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REGULAR ARTICLE

CHARACTERIZATION OF THE NATIVE FRESHWATER MUSSEL ASSEMBLAGE ACROSS A REACH OF THE RAPPAHANNOCK RIVER, VIRGINIA

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ABSTRACT

Native freshwater mussels occur in rivers of all sizes, yet much of the literature focuses on small- to medium-sized rivers, likely because of logistic challenges of sampling deep, fast, and turbid large rivers. As large-river surveys become more common, the information resulting from a systematic sampling design can provide baseline data on population sizes to inform decision making by resource managers. We collected baseline data on mussel resources in the Rappahannock River, Virginia, in August 2024. This Atlantic coast river, which drains into the Chesapeake Bay, is ~320 km long, up to 1.6 km wide, and up to 35 m deep. We conducted a systematic quantitative survey across the 75-km reach of the river from Fredericksburg to Leedstown, Virginia. Divers obtained 187 whole substrate samples to estimate the species richness, density, population size, size distribution, community composition, and longitudinal spatial distribution of the native mussel assemblage. Six species were found, and the community was dominated by Eastern Elliptio (*Elliptio complanata*). Mean reach density (± 1 standard error) and population size was 1.25 (0.21) mussels m^{-2} and 19.3 (3.3) million mussels, respectively. The presence of few fresh dead mussels indicated low to moderate natural mortality. Shell length ranged from 32 to 122 mm, and multiple size classes were observed in *E. complanata*. Species richness and density had similar longitudinal patterns, with the highest values in the middle of the sampled reach (river kilometers 60–95). These data provide resource managers with baseline information on the spatial distribution, density, length demography, diversity, and evenness of native freshwater mussels across this reach of the Rappahannock River. Identification of mussel occurrence, density, and evidence of reproduction can be used by managers to aid conservation and management decisions such as prioritizing areas for reintroductions and habitat restoration.

KEY WORDS: density, population size, native mussels, large rivers, diversity

INTRODUCTION

Native freshwater mussels (Family Unionidae; hereafter mussels) are benthic filter-feeding organisms that provide important ecological and cultural functions in rivers. Dense assemblages of mussels influence nutrient cycling and storage, create and modify habitats for other species, support aquatic food webs, and sequester contaminants (Vaughn and Hoellein 2018). In addition, mussels are a part of Native American tribes' traditional foodways and crafts (Strickland et al. 2016; Wertz 2020). With more than 30% of mussel species in the USA federally listed as threatened or endangered (USFWS 2025), mussels are a substantial resource of concern to the Virginia Department of Wildlife Resources (VADWR) and the U.S. Fish and Wildlife Service (USFWS). The VADWR mission is to conserve wildlife populations and habitat for the benefit of present and future generations; the USFWS mission is to conserve, protect, and enhance fish, wildlife, plants, and their habitats (USFWS 2023; VADWR 2025a). A knowledge of extant populations in understudied rivers can inform the decision making that supports these missions (USFWS 2023; VADWR 2025a).

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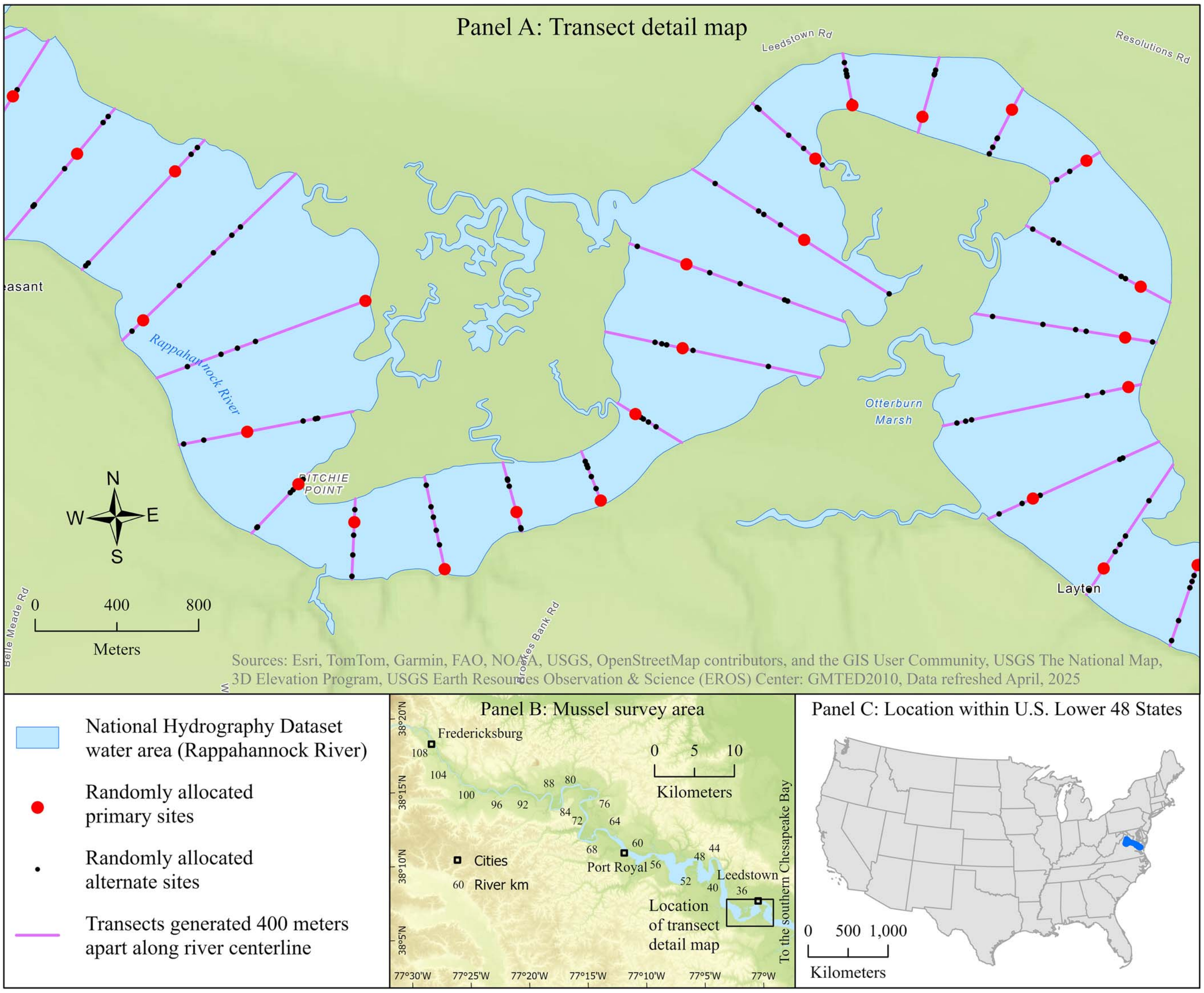

Figure 1. Map illustrating a systematic sampling design for native freshwater mussels across the 75-km reach of the Rappahannock River between Fredericksburg and Leedstown, Virginia (rkm 110 to 36) (Panel B) and the location of the Rappahannock River watershed in the conterminous United States (Panel C). Pink lines are transects generated 400 m apart along the river centerline, red circles are the randomly allocated primary sampling sites, and black circles are the randomly allocated alternate sites in cases where sampling the primary site is unsafe (Panel A).

Mussel assemblages in the lower Rappahannock River, Virginia, are understudied. The 314-km Rappahannock River flows into the southern Chesapeake Bay, and its river basin covers an area of 7,380 km^2 or about ~6% of the state of Virginia (Fig. 1) (Zhu et al. 2023). The river downstream of Fredericksburg, Virginia, at river kilometer (rkm) 108 (measuring from its confluence with the Chesapeake Bay) is tidal and transitions to brackish downstream of Port Royal, Virginia (rkm 60) (Fig. 1B). The river and its biota change abruptly in Fredericksburg at the fall line (where the river crosses from bedrock to soft sediments). Below Fredericksburg, the substrate is sand and silt, the water is turbid, and the fish assemblage comprises *Micropterus salmoides* (largemouth bass), catfish (order Siluriformes), and anadromous species (VADWR 2025b). In prior surveys, abundances of aquatic macroinvertebrates peaked between rkm 87 and 93 (Massmann et al. 1952). Thirteen mussel species have been documented in the Rappahannock River basin (Jones 2015; Black and Medlin 2020). Our objective was to quantitively characterize the mussel assemblage in the lower Rappahannock River downstream of Falmouth, Virginia (rkm 110), just upstream of Fredericksburg, Virginia.

METHODS

We designed a systematic quantitative survey to sample mussels across a 75-km reach of the lower Rappahannock River (Fig. 1). First, we created transects every 400 m perpendicular to the centerline of the river based on the National Hydrography Dataset (Moore et al. 2019). Second, we clipped the transects by river area and randomly allocated sites along each transect. As an example, Figure 1A depicts a small segment of the total study area and the clipped transects. A single (primary) site was sampled at each transect; alternate (secondary) site locations were provided in case the primary site was inaccessible or unsafe to sample. Divers surveyed 187 sites over the 75-km reach from rkm 110 to 36 (Fig. 1B).

The newly created USFWS Mussel Strike Team, consisting of divers and staff from eight states, conducted the survey August 19–22, 2024. At each site, divers placed two 0.25-m^2 quadrat frames on the river bottom about 0.5 m apart to increase the area sampled. They excavated the substrate within each quadrat to a depth of ~15 cm and placed all material into a 6-mm mesh bag (Newton et al. 2011). The contents in the bag were rinsed, and the bag was brought to the surface for processing. All mussels were categorized as alive or dead; dead shells were further categorized as fresh dead or weathered dead. Fresh dead mussels were defined by shiny nacre and an intact hinge, and weathered dead mussels were defined by chalky nacre (Newton et al. 2023b). The percent of fresh dead mussels has been used as a measure of mortality (Dunn et al. 2020). Individual mussels were identified to species, measured for shell length, and sexed if possible. Nomenclature follows the Integrated Taxonomic Information System (https://www.itis.gov/) and guidelines from the Freshwater Mollusk Conservation Society (https://www.molluskconservation.org/MServices_Names-Bivalves.html).

Divers recorded physical habitat conditions. Water depth was recorded to the nearest 0.1 m. Divers visually or tactilely assessed the substrate in each quadrat. Substrate composition was assessed inconsistently across sites. At 146 sites, divers assessed substrate composition as percentage across 10 substrate types (bedrock, boulder, cobble, gravel, sand, silt, clay, detritus, shells, and vegetation). At 37 sites, divers assessed substrate composition by recording the primary, secondary, and tertiary substrate type in the quadrat. At four sites, substrate data were not recorded. To reconcile substrate composition at the 37 sites with categorized substrate, we conservatively assigned 50% for the primary category, 35% for the secondary category, and 15% for the tertiary category.

We estimated species richness, total and species-specific density, reach-wide estimates of total and species-specific population size, and size distribution. Species richness was reported as the number of live species across all sites. Mussel data from the two quadrats at each site were summed for density and population estimation. We calculated total and species-specific density and population size using design-based statistical inference that incorporates spatial information (R package *spsurvey* ver. 5.5.1; Dumelle et al. 2023; Stevens and Olsen 2003). We calculated reach area by buffering site locations by 200 m in the NAD83 coordinate reference system, finding the rectangle that included all buffered site locations (i.e., the bounding box), cropping the polygon of the river from the National Hydrography Dataset Plus V2 (R package *nhdplusTools* ver. 1.2.1), and estimating the area of the resulting polygon (R package *sf* ver. 1.0-16) (Pebesma 2018; Moore et al. 2019; Blodgett and Johnson 2022). The river area was used to calculate inclusion probabilities of each site when estimating total and species-specific density.

Table 1. Life history (Haag 2012), reproductive (Watters et al. 2009; Hopper et al. 2023), and phylogenetic (Graf and Cummings 2021) guilds of the five species of native freshwater mussels found live during a systematic survey of the 75-km reach of the Rappahannock River between Fredericksburg and Leedstown, Virginia (rkm 110 to 36). Nomenclature follows the Integrated Taxonomic Information System (https://www.itis.gov/).

Species	Life history	Reproduction	Tribe
Atlanticoncha ochracea	Opportunistic	Long term	Lampsilini
Elliptio complanata	Equilibrium	Short term	Pleurobemini
Pyganodon cataracta	Opportunistic	Long term	Anodontini
Utterbackia imbecillis	Opportunistic	Long term	Anodontini
Utterbackiana implicata	Opportunistic	Long term	Anodontini

We depicted the size distribution of the two most abundant species separately using the frequency of individuals in 5-mm shell-length bins.

Community composition was assessed based on multiple metrics (Table 1). First, we categorized each species as an opportunistic, equilibrium, or periodic strategist following Haag (2012). Second, we categorized species based on the length of time glochidia are sustained in the marsupium as short-term or long-term brooders (Watters et al. 2009). Third, we classified the phylogenetic diversity of mussels into five tribes (Amblemini, Anodontini, Lampsilini, Pleurobemini, and Quadrilini) (Graf and Cummings 2021). Fourth, we estimated diversity (Simpson's D, Shannon's entropy H) and evenness (Pielou's J) indices (R package *vegan* ver. 2.6-6.1; Oksanen et al. 2024; R Core Team 2024).

The spatial distribution of mussels was portrayed based on species richness per river kilometer (in 5-km bins) and by plotting total mussel density across the longitudinal gradient of the river. We interpolated densities in areas not sampled using the *Topo to Raster* function in ArcGIS (ArcGIS Pro 3.3.1; Environmental Systems Research Institute, Redlands, California).

RESULTS

The 75-km reach of the lower Rappahannock River encompasses 3,079 ha of aquatic area; divers surveyed 187 sites from rkm 110 to 36. Although a larger survey was planned, the effort was terminated at rkm 36 because samples there comprised exclusively *Rangia cuneata*, an invasive clam that can tolerate salinities from 0 to 18 parts per thousand (Tang and Aldridge 2021). Across all sites, water depth averaged 4.1 m (range, 0.5–10 m) and the substrate was predominantly silt, followed by sand and gravel (Table 2).

Species Richness

Thirty-eight percent of the sites yielded a total of 117 live mussels and 34 dead mussels; 68% of the sites had no live mussels at all (Table 3). Of the dead mussels found, seven were fresh dead and 27 were weathered dead. There were five live species: *Atlanticoncha ochracea* (formerly *Leptodea*), *Elliptio complanata*, *Pyganodon cataracta*, *Utterbackia imbecillis* (formerly *Anodonta*), and *Utterbackiana implicata* (formerly

Table 2. Average water depth and substrate type (± 1 standard error) at sites sampled for native freshwater mussels across the 75-km reach of the Rappahannock River between Fredericksburg and Leedstown, Virginia (rkm 110 to 36).

Metric	Value (± 1 standard error)
Water depth (m)	4.1 ± 0.2
Bedrock (%)	1.4 ± 0.8
Boulder (%)	0.3 ± 0.3
Cobble (%)	2.0 ± 0.8
Gravel (%)	8.4 ± 1.5
Sand (%)	19.5 ± 2.5
Silt (%)	51.8 ± 3.1
Clay (%)	6.8 ± 1.4
Detritus (%)	5.0 ± 1.3
Shells (%)	0.5 ± 0.3
Vegetation (%)	1.7 ± 0.9

Anodonta). No additional species were found as fresh or weathered dead. *Elliptio complanata* had the highest relative abundance, comprising 55% of the live mussels found, followed by *U. implicata* at 33% (Table 4). Two of the five species, *A. ochracea* and *U. implicata*, are of high or moderate conservation need, respectively (VADWR 2025a).

Incidental to the systematic survey, we observed a 31-mm live *Lasmigona subviridis*, a species currently listed as in need of critical conservation in Virginia (https://ecos.fws.gov/ecp/report, accessed on February 20, 2026; VADWR 2025a) that is also proposed for federal listing as threatened. Found in an eddy behind a bridge pier at rkm 110, this individual was not included in statistical analyses.

Density and Population Size

Site density across the sampled reach averaged 1.25 mussels m^{-2} (95% confidence interval [CI], 0.83–1.67 mussels m^{-2}) and ranged from 0 to 36 mussels m^{-2} (Table 3). Across the 75-km reach, there were an estimated 19.3 million mussels (12.9–25.7 million; Table 3). Species density ranged from 0.03 mussels m^{-2} for *U. imbecillis* to 0.68 mussels m^{-2} for *E. complanata* (Table 4). Estimates of species-specific population sizes were approximately 11 million *E. complanata* (7.2–13.8 million), 6 million *U. implicata* (2.7–10.2 million), 1 million *A. ochracea* (0.3–1.6 million), 0.8 million *P. cataracta* (0–1.7 million), and 0.5 million *U. imbecillis* (0–1.3 million).

Size Distribution

Shell lengths of the most abundant species, *E. complanata*, ranged from 32 to 122 mm (Fig. 2 and Table 4). However, about 81% of the individuals were 76–100 mm in length (Fig. 2). In contrast, shell lengths of *U. implicata* were negatively skewed, indicating that mostly larger individuals were found (Fig. 2 and Table 4). Specifically, 67% of the individuals were 108–124 mm in length (Fig. 2).

Table 3. Population and density estimates (± 1 standard error) and community characteristics of native freshwater mussels across the 75-km reach of the Rappahannock River between Fredericksburg and Leedstown, Virginia (rkm 110 to 36).

Parameter	Value
Number of sites sampled	187
Number of live mussels obtained	117
Number (%) of sites without live mussels	127 (68)
Total population estimate (millions)	19.3 ± 3.3
Total density (no. m^{-2})	1.25 ± 0.21
Range of densities (no. m^{-2})	0–36
Number of live species	5
Equilibrium strategists (%)	55
Opportunistic strategists (%)	45
Anodontini (%)	40
Lampsilini (%)	5
Pleurobemini (%)	55
Community diversity (Simpson's D)	0.41
Community diversity (Shannon's entropy H)	1.08
Community evenness (Pielou's J)	0.67

Diversity and Evenness

The mussel assemblage had moderate diversity and evenness. Simpson's D was 0.4 on a scale of 0 (not diverse) to 1 (infinitely diverse), and Shannon's entropy H was 1.08, where higher numbers indicate more diverse communities (Table 3). Similarly, evenness was 0.7 on a scale of 0 (uneven) to 1 (even) (Table 3). The assemblage was dominated by *E. complanata*, an equilibrium strategist with a short-term brooding strategy. The remaining four species were opportunistic strategists with long-term breeding strategies. Three of the five phylogenetic tribes in Unionidae were represented (Table 1). The only species that was sexually dimorphic was *A. ochracea*; of the six individuals found, two were females, one was male, and three were unknown.

Spatial Distribution

Species richness and mussel density peaked in the middle of the sampled reach. Species richness of live mussels showed few mussels in the most upstream (rkm 95–110) and most downstream (rkm 35–60) stretches, with greatest richness (three species) in the middle stretch (rkm 60–95) (Fig. 3). A similar pattern was observed for density (Fig. 4). In the middle stretch (rkm 60–95), there were 10 pockets of high mussel density (>8 mussels m^{-2}). Greatest densities were observed near rkm 73 (12 mussels m^{-2}), rkm 71 (14 mussels m^{-2}), and rkm 86 (36 mussels m^{-2}).

DISCUSSION

The lower Rappahannock River contained relatively low species richness and density, and many species were represented by older individuals (based on shell length); however, diversity and evenness were moderate, and natural mortality

Table 4. Species-specific characterization of the live native freshwater mussel assemblage (mean ± 1 standard error) across the 75-km reach of the Rappahannock River between Fredericksburg and Leedstown, Virginia (rkm 110 to 36). *Atlanticoncha ochracea* (formerly *Leptodea*) and *Utterbackiana implicata* (formerly *Anodonta*) are species of greatest conservation need in Virginia (VADWR 2025a).

Species	Number alive	Percent of total	Length (range, mm)	Density (no. m^{-2})	Population estimate (millions)
Elliptio complanata	64	55	32–122	0.68 ± 0.11	10.54 ± 1.70
Utterbackiana implicata	39	33	50–138	0.42 ± 0.12	6.42 ± 1.91
Atlanticoncha ochracea	6	5	76–106	0.06 ± 0.02	0.99 ± 0.34
Pyganodon cataracta	5	4	96–122	0.05 ± 0.03	0.82 ± 0.50
Utterbackia imbecillis	3	3	58–67	0.03 ± 0.03	0.49 ± 0.43
Total	117	—	—	1.25 ± 0.21	19.26 ± 3.27

was low to moderate. Thus, mussels persist in this reach, but "evidence of them still existing in large numbers is rare" as in many Chesapeake Bay tributaries (Kreeger et al. 2018).

Seventy-seven species of native freshwater mussels have been recorded in Virginia, with 12 extant species reported in the Rappahannock River (Johnson 1970; Jones 2015; Black and Medlin 2020). The six species observed in this study (five in the systematic survey and one incidental observation) were reported by Jones (2015), and the five species in the systematic survey are represented by museum records spanning 1973–2012 (Pfeiffer et al. 2024). Although *Alasmidonta undulata*, *Elliptio fisheriana*, *Elliptio lanceolata*, *Pyganodon grandis*, and *Strophitus undulatus* were reported in the Rappahannock River drainage, we did not find these species in the 2024 survey. Given the difficulty separating mussels in the anodontini phylogenetic tribe and the lack of *P. grandis* museum records located in the Rappahannock River (Pfeiffer et al. 2024), reports of *P. grandis* are dubious (B. Watson, VADWR, written communication, April 21, 2025). Of the five species not found in the current survey but reported by Pfeiffer et al. (2024), only one (*S. undulatus*) was found in the 75-km reach we sampled (it was last found in 1945). *Elliptio fisheriana* museum records include observations above and below our reach, and the remaining three species were found in upstream reaches and tributaries.

Quantitative sampling can underestimate the number of species present, thus, at sites where no mussels were found in quadrats, divers conducted 92 radial searches (5–10 min in an area about 3 m in diameter) and 18 timed searches (10–15 min) in areas of dense aggregations to increase search effort. Additional searches did not produce more species. Two recent surveys

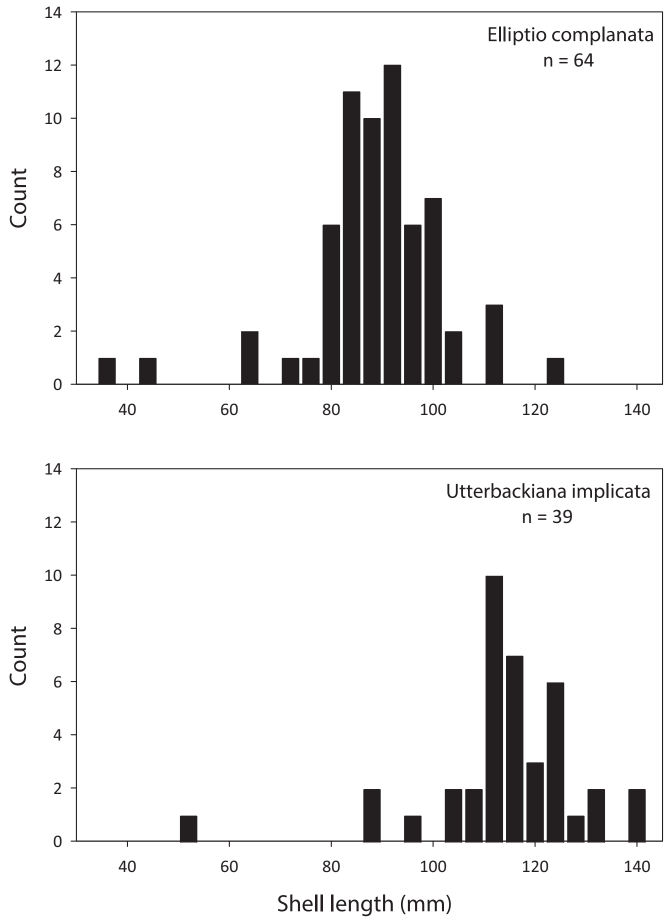

Figure 2. Size distribution of live individuals across the two most abundant species of native freshwater mussels across the 75-km reach of the Rappahannock River between Fredericksburg and Leedstown, Virginia (rkm 110 to 36). Bars represent (upper) bins of 4 mm.

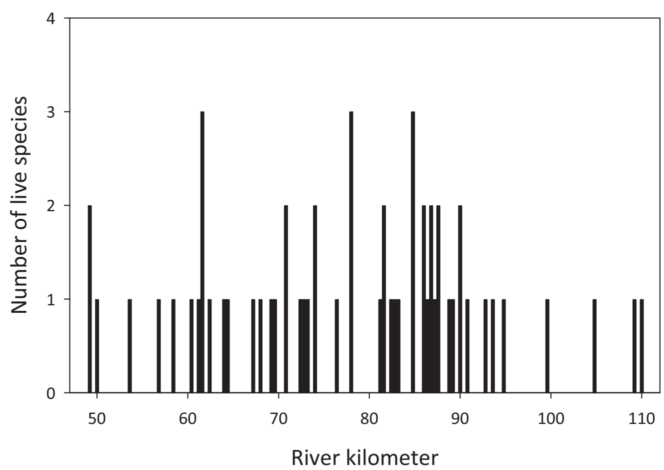

Figure 3. Species richness (number of live species) of native freshwater mussels across the 75-km reach of the Rappahannock River between Fredericksburg and Leedstown, Virginia (rkm 110 to 36). Note there were no live species between rkm 35 and rkm 49.

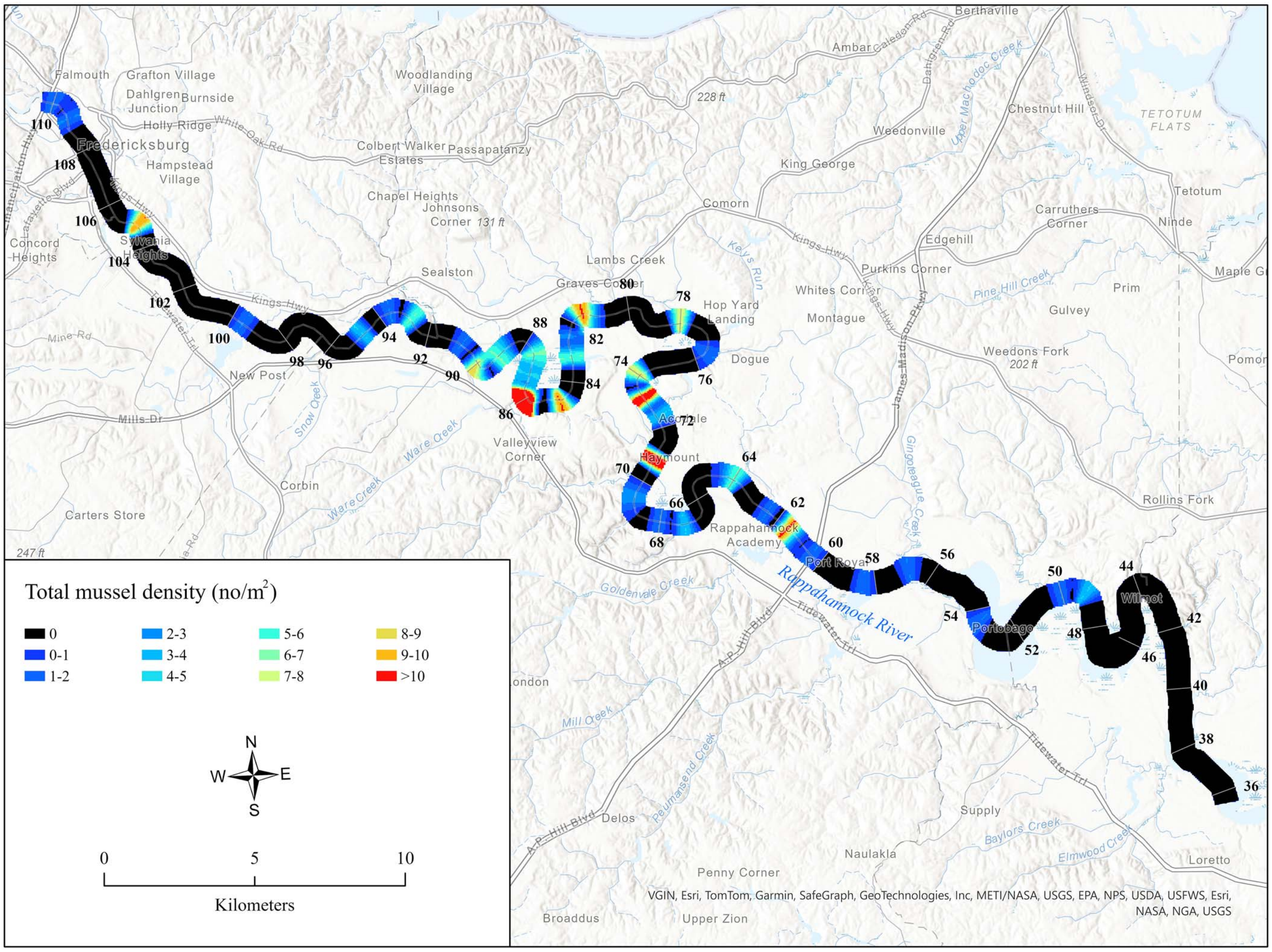

Figure 4. Spatial distribution of total density (mussels m^{-2}) of native freshwater mussels across the 75-km reach of the Rappahannock River between Falmouth (rkm 110), just upstream of Fredericksburg, and Leedstown (about rkm 36), Virginia.

increased the species list of the lower Rappahannock River. Qualitative surveys by Neves and Henley (2019) near rkm 110 found the first record of *L. subviridis* downstream of the fall line. Black and Medlin (2020) found seven *E. fisheriana*, and a single, gravid *Lampsilis radiata*, the only record of this species in the river. In addition, since 2007, the Virginia Fisheries and Aquatic Wildlife Center has released between 3,000 and 62,000 mussels annually into Virginia rivers, including almost 38,000 *U. implicata* and 300 *L. subviridis* in the Rappahannock River (Kreeger et al. 2018; B. Watson, VADWR, written communication, April 22, 2025). Our quantitative survey highlights the rarity of *L. subviridis*, *E. fisheriana*, and *L. radiata* in the lower section of the river and produces robust population size and density estimates for the five species found during the systematic survey.

We chose a quantitative systematic survey design because it met our objective of providing robust estimates of population size and density in this reach (Strayer and Smith 2003). Other survey designs (e.g., adaptive sampling, stratified random sampling) are available, but each has advantages and disadvantages. We recognize that the design we chose can underestimate species richness (Strayer and Smith 2003), but it does provide important baseline information. Our findings can be used to conduct additional complementary surveys to address different objectives. Mean total density in the Rappahannock River is low compared to systematic studies of mussels in other large rivers. For example, in the upper Hudson River (another large river in the Atlantic Slope drainage), mean density in strata that were unremediated or sampled before remediation for polychlorinated biphenyls was >15 mussels m^{-2}; in contrast, strata that were sampled after remediation had densities <1 mussel m^{-2} (Newton et al. 2023b). Similarly, mean density of mussels in the lower Hudson River prior to the invasion of *Dreissena polymorpha* was 8 mussels m^{-2} (Strayer et al. 1994). The total population estimate in the Rappahannock River (19 million mussels) is low relative to other large rivers. In the upper Hudson River study, estimates of population size ranged from 0.1 million to 156 million across all strata, with population size estimates >10 million in 8 (of 17 total) nonremediated strata (Newton et al. 2023b).

The size distribution of live mussels and number of fresh dead mussels can reflect population age and mortality (Haag 2012;

Dunn et al. 2020). We predominantly found larger and thus older individuals. For example, *A. ochracea* shell lengths observed in our study (76–106 mm) are between the maximum shell lengths of *A. ochracea* reported in Maine and Massachusetts (Nedeau et al. 2000; Massachusetts Division of Fisheries and Wildlife 2015). In all species, low recruitment could be related to reduced bottom dissolved oxygen associated with eutrophication in the lower Rappahannock River (Sullivan et al. 2024), but we cannot rule out other causes. In contrast, the seven fresh dead mussels observed indicate a mortality rate of ~4%, which in the upper Mississippi River is indicative of a mussel assemblage at the transition between "good" and "fair" condition (Dunn et al. 2020). Thus, our data indicate low recruitment and low to moderate natural mortality in this reach.

Assemblages in Atlantic Slope rivers are dominated by *E. complanata* (Haag 2012; Kreeger et al. 2018), and the assemblage observed in the lower Rappahannock River was no exception. This species is widely distributed across the Atlantic coast and can reach high densities (Nedeau et al. 2000). Its widespread distribution could be due to its glochidia's ability to complete transformation on many host species (Kneeland and Rhymer 2008; Lellis et al. 2013). The dominance of *E. complanata* could be attributed to its life history strategy: equilibrium strategists are often found in medium-sized and large rivers (Haag 2012). The remaining species are widespread across the Atlantic Slope region but are uncommon.

Even though the mussel assemblage was dominated by a single species (*E. complanata*), species diversity and evenness were moderate in the sampled reach. Diversity indices are forms of the same entropy equation but weigh abundant and rare species differently. Simpson's D ignores rare species, Pielou's evenness equally weighs rare and abundant species, and Shannon's entropy acts intermediately to the two other indices (Hill 1973). The moderate relative abundance of *U. implicata* and low species richness offset the numerical dominance of *E. complanata* to contribute to a community with moderate diversity. Similar frequencies among the three rarer species contributed to moderate evenness. Diversity was comparable to that reported in two Midwest rivers and evenness was fourfold higher than the median of 0.19 reported for the Atlantic region (Haag 2012; Hornbach et al. 2018; McMurray et al. 2018).

In the lower Rappahannock River, we observed longitudinal patterns in species richness and total density of mussels, which aligns with patterns in fish and other invertebrate assemblages related to the fall line (Massmann et al. 1952; Maurakis et al. 1987). Some mussel species found in the survey use migratory fish as hosts for their glochidia (*E. complanata*, *U. implicata*, and *A. ochracea*) (Kneeland and Rhymer 2008; Lellis et al. 2013); the absence of barriers in this reach of the river (and lower portions of large rivers in general) contributes to the similar patterns between mussel and fish assemblages and reduces the chance of host-loss–induced extirpation. Concordance between mussel and other invertebrate assemblages could be due to similar habitat requirements or the ecosystem engineering of freshwater mussels (hard-substrate, food, and flow-refugia generation; *sensu* DuBose et al. 2024). Although most of the lower Rappahannock River watershed has natural land use (Sullivan et al. 2024), high-density areas of mussels were often located near the Pettigrew Wildlife Management Area (rkm 86).

The quality of mussel assemblages is often based on a suite of biological metrics, including species richness, density, and demography (Dunn et al. 2020; Haag et al. 2024). The surveyed reach of the Rappahannock River supported low species richness, low density, low to moderate natural mortality, potential evidence of recruitment in *E. complanata* (based on size demography with individuals likely <10 years old), and moderate diversity and evenness. Systematic sampling designs and quantitative whole substrate samples, like those used on this reach of the Rappahannock River, can provide resource managers with robust information on mussel assemblages. Specifically, these data provide managers with baseline information on the spatial distribution, density, size demography, diversity, and evenness of mussels across a 75-km reach of the Rappahannock River. This information can be used to aid conservation and management efforts, such as identifying and prioritizing locations with rich and dense assemblages for reintroduction efforts (i.e., Cope and Waller 1995), and they are well suited as input data for models of mussel habitat (i.e., Zigler et al. 2012). Surveys of mussel assemblages in large rivers can inform management decisions in three ways. First, systematic longitudinal surveys detail mussel spatial distribution, including hot spots for biodiversity and density. Second, systematic surveys provide baseline abundance estimates that can be used in population viability or trend assessments. Third, by quantifying abundance and size, data from systematic surveys can be used to estimate the ecosystem services provided by mussels, which can be substantial in large rivers (Newton et al. 2011, 2023a). Importantly, resource managers can use baseline information on spatial distribution, size and age demography, density, and population size to assess how future management actions could affect this imperiled resource.

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