobites) cannot be entirely dismissed. Notwithstanding, by exerting selective pressures on populations of juvenile trilobites and other small, thin-shelled prey, *S. inexpectans* potentially drove selection for more fortified shells or other novel defences in biomineralized prey within the Burgess Shale community over time [19,64]. However, despite strong evidence that *S. inexpectans* was a durophagous predator [19], scavenging as a commensurate or secondary feeding mode cannot be discounted, which would have downplayed its escalatory role in the phenotypic evolution of shelly prey.

Similarity of bite reaction forces to FEM reaction forces shows that FEMs of arthropods can produce results comparable to real-world values [32]. FEM values that are higher than the validation data reflect the upper limit of *L. polyphemus* bite force, demonstrating that even arthropods will not process with maximized force unless required [65]. The peak bite force value acquired from the validation test is lower than the maximum FEM reaction force values (figure 4). The food used to induce processing during the test explains this: lobster meat requires much less force than shells during mastication, resulting in lower forces than values predicted by the FEM. This is an important outcome, as FEMs can occasionally produce mixed results, with VM microstrain and stress magnitudes inconsistently reflecting reality [38,65–69]. One potential issue with the methodology is that MCSA values were used to inform the FEM. Muscle force values have errors ranging between 4.5 and 12.4%, and muscle staining may have shrunk muscle tissues [46]. However, agreement between the validation test and FEM reaction force data confirms that MCSA values obtained from iodine-stained specimens and micro-CT scans are reliable for arthropod FEA studies.

5. Conclusion

FE models of masticatory appendage structures of the Cambrian euarthropod *S. inexpectans* and its closest modern analogue *L. polyphemus* are presented. This premier comparative study demonstrates the mechanical performance of two durophagous arthropods with similar appendage morphology that are separated by more than 500 Myr. The FE microstrain map of the *L. polyphemus* coxa is comparable to the *S. inexpectans* protopodite, suggesting similar mechanical performance. However, the *S. inexpectans* model lacks concentrated areas of very high VM microstrain (compared to the coxal kink of *L. polyphemus*), suggesting that this Cambrian species may have been a more efficient durophage than the modern counterpart. When combined with other evidence, such as gnathobasic cuticle thickness and shelly gut contents, the FEA results convincingly demonstrate that *S. inexpectans* was an effective Cambrian shell-crushing arthropod. Furthermore, the effective use of heavily sclerotized masticatory structures would have impacted the benthic community of the Burgess Shale marine ecosystem, placing considerable selective pressures on shelly prey. Similarity of reaction force values from the *L. polyphemus* FEA to a bite force test on a live specimen validates the methodology developed here, demonstrating that FEA can be applied to studies on large modern arthropods. Our results show how useful 3D FEA is for not only understanding the biomechanics of modern arthropods, but also testing ideas regarding the functional morphology and lifestyles of extinct taxa.

7

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