

Hydrodynamic Performance of *Euplectella aspergillum*: Simulating Real Life Conditions in the Abyss

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Abstract. We detail some of the understudied aspects of the flow inside and around the Hexactinellid Sponge *Euplectella aspergillum*. By leveraging the flexibility of the Lattice Boltzmann Method, High Performance Computing simulations are performed to dissect the complex conditions corresponding to the actual environment at the bottom of the ocean, at depths between 100 and 1,000 m. These large-scale simulations unveil potential clues on the evolutionary adaptations of these deep-sea sponges in response to the surrounding fluid flow, and they open the path to future investigations at the interface between physics, engineering and biology.

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1 Introduction

Discovered at the end of the XIX Century [1, 2], the silica sponge *Euplectella aspergillum* has seized the attention of scientists ever since, for its remarkable structural properties and mesmerizing beauty. The skeletal system of this hexactinellid sponge, in fact, is characterized by a regular and hierarchical cylindrical lattice, which confers flexibility and resistance, notwithstanding its composition of amorphous hydrated silica [3–6]. Despite such a long-standing interest in the structural properties of these dwellers of the abyss, the study of the hydrodynamic fields surrounding the glass sponge has remained largely unexplored until very recently, [7].

In [8], some of these authors have conducted massively-parallel fluid dynamic simulations [9] using the Lattice Boltzmann Method (LBM) [10], to explore the role of the sponge skeletal structure for different values of the external velocity, corresponding to different Reynolds numbers. For the first time, compelling evidence was provided that the skeletal structure of *E. aspergillum* delivers a twofold benefit to the organism, by reducing the hydrodynamic drag and increasing the residence time inside the sponge body cavity, thereby enhancing the possibility of selective filter feeding and sexual reproduction.

In this paper, we provide additional details to the investigation in [8] along three main directions: i) we present new insights on the local, micro-scale features of the flow through *E. aspergillum* skeleton; ii) we clarify the possibility of employing different characteristic residence times within the body cavity; and iii) we offer further evidence to the complexity of the fluid motion within the body cavity and its connection to the technical literature on deep-sea sponges. The proposed results unveil potential clues on the evolutionary strategy that has led to the formation of such a complex structure, driven by stimuli from the surrounding hydrodynamic environment.

2 Reconstruction of *E. aspergillum* skeletal structure

E. aspergillum exhibits a remarkably beautiful skeletal structure, characterized by a complex hierarchical architecture, [3], which can be schematized in four main parts: i) the bottom bulb, which anchors the sponge to the sea floor, ii) the main cylindrical body, iii) a curved section connecting the two, and iv) the sieve plate at the top of the structure, called *osculum* (see Fig. 1(a)). In [8], we accurately described the process of creating five digital mock-ups: one corresponding to the complete geometry of the deep-sea sponge and four simplified models derived from its main body.

The complete geometry has been rendered with a resolution of 200 μm , reproducing the primary and secondary patterns of external ligaments and the helical ridges that decorate its outer surface. Concerning the four simplified models, two solid (a smooth cylinder and a cylinder with helical ridges) and two porous (hollow cylindrical lattice and hollow cylindrical lattice with helical ridges) geometries were generated, as reported in Fig. 1(b).

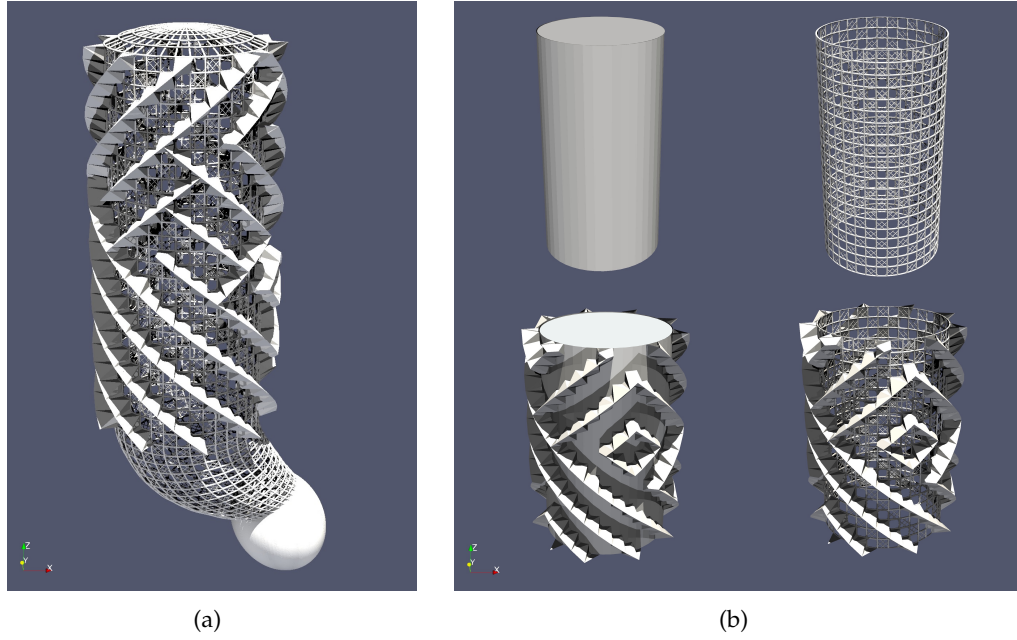


Figure 1: Details of the reconstructed mock-up geometries: (a) complete *E. aspergillum*, and (b) four *derived* models, with periodic boundary conditions at top and bottom of the computational domain.

3 Numerical methodology

In the following, we summarize our numerical methodology, implementation of boundary conditions and selection of fluid dynamic quantities; more details can be found in [8].

We consider a D3Q19 lattice Boltzmann implementation [11], in which the fluid fields evolve in time according to the following equation:

$$f_i(\vec{x} + \vec{c}_i, t + 1) - f_i(\vec{x}, t) = \frac{1}{\tau} [f_i^{\text{eq}}(\vec{x}, t) - f_i(\vec{x}, t)]. \quad (3.1)$$

In the above, $f_i(\vec{x}, t)$ is the probability density function of finding a representative fluid particle at site \vec{x} and discrete time t , moving along the \vec{c}_i lattice directions (in the D3Q19 scheme, $i = 0, \dots, 18$). In Eq. (3.1), τ is the characteristic time for the relaxation towards local Maxwellian equilibrium, represented by f_i^{eq} [11, 12]

$$f_i^{\text{eq}} = \rho w_i \left[1 + \frac{\vec{c}_i \cdot \vec{u}}{c_s^2} + \frac{(\vec{c}_i \cdot \vec{u})^2}{2c_s^4} - \frac{\vec{u} \cdot \vec{u}}{2c_s^2} \right], \quad (3.2)$$

where \vec{u} and ρ are the fluid macroscopic velocity and density, respectively.

The handling of complex geometries is among the most peculiar *atouts* of the LBM: we implement second-order accurate, no-slip wall boundary conditions on the surface of the various mock-ups, by using the algorithms proposed in [10, 13]. For what concerns the rest of the domain, we impose the following boundary conditions [13]:

- *Inflow*: a fix-velocity condition, in order to achieve the desired Reynolds number (Re) at the inlet;
- *Outflow*: a zero-gradient condition for both velocity and density;
- *Side boundaries*: periodic boundary conditions; and
- *Top and bottom boundaries*: the complete geometry of *E. aspergillum* has wall free-slip at the top and wall no-slip at the bottom, representing the sea floor, and the four derived mock-ups have periodic boundaries at both top and bottom.

Besides the density and velocity fields, we focus on the flow enstrophy density $|\vec{\omega}|^2$, and helicity \mathcal{H} to gain insight into the flow structure within the body cavity and downstream of the sponge. We use these quantities to compute the parameter Q that identifies the presence of vortical structures [14], and the non-dimensional residence time t^* , within the body cavity, [8].

We compute enstrophy from the magnitude of the vorticity, through the following expression:

$$|\vec{\omega}|^2 = |\vec{\nabla} \times \vec{u}|^2 = \left(\frac{\partial u_z}{\partial y} - \frac{\partial u_y}{\partial z} \right)^2 + \left(\frac{\partial u_x}{\partial z} - \frac{\partial u_z}{\partial x} \right)^2 + \left(\frac{\partial u_y}{\partial x} - \frac{\partial u_x}{\partial y} \right)^2. \quad (3.3)$$

Helicity is given by

$$\mathcal{H} = \vec{u} \cdot (\vec{\nabla} \times \vec{u}) = u_x \left(\frac{\partial u_z}{\partial y} - \frac{\partial u_y}{\partial z} \right) + u_y \left(\frac{\partial u_x}{\partial z} - \frac{\partial u_z}{\partial x} \right) + u_z \left(\frac{\partial u_y}{\partial x} - \frac{\partial u_x}{\partial y} \right). \quad (3.4)$$

Enstrophy is directly related to the vortical patterns inside the body cavity, while helicity provides information on the local degree of swirling of the fluid, namely the projection of the fluid velocity along the axis of rotation.

To properly identify the presence of vortical structures, we compute Q through the anti-symmetric (vorticity tensor) and symmetric (rate-of-strain tensor) components of the velocity gradient tensor, defined as follows:

$$\bar{\Omega} = \frac{1}{2} [\nabla \vec{u} - (\nabla \vec{u})^T] = \frac{1}{2} \left(\frac{\partial u_\alpha}{\partial x_\beta} - \frac{\partial u_\beta}{\partial x_\alpha} \right), \quad (3.5)$$

$$\bar{S} = \frac{1}{2} [\nabla \vec{u} + (\nabla \vec{u})^T] = \frac{1}{2} \left(\frac{\partial u_\alpha}{\partial x_\beta} + \frac{\partial u_\beta}{\partial x_\alpha} \right), \quad (3.6)$$

where T denotes tensor transposition, and Greek subscripts α, β label the Cartesian components. Finally, Q is given by

$$Q = \frac{1}{2} [||\bar{\Omega}||^2 - ||\bar{S}||^2], \quad (3.7)$$

where $||\cdot||$ is the tensor norm. Vortical structures are defined as the regions in which rotational energy exceeds dissipation so that $Q > 0$.

4 Results & discussion

We consider five flow regimes represented by $Re = \frac{u_{in} D}{\nu} = 100, 500, 1000, 1500$, and 2000 ; D is the sponge diameter, u_{in} and ν are the flow velocity at inlet and kinematic viscosity (evaluated at 100 – 1,000 m below sea surface [15]). These *global* values of Re represent the undisturbed flow regime.

Of course, it is possible evaluate the *local* values of Reynolds in the flux through the skeletal structure of *E. aspergillum* by considering the velocity *through* the holes of the sponge, u_{th} , and the diameters of the smaller silica struts, l , [16]:

$$Re_l = \frac{u_{th} l}{\nu}. \quad (4.1)$$

With this definition, we retrieve local values of $Re_l = 0 - 10$, as shown in Fig. 2. This range of *local* Re is in agreement with the scientific literature in the field, which points at values of Re associated with the flux through the sponge walls on the order of the unity [17, 18].

Fig. 3 reports the velocity field through the cylindrical structure of the skeletal apparatus of *E. aspergillum*, compared to that of the hollow cylindrical lattice: the flow through the larger and smaller *fenestræ* of the sponge is apparent, as well as the impact of the helical ridges on the flow dynamics. The figure reports the contours of $Q > 0$ (in *lilac*) and provides evidence of the swirling patterns of the streaklines inside the body cavity of the sponge model.

In order to provide a quantitative measure of the confining effects of the vortical structures inside the cavity of sponge, we begin by considering the relevant time scales in action, namely the transit time across the body cavity, $t_t = D/u_x$ and the rotation time $t_r \sim 1/|\vec{\omega}|$. By definition, the condition $t_t/t_r > 1$ implies that the fluid has time to turn around before leaving the cavity, thereby providing a measure of the “*confinement*” of the

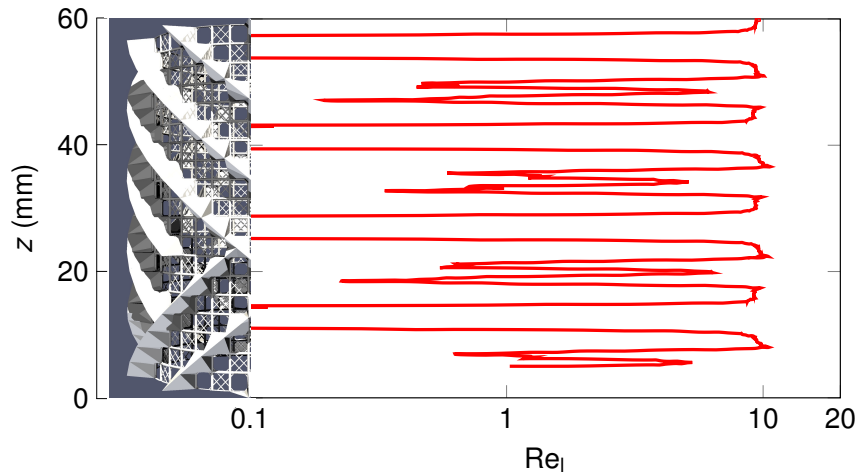


Figure 2: Local values of Re numbers, computed according to Eq. (4.1).

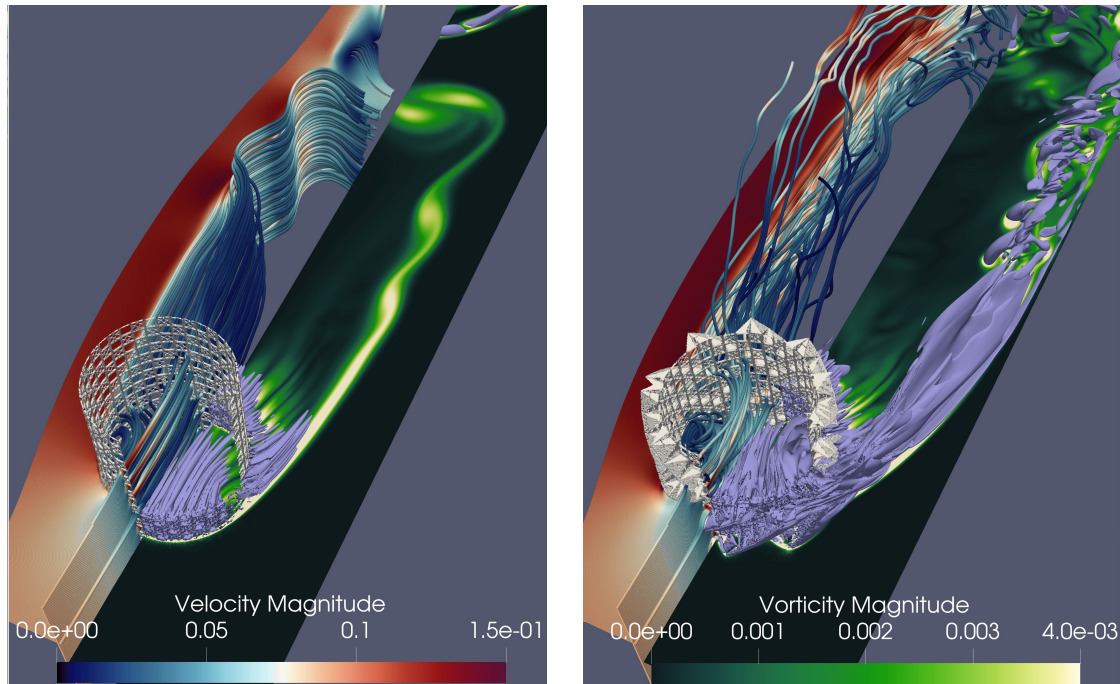


Figure 3: Detail of the velocity field contours in [m/s], vorticity magnitude and Q criterion for the hollow cylindrical structure (P1, on the left) vs the hollow cylindrical structure with helical ridges (P2, on the right) at $Re=2000$. The contours of $Q>0$ in lilac show the vortical structures generated by the two models.

flow within the body cavity. Confinement due to fluid rotation alone, however, is not effective in connecting regions at different altitudes within the sponge. To this purpose, a more informing time scale is provided by the ratio u_x/\mathcal{H} , which we may call the swirling time scale t_s . The dimensionless ratio $t^* \equiv t_t/t_s$ provides a combined measure of the flow propensity to turn around and move along the axial direction at the same time, delivering a measure of what we may call “cyclonic confinement”. In broad strokes, t^* is the number of swirls that a representative fluid particle can take before being swept away from the cavity by the mainstream motion. We wish to observe that such a dimensionless quantity t^* is obtained through a *global* statistics over the entire volume of *Euplectella*’s body cavity, providing a relevant information from the biological point of view.

The statistical distribution of t^* is shown in Fig. 4, from which it is apparent that most of the probability distribution in the hollow cylindrical lattice with helical ridges (model P2, which mimics the actual *E. aspergillum* structure) lies in the cyclonic confined sector $t^* > 1$. The relevance of considering the helicity \mathcal{H} in estimating the residence time inside the body cavity is further confirmed by the capability of our simulations to capture the outflow from the upper *osculum*, due to the complex fluid patterns inside the body cavity, as reported in Fig. 5. In this figure, we show contours of velocity magnitude and streaklines colored according to the vorticity magnitude. In accordance with the

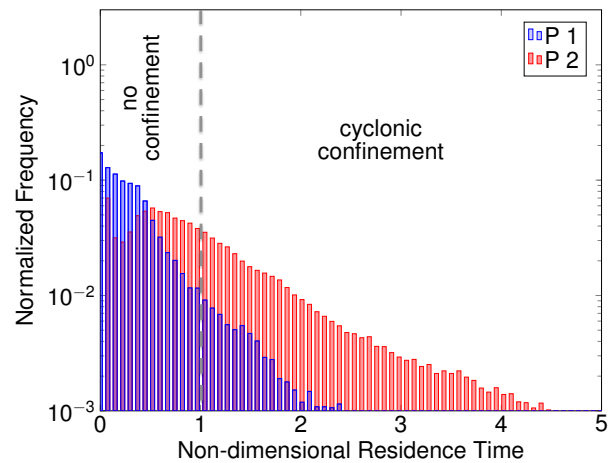


Figure 4: Normalized residence time inside the body cavity of the hollow cylindrical structure (P1) vs the hollow cylindrical structure with helical ridges (P2). In the panel, the vertical dotted line represents the value of $t^*=1$: the region characterized by $t > t^*$ corresponds to the cyclonic confinement regime, in which the representative fluid parcels swirl t^* times before leaving the cavity.

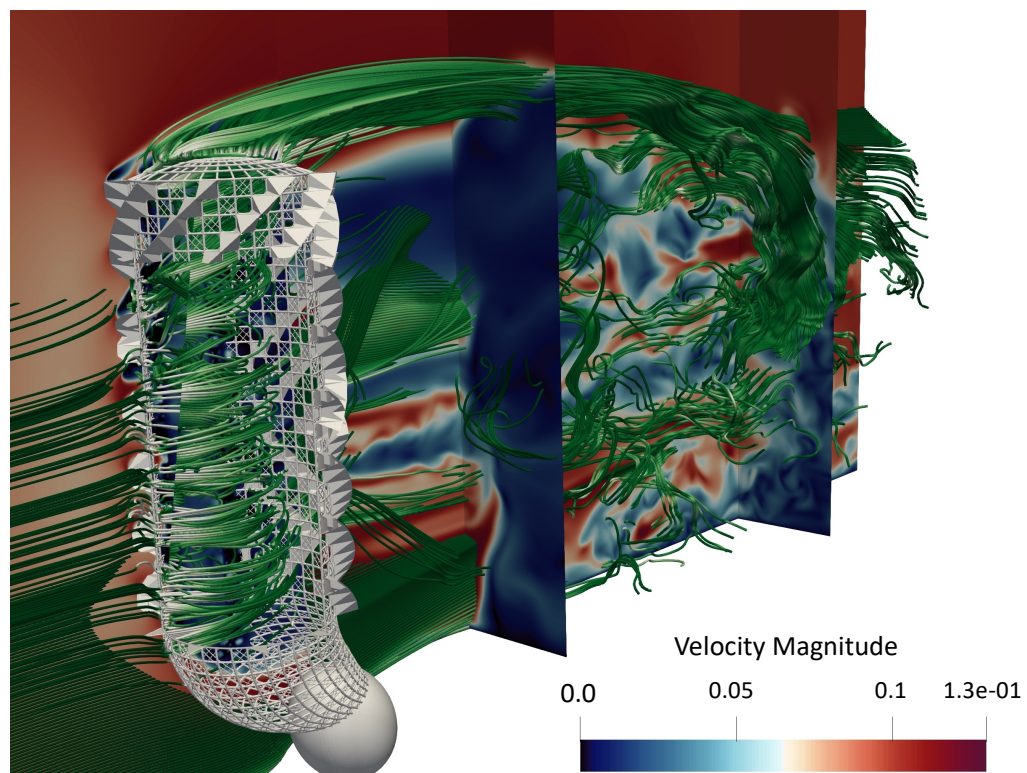


Figure 5: Contours of velocity magnitude in [m/s] at $Re=2000$ for the complete model of *E. aspergillum*. The streamlines are colored according to the vorticity magnitude and highlight the swirling motion inside the body cavity with upper outflow from the *osculum*, in accordance with the literature on hexatinellidæ, [20].

literature on hexactinellida [19], we find that part of the flow exiting from the body cavity is directed to the upper sieve plate.

Whether or not such a top-wards flow is a signature of the sponge *active* pumping is still an open issue; however, Vogel and Bretz in their seminal work [20], provide strong evidence that the same vertical flow is also found in passive (plastic) sponge mock-ups. Our results support this line of thinking, whereby our simulations clearly point to an outflow from the upper *osculum*, as found in the plastic mock-ups used by Vogel and Bretz in their experiments [20].

5 Computational performance

A few details on the computational performance of the present investigation are in order. Simulations were carried out on two High Performance Computing (HPC) facilities at CINECA, namely, “Marconi” (with a CPU-based architecture) and “Marconi100” (based on Nvidia V100 GPU accelerators). The simulations of the entire geometry of *E. aspergillum*, reaching up to 50 billion lattice sites over 5 million time-steps, were conducted on 128 computational nodes of “Marconi100”, corresponding to 1/8 of the entire HPC facility, yielding ~ 4 PFLOPS peak performance (*Peta Floating Point Operations Per Second*), corresponding to ~ 1.5 TLUPS (i.e., *Trillion Lattice Updates Per Second*), requiring 4,096 CPU cores, 40,960 Streaming Multiprocessors and 100 TB of central storage. The overall computational effort amounts to about $\sim 75,000$ GPU hours and $\sim 2,000,000$ CPU hours. The remarkable scalability shown by the LBM on both HPC architectures proved instrumental to enable the full-scale simulation of *E. aspergillum*, accounting for its microscopic geometric details, all the way up to the entire skeletal structure.

6 Conclusions & future outlook

Complementing our previous work [8], we have demonstrated that the flexibility and high computational efficiency of the LBM enables the investigation of bio-physical systems from microscale details all the way up to the full scale of the system. More specifically, we have conducted Petascale simulations on the skeletal systems of the deep sea glass sponge *E. aspergillum* with a spatial resolution of $200\ \mu\text{m}$, up to flow regimes corresponding to $\text{Re}=2,000$, typical of the actual living conditions in the abyss. We have investigated flow field characteristics around and inside the body cavity of the hexactinellid sponge, providing evidence of the roles of the skeletal features in raising such complex flow patterns.

The present study does not account for soft living tissues that surround the skeletal structure, thus raising the question as to their effects on the flow structure within the sponge cavity and around it. A detailed account of the soft tissues requires at least one more decade in spatial resolution, which is beyond the computational capability of even the most powerful present-day HPC facilities and must consequently await for Exascale

implementations [21]. Meanwhile, a viable approach is to homogenize the presence of such tissues through a global permeability coefficient, so as to provide an effective account for the flux through the body and the action of choanocytes and aquaporins, [16]. Work along these lines is currently in progress.

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