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Reevaluating fecundity of white perch (*Morone americana*) in Chesapeake Bay with modern stereological techniques

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Abstract—The white perch (*Morone americana*) is an abundant estuarine teleost in eastern North America, with its commercial and trophic importance creating a need for fecundity and recruitment data. In this study, we reevaluated the fecundity of subpopulations of white perch in Chesapeake Bay. Stereological sampling methods were used to determine if environmental changes in the Chesapeake Bay watershed over the last 60 years have altered average fecundity of this species. These methods were compared with automated gravimetric methods to determine the efficacy of using stereological fecundity sampling for white perch. The results of using both methods were statistically the same, as indicated by a Lin's concordance correlation coefficient of 0.98 and a favorable distribution on Bland–Altman plots. After the stereological methods were validated, archival histological samples from the Choptank River subestuary were evaluated for fecundity over a 4-year period of sampling. Results indicate that fecundity of white perch has been reasonably unchanged in the river system, with an average estimated fecundity of 69,379 oocytes per fish. These findings indicate the resiliency of the reproduction of white perch in mesohaline Chesapeake Bay, despite widespread environmental change.

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Much has changed in the Chesapeake Bay watershed since 1961, including growth in the estimated human population by more than 10 million residents (Chesapeake Bay Program[1]). This growth has led to a cascade of effects, including changes in land use, differences in nitrogen and phosphorous inputs, and increased contamination, that influence estuarine habitats (Brush, 1997, 2001; Kemp et al., 2005). The last published investigation of fecundity of white perch (*Morone americana*) in Chesapeake Bay, in the Patuxent River sub-estuary (Mansueti, 1961), was done in 1961. Since then, research on the species has been focused on life history strategy (Kraus and Secor, 2004; McGrath and Austin, 2009; McCauley et al., 2014), reproduction and growth (Mansueti, 1964; Jackson and Sullivan, 1995; Newhard et al., 2012), and the use of white perch as indicators of ecosystem health (McLaughlin et al., 2018; Matsche et al., 2020). Given that human actions have affected the reproductive health of other resident species in the region (Blazer et al., 2013, 2014), fecundity of white perch should be reevaluated as a way to monitor reproductive potential and to ensure continued survival of this commercially valuable species.

In the last 60 years, fish fecundity sampling has become more efficient and cost effective, thanks to advances in open-source computing (Friedland et al., 2005; Klibansky and Juanes, 2008). Sampling efficiency has enabled collection of larger data sets, which provide greater detail on links between fecundity and stock recruitment (Lambert, 2008; Armstrong and Witthames, 2012) and have allowed fecundity sampling to become

[1] Chesapeake Bay Program. 2023. Population growth. [Web page available at website, accessed 6 September 2023.].

more specific to oocyte development mode (Murua et al., 2003; Witthames et al., 2009). This improvement in understanding the relationship between stock recruitment and fecundity has resulted in a more accurate picture of stock health and recruitment when metrics that include fecundity data, such as total egg production, are coupled with more traditional measurements, such as spawning stock biomass (Lambert, 2008; Morgan et al., 2009; Witthames et al., 2009). This increase in accuracy makes a strong argument for the inclusion of population-level egg production in modeling of fish stocks, even those stocks with stable recruitment, such as Chesapeake Bay white perch (Piavis and Webb[2]).

Gravimetric methods remain a popular choice for fecundity sampling given that they involve simple counting of whole oocytes in gravid specimens caught prior to spawning, with little to no sample preparation (Murua et al., 2003; Klibansky and Juanes, 2008). Therefore, early studies of reproduction of white perch relied on such methods to estimate relative fecundity (Mansueti, 1961; Taub, 1969; Zuerlein, 1981; Bur, 1986; Klauda et al., 1988). Although simple gravimetric counting has many advantages, gravimetric methods are not as effective at estimating fecundity of species in which vitellogenic and non-vitellogenic oocytes are similar in size or are uniformly mixed throughout an ovary (Murua et al., 2003). The white perch falls within this category of fish species (Jackson and Sullivan, 1995); therefore, other methods, such as stereological sampling, may be required to more accurately sample relative fecundity (Murua et al., 2003).

Stereological fecundity sampling methods for fish were developed by Emerson et al. (1990), who adapted stereometric principles used for counting lung alveoli developed by Weibel and Gomez (1962). By formulating specific equations to control for bias in oocyte size distribution and shape, Emerson et al. (1990) were able to accurately estimate fecundity in species employing both group-synchronous and asynchronous oocyte development strategies. In contrast to gravimetric methods, stereology can be used to estimate fecundity while simultaneously assessing reproductive health and oocyte developmental state (Emerson et al., 1990; Murua et al., 2003). Despite having been used with numerous species, stereological techniques have yet to be tested on white perch. If stereological methods can be validated for use with white perch, this new tool for reproductive health assessment not only will be added to the toolbox available for management of this species but also could be used in research that involves archival data to determine change over time.

In addition to monitoring general reproductive potential, monitoring for oocyte health and atresia is important for fish populations experiencing chronic stress. Research into the health of populations of white perch in Chesapeake Bay in response to anthropogenic stressors has yielded evidence of stress response in select populations (Morgan et al., 1973; McLaughlin et al., 2018; Matsche et al., 2020). Although severity and presentation of stress response has varied, noted responses to hypoxia and sediment contamination in the Choptank River watershed have included increased parasite burden, decreased white blood cell counts, and more observations of lesions (McLaughlin et al., 2018; Matsche et al., 2020). Reproductive effects of stress, however, have not been investigated beyond simple somatic index scores. Hypoxia and contamination have been determined to affect reproduction in a number of teleost species (Barton et al., 2002; Blazer et al., 2013, 2014), with specific reproductive effects that include increased atresia and greater incidence of intersex. Given the presence of these specific stressors in the habitats of white perch, it is highly possible that the reproduction of white perch in the Chesapeake Bay watershed has been affected.

We opportunistically used specimens already being collected for this health assessment work to reinvestigate fecundity in Chesapeake Bay populations of white perch by using stereological techniques. If stereological tools are accurate for this species, they not only will yield new data for the study of temporal change in reproductive potential but also will provide useful and efficient means for future studies of reproductive health in response to environmental change.

Materials and methods

Field collections for this study focused on gravid white perch from the Choptank River of Chesapeake Bay in Maryland, with an additional small sample collected from the Saluda River in South Carolina to account for geographical fecundity variation in method testing. Specimens from the Choptank River were captured by using either hook and line or standing fyke nets that collected fish for no more than 24 h (Table 2). Following capture, fish were transported live in river water with supplemental oxygen and held for 18–24 h before being euthanized with a lethal dose of buffered tricaine methanesulfonate (Syndel[3], Ferndale, WA) immediately before necropsy, as per animal use protocols of the Maryland Department of Natural Resources (UFRC, 2014). Specimens collected on the Saluda River were captured by using electrofishing techniques and were euthanized at the time of capture by severing the spinal cord, as per Maryland Department of Natural Resources animal use protocols for animals that cannot be transported alive (UFRC, 2014). Fish were checked by palpation of the abdomen for sex and spawning state at time of capture to mitigate the collection of postspawning specimens. Males and postspawning females were returned to the waters where they were captured.

Before necropsy, morphological data, including total length (TL, in millimeters) and total fish weight (in grams) prior to evisceration, were recorded. Age was determined

[2] Piavis, P., and E. Webb III. 2018. Population assessment of white perch in select regions of Chesapeake Bay, Maryland. Md. Dep. Nat. Resour., Vol. Rep. F-61-R, 46 p. [Available from Md. Dep. Nat. Resour., 580 Taylor Ave., Annapolis, MD 21401.]

[3] Mention of trade names or commercial companies is for identification purposes only and does not imply endorsement by the Maryland Department of Natural Resources or the National Marine Fisheries Service, NOAA.

after necropsy by submerging dry, whole otoliths in glycerol and counting annuli at 10× magnification. During necropsy examination, ovaries were excised, measured for mass and volume, and then sectioned and fixed in 10% neutral buffered formalin before subsamples were counted gravimetrically and stereometrically. Volume was measured by using the wet-weight method, described by Scherle (1970), in which ovaries are suspended in a tared water bath and weighed. Ovaries were sectioned by using a multiblade knife with blade spacing of 4 mm. Alternating sequential sections of 4 mm from both ovaries were used for gravimetric and stereometric analysis, with no less than 3 sections used for stereometry depending on ovary size. Because differences in oocyte distribution between ovarian regions were not considered in previous studies (Mansueti, 1961; Taub, 1969; Klauda et al., 1988; Okoye et al., 2008), a subset of sequential histological samples from 10 specimens were placed in individual histology cassettes and examined to confirm the lack of locational bias. Data confirm that oocyte size distribution was uniform throughout examined ovaries.

To test the efficacy of using stereological methods to estimate relative fecundity in white perch, data obtained from stereological counts were compared to fecundity estimated gravimetrically. Gravimetric oocyte counting was selected as the comparative method because prior fecundity estimations for populations of white perch all were made with gravimetric techniques (Taub, 1969; Zuerlein, 1981; Bur, 1986; Klauda et al., 1988; Okoye et al., 2008). For gravimetric sampling, we used techniques described by Klibansky and Juanes (2008), specifically their method for the automated counting of oocytes with ImageJ, vers. 1.53k (Schneider et al., 2012).

Gravimetric counting procedures started with collection of oocyte samples that were separated from ovarian connective tissue by using a series of sieves. From this subset, a sample of 1 g (±0.001 g) was taken, placed in 70% ethanol, and vortexed for 15 s at 1000 rpm to further separate individual oocyte particles. Following separation, oocyte samples were placed on a standard petri dish that had a diameter of 100 mm and had been painted black, and the samples were photographed with a Nikon D5100 camera that had an AF-S Micro Nikkor 60-mm lens (Nikon Corp., Tokyo, Japan). After photography, ImageJ was used to automate particle counts, with macro scripts automatically adjusting image attributes and recording number and size of particles in the sample. Particles that were larger than the 95th quartile of the size–frequency distribution were considered groups of oocytes. The area of these groups was divided by the mean particle area of the sample to estimate how many individual oocytes were present in the group.

Stereometric methods followed those of Emerson et al. (1990), as described by Murua et al. (2003), with point-counting techniques used to estimate fecundity. Stereological samples were prepared for analysis by using standard paraffin embedding protocols with sectioning done at 5-µm increments (Hinton, 1990). Before point counting, samples were checked for signs of ovulation by using light microscopy.

The white perch is a batch-spawning species with a group-synchronous oocyte development mode; therefore, oocytes are present in ovaries at multiple different developmental stages during spawning (Jackson and Sullivan, 1995). Samples with post-ovulatory oocytes were removed from consideration, as active spawning would affect the accuracy of fecundity estimates. For point counting, the grid area was adjusted to 3000 μm^2, 4× magnification was used, and a minimum of 10 full grids were counted, to ensure a balance between sampling efficiency and accuracy. Because of constraints in available equipment, the grid style was changed from the Weibel multipurpose grid as pictured in figure 4 of Murua et al. (2003), to a 10-line-by-10-line standard grid of 81 cells (Fig. 1). All method changes were tested for precision by monitoring observed coefficient of

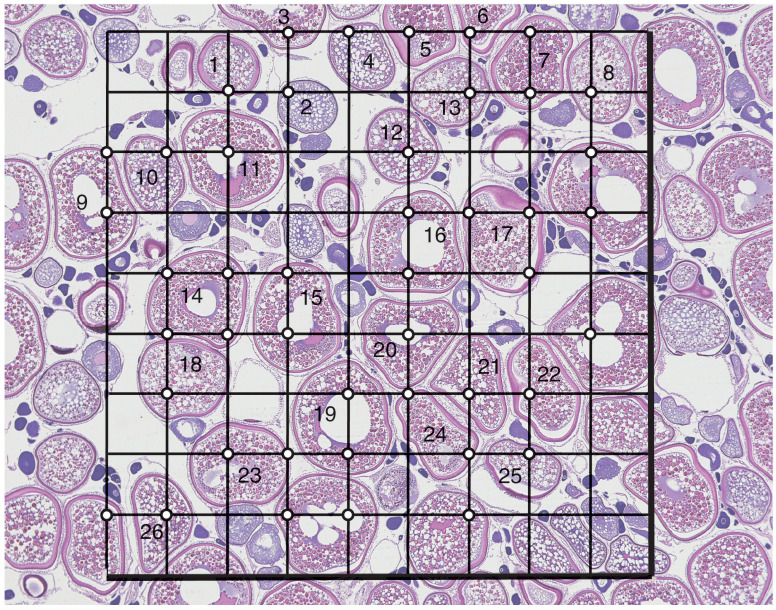

Figure 1

Image of the grid used for stereological fecundity sampling of white perch (*Morone americana*) caught from 2015 through 2018 in the Choptank River in Maryland. The grid differs from the Wiebel multipurpose grid used in other studies, but results from pilot studies indicate that the difference in grids did not affect the accuracy of estimates. The thick lines on the right side and bottom of the grid indicate exclusionary boundaries (the oocytes that overlap these boundaries were not counted), numerals indicate the number of counted whole oocytes, and white dots indicate grid intersection points that fall over oocyte tissue and were counted.

error (OCE) while sampling to verify that error rates were below 10% (West, 2012).

Following point counts, relative fecundity was calculated by multiplying the number of oocytes per unit volume by total volume of the ovaries (Emerson et al., 1990; Murua et al., 2003). Coefficients used to correct for variance in size distribution (K) and shape of oocytes (β) used by Emerson et al. (1990) were calculated for each sample by using ImageJ to count and measure particles on images taken at 4× magnification.

Method agreement was assessed by using Lin's concordance correlation coefficient (Lin, 1989) interpreted on McBride's strength of agreement criteria (McBride[4]). This assessment was undertaken in order to simultaneously measure agreement between the methods and potential bias (Lin, 1989), as opposed to using a Pearson's correlation, which can fail at assessing certain sampling biases, such as scale and location shift, when the desired outcome is reproducibility. Results from concordance correlation coefficient assessments were then combined with plotting of data by using Bland–Altman techniques and by calculating Deming and Passing–Bablok regressions to further assess potential bias (Deming, 1943; Passing and Bablok, 1983; Bland and Altman, 1986). The Bland–Atlman difference plot is a common means of visualization to compare 2 methods of collecting the same data (Bland and Altman, 1986; Westgard, 2008) and allows additional qualitative review of bias between the 2 different methods. If plotted differences approximate zero, are evenly distributed around the mean of differences, and fall within Bland–Altman accepted limits of agreement (1.96 standard deviation), it is assumed that there is no measurement bias from either method. A lack of such bias is critical for the reproducibility of data and interchangeability of methods.

Relationships between morphological data and fecundity were investigated by using linear regression techniques. Regression models were created for the entire sample and for individual years. To assess interannual variability in fecundity, analysis of variance with log transformation of fecundity data was used to compare fecundity between the 4 sampling years.

Results

Methods testing

In 2018, 42 white perch were sampled from 2 geographically isolated river systems for the purpose of testing stereological fecundity methods (Table 1). The OCE calculations indicate that a grid size of 3000 μm^2 and the minimum of 10 full grids per sample counted was sufficient to keep the OCE below 0.1. Average OCE was 0.047 for particle-area counts and 0.068 for particle-enumeration counts. In assessment of the correlation between the methods, Lin's concordance correlation coefficient was 0.98, indicating "substantial" agreement as per McBride's scale (McBride[4]). Bland–Altman plots indicate that 95% of data points are within 1.96 standard deviation confidence intervals as recommended (Fig. 2). There was no visual indication of constant bias between methods, corroborated by results from Passing–Bablok and Deming regressions (Table 1). As archival data included only dry mass ovarian weight, volumes were estimated for calculations by using the formula obtained by comparing a subset of whole ovaries measured for dry mass and wet weight:

$$V = 0.58110 + (0.96842 \times M) + 1.233,$$

where V = ovarian volume; and

M = dry mass.

Differences in fecundity estimates between the Saluda River in South Carolina and the Choptank River in Maryland were negligible. In analysis of samples collected from specimens caught in 2018 for comparison of methods, specimens from the Saluda River had an average estimated fecundity of 42,761 oocytes per fish, and specimens from the Choptank River had an average estimated fecundity of 54,406 oocytes per fish.

Table 1

Results from analysis with Lin's concordance correlation coefficient (CCC), Deming regression, and Passing–Bablok regression to compare stereological and gravimetric fecundity sampling methods used to evaluate fecundity in white perch (*Morone americana*) sampled in 2018 from the Choptank River in Maryland and the Saluda River in South Carolina. Confidence intervals are provided in parentheses. Intervals contain 0.00 for both intercepts and 1.00 for both slopes; therefore, there is no statistical evidence of bias. n=sample size.

n	Lin's CCC	Deming regression	Passing–Bablok regression
42	0.979	Intercept: –107.91 (–5786.51–5583.98) Slope: 1.01 (0.94–1.07)	Intercept: –2717.75 (–9081.37–2745.47) Slope: 1.02 (0.95–1.10)

Fecundity sampling

Following the favorable results from the methods comparison, stereological methods were used to reevaluate the fecundity of Chesapeake Bay white perch, by using the Choptank River subpopulation as a proxy for the population of the entire system. From 2015 through 2018, 182 gravid white perch were collected (Table 2). Ovarian tissue

[4] McBride, G. 2005. A proposal for strength-of-agreement criteria for Lin's concordance correlation coefficient. NIWA Client Rep. HAM2005-062, 7 p. N.Z. Natl. Inst. Water Atmos. Res., Hamilton, New Zealand. [Report on NIWA project MOH05201 prepared for the Ministry of Health.] [Available from website.]

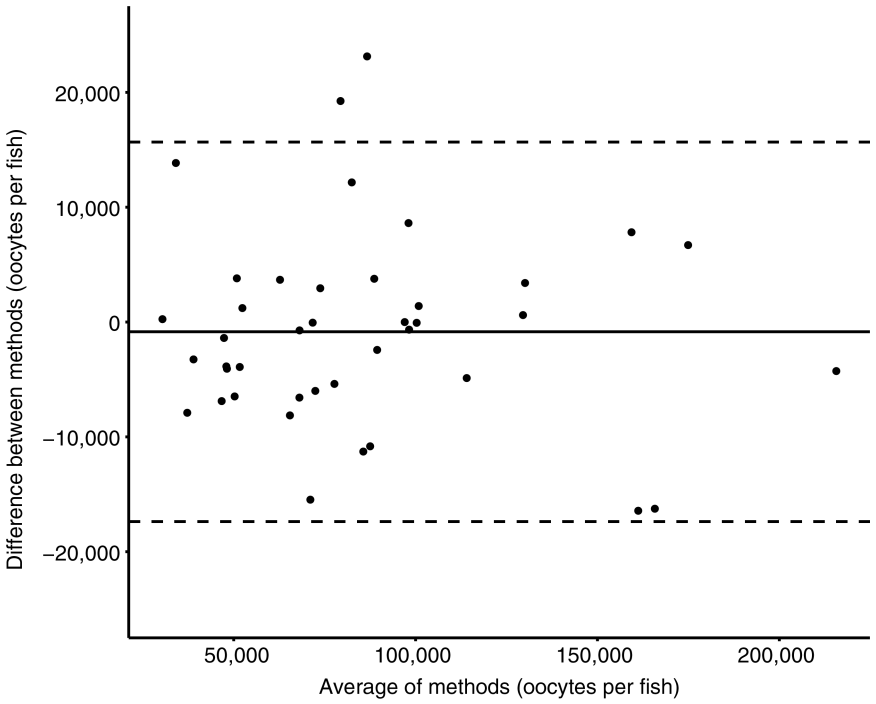

Figure 2

Bland–Altman plot comparing gravimetric and stereological sampling methods used to estimate fecundity of white perch (*Morone americana*) caught in 2018 in the Choptank River in Maryland. Dashed lines indicate 95% confidence intervals (1.96 standard deviation). The solid line indicates the mean of the differences between the 2 methods. A mean of differences near zero indicates a general lack of bias between the measurements and random variability.

Table 2

Estimated average, minimum, and maximum fecundity of white perch (*Morone americana*) caught during 2015–2018 in the Choptank River in Maryland. Hook-and-line gear were used to sample fish in 2015 at site 1 (top set of coordinates) and in 2016. Standing fyke nets were used to sample fish in 2015 at site 2 (bottom set of coordinates) and in 2017 and 2018. *n*=sample size.

			Fecundity (oocytes per fish)		
Year	Sampling location	*n*	Average	Min	Max
2015	38.9985, −75.7857; 38.7800, −75.9602	51	38,811.63	9399	13,8157
2016	38.9735, −75.8009	30	25,340.43	7691	84,345
2017	38.7800, −75.9602; 38.8072, −75.9113	35	65,520.77	28,592	146,092
2018	38.7800, −75.9602	66	117,164.30	57,184	280,537

samples from each fish were sectioned, placed on microscope slides, and archived. Mean total fish weight for all collected specimens is 140.9 g, and mean TL of fish is 211.3 mm. Mean fish age was 5 years, with a range of 2–14 years. Estimated fecundity, determined from archival histological samples, was an average of 69,379 oocytes per fish for all 4 years combined, with a maximum value of 280,537 oocytes per fish in 2018 and a minimum of 7691 oocytes per fish in 2016 (Table 2). Averages from this study fall within the range of historically reported fecundity

estimates of 50,000–150,000 oocytes per fish for populations in Chesapeake Bay and the range of reported total fecundity of 5000–320,000 oocytes per fish for all populations of this species (Setzler-Hamilton, 1991).

Results from investigations of the relationship between length and fecundity in the sample indicate a positive correlation between TL and estimated fecundity (Fig. 3). As shown in Table 2, fecundity estimates for 2018 were notably higher than fecundity values for any of the previous 3 years of sampling. Total lengths in the sample were similar in range, with lengths in 2018 ranging from 185 to 255 mm TL, with an average of 217 mm TL, and with lengths of 159–265 mm TL, 161–245 mm TL, and 189–267 mm TL in 2015, 2016, and 2017, respectively. Use of the linear model of length by fecundity yielded a moderately positive relationship, with a coefficient of multiple determination (R^2) of 0.48 (Fig. 3). Interannual variability among fish in the sample is indicated by the different average fecundity values (Table 2). Comparison of the relationship between length and fecundity by year yielded positive relationships, with R^2 values of 0.71, 0.68, 0.80, and 0.66 for 2015, 2016, 2017, and 2018, respectively. Results from the analysis of variance following log transformation of fecundity data indicate significant differences in fecundity between sampling years (P<0.001).

Discussion

Our study represents the most comprehensive investigation of the fecundity of white perch in Chesapeake Bay since the early 1960s. We used a novel approach for this species: stereological fecundity sampling. Stereological methods were proven to be efficient and accurate when results were compared to results from use of established gravimetric oocyte counting methods. This favorable outcome allowed us to expand the available fecundity data for Choptank River white perch to include information from archival histological samples. With these expanded data, we could conduct a robust, multiyear analysis of fecundity in this subpopulation of white perch. Findings from this study regarding reproductive potential further indicate the resiliency of the reproduction of Chesapeake Bay white perch in the face

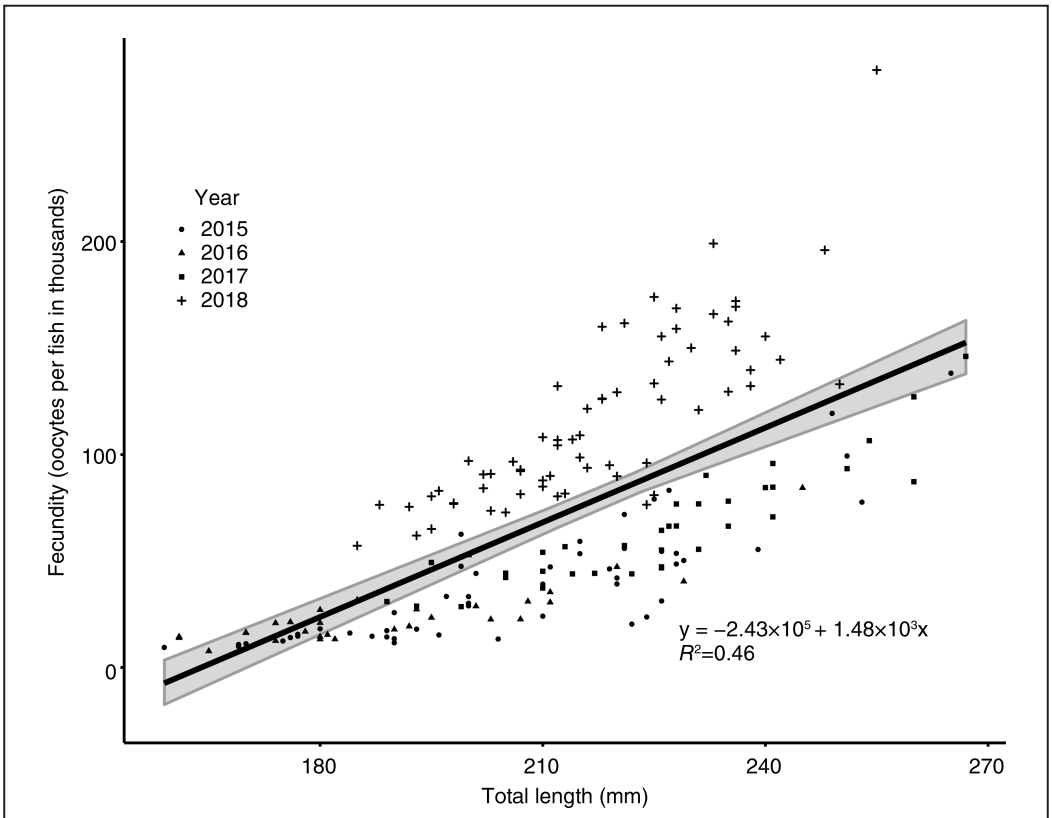

Figure 3

Relationship between estimated fecundity and total length, by year, for white perch (*Morone americana*) caught in the Choptank River in Maryland from 2015 through 2018. The shaded area indicates the estimated standard error. The equation of the line and the coefficient of multiple determination (R^2) are provided. The high fecundity values in 2018 indicate interannual variability in average fecundity of Choptank River white perch.

of environmental change and fluctuations in fishing pressure and predation over time.

When coupled with basic automation of repetitive procedures and slight changes to techniques, stereological methods appear well suited for use with white perch. Although stereological methods are well established and could be assumed to work reasonably for white perch, initial testing was needed on the basis of the oocyte development mode of white perch. Because white perch have a group-synchronous spawning strategy, ovaries of gravid fish have a well-mixed size distribution of oocytes (Jackson and Sullivan, 1995) that could confound calculations of size and shape if oocytes were not properly bounded. Results from comparisons between gravimetric and stereological methods, however, indicate that bounded gravimetric counts are just as accurate as stereometric counts and, therefore, that the size distribution of oocytes did not affect counting of whole oocytes. Although counting of whole oocytes, especially with automated image analysis, is rapid and effective (Klibansky and Juanes, 2008), performing counts stereologically has advantages, such as the abilities to cross-validate field assessments of spawning state and to investigate ovarian health.

Because of their accuracy, efficiency, and cost-effective nature, we expect stereological methods to become another tool for resource managers to more accurately assess change in reproductive potential of white perch. Despite a ubiquitous presence of the white perch in estuaries of eastern North America and the Great Lakes region, most fecundity estimates for the species were reported more than 30 years ago (Setzler-Hamilton, 1991). Having updated methods with which to retest fecundity estimates will be useful in the reevaluation of fecundity over the range of white perch, and examining fecundity stereologically will increase knowledge of reproductive health and temporal change in fecundity. Advantages of the stereological method include the abilities to simultaneously determine oocyte developmental state and sample fecundity, to monitor for reproductive health pathology, such as intersex and atresia, and to study change in fecundity over time by using archival samples. Monitoring atresia is especially important considering the relationship of this condition with environmental stress (Schreck et al., 2001; Barton et al., 2002).

In comparisons of data between the previous study conducted in the Patuxent River sub-estuary in Maryland (Mansueti, 1961) and this study, no apparent change was found in reproductive potential for white perch in Chesapeake Bay in Maryland. It is worth noting that direct comparisons are impossible because study methods for the original work were not recorded (Mansueti, 1961) and samples were not acquired from the Patuxent River for our study. Geographical isolation is an important consideration in the Chesapeake region, as white perch have discrete home ranges (McGrath and Austin, 2009), which, in conjunction with salt regimes in Chesapeake Bay, typically keep populations of white perch in the larger sub-estuaries from mixing. Therefore, a truly direct comparison between historical data would require specimens from the Patuxent River, and a truly holistic evaluation of fecundity of Chesapeake Bay white perch would require larger geographical coverage of multiple sub-estuaries of the tidal region of Maryland.

Although characteristics of the Choptank River are similar to those of the Patuxent sub-estuary, the populations in both systems are distinct and, therefore, have potentially different average reproductive potentials. We contend, however, that the Choptank River, with characteristics similar to those of the Patuxent River, serves as an effective proxy in our study. Land use in the Patuxent River watershed is markedly different, with approximately 23% of the watershed developed compared to only 5% of the watershed developed for the Choptank River (NOAA Office for Coastal Management, Coastal Change Analysis Program Landcover Atlas, available from website, accessed September 2023), but the general latitudinal and climactic locations for both sub-estuaries in the Chesapeake Bay watershed are nearly identical, making comparisons between the 2 systems a reasonable approach.

Investigating the relationship between TL and estimated fecundity was also a novel approach for populations of white perch in Chesapeake Bay (Mansueti, 1961). Although length and fecundity of the entire sample had a moderately positive relationship (R^2=0.48), relationships between length and fecundity for each year had greater correlation. Findings of interannual variability were confirmed by using analysis of variance, indicating that unknown drivers are affecting egg production.

Fecundity has been reported to vary in other species as a result of numerous factors, including food availability, fish condition, and climate (Rideout and Morgan, 2007; Lambert, 2008). Other possible explanations for the variability in fecundity found for specimens in our study are differences in reproductive potential between resident freshwater subpopulations and migratory populations in the Choptank River system. Research into the interestuarine movements of white perch in the neighboring Patuxent River has revealed the presence of resident, non-migratory freshwater population contingents (Kraus and Secor, 2004; Kerr and Secor, 2012). Although these contingents contribute to system-wide recruitment (Kraus and Secor, 2005), it is not known whether fecundity varies between migratory and resident populations. For this study, sampling in 2015–2017 included work in freshwater areas in the upper limits of the Choptank River system, increasing the potential of sampling freshwater residents. Further study would need to incorporate chemical otolith analysis to determine the source populations for individuals before it could be possible to determine whether resident populations have lower average fecundity than migratory populations.

Another explanation could be a greater influence of age, in comparison to that of length, on individual fecundity in the Choptank River population, possibly the result of a truncated age-at-length population structure due to fishing pressure. White perch are commercially collected in the Choptank River system through winter gill-net fishing (Piavis and Webb[2]). If fishing was selective for larger white

perch (>200 mm TL), as has been reported for numerous stocks with commercial fishing pressure (Bianchi et al., 2000; Ward and Myers, 2005), older females might be shorter in length but more fecund, possibly accounting for the greater fecundity (average fecundity was 117,164 oocytes per fish in 2018, versus 65,520 oocytes per fish in 2017) but not greater length (average TL was 217 mm in 2018, versus 225 mm in 2017) in specimens caught in 2018. Results from year-class investigation in the Choptank River indicate that the 2011 year class is a dominant class (Piavis and Webb[2]). Age data from this study indicate that the majority of fish collected in 2018 and 2017 were of this age class; therefore, the fish may not be growing longer but are instead producing more eggs with age.

Conclusions

In this study, we were able not only to effectively reevaluate fecundity in white perch from the Chesapeake Bay watershed but also to demonstrate the utility and accuracy of modern stereological methods of sampling for this species. The white perch is an important species in estuarine food webs in eastern North America, and the ability of this species to maintain reproductive potential and population abundance will be critical for commercially and environmentally important anadromous species of this region that use white perch as food in their early life stages (Walter and Austin, 2003). In addition, it has been demonstrated that the abundance and health of white perch are useful proxies for general habitat health (McLaughlin et al., 2018). Therefore, the ability to monitor reproductive health and production of this species can be useful in study of habitat quality for all resident species of a given mesohaline area. Given the abundance of white perch in the estuaries of eastern North America, studying changes in the reproductive potential of populations of this species over time and in relation to environmental shifts could provide insights into the health and resiliency of teleost communities in this region.

Resumen

La perca blanca (*Morone americana*) es un teleósteo estuarino abundante en el este de Norteamérica, y su importancia comercial y trófica crea la necesidad de disponer de datos sobre fecundidad y reclutamiento. En este estudio, reevaluamos la fecundidad de subpoblaciones de perca blanca en la bahía de Chesapeake. Se utilizaron métodos de muestreo estereológico para determinar si los cambios medioambientales en la cuenca de la bahía de Chesapeake durante los últimos 60 años han alterado la fecundidad media de esta especie. Estos métodos se compararon con los métodos gravimétricos automatizados para determinar la eficacia del uso del muestreo estereológico de fecundidad para la perca blanca. Los resultados de la utilización de ambos métodos fueron estadísticamente iguales, como lo indica el coeficiente de correlación de concordancia de Lin de 0.98 y una distribución favorable en los gráficos de Bland–Altman. Una vez validados los métodos estereológicos, se evaluó la fecundidad de muestras histológicas almacenadas del estuario del río Choptank durante un período de muestreo de 4 años. Los resultados indican que la fecundidad de la perca blanca se ha mantenido razonablemente inalterada en el sistema fluvial, con una fecundidad media estimada de 69,379 oocitos por pez. Estos resultados indican la resistencia de la reproducción de la perca blanca en la bahía mesohalina de Chesapeake, a pesar de los cambios ambientales generalizados.

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Literature cited

Armstrong, M. J., and P. R. Witthames.
2012. Developments in understanding of fecundity of fish stocks in relation to egg production methods for estimating spawning stock biomass. Fish. Res. 117–118:35–47. Crossref

Barton, B. A., J. D. Morgan, and M. M. Vijayan.
2002. Physiological and condition-related indicators of environmental stress in fish. *In* Biological indicators of aquatic ecosystem stress (S. M. Adams, ed.), p. 111–148. Am. Fish. Soc., Bethesda, MD.

Bianchi, G., H. Gislason, K. Graham, L. Hill, X. Jin, K. Koranteng, S. Manickchand-Heileman, I. Paya´, K. Sainsbury, F. Sanchez, et al.
2000. Impact of fishing on size composition and diversity of demersal fish communities. ICES J. Mar. Sci. 57:558–571. Crossref

Bland, J. M., and D. Altman.
1986. Statistical methods for assessing agreement between two methods of clinical measurement. Lancet 327:307–310. Crossref

Blazer, V. S., A. E. Pinkney, J. A. Jenkins, L. R. Iwanowicz, S. Minkkinen, R. O. Draugelis-Dale, and J. H. Uphoff.
2013. Reproductive health of yellow perch *Perca flavescens* in selected tributaries of the Chesapeake Bay. Sci. Total Environ. 447:198–209. Crossref

Blazer, V. S., D. D. Iwanowicz, H. L. Walsh, A. J. Sperry, L. R. Iwanowicz, D. A. Alvarez, R. A. Brightbill, G. Smith, W. T. Foreman, and R. Manning.
2014. Reproductive health indicators of fishes from Pennsylvania watersheds: association with chemicals of emerging concern. Environ. Monit. Assess. 186:6471–6491. Crossref

Brush, G. S.
1997. History and impact of human activities on Chesapeake Bay. *In* Ecosystem function and human activities (R. D. Simpson and N. L. Christensen, eds.), p. 125–145. Springer, Boston, MA.
2001. Natural and anthropogenic changes in Chesapeake Bay during the last 1000 years. Hum. Ecol. Risk Assess. 7:1283–1296. Crossref

Bur, M. T.
1986. Maturity and fecundity of the white perch, *Morone americana*, in western Lake Erie. Ohio J. Sci. 86:205–207.
Deming, W. E.
1943. Statistical adjustment of data, 269 p. John Wiley and Sons, New York.
Emerson, L. E., M. G. Walker, and P. R. Witthames.
1990. A stereological method for estimating fish fecundity. J. Fish Biol. 36:721–730. Crossref
Friedland, K. D., D. Ama-Abasi, M. Manning, L. Clarke, G. Kligys, and R. C. Chambers.
2005. Automated egg counting and sizing from scanned images: rapid sample processing and large data volumes for fecundity estimates. J. Sea Res. 54:307–316. Crossref
Hinton, D. E.
1990. Histological techniques. *In* Methods for fish biology (C. B. Schreck and P. B. Moyle, eds.), p. 191–209. Am. Fish. Soc., Bethesda, MD.
Jackson, L. F., and C. V. Sullivan.
1995. Reproduction of white perch: the annual gametogenic cycle. Trans. Am. Fish. Soc. 124:563–577. Crossref
Kemp, W. M., W. R. Boynton, J. E. Adolf, D. F. Boesch, W. C. Boicourt, G. Brush, J. C. Cornwell, T. R. Fisher, P. M. Glibert, J. D. Hagy, et al.
2005. Eutrophication of Chesapeake Bay: historical trends and ecological interactions. Mar. Ecol. Prog. Ser. 303:1–29. Crossref
Kerr, L. A., and D. H. Secor.
2012. Partial migration across populations of white perch (*Morone americana*): a flexible life history strategy in a variable estuarine environment. Estuar. Coasts 35:227–236. Crossref
Klauda, R. J., J. B. McLaren, R. E. Schmidt, and W. P. Dey.
1988. Life history of white perch in the Hudson River estuary. Am. Fish. Soc. Monogr. 4:69–88.
Klibansky, N., and F. Juanes.
2008. Procedures for efficiently producing high-quality fecundity data on a small budget. Fish. Res. 89:84–89. Crossref
Kraus, R. T., and D. H. Secor.
2004. Dynamics of white perch *Morone americana* population contingents in the Patuxent River estuary, Maryland, USA. Mar. Ecol. Prog. Ser. 279:247–259. Crossref
2005. Application of the nursery-role hypothesis to an estuarine fish. Mar. Ecol. Prog. Ser. 291:301–305. Crossref
Lambert, Y.
2008. Why should we closely monitor fecundity in marine fish populations? J. Northwest Atl. Fish. Sci. 41:93–106. Crossref
Lin, L. I.-K.
1989. A concordance correlation coefficient to evaluate reproducibility. Biometrics 45:255–268. Crossref
Mansueti, R. J.
1961. Movements, reproduction, and mortality of the white perch, *Roccus americanus*, in the Patuxent estuary, Maryland. Chesap. Sci. 2:142–205. Crossref
1964. Eggs, larvae, and young of the white perch, *Roccus americanus*, with comments on its ecology in the estuary. Chesap. Sci. 5:3–45.
Matsche, M. A., V. S. Blazer, E. L. Pulster, and P. M. Mazik.
2020. High prevalence of biliary neoplasia in white perch *Morone americana*: potential roles of bile duct parasites and environmental contaminants. Dis. Aquat. Org. 141:195–224. Crossref
McCauley, M. M., R. M. Cerrato, M. Sclafani, and M. G. Frisk.
2014. Diel behavior in white perch revealed using acoustic telemetry. Trans. Am. Fish. Soc. 143:1330–1340. Crossref
McGrath, P., and H. A. Austin.
2009. Site fidelity, home range, and tidal movements of white perch during the summer in two small tributaries of the York River, Virginia. Trans. Am. Fish. Soc. 138:966–974. Crossref
McLaughlin, S. M., A. K. Leight, J. E. Spires, S. B. Bricker, J. M. Jacobs, G. A. Messick, and S. Skelley.
2018. Coastal ecosystem assessment to support NOAA's Choptank River complex habitat focus area: Tred Avon River. NOAA Tech. Memo. NOS NCCOS 251, 118 p.
Morgan, M. J., H. Murua, G. Kraus, Y. Lambert, G. Marteinsdóttir, C. T. Marshall, L. O'Brien, and J. Tomkiewicz.
2009. The evaluation of reference points and stock productivity in the context of alternative indices of stock reproductive potential. Can. J. Fish. Aquat. Sci. 66:404–414. Crossref
Morgan, R. P., R. F. Fleming, V. J. Rasin, and D. R. Heinle.
1973. Sublethal effects of Baltimore Harbor water on the white perch, *Morone americana*, and the hogchoker, *Trinectes maculatus*. Chesap. Sci. 14:17–27. Crossref
Murua, H., G. Kraus, F. Saborido-Rey, P. R. Witthames, A. Thorsen, and S. Junquera.
2003. Procedures to estimate fecundity of wild collected marine fish in relation to fish reproductive strategy. J. Northwest Atl. Fish. Sci. 33:33–54. Crossref
Newhard, J. J., J. W. Love, and J. Gill.
2012. Do juvenile white perch *Morone americana* grow better in freshwater habitats of the Blackwater River drainage (Chesapeake Bay, MD, USA)? Estuar. Coasts 35:1110–1118. Crossref
Okoye, A. O., A. S. Overton, M. Loeffler, and S. E. Winslow.
2008. White perch fecundity relationships in western Albemarle Sound, North Carolina. J. N.C. Acad. Sci. 124:46–50.
Passing, H., and W. Bablok.
1983. A new biometrical procedure for testing the equality of measurements from two different analytical methods: application of linear regression procedures for method comparison studies in clinical chemistry, Part 1. J. Clinical Chem. Lab. Med. 21:709–724. Crossref
Rideout, R. M., and M. J. Morgan.
2007. Major changes in fecundity and the effect on population egg production for three species of north-west Atlantic flatfishes. J. Fish Biol. 70:1759–1779. Crossref
Scherle, W.
1970. A simple method for volumetry of organs in quantitative stereology. Mikroskopie 26:57–60.
Schneider, C. A., W. S. Rasband, and K. W. Eliceiri.
2012. NIH Image to ImageJ: 25 years of image analysis. Nat. Methods 9:671–675. Crossref
Schreck, C. B., W. Contreras-Sanchez, and M. S. Fitzpatrick.
2001. Effects of stress on fish reproduction, gamete quality, and progeny. Aquaculture 197:3–24. Crossref
Setzler-Hamilton, E. M.
1991. White perch, *Morone americana*. *In* Habitat requirements for Chesapeake Bay living resources, 2nd ed., p. 12.1–12.20. Chesap. Res. Consort., Solomons, MD.
Taub, S. H.
1969. Fecundity of the white perch. Progress. Fish-Cult. 31:166–168. Crossref
UFRC (Use of Fishes in Research Committee).
2014. Guidelines for the use of fishes in research, 86 p. Am. Fish. Soc., Bethesda, MD.
Walter, J. F., III, and H. M. Austin.
2003. Diet composition of large striped bass (*Morone saxatilis*) in Chesapeake Bay. Fish. Bull. 101:414–423.
Ward, P., and R. A. Myers.
2005. Shifts in open-ocean fish communities coinciding with the commencement of commercial fishing. Ecology 86:835–847. Crossref

Weibel, E. R., and D. M. Gomez.
1962. A principle for counting tissue structures on random sections. J. Appl. Physiol. 17:343–348. Crossref
West, M. J.
2012. Basic stereology for biologists and neuroscientists, 206 p. Cold Spring Harbor Lab. Press, Cold Spring Harbor, NY.
Westgard, J. O.
2008. Basic method validation: training in analytical quality management for healthcare laboratories, 3rd ed., 320 p. Westgard Quality Corp., Madison, WI.
Witthames, P. R., A. Thorsen, H. Murua, F. Saborido-Rey, L. N. Greenwood, R. Dominguez, M. Korta, and O. S. Kjesbu.
2009. Advances in methods for determining fecundity: application of the new methods to some marine fishes. Fish. Bull. 107:148–164.
Zuerlein, G.
1981. The white perch, *Marone americana* (Gmelin) in Nebraska. Neb. Tech. Ser. 8, 108 p.