VAMPIRELLIDS (order Vampyrellida) are predatory, naked amoebae that form a genetically diverse clade within Rhizaria, most closely related to the parasitic Phytomyxea (Bass et al., 2009; Hess, 2017a; Hess et al., 2012; Sierra et al., 2016). Known vampyrellids typically feed on other eukaryotes by extracting the protoplast or engulfing the entire prey cell, and have an obligatory “digestive cyst” stage in which cell division takes place (Cienkowski, 1865; Hess, 2017b; Hess et al., 2012; Hülsmann, 1993; More et al., 2019; Zopf, 1885). Currently, there are three well-defined vampyrellid families, namely Vampyrellidae Zopf, 1885, Leptophryidae Hess et al., 2012, and Placopodidae Jahn, 1928 (the latter...
containing only the genus *Placopus*; More et al., 2019), plus the genus *Thalassomyxa*, which represents a separate clade in SSU rRNA gene phylogenies (More et al., 2019). Their members differ markedly in gross morphology and locomotive behavior, and can be assigned to one or more of the three established vampyrellid morphotypes (Hess et al., 2012). “Isodiometric” amoebae (known Vampyrellidae, some Leptophryidae) have a spherical morphology and tend to float in the water column (Hess, 2017b; Hess et al., 2012; Hülsmann, 1985), while “expanded” amoebae (some Leptophryidae, *Thalassomyxa*) may be branched, network-forming, or sheet-like, and creep over surfaces (Berney et al., 2013; Grell, 1992; Hess, 2017b). “Filoflabellate” amoebae (*Placopus*) are characterized by the formation of a pseudopodial lamella and a peculiar rolling locomotion (Hertwig & Lesser, 1874; Hess, 2017a; More et al., 2019). However, much of the vampyrellid diversity that has been detected in molecular environmental studies is still poorly characterized. There are two family-level clades (clades B5 and C) with very limited phenotypic information, and others (clades B1, B2, and B4) whose morphology and ecology remain completely unknown (Berney et al., 2013).

Here, we describe a new vampyrellid amoeba, *Sericomysmyx perlucida* gen. et sp. nov., discovered in the brackish sediment of Bras D’Or Lake in Nova Scotia, Canada, and cultivated in marine media. This amoeba differs markedly from known vampyrellid taxa in having an expanded cell body with lamellate pseudopodia that are fringed with very delicate, unbranched filipodia. Using SSU rRNA gene phylogenies, we show that *S. perlucida* belongs to the deepest branching lineage of the order Vampyrellida, formerly referred to as “clade C” (Berney et al., 2013) and here defined as a new family, Sericomysmyxidae. We characterize the new vampyrellid with light and electron microscopy and show that it consumes diverse marine microalgae using two different feeding strategies.

**MATERIALS AND METHODS**

**Establishment and maintenance of cultures**

Samples of submerged sediment were taken from the saline Bras D’Or Lake, NS, Canada (25 ppt; 46°06′000.4″ N, 60°44′054.3″ W) at low tide (though Bras D’Or is referred to as a lake, it is connected to the Atlantic Ocean and has small tides). A few milliliters of sample was added to Petri dishes containing the medium F/8 (a four-fold dilution of F/2 (Guillard, 1975) with sterile local seawater) and a mixture of cultivated marine microalgae (*Amphiprora* sp. CCMP467, *Entomoneis* sp. CCMP1552, *Navicula* sp., *Storeatula* sp. CCMP1868, *Tetraselmis* sp. CCAC6920, and an unidentified small pennate diatom, MSH07) to promote the growth of algivorous amoebae. These plates were kept at ambient temperature (approx. 23°C) under dim light (about 3 small pennate diatom, MSH07) to promote the growth of algivorous amoebae. These plates were kept at ambient temperature (approx. 23°C) under dim light (about 3 μmol/m²/s) on a 14:10 h light/dark cycle, and monitored for the presence of amoebae displaying vampyrellid-like characteristics (filipodia, digestive cysts). Single digestive cysts of a diatom-feeding vampyrellid were isolated with a glass micropipette into the wells of a microtiter plate containing F/8 medium with cells of the small pennate diatom MSH07. Resulting co-cultures of vampyrellid strain BDO1-7 and the prey diatom were kept in vented 50 ml flasks (Falcon, Corning, NY, USA) with ~25 ml sterile F/8 and maintained at 16°C with dim light on a 14:10 h light/dark cycle. Every 3 weeks, two drops of an active vampyrellid culture were transferred to a new flask containing fresh F/8 medium and prey algae. For long-term cultivation, the prey alga was transferred to a new flask containing fresh F/8 medium and prey algae. For long-term cultivation, the prey alga was changed to *Phaeodactylum tricornutum* (CCMP1327), which produced more consistent growth. Algae for feeding experiments (for details see in the following sections) were grown in F/2 medium as described in More et al. (2019). The vampyrellid culture is available from the corresponding author, whereas the algal cultures used here can be obtained from the relevant culture collections (except for strain MSH07, which is deceased).

**DNA amplification, sequencing, and phylogenetic analyses**

Single cells of starved, motile amoebae were isolated with a glass micropipette into 10 μl of Milli-Q water and subjected to whole genome amplification (WGA) with the illustra Ready-To-Go GenomiPhi V3 DNA Amplification Kit (GE Healthcare Life Sciences; now known as Cytiva, Marlborough, MA, USA). As described in More et al. (2019), the SSU rRNA gene was amplified from successful WGA reactions, sequenced by commercial Sanger sequencing (Genome Québec, Montréal, Québec, Canada), and assembled into a near-full-length gene sequence using Geneious 10.0.8 (https://www.geneious.com). Preliminary BLAST searches to the nr/nt database (https://blast.ncbi.nlm.nih.gov/Blast.cgi) returned hits with relatively low genetic identity from vampyrellid amoebae (e.g. *Placopus melkonianii* MH235264, 82.21% identity), but also from other eukaryotes (e.g. *Takayama* cf. *pulchellum* AY800130, 80.79% identity). The affiliation of strain BDO1-7 to the Vampyrellida was confirmed by a maximum likelihood (ML) phylogenetic analysis of a curated alignment of 357 eukaryotes from diverse supergroups (not shown). This analysis, using RAxML 8.2.6 (Stamatakis, 2014) with 100 starting trees and 1000 ultra-fast pseudoreplicate bootstraps under the GTR + Γ + I model, placed strain BDO1-7 at the base of the included vampyrellids. For the main phylogenetic analysis of this work,
the sequence of strain BDO1-7 was added to the curated alignment of Vampyrellida + Phytomyxea + “novel clade 9” as used by More et al. (2019). The initial alignment was performed with MUSCLE in Seaview v4.5.4 (Edgar, 2004; Gouy et al., 2010), followed by manual correction. To test the influence of more variable sites on the tree topology, two site selections were made for the final analyses comprising 55 selected sequences: Alignment 1 (conservative) with 1451 unambiguously aligned sites, and Alignment 2 with 1579 sites (including more variable regions). ML analyses were performed with RAxML as described above, except with 1000 conventional bootstrap replicates. Bayesian inference was performed using MrBayes 3.2.7a (Ronquist et al., 2012) with two runs of four MCMC chains, 5,000,000 generations, 25% burn-in, and a sampling frequency of 1000 generations. Stationarity was confirmed by examining log likelihoods in Tracer v1.7.1 (Rambaut et al., 2018). The SSU rRNA gene sequence of strain BDO1-7 generated in this study was deposited at GenBank (https://www.ncbi.nlm.nih.gov/genbank/) under accession number MW969735.

Light microscopy

Enrichments, long-term cultures, and feeding experiments (see in the following sections) were observed using phase contrast optics on a Nikon ECLIPSE TS 100 inverted microscope (Nikon, Tokyo, Japan). High-resolution imaging was performed with a Zeiss Axiovert 200 M inverted microscope and a Zeiss IM35 inverted microscope (ZEISS, Oberkochen, Germany), both equipped with differential interference contrast optics, high-resolution immersion objectives, and digital cameras (Zeiss AxioCam Icc5 and Canon EOS 6D, respectively). Cell dimensions were measured with the software Fiji (Schindelin et al., 2012), while Adobe Photoshop CS4 and Illustrator CS4 (Adobe Systems, Munich, Germany) were used to adjust color balance and contrast of light micrographs, and to prepare figures and plates, respectively.

Transmission electron microscopy

Amoebae and digestive cysts of strain BDO1-7 were scraped from the bottom of a culture flask, injected into a fixative consisting of seawater, HEPES (1 mM), glutaraldehyde (2.5%) and osmium tetroxide (2%), and incubated for 1 min at RT, thereafter for 1 h on ice. Cells were then briefly washed with demineralized water, dehydrated with a graded series of acetone/water mixtures and pure acetone, and infiltrated with EPON/acetone (1:1) overnight at 4°C. Acetone was then evaporated from the opened sample under a fume hood for 1 day. The infiltrated cells were then mixed with fresh EPON and cured for 2 days at 65°C. The resulting sample (representing the type material for Sericomyma perlucida) was sectioned (60–100 nm thickness) with a Leica EM UC7 ultramicrotome (Leica Microsystems GmbH, Wetzlar, Germany). Sections were stained with UranyLess (10 min; Benmeradi et al., 2015) and lead citrate (3.5 min; Reynolds, 1963), and finally examined and imaged with the transmission electron microscope CM 10 (FEI) equipped with an ORIUS SC200W TEM CCD camera (Gatan Inc., Pleasanton, CA, USA). Transmission electron micrographs were processed (brightness, contrast) with Adobe Photoshop CS4.

Feeding experiments

Well-growing cultures of marine microalgae (Table 1) were suspended in sterile F/8 medium and distributed into 12-well microtiter plates (approx. 3 ml per well). After the addition of starved amoebae of strain BDO1-7 (a few drops per well), wells were monitored every day for a week to determine the following, as per More et al. (2019): (i) whether vampyrellids were feeding, (ii) whether vampyrellid populations were growing (assessed qualitatively), and (iii) whether growth of vampyrellids was persistent (i.e. amoebae did not die before the food source was depleted). Feeding was identified based on ingested prey cells or plastid material in the amoebae and the presence of digestive cysts. The results were summarized in three categories: no growth (−), growth (+), and fast growth and depletion of food (++)

Nomenclatural acts

This published work and the nomenclatural acts it contains have been registered in ZooBank (http://zoobank.org/), the proposed online registration system for the ICZN. The ZooBank LSIDs (Life Science Identifiers) can be resolved and the associated information can be viewed through any standard web browser by appending the LSID to the prefix “http://zoobank.org/.” The LSID for this publication is as follows: urn:lsid:zoobank.org:pub:16EFD352-F627-44E7-87FA-E965EAB444C1
RESULTS

Phylogenetic position of *Sericomyxa perlucida* (strain BDOI-7)

The topology of the ML trees of Vampyrellida (with Phytomyxea + NC 9 as outgroups) was robust to site selection. With the liberal selection of sites (i.e. 1579 sites), all “family-group level” major lineages within Vampyrellida received bootstrap support ≥ 75% and posterior probability ≥ 0.99 (Figure 1). *Sericomyxa perlucida* (strain BDOI-7) fell within “clade C” (Berney et al., 2013), which represents the deepest branching clade within vampyrellids, with full support. *S. perlucida* is phylogenetically distinct from known “clade C” sequences, including that of “New Isolate NVam1” (KC779511; Berney et al., 2013), another brackish vampyrellid that has not been cultivated or studied in detail.

Trophozoite morphology and motility of *Sericomyxa perlucida* (strain BDOI-7)

The trophozoites of *S. perlucida* were most often small and inconspicuous with extremely dynamic and variable cell bodies. Motile trophozoites were generally roughly fan-shaped, with a ragged anterolateral lamella and posterior cytoplasmic hump, or linearly extended with lamellae at both the leading and trailing edge of the cell body (Figure 2A). Long, rarely branching filopodia extended from the ventral surface of the lamella and contacted the substrate (Figure 2B), and sometimes from the dorsal surface and into the water column. The lamellae and filopodia were extremely delicate in appearance and were difficult to observe under low-power microscopy. The lamellae lacked the conspicuous “membranosomes” seen in some other vampyrellids (e.g. *Placopus*, *Vampyrella*), but contained numerous smaller granules, < 0.5 µm in size (Figure 2B,C). The cells generally measured 10–20 µm in length and width when in a compact form, excluding filopodia (Figure 2A,B). The largest cells were approximately 10 × 40 µm in length and width (Figure 2D). The filopodia sometimes extended more than 20 µm past the lamella margins of the cell. The cell body was colorless with granular cytoplasm, numerous rod-like inclusions (possibly symbiotic bacteria—see in the following sections), and a few discernible vacuoles (Figure 2C). The nuclei were difficult to see and occasionally spherical, but more often deformed into more complex shapes (Figure 2E). These nuclei measured 3.5–5.3 µm in their longest dimension with a subspherical nucleolus of 0.9–1.5 µm diameter. Multinucleate cells were occasionally observed (Figure 2E). Movement occurred through amoeboid extension of the anterior lamella (Movie S1). The cell

### TABLE 1 Results of the feeding experiment of *Sericomyxa perlucida* gen. et sp. nov. (strain BDOI-7) on various marine microalgae.

| Lineage          | Algal species       | Algal strain | Feeding  |
|------------------|---------------------|--------------|----------|
| Chlorophyta      | *Chlamydomonas* sp. | CCMP222      | −        |
|                  | *Dunaliella tertiolecta* | CCMP1320 | −        |
|                  | *Pyramimonas* parkeae | CCMP725    | +        |
|                  | *Tetraselmis* sp.   | CCAC 6920   | +        |
|                  | *Tetraselmis* sp.   | MSH01#      | +        |
| Cryptophyceae    | *Chroomonas mesostigma*eta | CCMP 1168 | ++       |
|                  | *Guillardia* theta | CCMP 2712   | −        |
|                  | *Storeatula* sp.    | CCMP1868    | −        |
| Diatomeae        | *Amphiprora* sp.    | CCAC 1300B  | ++       |
|                  | *Amphiprora* sp.    | CCMP467     | ++       |
|                  | *Attheya* sp.       | CCAC 6914B  | ++       |
|                  | *Cylindrotheca* sp. | CCAC 6913B  | +        |
|                  | *Entomoneis* cf. alata | CCMP1522 | −        |
|                  | *Entomoneis* sp.    | MSH03#      | −        |
|                  | *Pennate diatom*    | MSH07#      | ++       |
|                  | *Phaeodactylum tricornutum* | CCMP1327 | ++       |
|                  | *Surirella* sp.     | MSH12#      | −        |
|                  | *Thalassiosira* sp. | CCAC 6912   | −        |
| Haptophyta       | *Pavlova* sp.       | CCAC 1328   | +        |

*Strains isolated in More et al. (2019) (strains now deceased).
outline was dynamic throughout movement: periods of forward movement were relatively short, and often ended with the anterior portion of the lamella being reabsorbed, forming linearly extended cells that resumed amoeboid locomotion in the direction of one of the lateral lamellae (Figure 2A; Movie S1). In dense cultures deprived of food, plasmodia and branching networks are formed through fusion of cells (Figure 2F; Movie S2).
Feeding specificity and processes

*Sericomyxa perlucida* was able to feed on microalgae from four different lineages, namely, haptophytes, chlorophytes, cryptophytes, and diatoms (Table 1). The diatoms *Attheya* sp., *Amphipora* sp. (two strains), *Phaeodactylum tricornutum*, and the unidentified small pennate diatom MSH07 supported vigorous growth and were fed upon to elimination. The other tested diatoms supported slower growth (*Cylindrotheca* sp.) or no growth at all (*Entomoneis* sp., *Surirella* sp.,...
Thalassiosira sp.). There was also considerable variability among the cryptophyte trials: Chroomonas mesostigmatica was fed on quickly and to elimination, while Guillardia theta and Storeatula sp. were only occasionally ingested and did not support growth of the population. The chlorophytes Tetraselmis sp. (two strains) and Pyramimonas parkeae supported minimal growth, while Dunaliella tertiolecta and Chlamydomonas sp. did not serve as suitable food. Pavlova sp. was the sole haptophyte tested during this study, and it supported growth and these amoebae often contained multiple algal cells.

Depending on the prey species, S. perlucida had different feeding strategies. Small diatoms such as Phaeodactylum tricornutum were grazed from surfaces (Figure 3A), similar to the observations reported for Thalassomyxa species (Berney et al., 2013; Grell, 1992). These small diatoms were taken up by conventional phagocytosis of entire cells, as shown by time-lapse video (Movie S3) and micrographs of trophozoites and digestive cysts (Figure 3B,C). Intact Phaeodactylum cells were often visible inside trophozoites and young digestive cysts (Figure 3B,C), while their frustules remained in older cysts (Figure 3D). S. perlucida was also able to ingest motile flagellates (Chroomonas mesostigmatica) by conventional phagocytosis with an extended feeding pseudopodium (Figure 4A). After the initial attachment of the pseudopodium to the alga and closure of the food vacuole, the Chroomonas cell was incorporated in the main cell body and quickly started to degrade. If and how S. perlucida immobilized the Chroomonas cells remains unclear. Young digestive cysts of S. perlucida feeding on Chroomonas contained bright blue-green inclusions that turned yellow over time, with orange material being left behind within the abandoned cyst wall after reproduction and excystment (Figure 4B–D).

**Figure 3** Feeding process and digestive cysts of Sericomyxa perlucida gen. et sp. nov., feeding on Phaeodactylum tricornutum; phase contrast (A) and differential interference contrast (B–D). (A) Time course of a culture depicted over 16 h. Note the formation of large plasmodia in later stages. (B) Trophozoite with ingested diatoms. (C) Young digestive cyst containing several diatoms with typical color. (D) Digestive cyst containing digested diatoms with orange remnants of the plastids. Scale bars: 100 µm in A; 10 µm in B–D.
When confronted with the larger diatoms, *Attheya* sp. and *Amphiprora* sp., *S. perlucida* applied a different feeding strategy: protoplast feeding. After initial contact, the trophozoites invaded the diatom cells with very inconspicuous pseudopodia, probably through the girdle region (we frequently observed missing girdle bands in emptied frustules), and subsequently removed the protoplast from the frustule by pseudopodial retraction (Figure 5A; Movie S4). The cell contents were typically packaged into several food vacuoles, as seen by the distribution of golden plastid material in the predator (Figure 5A). In late cultures of *S. perlucida*, numerous emptied diatom frustules remained (Figure 5B). In contrast to the digestive cysts observed with smaller prey diatoms, cysts formed after protoplast feeding contained numerous small food vacuoles and no frustule was seen (Figure 5C). The food contents changed color from golden to reddish during the digestive period (Figure 5C-E). After division of the nuclei (Figure 5E), the vampyrellid cytoplasm typically divided into several cells (Figure 5F) and up to eight small amoebae excysted (Figure 5G).
Ultrastructure

As typical for other vampyrellid amoebae, the trophozoites of *S. perlucida* were truly naked, that is, they did not exhibit any extracellular structures covering the plasma membrane (Figure 6A,B). The trophozoites contained numerous vesicles and occasionally food vacuoles with engulfed diatoms (amoebae for this preparation were fed with the small pennate diatom, strain MSH07). The cytoplasm of *S. perlucida* was populated by mitochondria with round cross-sections and tubular cristae (Figure 6B,C) and by numerous rod-shaped bacteria (Figure 6B,D), representing potential endosymbionts of unknown identity. These bacteria may represent the rod-shaped inclusions observed by light microscopy (see in the earlier sections). Sections of digestive cyst remains left behind by *S. perlucida* revealed a single cyst wall (Figure 6E), which is consistent with our light microscopy observations.
DISCUSSION

Our phylogenetic analyses revealed that *S. perlucida* (strain BDO1-7) belongs to “clade C,” one of the poorly characterized vampyrellid lineages. Multiple independent studies indicate that this clade is the sister group to all other vampyrellids (Berney et al., 2013; Hess, 2017a), making it especially interesting from an evolutionary point of view.
Prior to our study, just a single representative of “clade C” had been documented with a few light micrographs, but not described in detail (“New Isolate NVam1,” Berney et al., 2013). Interestingly, this amoeba was also found in brackish sediment, but differs clearly from S. perlucida in terms of trophozoite morphology in having anastomosing and branching filopodia. Previously, “New Isolate NVam1” had been tentatively assigned to the genus Penardia Cash, 1904 (Berney et al., 2013). However, we consider Penardia mutabilis Cash, 1904 (the type species of the genus) a junior synonym of Chlamydomyxa labrithuloides Archer, 1875, a well-characterized amoeboid alga that branches at the base of the Chrysophyceae (Grant et al., 2009; Wenderoth et al., 1999). This synonymy is supported by their isolation from the same environment (Sphagnum-dominated bogs), the presence of spindle-shaped granules shuttled along the anastomosing pseudopodia, and a cell body packed with yellow-green plastids (Archer, 1875; Cash, 1904; Cash & Hopkinson, 1905). Therefore, the name Penardia is not appropriate for vampyrellids, and “New Isolate NVam1” documented by Berney et al. (2013) likely represents a yet-undescribed genus, given the marked genetic distance from S. perlucida as well as the substantial morphological differences.

Our feeding experiments suggest that S. perlucida is a versatile predator with multiple approaches to handling its prey. While most algae were engulfed through conventional phagocytosis, S. perlucida consistently dealt with larger diatoms by extracting the protoplast and leaving behind the empty frustule. At first glance, this resembles the “protoplasm feeding” observed in Vampyrella, Placopus, and Platyreta species, which locally dissolve the carbohydrate cell walls of green algae and fungi (Cienkowski, 1865; More et al., 2019; Pakzad & Schlösser, 1998). However, diatoms differ drastically from green algae and fungi in terms of cell wall structure and biochemistry. The diatom cell wall (frustule) is formed by two silicified thecae, each composed of valves and girdle bands, and coated in mucilaginous organic polymers (Aumeier & Menzel, 2012; Schmid et al., 1981). Thus, it seems unlikely that the penetration of the diatom cell wall is mainly based on enzymatic dissolution, as is suspected for the protoplasm feeders that consume green algae and fungi (Busch & Hess, 2017; Old et al., 1985). Similar feeding mechanisms to that of S. perlucida were observed for the putative amoebozoan Rhizamoeba schnepfii and the cercozoan flagellate Cryothecomonas longipes, both of which penetrate marine planktonic diatoms in the girdle region and subsequently phagocytose the cell contents (Kühn, 1997; Schnepf & Kühn, 2000). In the distantly related viridiraptorid amoeboflagellates (Viridiradiatoridae, Rhizaria), which perforate the cell walls of zygnematophycean green algae, the actomyosin system seems to be crucial for the removal of an excised disc of the algal cell wall (Oreiraptor agilis) and infiltration of the cell (Viridiradiator invadens) (Busch & Hess, 2017). These processes typically start with the insertion of a minute pseudopodium, which then enlarges and (very likely) exerts the required force. Although we yet lack a detailed documentation of the early penetration process in S. perlucida, a similar pseudopodium-based mechanism may be employed to invade diatoms in the girdle region. Interestingly, an undescribed marine Placopus-like amoeba has also been reported to extract cytoplasm from Atteya decora (unpublished diploma thesis of D. Kaufmann, 2010, Berlin), suggesting that there are vampyrellids of other families (Placopodidae at least) with similar feeding habits.

From the gross morphological point of view, S. perlucida does not fit neatly into the previously established vampyrellid morphotypes (see Introduction), and instead displays features of both “filoflagellate” and “expanded” forms. Small cells of S. perlucida bear a superficial resemblance to fan-shaped filoflagellate amoebae (e.g. Placopus pusillus), as both can exhibit a hyaline anterolateral lamella (lamellipodium) and a posterior cell hump. However, there are key differences, such as the absence of rolling locomotion in S. perlucida, which instead advances by the extension of the frontal lamella and filopodia. This cell motility, combined with the tendency of S. perlucida to form branching cell bodies and large plasmodia (which has not yet been observed in true filoflagellate amoebae), makes S. perlucida more closely resemble the expanded morphotype. Compact, creeping trophozoites are known from other expanded vampyrellids, especially from the leptophryids Arachnomyxa cryptophaga and Planctomyxa polycarya (Hess, 2017b). Even though lamellae as seen in S. perlucida are not a conspicuous feature in previously described expanded vampyrellids, especially small cells, a number of leptophryid amoebae have similar concentrations of filopodial “fringes” extending from thin sheets of cytoplasm (see figure 8D in Bass et al., 2009 and figure 4G in Hess et al., 2012). Hence, the filopodial arrangement and motility in S. perlucida resembles that of some expanded vampyrellids, while it shows clear differences to the known filoflagellate amoebae with short filopodia that move under the cell body during their rolling locomotion (Hess, 2017a; More et al., 2019). We therefore regard S. perlucida as an “expanded” vampyrellid.

Yet, S. perlucida exhibits a combination of characters unique among known vampyrellid species, namely, the prominent lamellae with long frontal filopodia, dorsal filopodia, and branching cell bodies. To the best of our knowledge, the only described taxon showing a superficial resemblance to smaller cells of S. perlucida is Hyalodiscus korotnevi Mereschkowsky, 1879. This potential vampyrellid, discovered in the White Sea, was described with a compact, colorless cell body, pointed pseudopodia connected by “membrane-like” lamellae, and an exceedingly variable cell shape (Mereschkowsky, 1879). In a conservative revision of filoflagellate vampyrellid amoebae (Hess, 2017a), this species was excluded from the genus Placopus (the accepted synonym of Hyalodiscus; More et al., 2019) and is currently of uncertain affinity. Even though H. korotnevi bears some superficial resemblance to S. perlucida, we are confident
that they represent distinct species. The trophozoites of *S. perlucida* (strain BDO1-7) are markedly larger than those of *H. korotnewi* (10–20 µm vs. 9–10 µm), and lack several characters of the latter, namely, the tapering pseudopodia, conspicuous nucleus, and visible contractile vacuole. To the best of our knowledge, the vampyrellid amoeba studied here does not correspond to any previously described species. Given its phylogenetic distance from other described vampyrellid genera and families, we describe it as *S. perlucida* gen. et sp. nov., and assign it a new vampyrellid family, Sericomyxidae fam. nov., corresponding to the “clade C” of Berney et al. (2013).

Vampyrellida West, 1901

**Sericomyxidae** fam. nov.

*LSID:* urn:lsid:zoobank.org:act:19DC9D7E-6367-4A73-8CE4-2AEFAB99B5CF

**Composition:** All members of “clade C,” including isolate NVam1 (both defined in Berney et al., 2013)

**Type genus:** *Sericomyxa* gen. nov.

*Sericomyxa* gen. nov.

*LSID:* urn:lsid:zoobank.org:act:A3BF34EE-A8C3-49D7-A6BE-73CA3A835F48

**Etymology:** *sērikós* [Greek] = silken, *múksa* [Greek] = mucus, slime. The genus name *Sericomyxa* f. refers to the cobweb-like appearance and delicate filopodia of the amoebae.

**Description:** Since *Sericomyxa* currently comprises a single species, the description of the genus corresponds to that of the species.

**Type species:** *Sericomyxa perlucida* sp. nov.

*Sericomyxa perlucida* sp. nov.

*LSID:* urn:lsid:zoobank.org:act:71B28AB8-168E-47B7-8869-6EFEA05ACDD2

**Etymology:** *per-*lūcidus, -a, -um [Latin] = transparent. The epithet *perlucida* refers to how difficult unfed trophozoites are to see.

**Description:** Trophozoites have compact, granular, and colorless cell body with hyaline anterolateral lamella, or anterior and posterior lamellae, with larger lamella in the direction of movement. Typical cell bodies 10–20 µm in length and width when compact, larger cells up to 10 × 40 µm in length and width. Outline variable throughout motion. Long, non-branching filopodia on both ventral and dorsal surface of lamella, contacting substrate or extending into water column. Movement is via extension of filopodia and lamellae. Nucleus with variable shape (3.5–5.3 µm in longest dimension) and subcircular nucleus, rarely visible, multinucleate cells exist. Feeds on a variety of algae: diatoms (*Attheya* sp., *Amphiprora* sp., *Cylindrotheca* sp., *Phaeodactylum tricornutum*), cryptophytes (*Chroomonas mesostigma*), haptophytes (*Pavlova* sp.), and chlorophytes (*Tetraselmis* sp., *Pyramimonas parkeae*), through conventional phagocytosis or protoplast extraction. Digestive cysts small and elongate or circular in outline to large and irregular; flattened towards substrate. Fed digestive cysts hyaline with inclusions colored by prey, which change color as digestion occurs. Large trophozoites much broader than long during movement. Stationary large cells forming branching networks. Plasmotomy observed.

**Differential diagnosis:** Differs from *Placopus* spp. in color of cell hump (colorless vs. orange or red tint), arrangement of filopodia (from ventral and dorsal vs. exclusively ventral), locomotion (advancement of lamella via regular amoeboid locomotion vs. rolling locomotion). Differs from *Hyalodiscus korotnewi* in size (10–20 µm vs. 9–10 µm), shape of the nucleus (variable vs. rounded), and the presence of contractile vacuole under saline conditions (not present vs. present).

**Type material:** A permanent preparation (resin block for TEM), constituting the name-bearing hapantotype (article 73.3, ICZN), has been deposited in the “Protists Collection” at the Department of Life Sciences of the Natural History Museum in London (Cromwell Road, London, U.K.) with registration number NHMUK 2021.4.15.2. Cells of the hapantotype are shown in Figure 6.

**Type generating strain:** BDO1-7.

**Sequence of type generating strain (SSU rRNA gene):** MW969735.

**Type habitat and locality:** Sediment of brackish (25 ppt) embayment; Bras D’Or Lake, NS, Canada; 46°06’000.4″ N, 60°44’054.3″ W.

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AUTHOR CONTRIBUTIONS
SH and AGBS designed the study. KM and SH performed lab work, analyzed data and prepared figures. KM, SH, and AGBS wrote and edited the paper.

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**SUPPORTING INFORMATION**

Additional supporting information may be found online in the Supporting Information section.

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