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ANNUAL PROGRESS REPORT - 2006 Data collection and analysis in support of single and multispecies stock assessments in Chesapeake Bay: The Chesapeake Bay Multispecies Monitoring and Assessment Program

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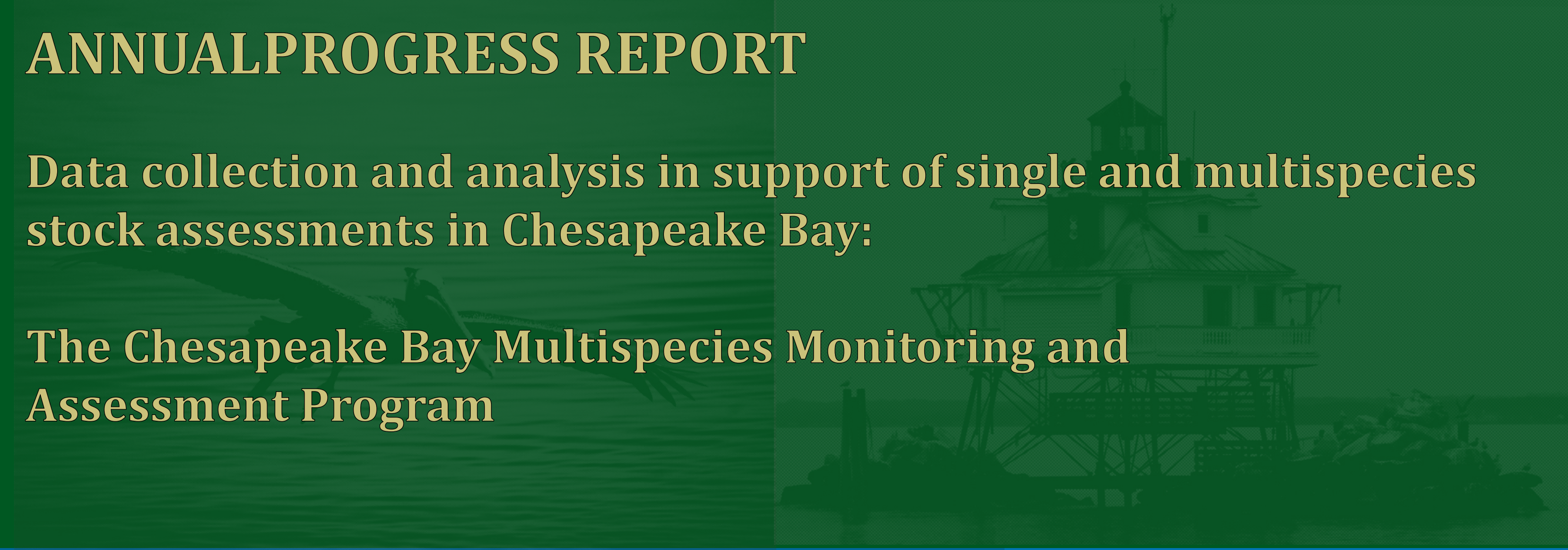

ANNUALPROGRESS REPORT

Data collection and analysis in support of single and multispecies stock assessments in Chesapeake Bay:

The Chesapeake Bay Multispecies Monitoring and Assessment Program

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June 2007

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Data collection and analysis in support of single and multispecies stock assessments in Chesapeake Bay:

The Chesapeake Bay Multispecies Monitoring and Assessment Program

U.S. Fish and Wildlife Service Sportfish Restoration Project F-130-R-2

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Introduction

Historically, fisheries management has been based on the results of single-species stock assessment models that focus on the interplay between exploitation level and sustainability. There currently exists a suite of standard and accepted analytical frameworks (e.g., virtual population analysis (VPA), biomass dynamic production modeling, delay difference models, etc.) for assessing the stocks, projecting future stock size, evaluating recovery schedules and rebuilding strategies for overfished stocks, setting allowable catches, and estimating fishing mortality or exploitation rates. A variety of methods also exist to integrate the biological system and the fisheries resource system, thereby enabling the evaluation of alternative management strategies on stock status and fishery performance. These well-established approaches have specific data requirements involving biological (life history), fisheries-dependent, and fisheries-independent data (Table 1). From these, there are two classes of stock assessment or modeling approaches used in fisheries: partial assessment based solely on understanding the biology of a species, and full analytical assessment including both biological and fisheries data.

Table 1. Summary of biological, fisheries-dependent and fisheries-independent data requirements for single-species analytical stock assessment models.

Data Category	Assessment Type	Data Description
Biological / Life History	Partial	Growth (length / weight)
		Maturity schedule
		Fecundity
		Partial recruitment schedules
		Longevity
		Life history strategies (reproductive and behavioral)
Fishery-Dependent Data	Analytical	Catch, landings, and effort
		Biological characterization of the harvest (size, sex, age)
		Gear selectivity
		Discards/bycatch
Fishery-Independent Data	Analytical	Biological characterization of the population (size, sex, age)
		Mortality rates
		Estimates of annual juvenile recruitment

Although single-species assessment models are valuable and informative, a primary shortcoming is that they generally fail to consider the ecology of the species under management (e.g., habitat requirements, response to environmental change), ecological interactions (e.g., predation, competition), and technical interactions (e.g., discards, bycatch) (NMFS 1999, Link 2002a,b). However, inclusion of ecological processes into fisheries management plans is now strongly recommended (NMFS 1999, NRC 1999, Pew Commission 2003, U.S. Oceans Commission 2004) and in some cases even mandated (NOAA 1996). Multispecies assessment models have been developed to move towards an ecosystem-based approach to fisheries management (Hollowed et al. 2000, Whipple et al. 2000, Link 2002a,b). Although such models are still designed to yield information about sustainability, they are structured to do so by explicitly incorporating the effects of ecological processes among interacting populations.

Over the past several years, the number and type of multispecies models designed to provide insight about fisheries questions has grown significantly (Hollowed et al. 2000, Whipple et al. 2000). This growth has been fueled by the need to better inform fisheries policy makers and managers, however, recent concerns about effects of fishing on the structure of ecosystems have also prompted research activities on multispecies modeling and the predator-prey relationships that are implied. From a theoretical perspective, basing fisheries stock assessments on multispecies rather than single-species models certainly appears to be more appropriate, since multispecies approaches allow a greater number of the processes that govern population abundance to be modeled explicitly. However, this increase in realism leads to an increased number of model parameters, which in turn, creates the need for additional types of data.

In the Chesapeake Bay region, there has been a growing interest in ecosystem-based fisheries management, as evidenced by the recent development of fisheries steering groups (e.g., ASMFC multispecies committee), the convening of technical workshops (Miller et al. 1996; Houde et al. 1998), publication of the Fisheries Ecosystem Planning document (Chesapeake Bay Fisheries Ecosystem Advisory Panel 2006), and the goals for ecosystem-based fisheries management set by the Chesapeake Bay 2000 (C2K) Agreement. In many respects, it can be argued that the ecosystem-based fisheries mandates inherent to the C2K Agreement constitute the driving force behind this growing awareness. The exact language of the C2K agreement, as it pertains to multispecies fisheries management, reads as follows:

1. By 2004, assess the effects of different population levels of filter feeders such as menhaden, oysters and clams on Bay water quality and habitat.

2. By 2005, develop ecosystem-based multispecies management plans for targeted species.

3. By 2007, revise and implement existing fisheries management plans to incorporate ecological, social and economic considerations, multispecies fisheries management and ecosystem approaches.

If either single-species or ecosystem-based management plans are to be developed, they must be based on sound stock assessments. In the Chesapeake Bay region,

however, the data needed to perform single and multispecies assessments is either partially available or nonexistent.
The Chesapeake Bay Multispecies Monitoring and Assessment Program (ChesMMAP) was developed to assist in filling these data gaps, and ultimately to support bay-specific stock assessment modeling activities at both single and multispecies scales. While no single gear or monitoring program can collect all of the data necessary for both types of assessments, ChesMMAP was designed to maximize the biological and ecological data collected for several recreationally, commercially, and ecologically important species in the bay.

In general, ChesMMAP is a large-mesh bottom trawl survey designed to sample late juvenile-to-adult fishes in Chesapeake Bay. This field program currently provides data on relative abundance, length, weight, age, and trophic interactions for several important fish species seasonally inhabiting the bay. This report summarizes the field, laboratory, and preliminary data.

Among the research agencies in the Chesapeake Bay region, only VIMS has a program focused on multispecies issues involving the adult/harvested components of the exploited fish species that seasonally inhabit the bay. The multispecies research program at VIMS is comprised of three main branches: field data collection (ChesMMAP and the VIMS Seagrass Trammel Net Survey), laboratory processing (The Chesapeake Trophic Interactions Laboratory Services – CTILS, and ChesMMAP), and data analysis and multispecies modeling (The Fisheries Ecosystem Modeling and Assessment Program - FEMAP). In this report, we summarize the field, laboratory, and data analysis activities associated with the 2006 sampling year.

The following Jobs are addressed in this report:

- Job 1 – Conduct research cruises
- Job 2 – Synthesize data for single species analyses
- Job 3 – Quantify trophic interactions for multispecies analyses
- Job 4 – Estimate abundance

Methods

Job 1 – *Conduct research cruises*

In 2006, five research cruises were conducted bimonthly from March to November in the mainstem of Chesapeake Bay. The timing of the cruises was chosen to adequately characterize the seasonal abundances of fishes in the bay. The R/V Bay Eagle, a 19.8m aluminum hull, twin diesel vessel owned and operated by VIMS, served as the sampling platform for this survey. The trawl net is a 13.7m (headrope length) 4-seam balloon trawl manufactured by Reidar's Manufacturing Inc. of New Bedford, MA. The wings and body of the net are constructed of #21 cotton twine (15.2cm mesh), and the codend is constructed of #48 twine (7.6cm mesh). The legs of the net are 6.1m and connected directly to 1.3m x 0.8m steel-V trawl doors weighing 83.9kg each. The trawl net is deployed with a single-warp system using 9.5mm steel cable with a 37.6m bridle constructed of 7.9mm cable.

For each cruise, the goal was to sample 80 stations distributed in a stratified random design throughout the mainstem of Chesapeake Bay. The Bay was stratified by dividing the mainstem into five regions of 30 latitudinal minutes each (the upper and lower regions being slightly smaller and larger than 30 minutes, respectively). Within each region, three depth strata ranging from 3.0m-9.1m, 9.1m-15.2m, and >15.2m were defined. A grid of 1.9km^2 cells was superimposed over the mainstem, where each cell represented a potential sampling location. The number of stations sampled in each region and in each stratum was proportional to the surface area of water represented. Stations were sampled without replacement and those north of Pooles Island (latitude 39^o 17') have not been sampled since July 2002 due to repeated loss of gear. In the future, sidescan sonar will be used to identify potential sampling locations in this area.

Tows were conducted in the same general direction as the tidal current (pilot tows conducted using the net monitoring gear in November 2001 indicated that the gear performed most consistently when deployed with the current rather than against the current). The net was generally deployed at a 4:1 scope, which refers to the amount of cable deployed relative to depth. For shallow stations, however, the bridle was always deployed beyond the vessel's tow-point, implying that the scope ratio could be quite high. The target tow speed was 6.5 km/h but occasionally varied depending on wind and tidal conditions. Based on data collected from the net monitoring gear, tow speed and scope were also adjusted occasionally to ensure that the gear was deployed properly. Tows were 20 minutes in duration, unless obstructions or other logistical issues forced a tow to be shortened (if the duration of a tow was at least 10 minutes, it was considered complete). Computer software was used to record data from the net monitoring gear (i.e., wingspread and headrope height) as well as a continuous GPS stream during each tow. On occasions when the monitoring gear failed, the trawl geometry was assumed to follow cruise averages and beginning and ending coordinates were taken from the vessel's GPS system.

Job 2 – *Synthesize data for single species analyses*

Once onboard, the catch from each tow is sorted and measured by species or size-class if distinct classes within a particular species are evident. A subsample of each species or size-class is further processed for weight determination, stomach contents, ageing, and determination of sex and maturity stage. In addition, surface and bottom temperature, salinity, and dissolved oxygen readings are also recorded at each sampling location.

Single-species assessment models typically require information on (among others) age-length-, and weight-structure, sex ratio, and maturity stage. Data were synthesized to characterize age-, length-, and weight-frequency distributions across a variety of spatial and temporal scales (e.g., by year, season, or region of the bay) for each species. Sex ratio and maturity data are also be available to support sex-specific analyses.

Job 3 – *Quantify trophic interactions for multispecies analyses*

In addition to the population-level information described under Task 3, multispecies assessment models require information on predator-prey interactions across broad seasonal and spatial scales. In general, these procedures involve identifying each prey item to the lowest possible taxonomic level (Hyslop 1980). Several diet indices were calculated to identify the main prey types for each species: %weight, %number, and %frequency-of-occurrence. These indices were coupled with the information generated from Task 3 and age-, length-, and sex-specific diet characterizations were developed for each species. Efforts also focused on characterizing spatial and temporal variability in these diets.

Diet index values were calculated to identify the main prey in the diet of predators in the mainstem Chesapeake Bay. Since trawl collections essentially yield a cluster of fish at each sampling location, the aforementioned indices were calculated using a cluster sampling estimator (Buckel et al. 1999).

The contribution of each prey type to the diet ($\%Q_k$, where Q_k is any of the aforementioned index types) is given by:

$$\%Q_k = \frac{\sum_{i=1}^{n} M_i q_{ik}}{\sum_{i=1}^{n} M_i} \quad , \qquad (1)$$

where

$$q_{ik} = \frac{w_{ik}}{w_i} * 100 \, ,$$

and where n is the number of trawls containing the predator of interest, M_i is the number of that predator collected at sampling site i, w_i is the total weight, number, or frequency of all prey items encountered in the stomachs of that predator collected from sampling location i, and w_{ik} is the total weight, number, or frequency of prey type k in those stomachs. Accordingly, stomachs collected in the field were processed following standard diet analysis procedures (Hyslop 1980).

Job 4 – *Estimate abundance*

Time-series of relative abundance information can easily be generated from the basic catch data of a monitoring survey. For each species, a variety of relative abundance trends can be generated according to year, season, and location within the Bay. Absolute abundance estimates can be generated for each species by combining relative abundance data with area swept and gear efficiency information. Area swept was calculated for each tow by multiplying tow distance (provided by GPS equipment) by average wingspread (provided by net monitoring gear). Gear efficiency estimates are being derived by comparing the number of fish that encounter the gear (from the hydroacoustic data) with the fraction captured (from the catch data). To develop species-specific efficiency estimates, the hydroacoustic data will be partitioned according to the target strength distribution for each species. These distributions will be determined through ongoing cage experiments.

ChesMMAP utilizes two types of hydroacoustic gear in an effort to convert relative indices of abundance into estimates of total abundance. The equation necessary for this conversion is:

$$N=\frac{cA}{\frac{a}{e}}, \qquad (1)$$

where N is total population size measured in numbers (or biomass), c is the mean number (or weight) of fish captured per tow, a is the area swept by one trawl tow, A is the total survey area, and e is the net efficiency (dimensionless). Given that c is observed and A is easily determined, the hydroacoustic equipment is used to derive estimates of a and e. Estimation of the parameter e for a variety of species is a mid-to-long term goal. Until then, removal of that parameter from Equation 1 results in relative estimates of ‘minimum trawlable abundance.’ These estimates represent the smallest number (or biomass) of fish present within the sampling area that are susceptible to the sampling gear.

Results

Job 1 – *Conduct Research Cruises*

Throughout the five years of sampling, the number of fish collected each year by the ChesMMAP survey was fairly consistent and ranged from approximately 31,000 (in 2003) to 48,000 (in 2004 – Table 1). Each year, between 3,900 and 6,000 pairs of otoliths have been collected, the majority of which have been processed for age determination. Similar numbers of stomach have been collected and processed for diet composition information annually.

Table 1. The number of specimens collected, measured and processed for age determination and diet composition information from ChesMMAP 2002 – 2006.

Year	Fish collected	Fish measured	Otoliths collected	Otoliths processed	Stomachs collected	Stomachs processed
2002	32,018	23,605	5,487	4,382	4,555	2,638
2003	30,925	20,828	3,913	2,934	3,250	2,220
2004	47,623	31,245	5,169	3,431	4,271	3,137
2005	45,206	36,906	6,064	4,694	5,064	3,170
2006	43,959	31,239	5,412	In process	4,391	2,640

Jobs 2-4 – *Data Summaries*

The data summaries in this report essentially represent biological and ecological profiles of those species well sampled by the ChesMMAP survey. Our intent with these profiles is to maximize the amount of information available to fishery managers. The profiles that follow are organized first by species and then by type of analysis ('Task'). Each Task element (single-species stock parameter summarizations, trophic interaction summaries, and estimates of abundance) is included but is not labeled with a Task number and is not necessarily shown in Task number order (note also that not all analysis types are available for all species).

The species profiles contain the following information (note that some data/analyses may not be available for all species):

1) estimates of abundance, both in numbers and biomass, by year, month, and region within the bay
2) site-specific abundance maps (number per area swept) for each cruise, overlaid on depth strata
3) length-frequency data by year
4) age-class distributions by year (for those species where appreciable numbers have been captured and otoliths have been processed)
5) sex-ratio by year and where appropriate, by region, month, and/or by age.
6) statistically determined length-weight relationships for sexes combined and separately
7) sex-specific maturity ogives along with a single diet summary

Following the species profiles figures are a series of figures for each cruise containing data describing the following water quality parameters:

1) Water temperature at the surface and at the bottom.
2) Salinity at the surface and at the bottom.
3) Dissolved oxygen at the surface and at the bottom.

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<u>*Summer Flounder*</u> (pages 109 – 119)

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White Perch (pages 133 – 143)

Water Temperature (pages 144 – 153)

Salinity (pages 154 – 163)

Dissolved Oxygen (pages 164 – 173)

Additional Work Performed – *Serve as sampling platform for bay studies*

Since its inception, ChesMMAP has strived to be not just a state-of-the-art monitoring survey, but equally, a research platform from which numerous projects can benefit. We have participated in fish disease, tagging, and habitat related studies that otherwise either could not have been conducted, or would have had very substantially increased costs. For example, since 2003 ChesMMAP personnel have been collecting additional samples from striped bass to support a mycobacteriosis prevalence study conducted by scientists in the Fisheries and Environmental and Aquatic Animal Health (EAAH) Departments at VIMS. Specifically, spleen samples from these striped bass were analyzed histologically for the presence of granulomas, which are evident in diseased fish. The apparent prevalence data set derived from these samples is the most comprehensive apparent prevalence data set collected for striped bass in the bay. Subsequent modeling of those prevalence data has shown 1) the force-of-infection (rate of which disease-negative fish become disease positive) is age-dependent, 2) covariates sex and season are significant explanatory variables, and 3) that there is appreciable disease-associated mortality.

In 2006, ChesMMAP personnel collected 536 striped bass tissue samples to support a trophic ecology project led by members of the Center for Quantitative Fisheries Ecology (CQFE) at Old Dominion University. Stable isotope analysis is being used to investigate the trophic interactions and position of striped bass; ultimately these data will be compared to data from traditional stomach content analysis to provide a more comprehensive description of the predatory impacts of striped bass.

The costs associated with conducting both the disease monitoring and stable isotope studies in the absence of a sampling platform such as the ChesMMAP trawl survey would likely have been prohibitive.

In addition to the aforementioned striped bass projects, ChesMMAP also supported the Environmental Protection Agency's National Coastal Assessment (NCA) program by sampling 11 additional sites during the September 2006 survey. At each of these stations, up to 10 specimens of each of a number of species of interest were sacrificed for chemical and pathological analysis. Overall, 96 specimens were taken for this effort. Again, by contracting the ChesMMAP survey to conduct this relatively small amount of sampling, the cost of obtaining the resulting information was reduced substantially. And finally, ChesMMAP's sampling efforts supported four master's theses and a doctoral dissertation in 2006.

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Figure 1. Atlantic croaker minimum trawlable abundance estimates in numbers (A) and biomass (B) in Chesapeake Bay 2002-2006.

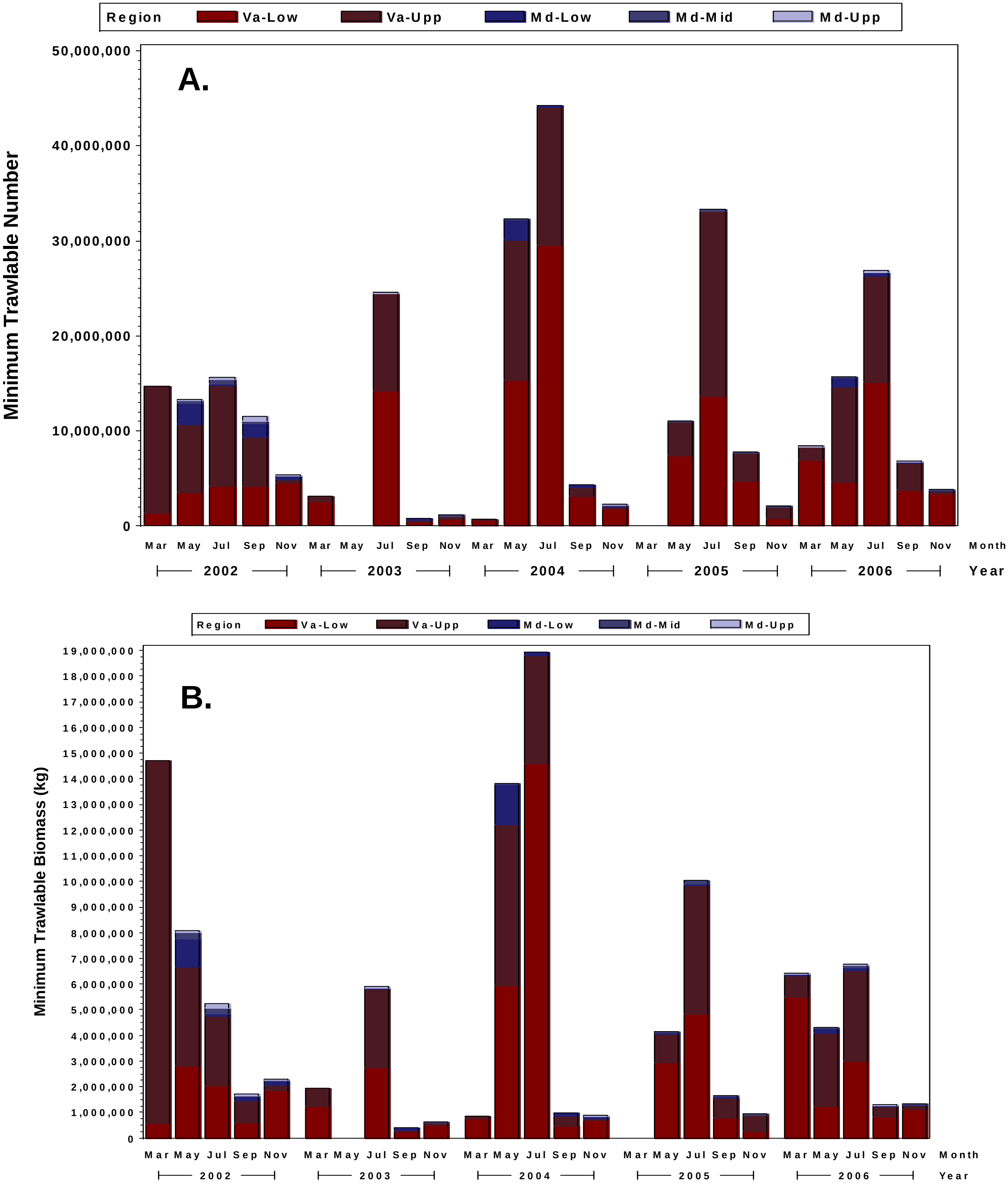


Figure 2. Abundance (number per hectare swept) of Atlantic croaker in Chesapeake Bay, 2002.

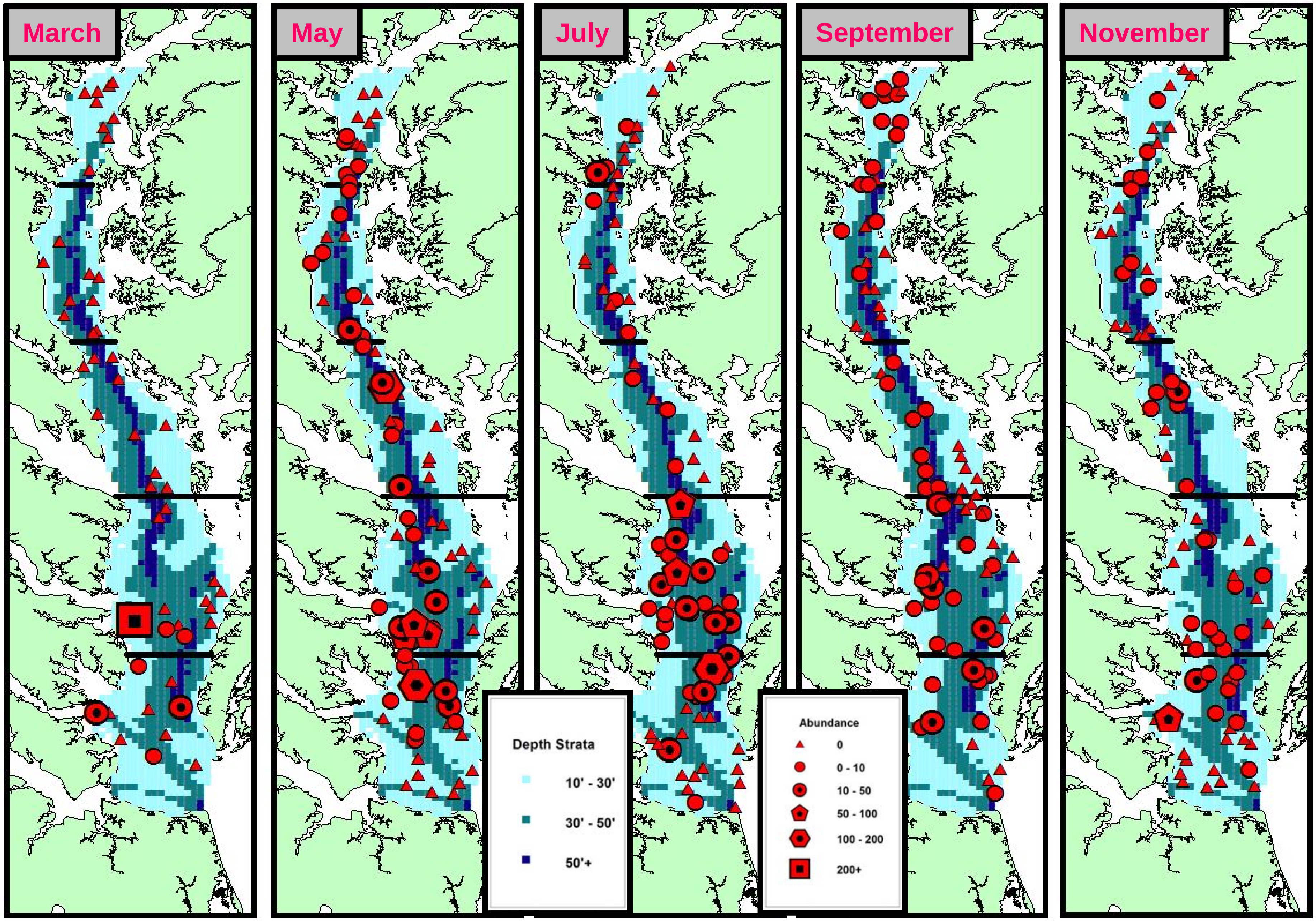


Figure 3. Abundance (number per hectare swept) of Atlantic croaker in Chesapeake Bay, 2003.

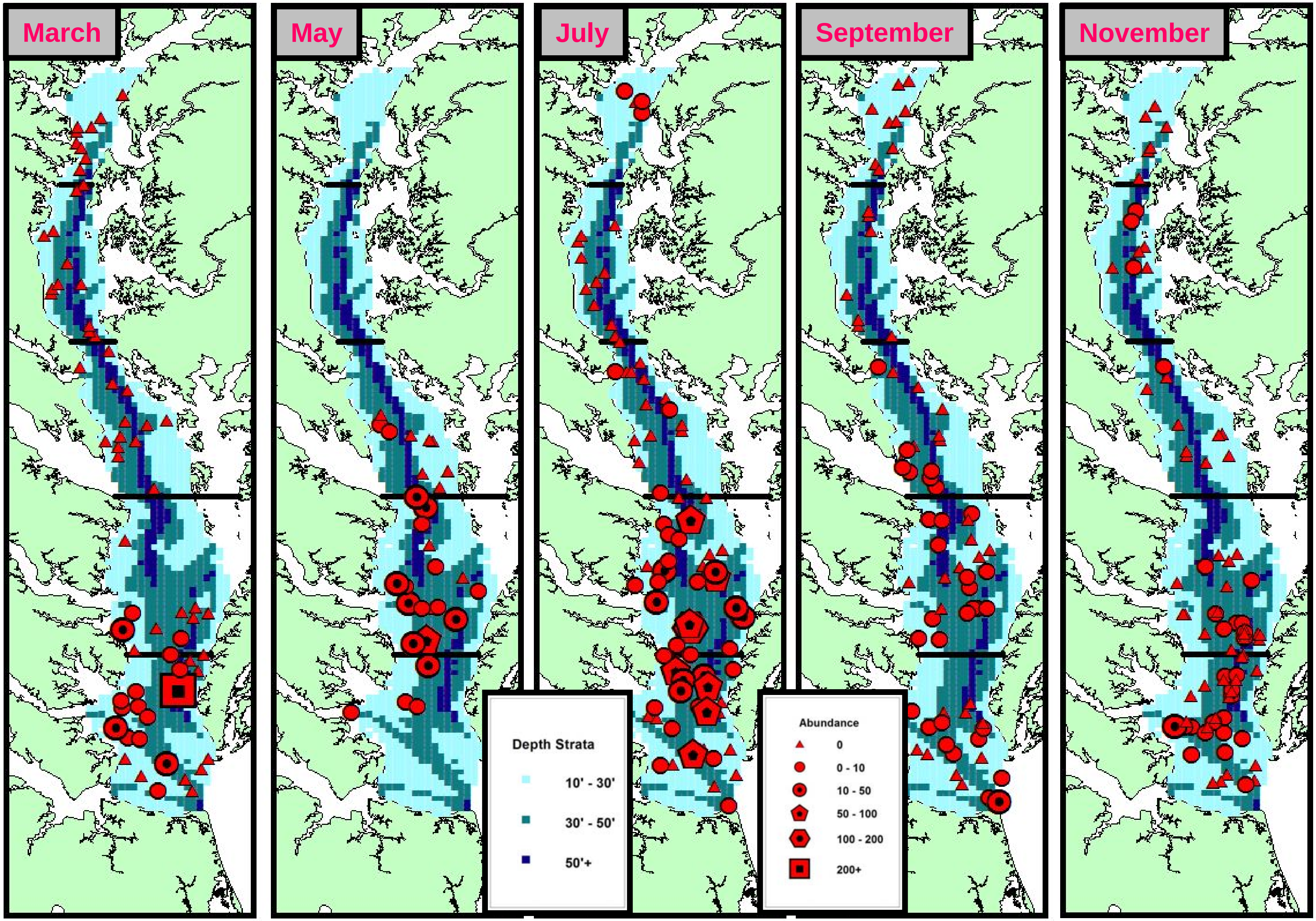


Figure 4. Abundance (number per hectare swept) of Atlantic croaker in Chesapeake Bay, 2004.

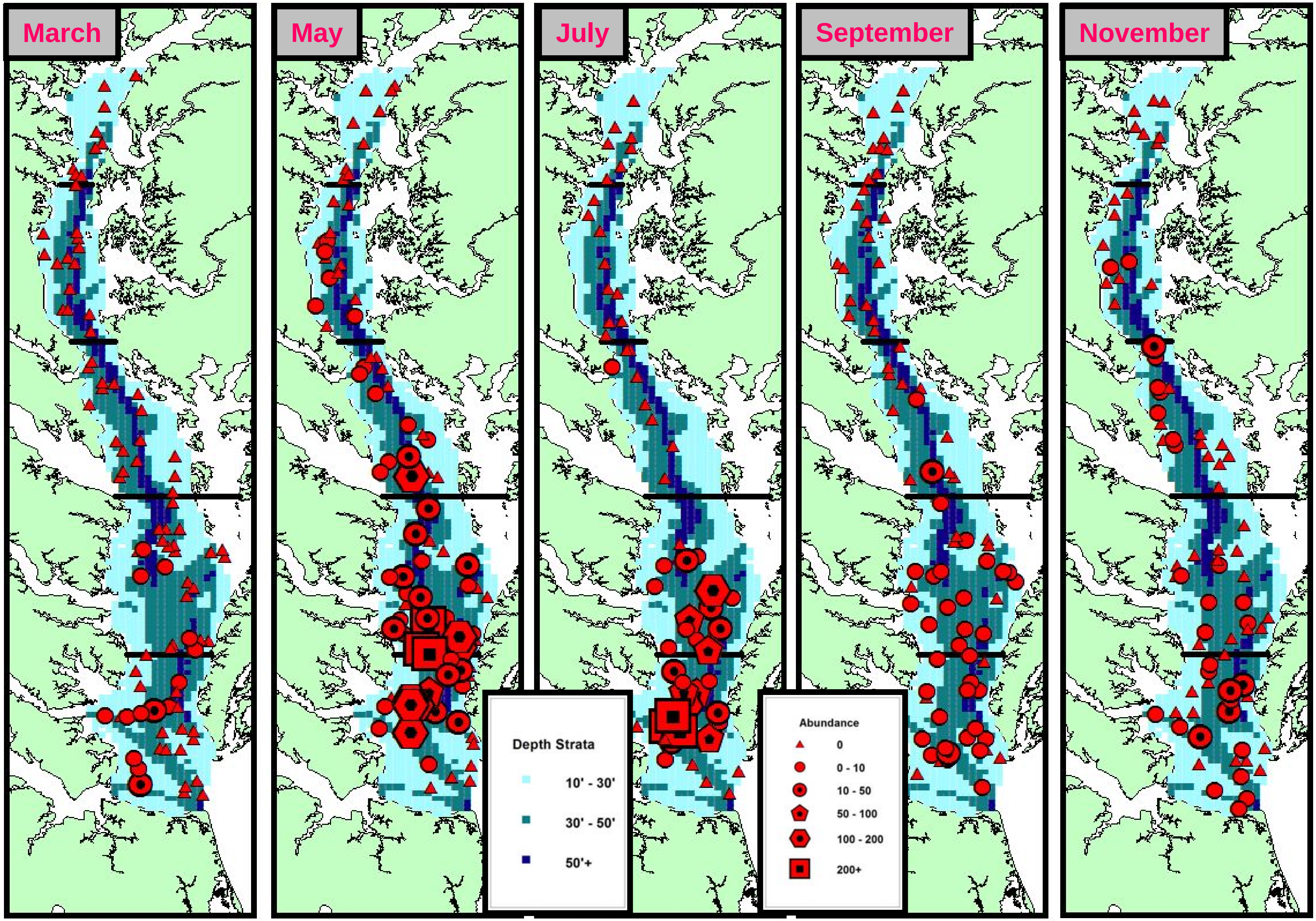


Figure 5. Abundance (number per hectare swept) of Atlantic croaker in Chesapeake Bay, 2005.

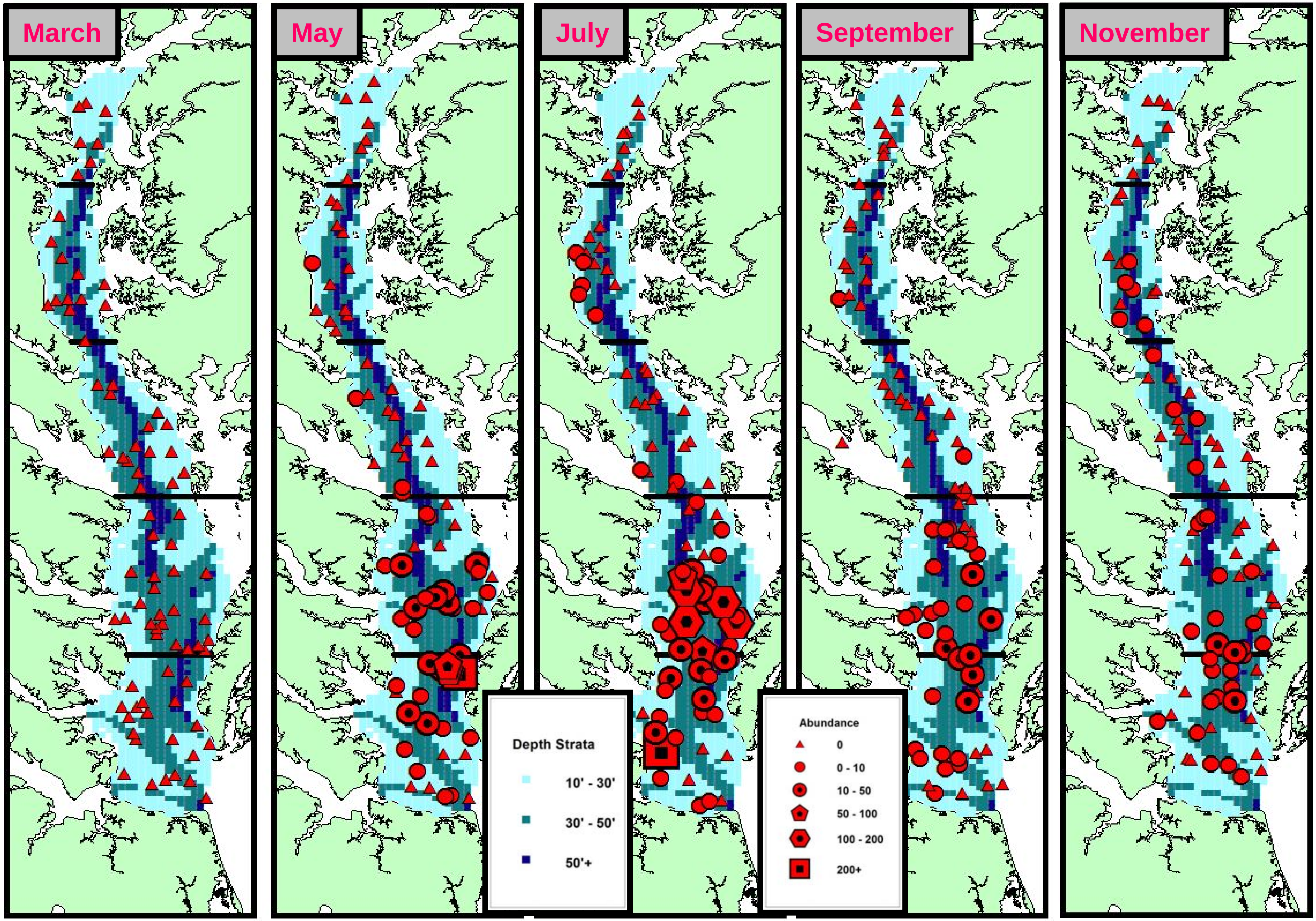


Figure 6. Abundance (number per hectare swept) of Atlantic croaker in Chesapeake Bay, 2006.

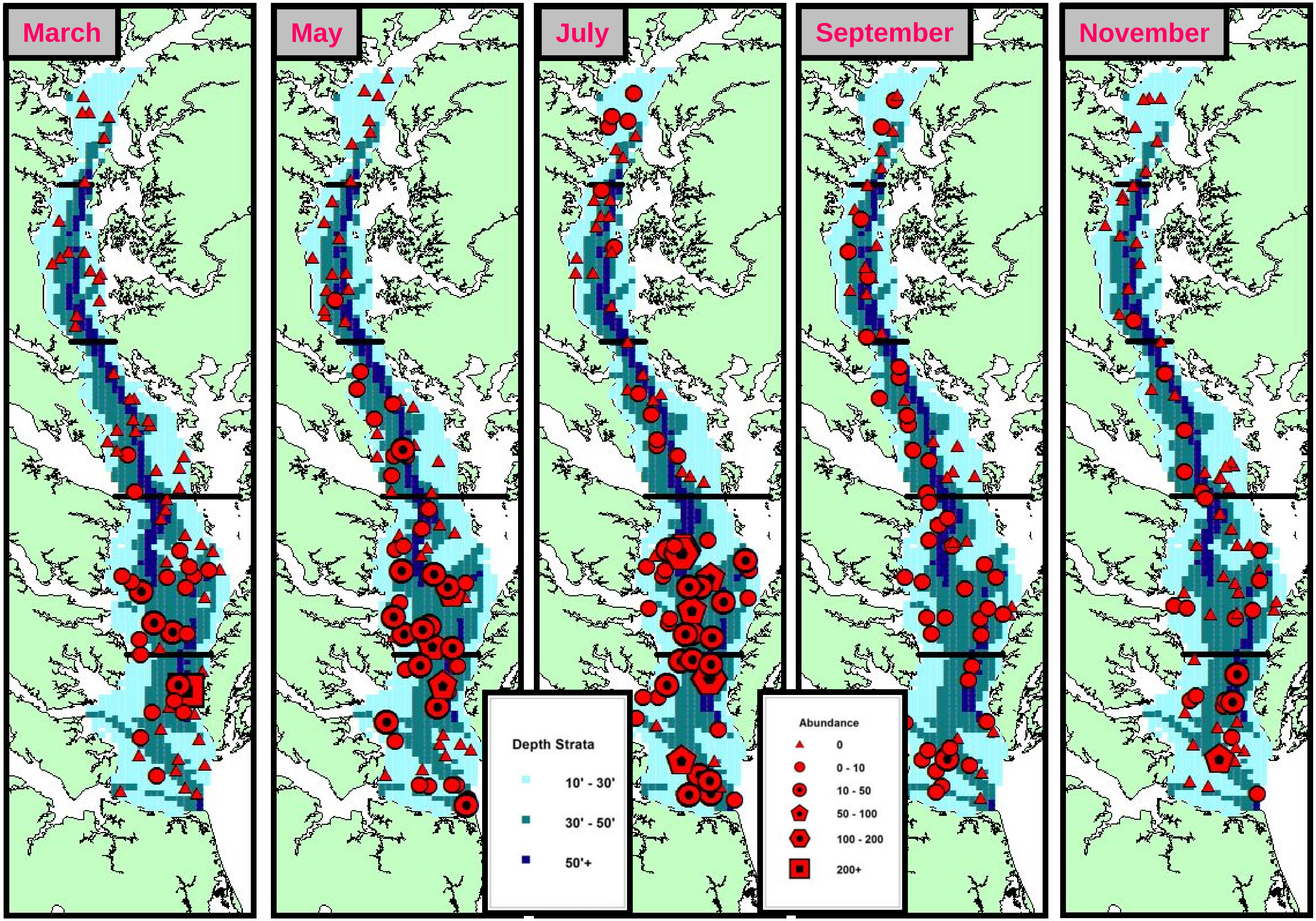


Figure 7. Atlantic croaker length-frequency in Chesapeake Bay 2002-2006.

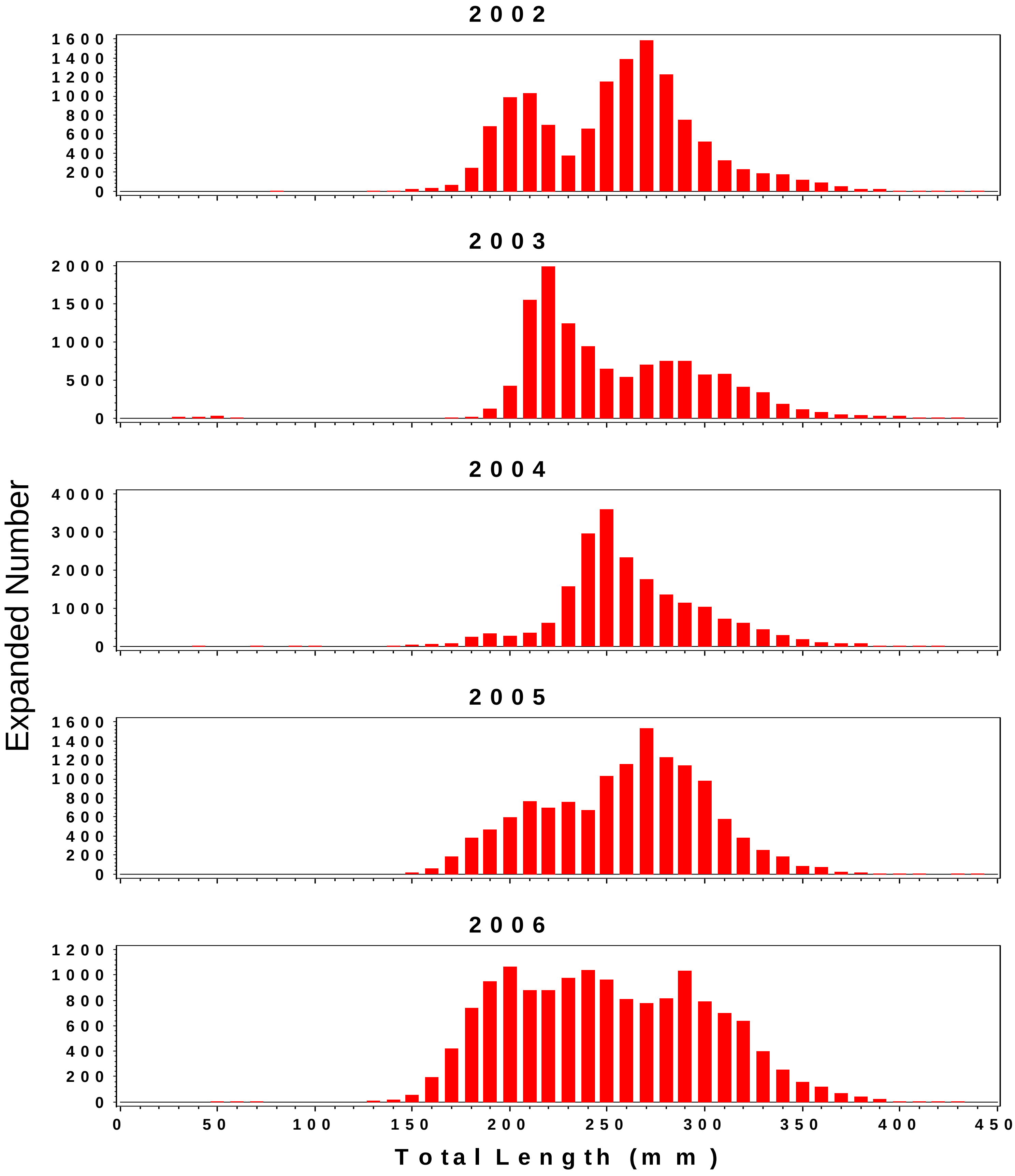
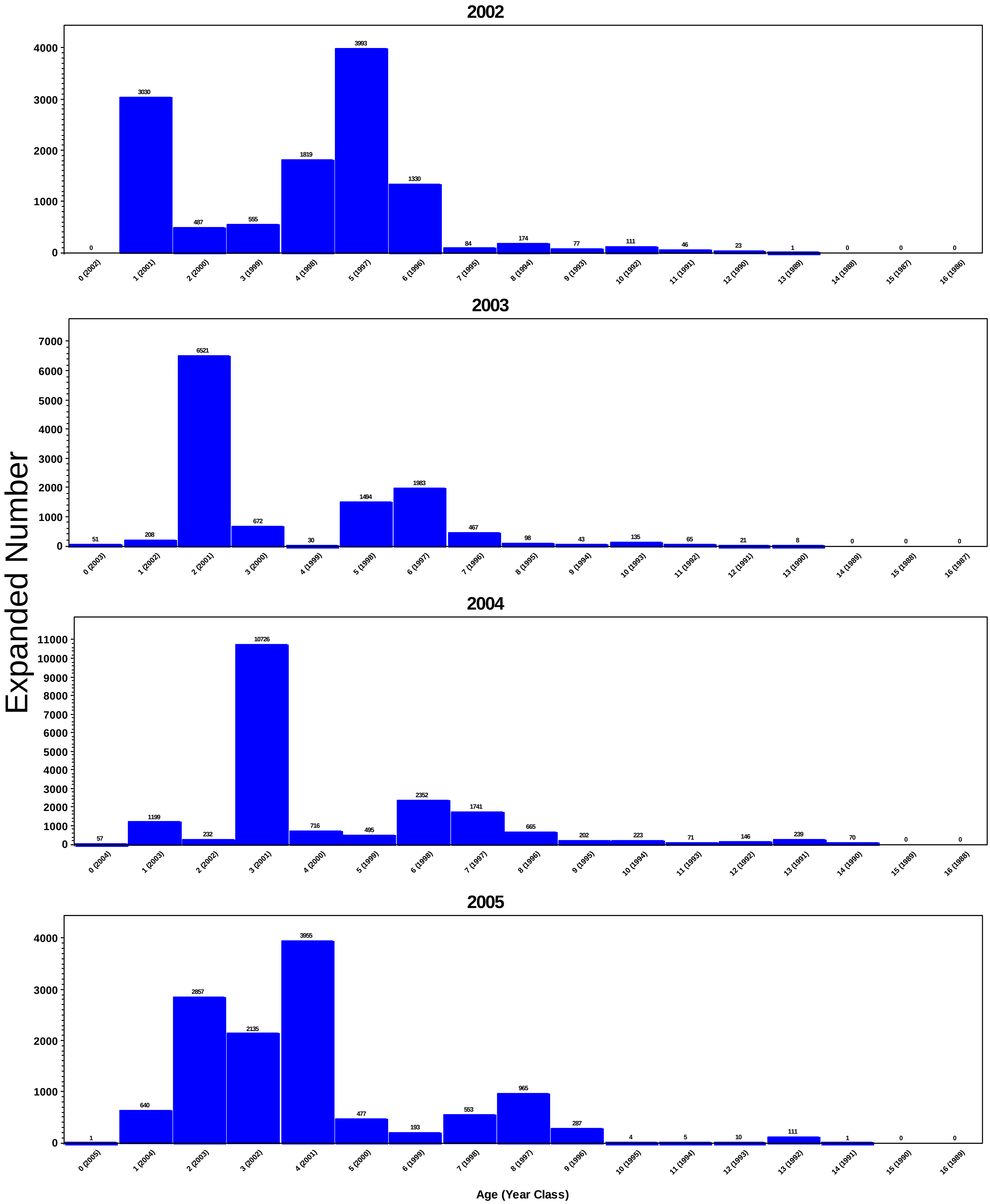


Figure 8. Atlantic croaker age-structure in Chesapeake Bay 2002-2005 (2006 ages not yet assigned).



2002

2003

2004

2005

Figure 9. Atlantic croaker sex-ratios in Chesapeake Bay 2002-2006, by region (A), age (B).

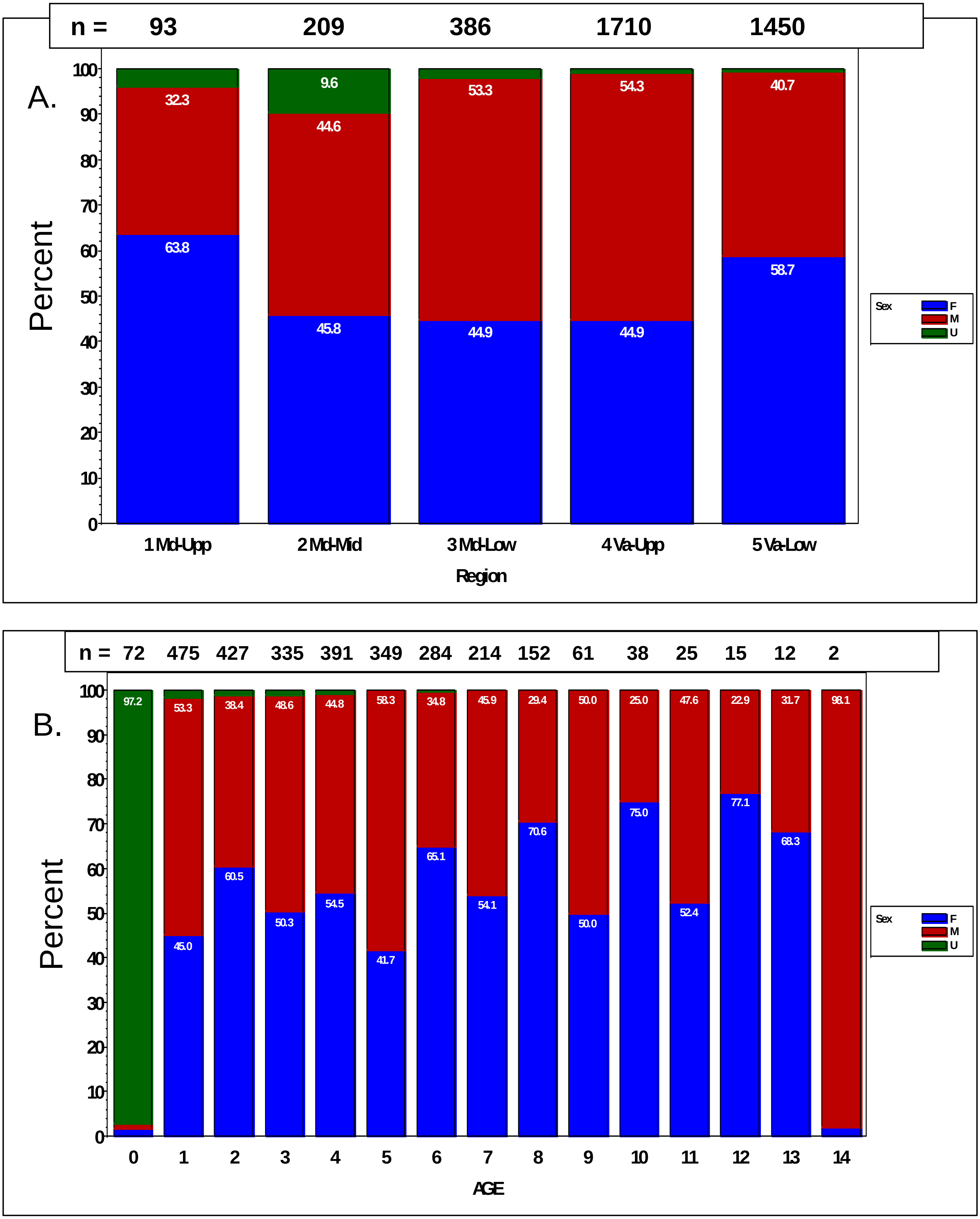


Figure 10. Atlantic croaker length-weight relationships in Chesapeake Bay 2002-2006 as calculated by power regression for sexes combined (A) and separately (B).

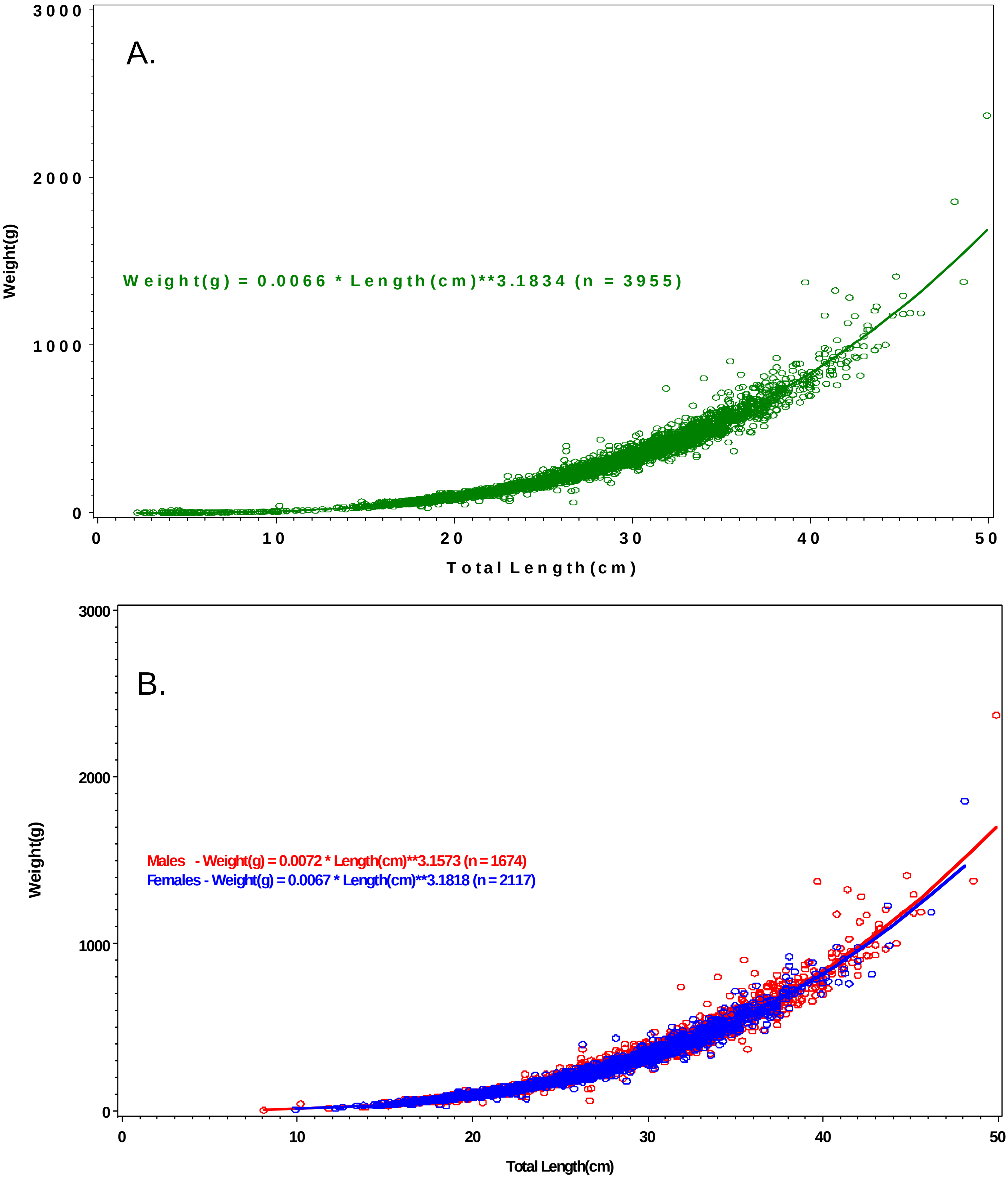


Figure 11. Atlantic croaker maturity schedule in Chesapeake Bay 2002-2006 combined, by sex.

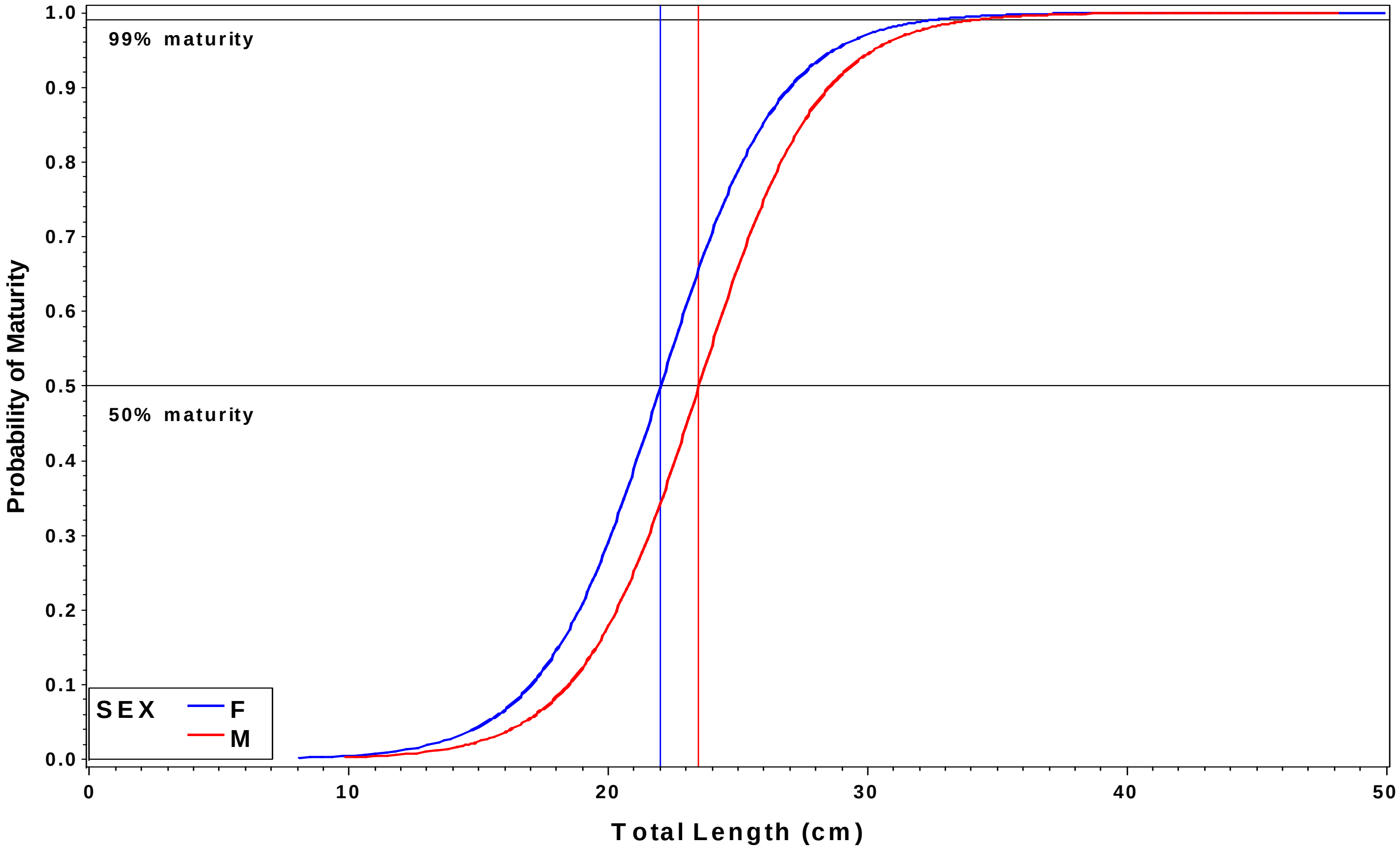
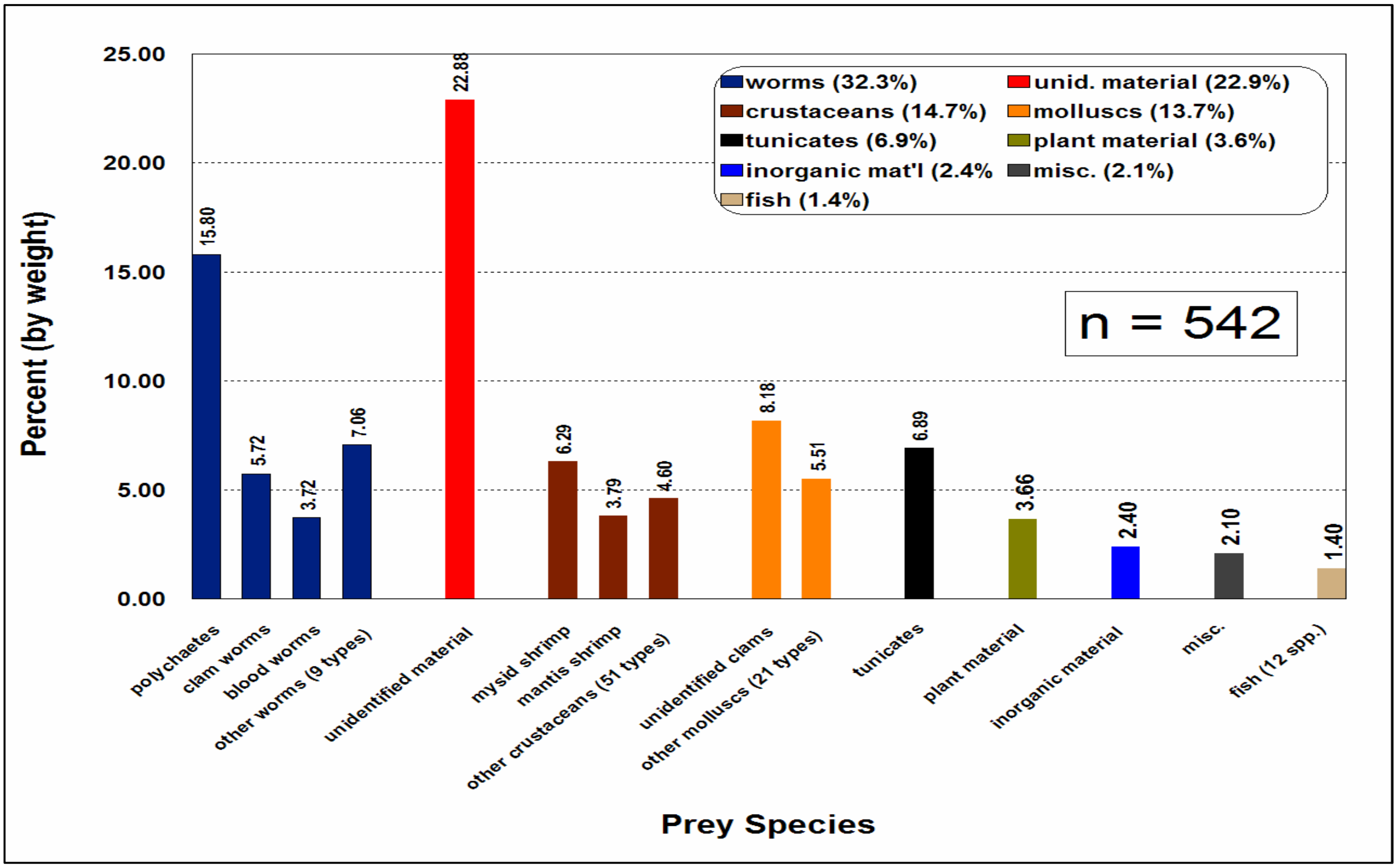
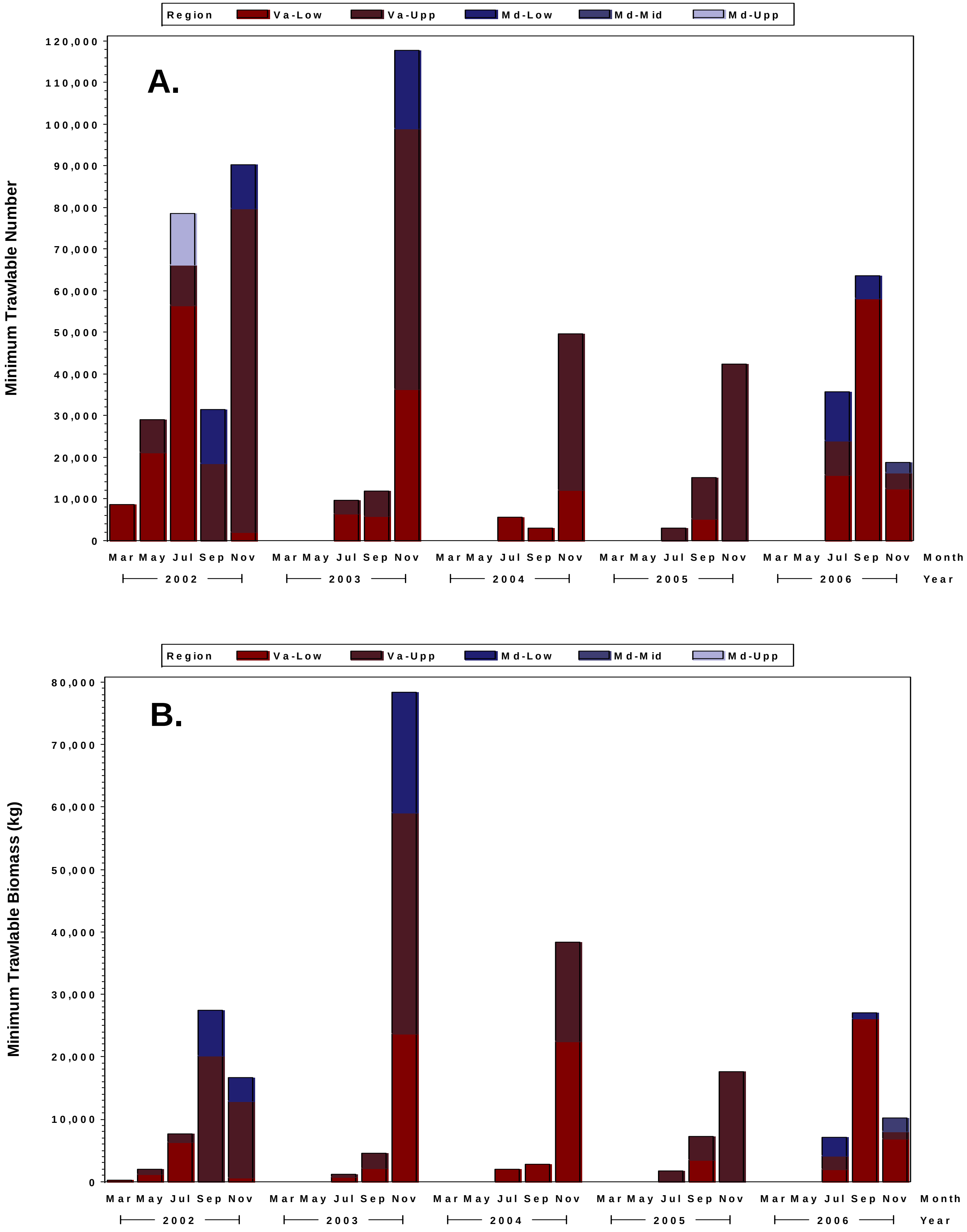


Figure 12. Atlantic croaker diet in Chesapeake Bay 2002-2006 combined*.



*All samples not analyzed.

Figure 13. Black seabass minimum trawlable abundance estimates in numbers (A) and biomass (B) in Chesapeake Bay 2002-2006 (Note: abundance estimates for this species not considered reliable).



Note: This species is not captured in enough abundance to create meaningful abundance maps.

Figure 14. Black seabass length-frequency in Chesapeake Bay 2002-2006.

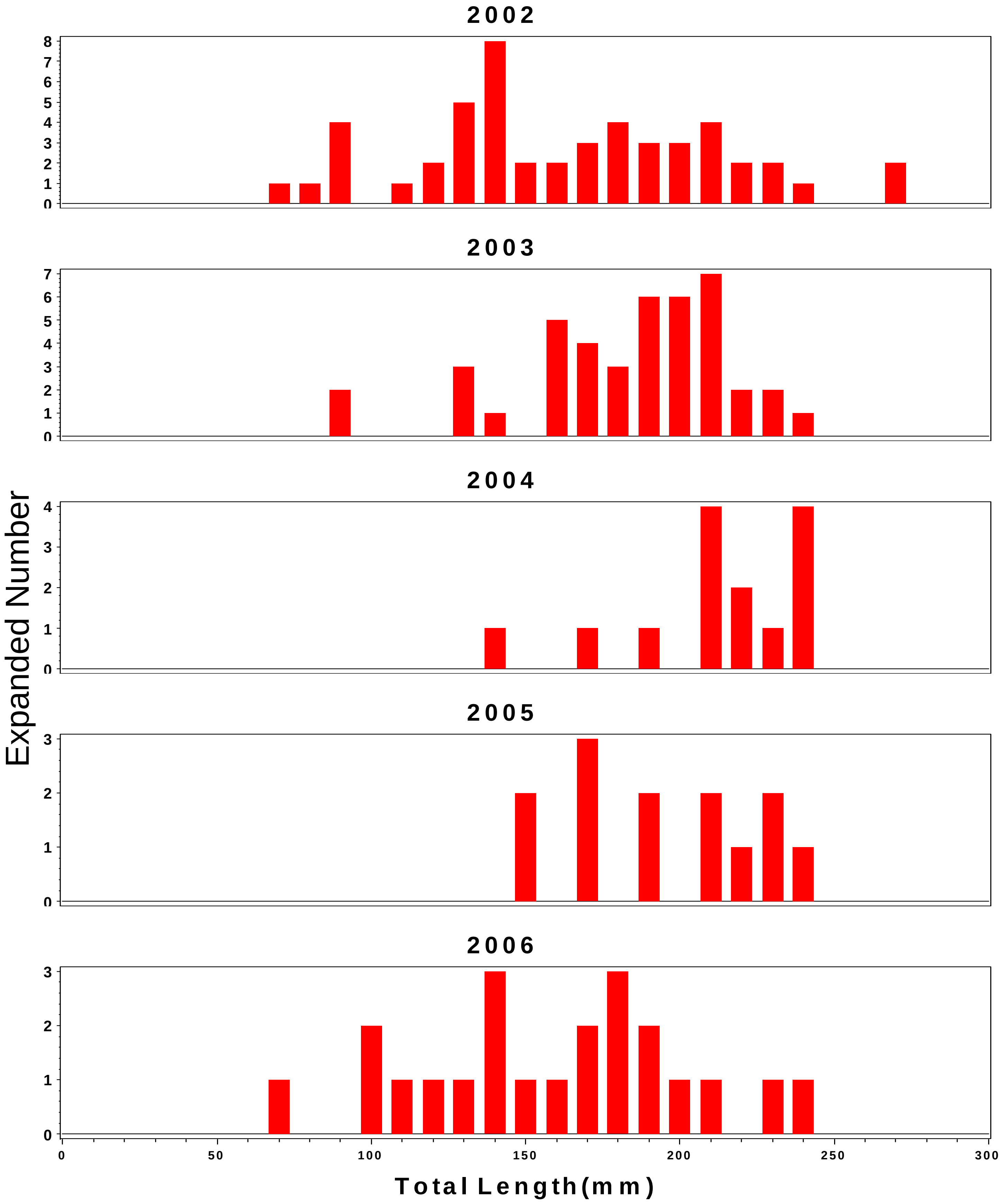


Figure 15. Black seabass age-structure in Chesapeake Bay 2002-2003 (2004-2006 ages not yet assigned).

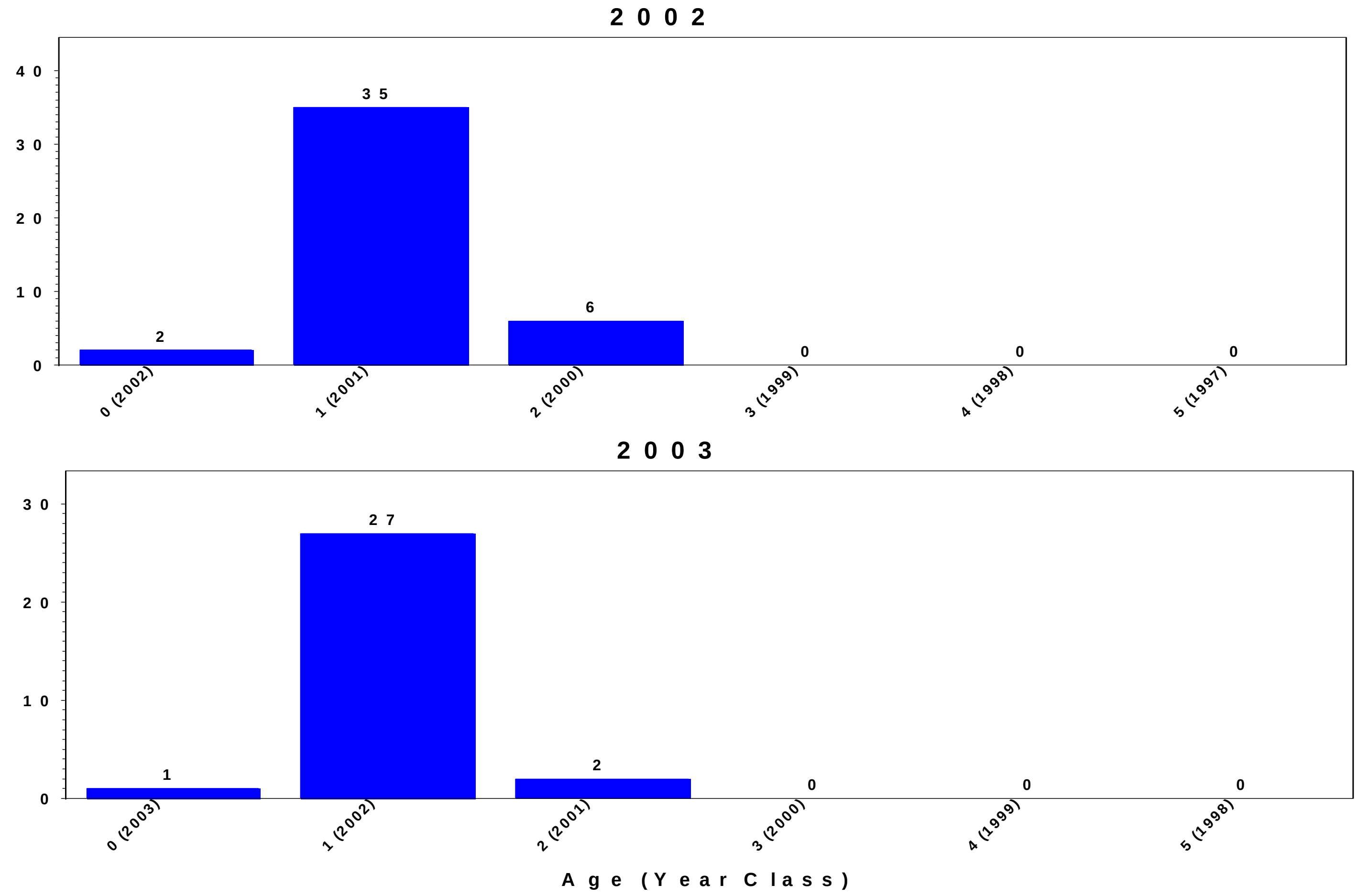


Figure 16. Black seabass sex-ratios in Chesapeake Bay 2002-2006, by year (A), month (B).

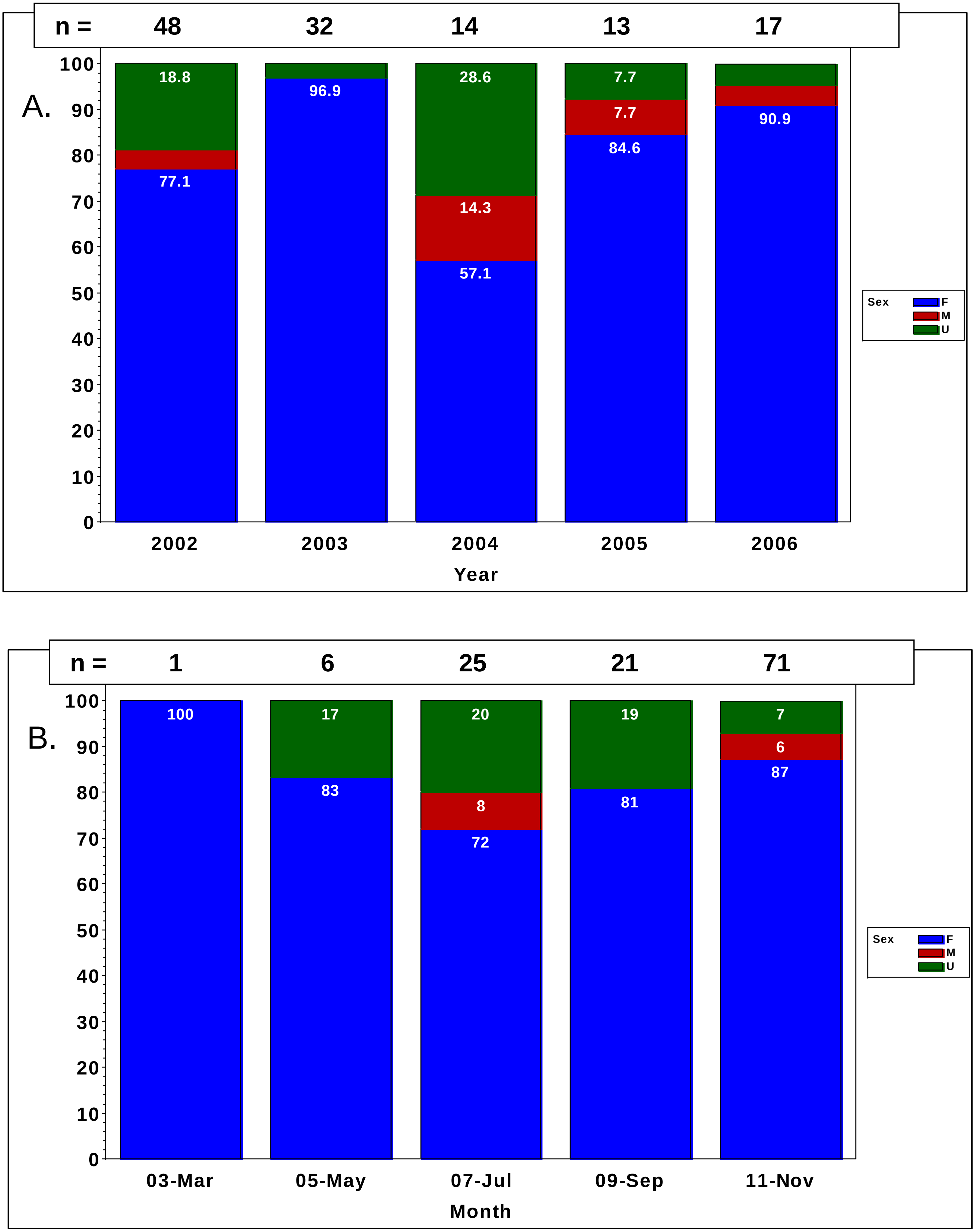
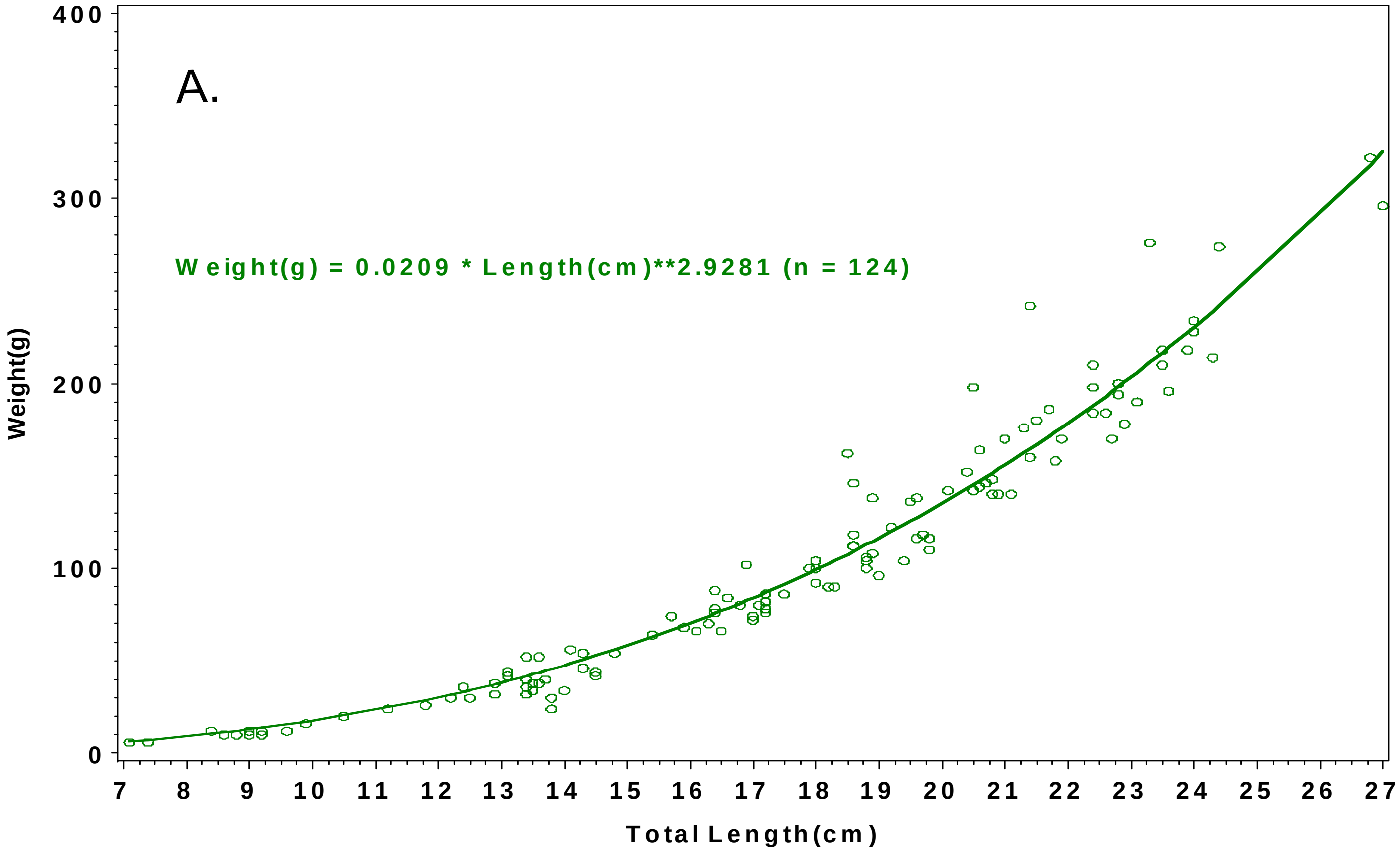


Figure 17. Black seabass length-weight relationships in Chesapeake Bay 2002-2006 as calculated by power regression for sexes combined (A) and separately (B).



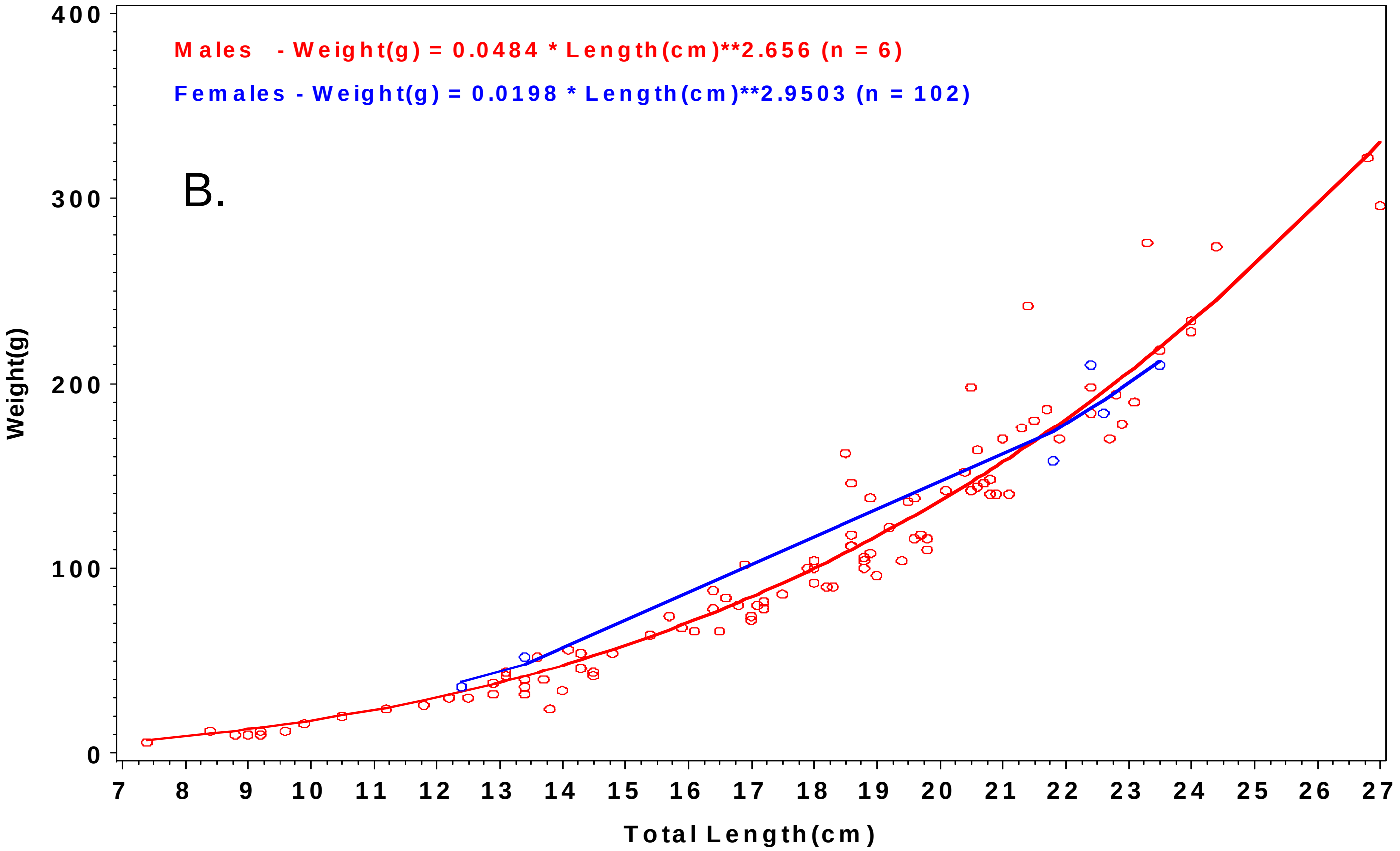


Figure 18. Black seabass maturity schedule in Chesapeake Bay 2002-2006 combined (females only).

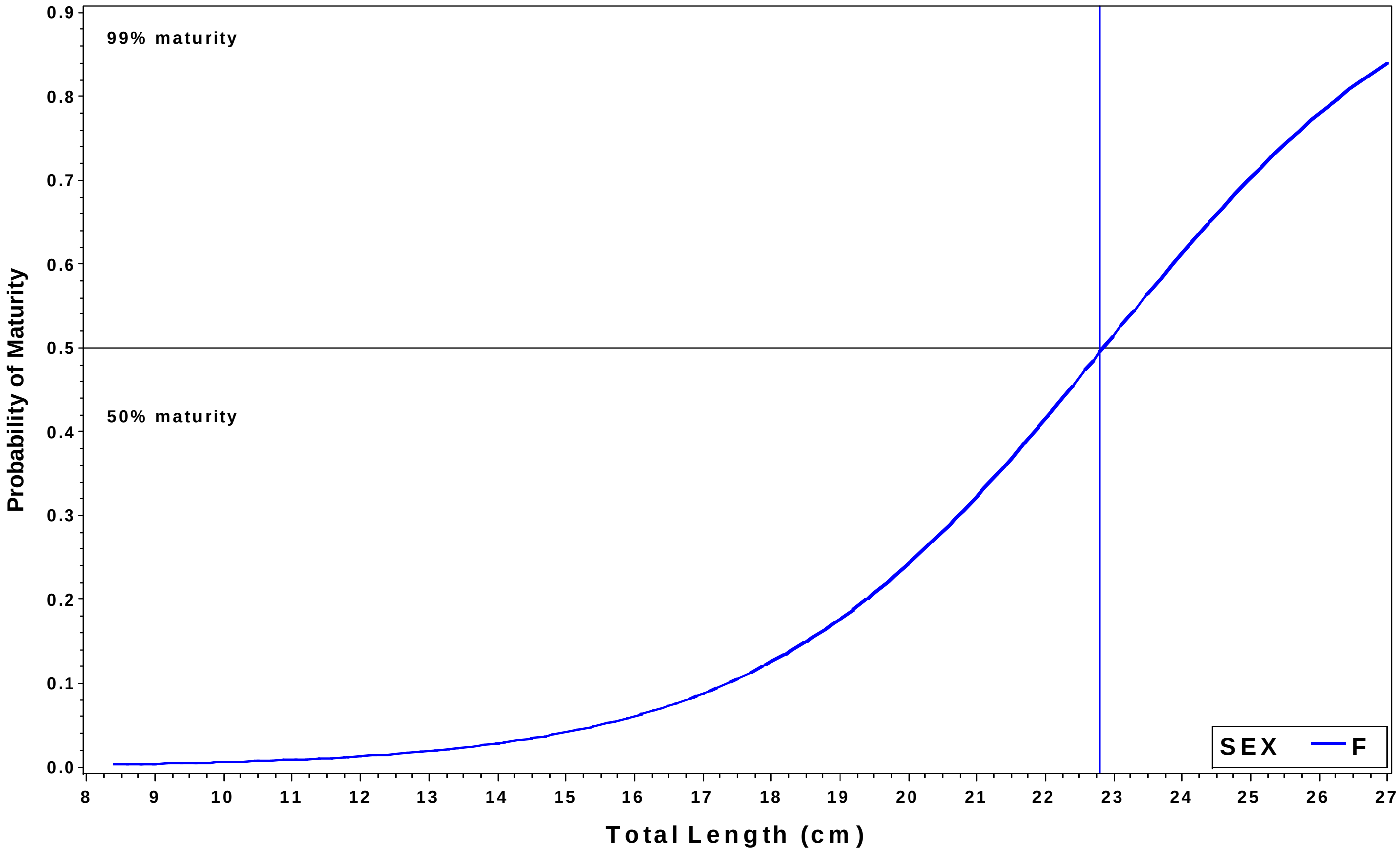


Figure 19. Black seabass diet in Chesapeake Bay 2002-2006 combined.

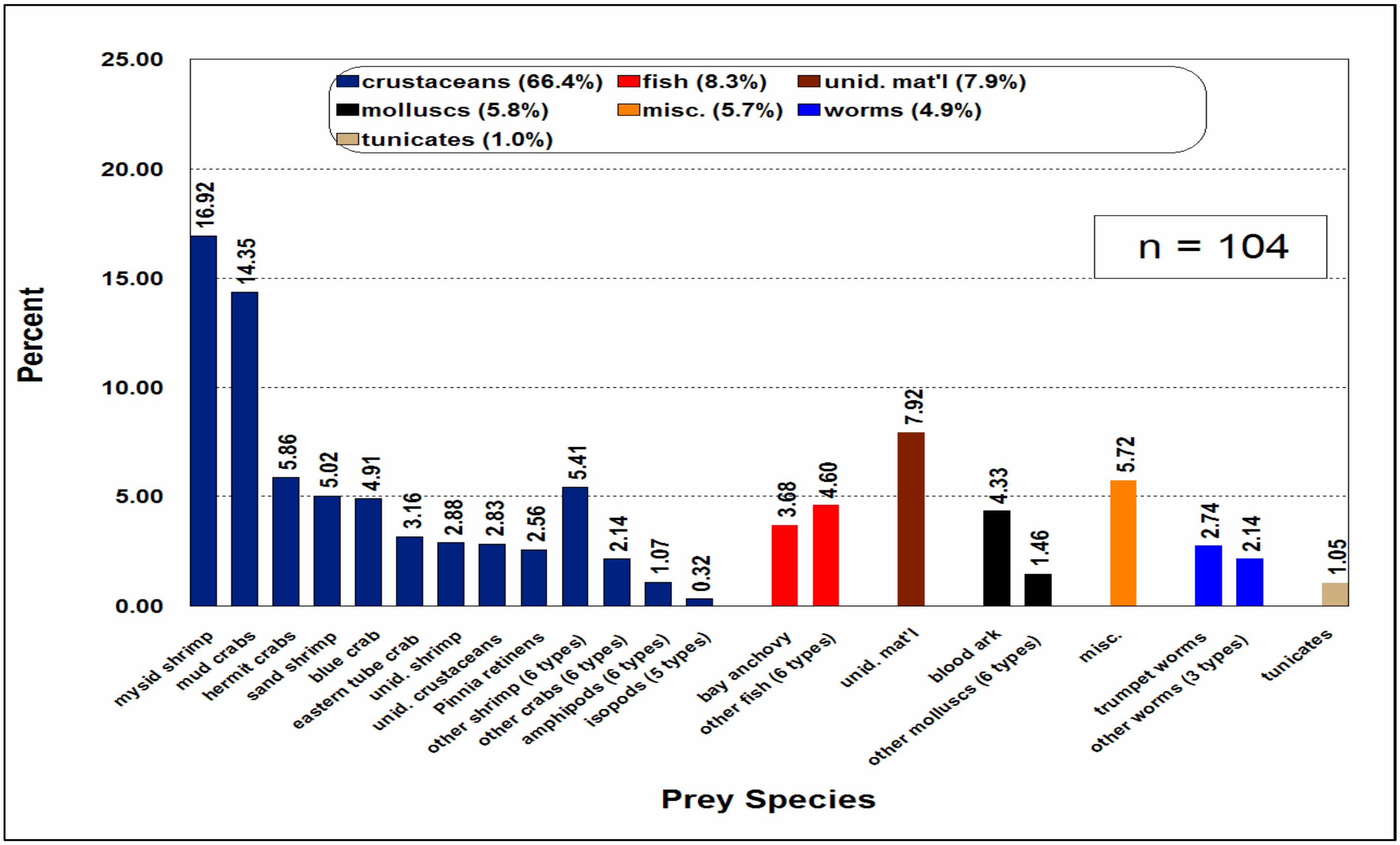


Figure 20. Bluefish minimum trawlable abundance estimates in numbers (A) and biomass (B) in Chesapeake Bay 2002-2006 (Note: abundance estimates for this species not considered reliable).

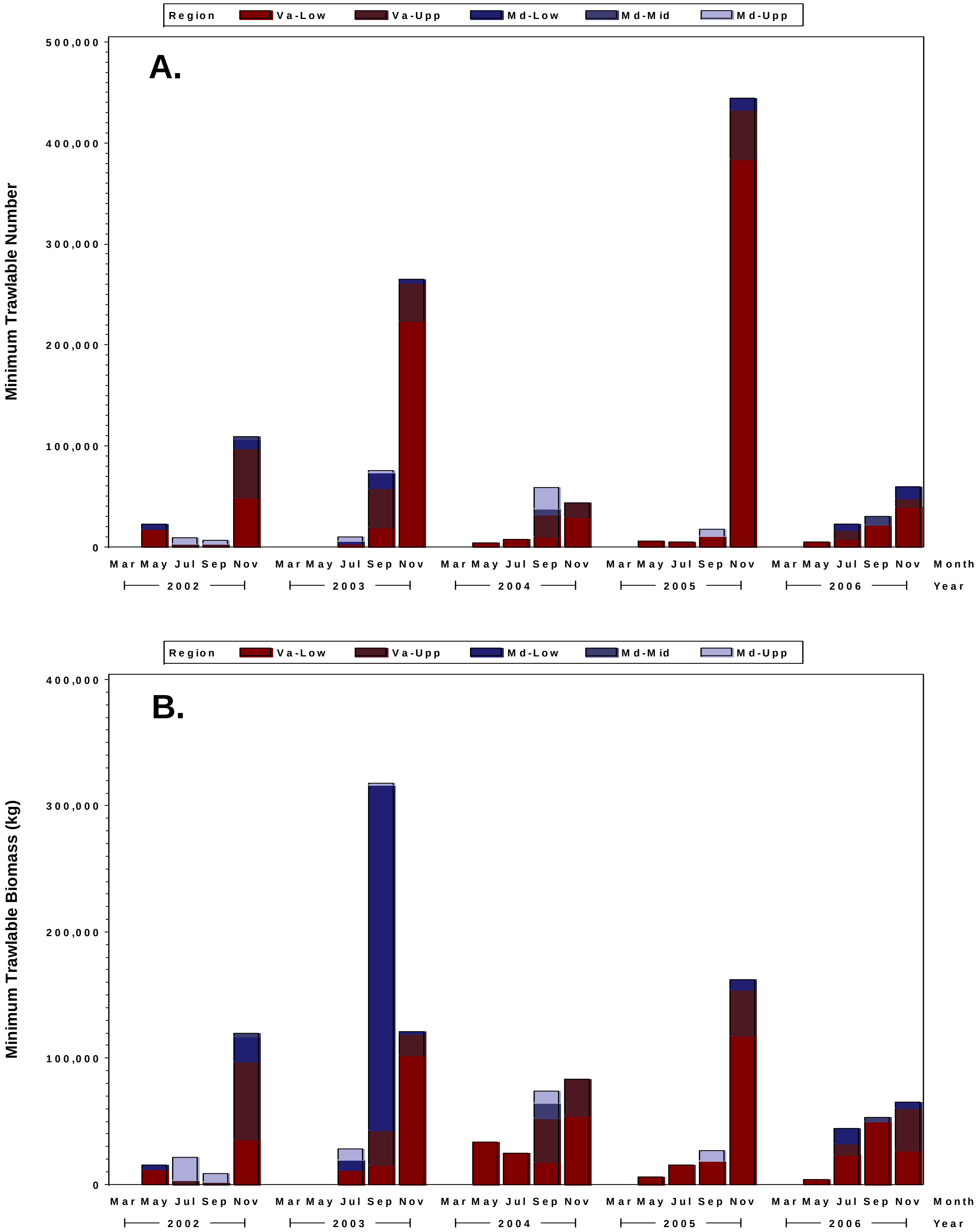


Figure 21. Abundance (number per hectare swept) of bluefish in Chesapeake Bay, 2002.

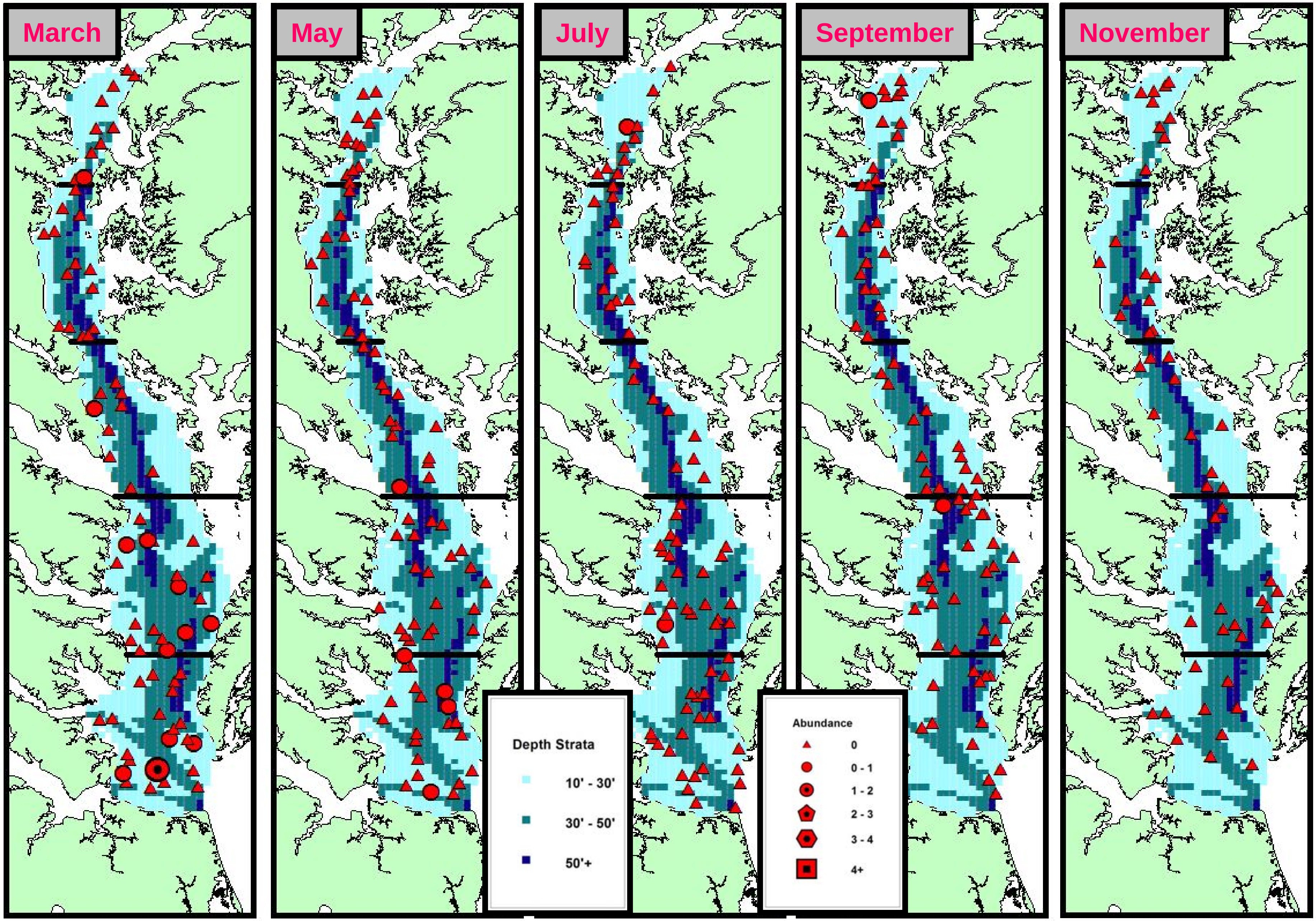


Figure 22. Abundance (number per hectare swept) of bluefish in Chesapeake Bay, 2003.

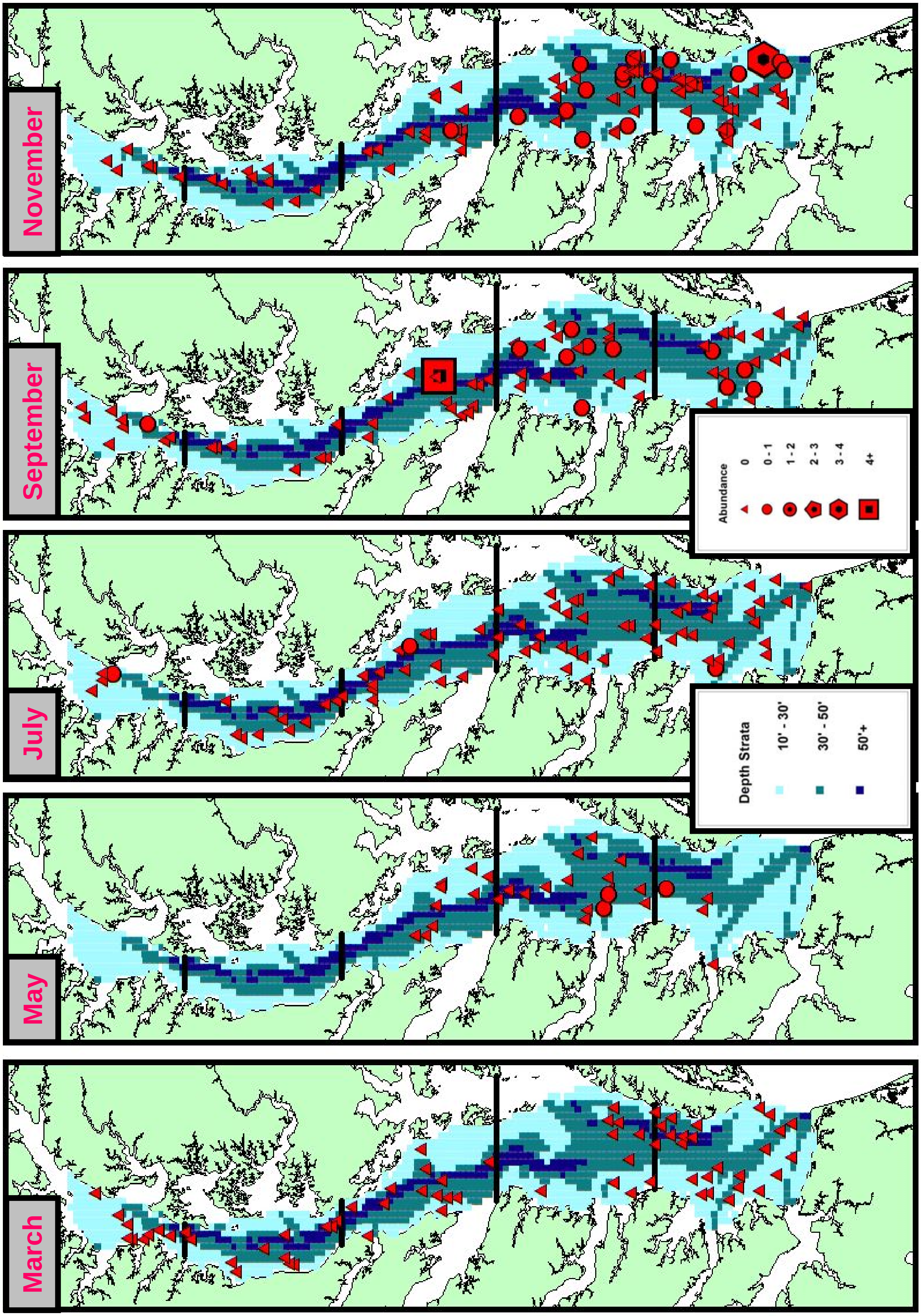


Figure 23. Abundance (number per hectare swept) of bluefish in Chesapeake Bay, 2004.

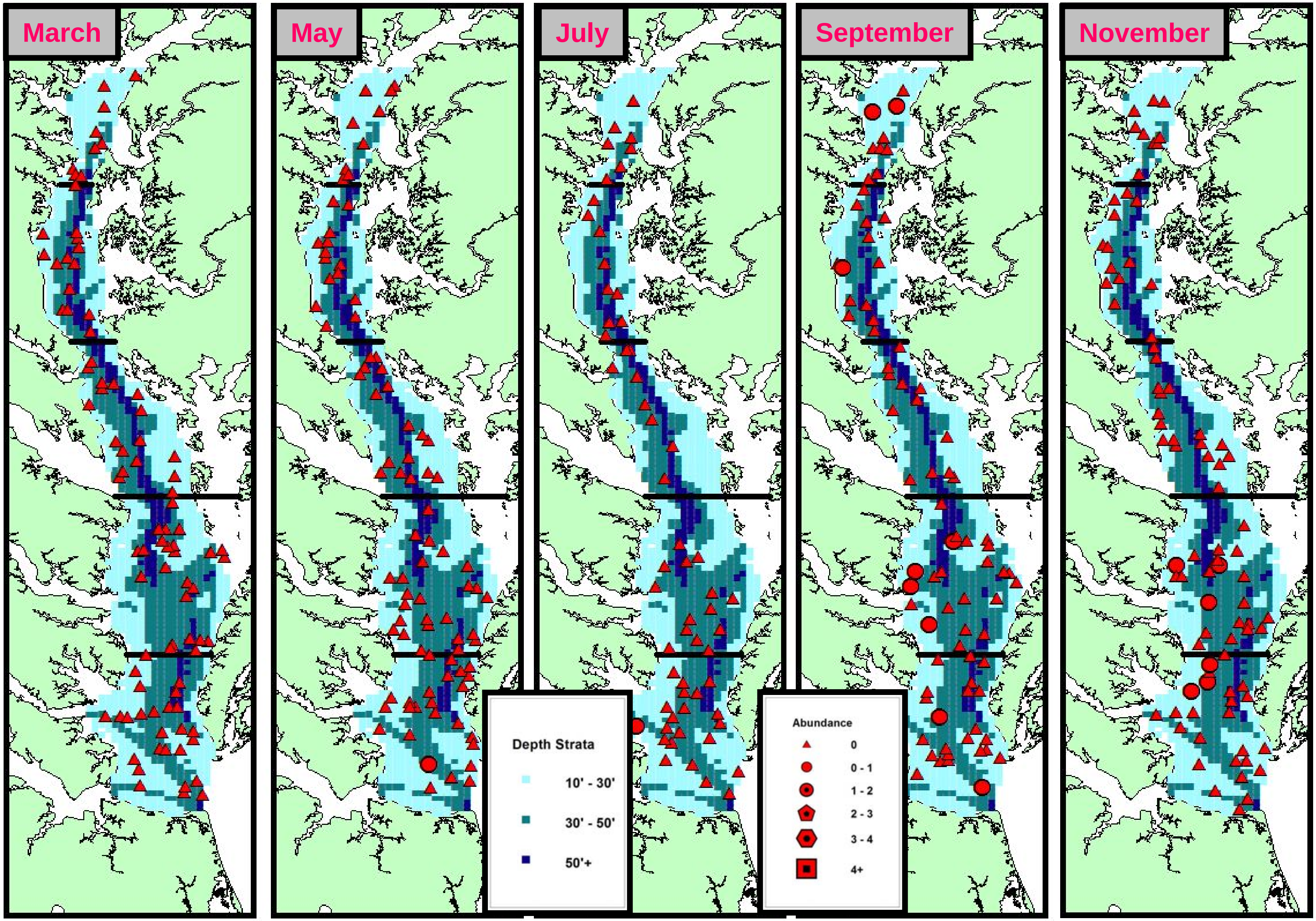


Figure 24. Abundance (number per hectare swept) of bluefish in Chesapeake Bay, 2005.

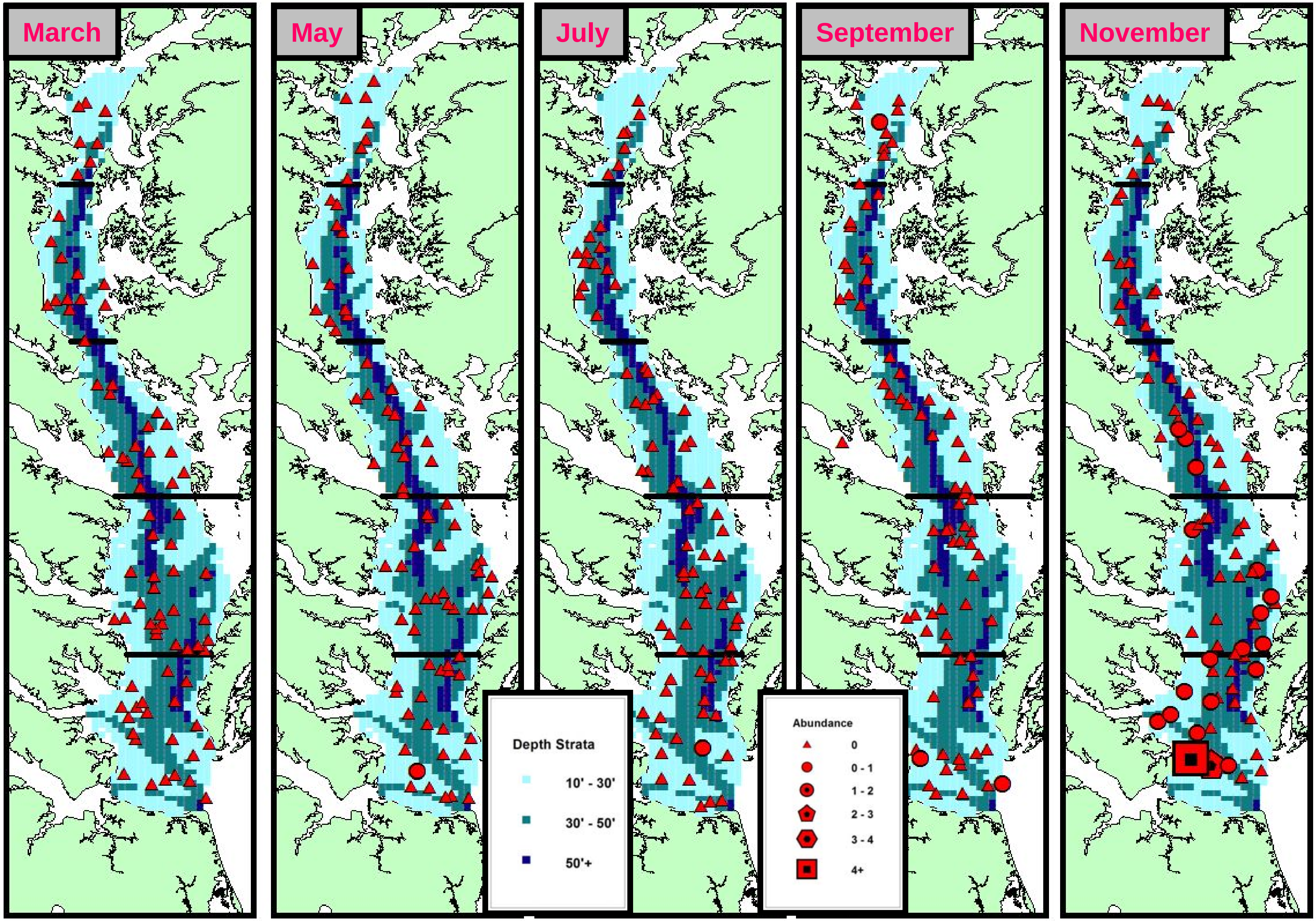


Figure 25. Abundance (number per hectare swept) of bluefish in Chesapeake Bay, 2006.

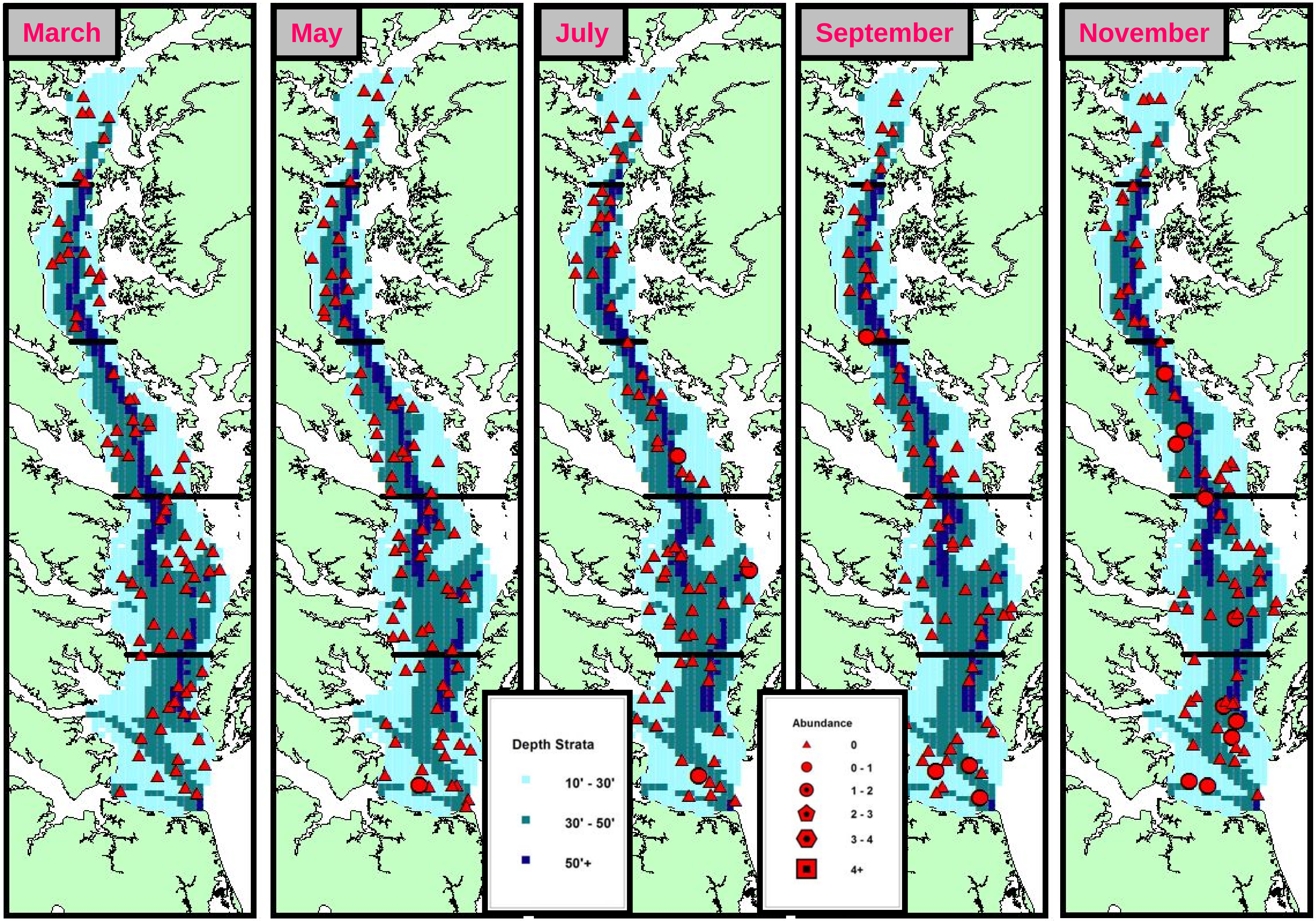


Figure 26. Bluefish length-frequency in Chesapeake Bay 2002-2006.

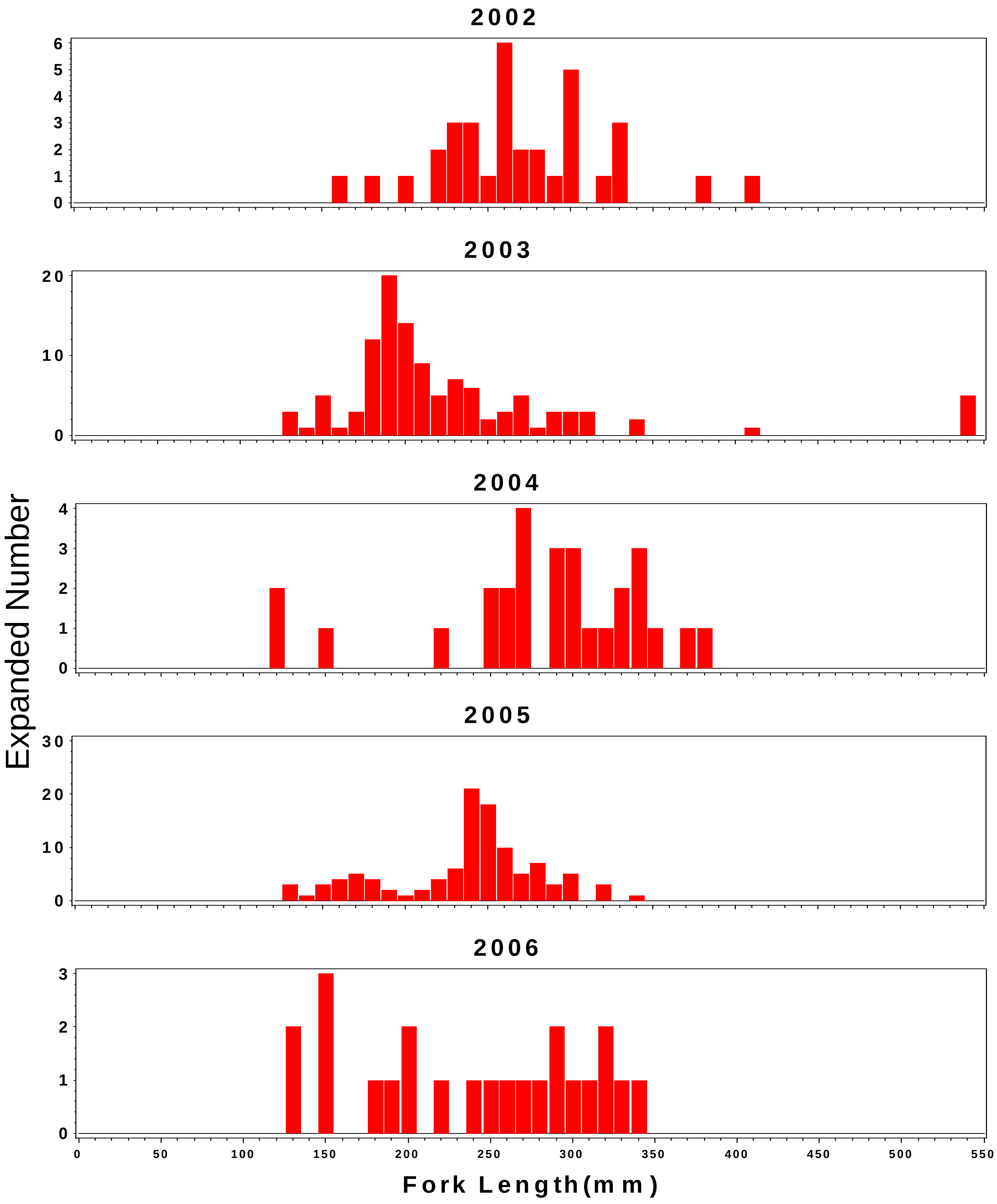


Figure 27. Bluefish age-structure in Chesapeake Bay 2002-2004 (2005-2006 ages not yet assigned).

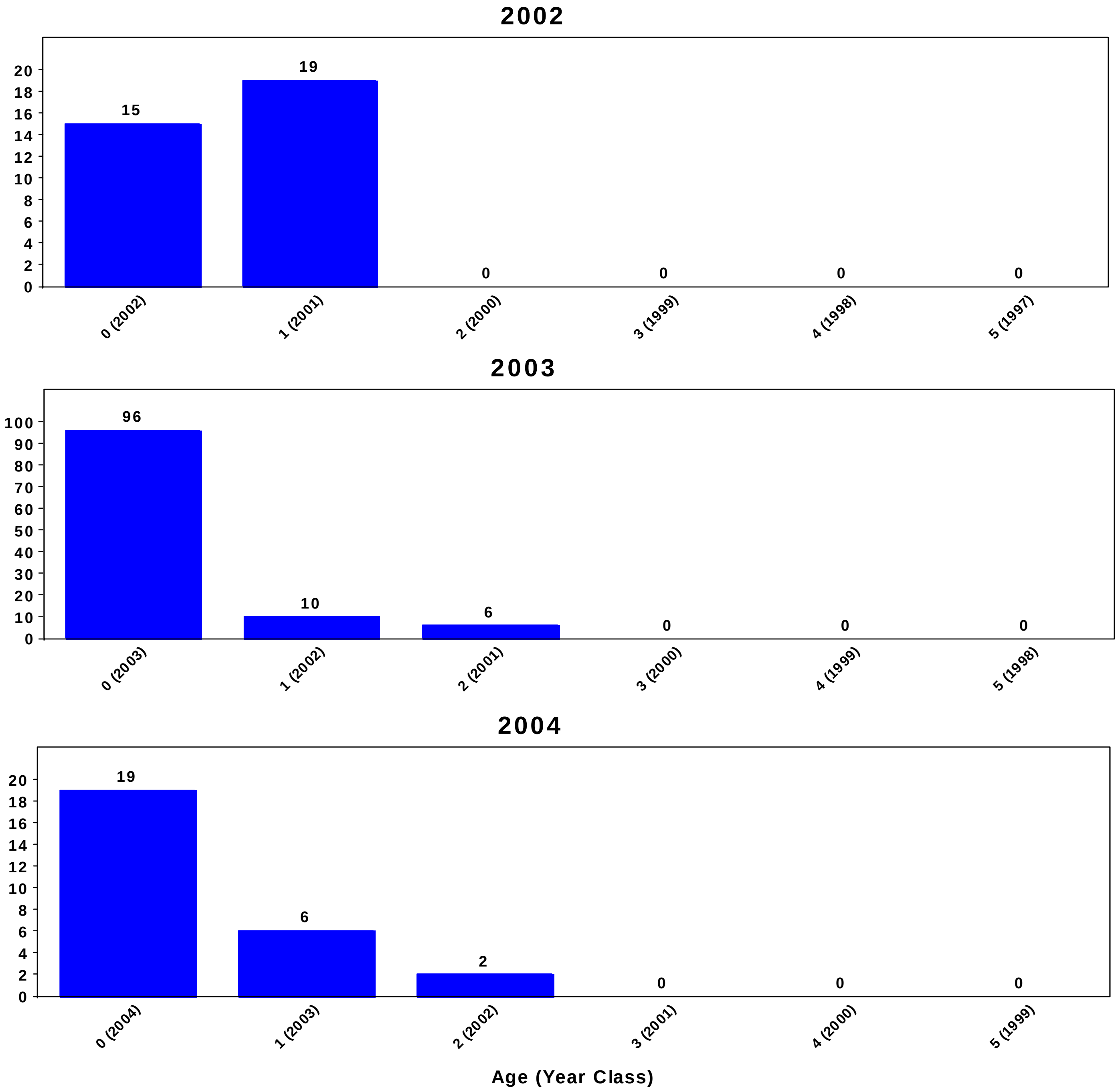


Figure 28. Bluefish sex-ratios in Chesapeake Bay 2002-2006, by year.

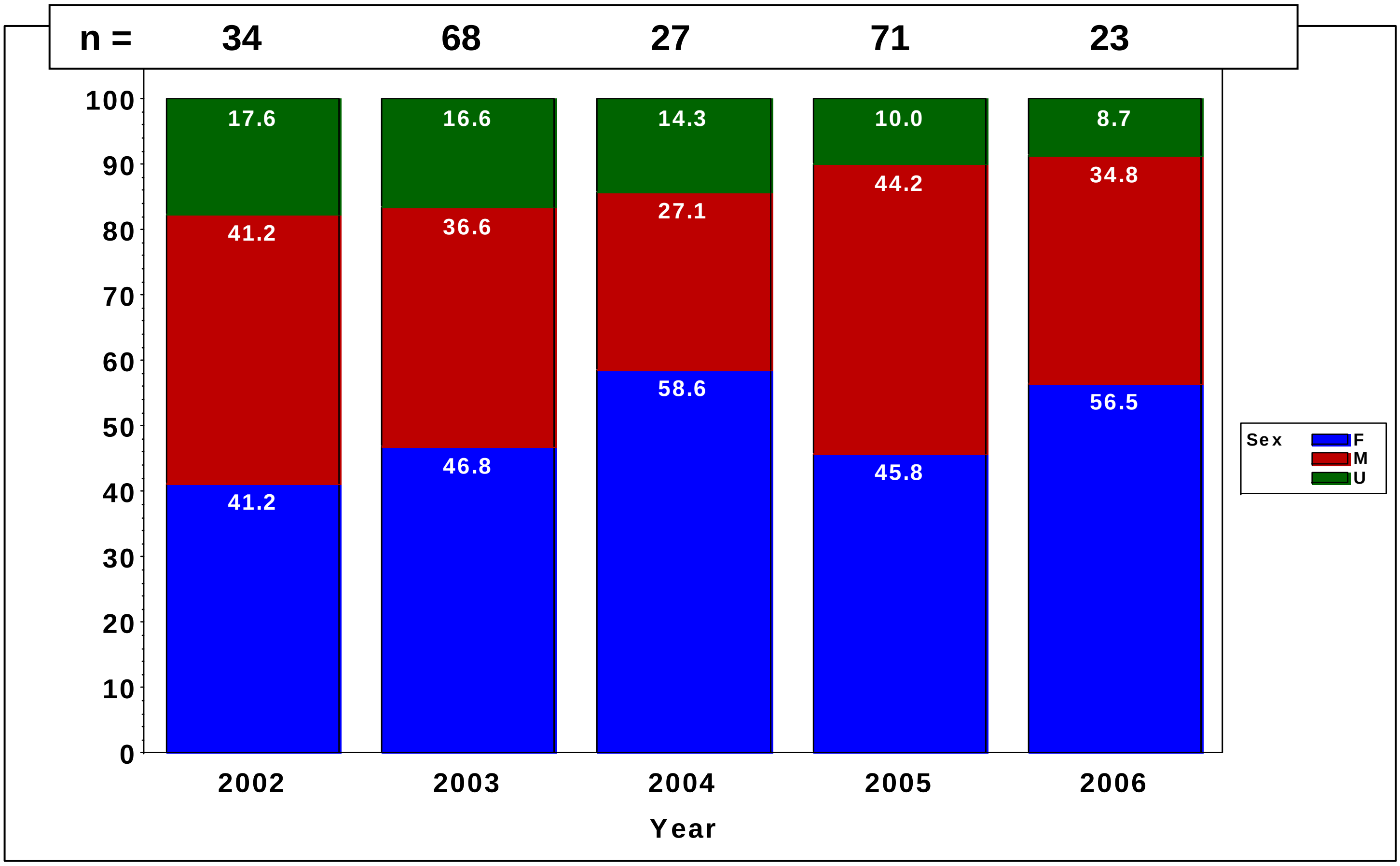


Figure 29. Bluefish length-weight relationships in Chesapeake Bay 2002-2006 as calculated by power regression for sexes combined (A) and separately (B).

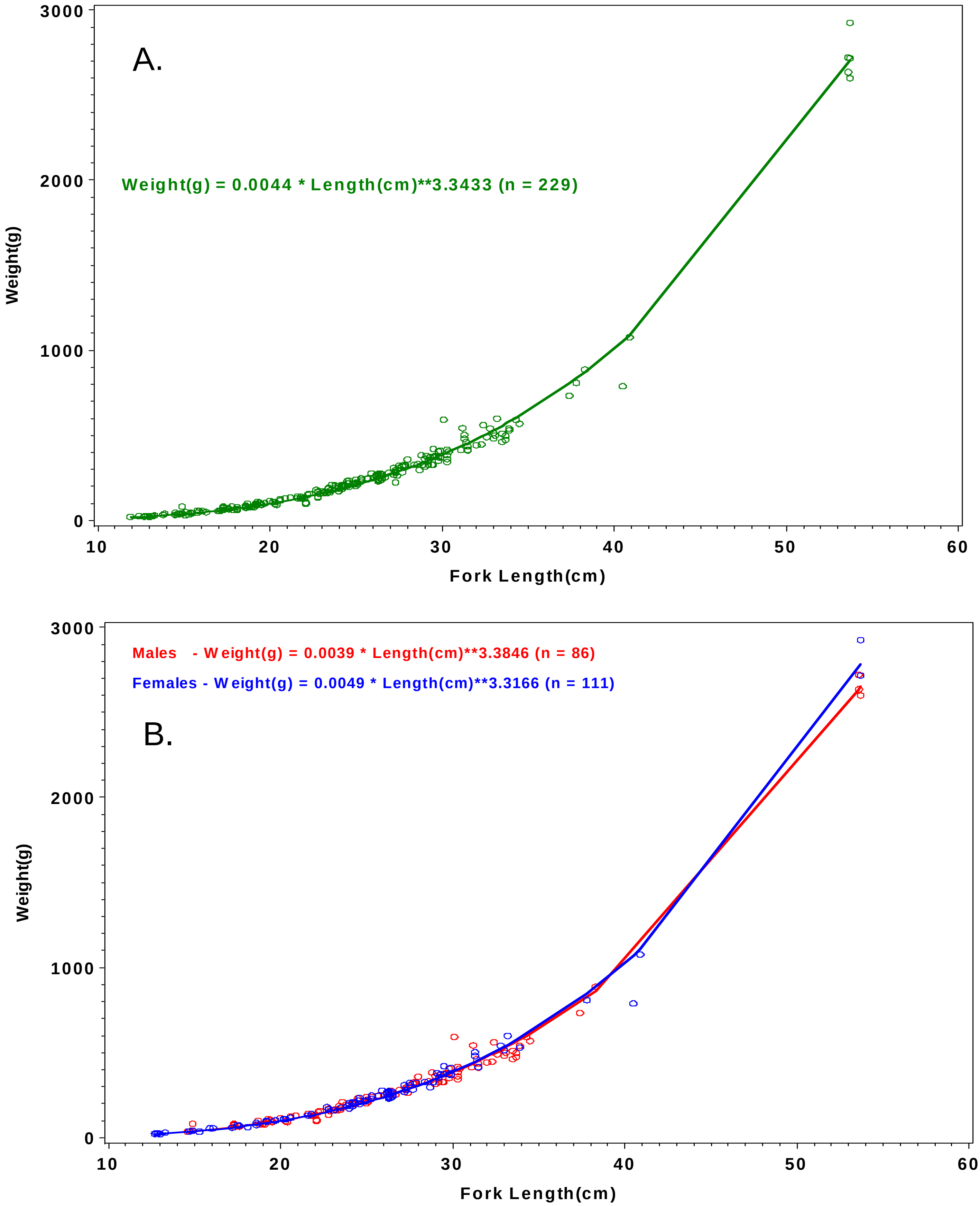


Figure 30. Bluefish maturity schedule in Chesapeake Bay 2002-2006 combined, by sex.

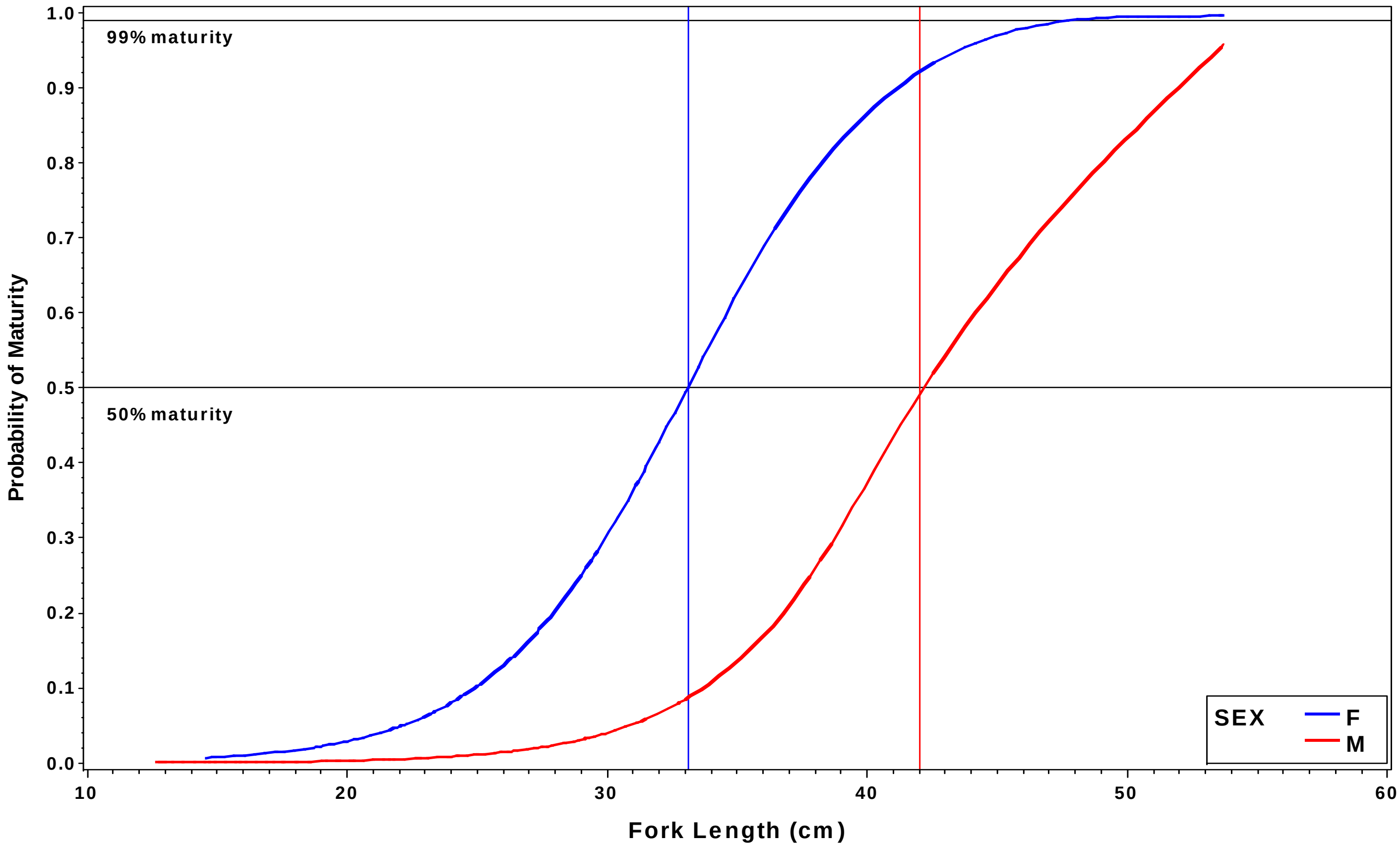


Figure 31. Bluefish diet in Chesapeake Bay 2002-2006 combined.

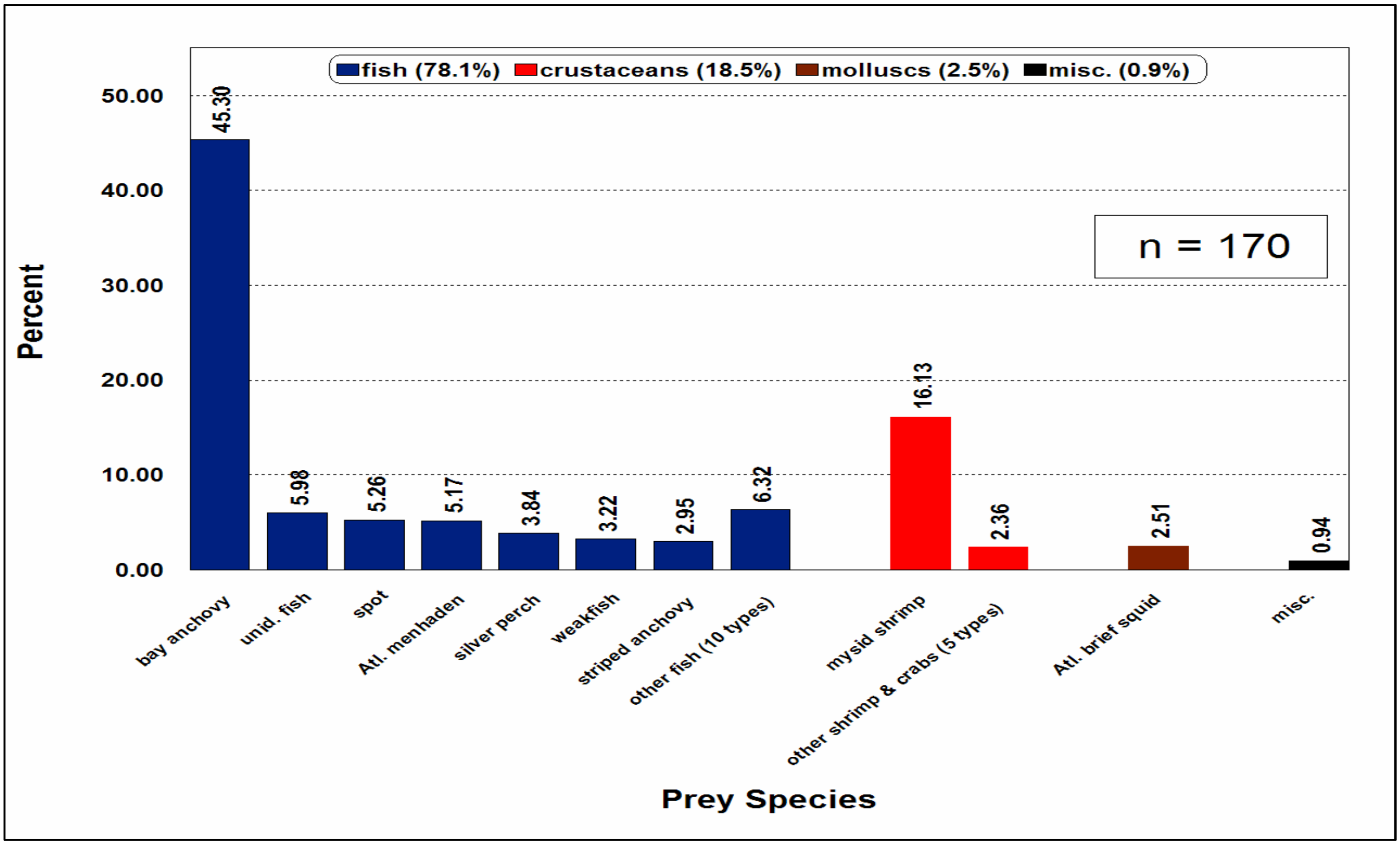


Figure 32. Butterfish minimum trawlable abundance estimates in numbers (A) and biomass (B) in Chesapeake Bay 2002-2006.

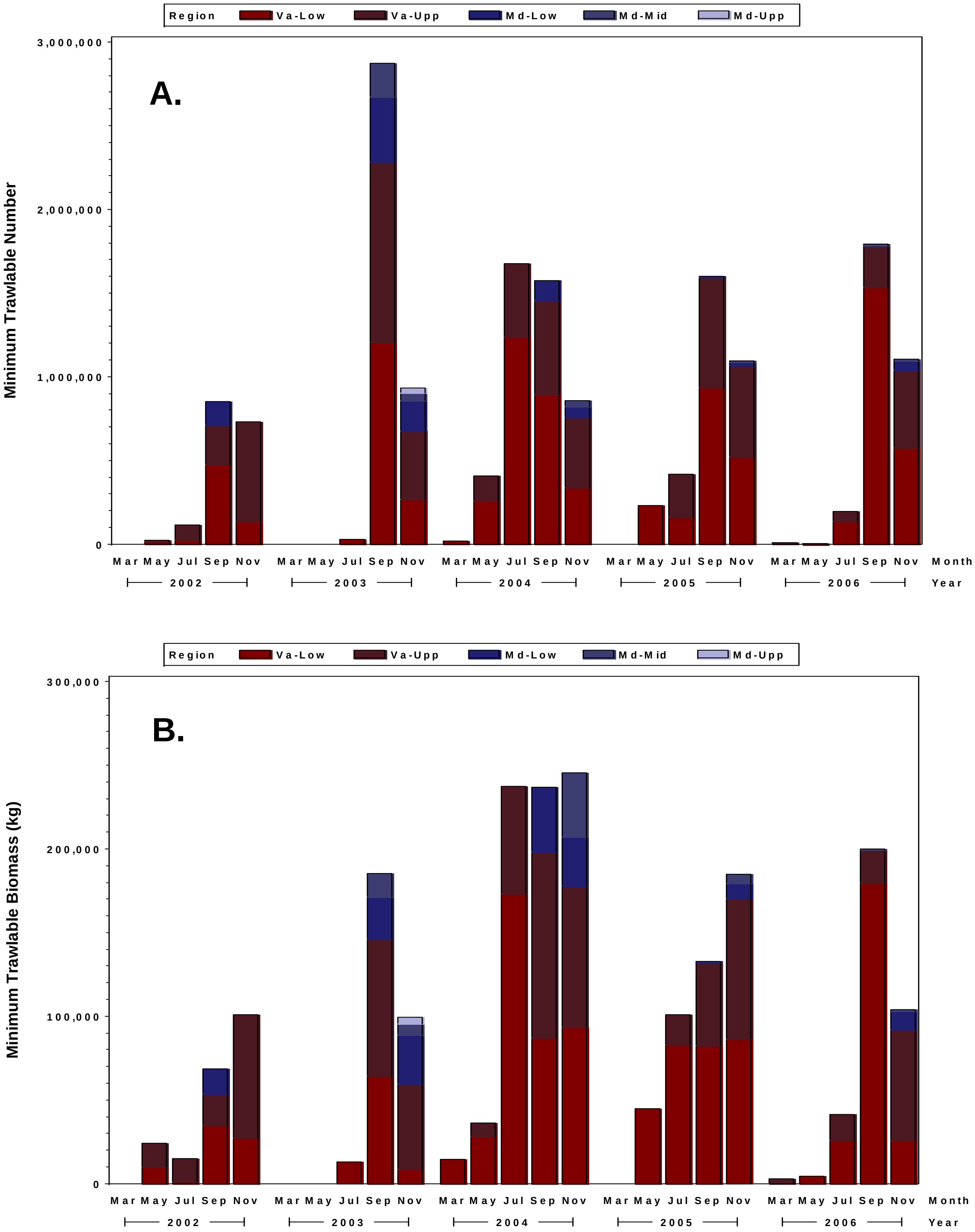


Figure 33. Abundance (number per hectare swept) of butterfish in Chesapeake Bay, 2002.

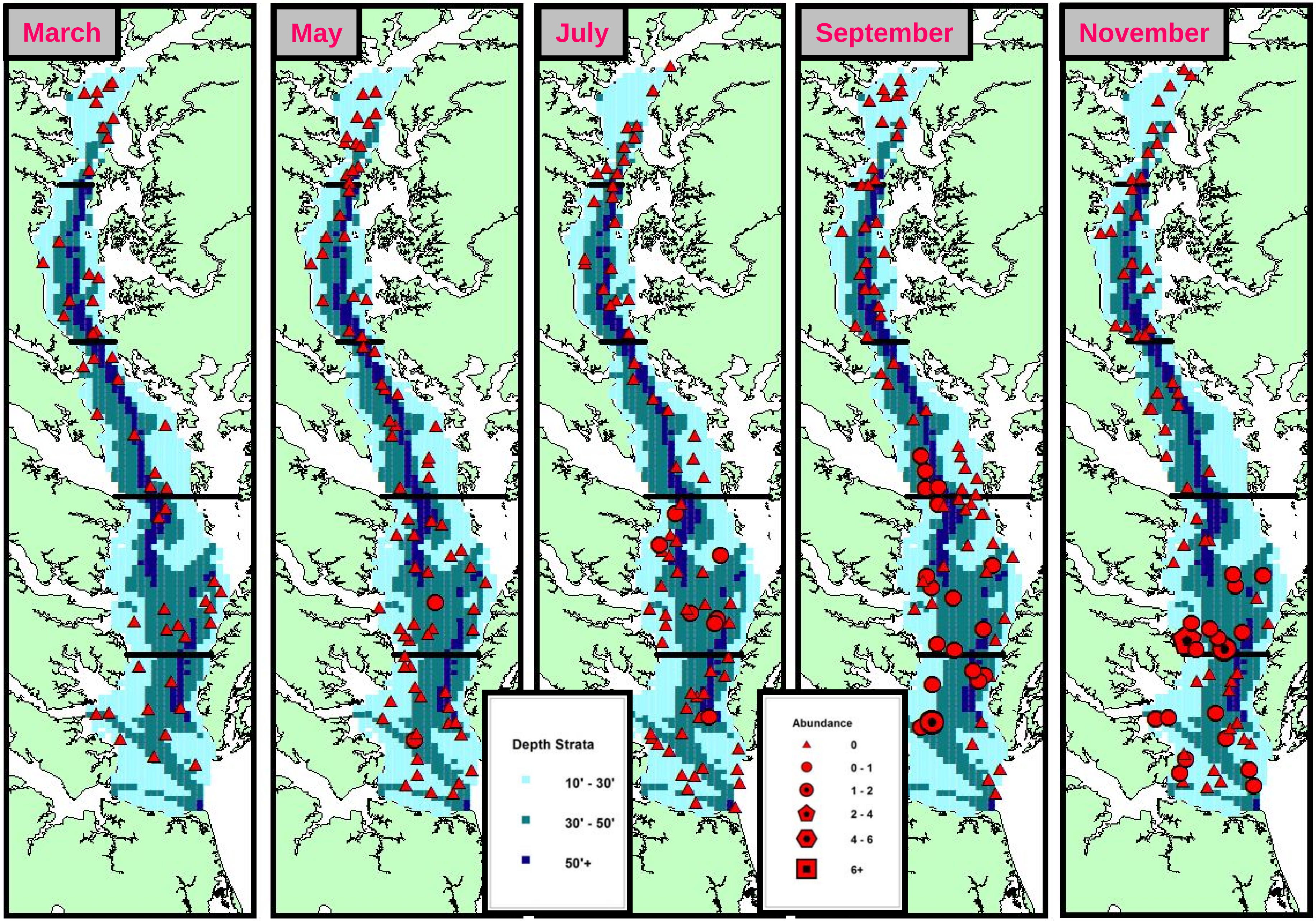


Figure 34. Abundance (number per hectare swept) of butterfish in Chesapeake Bay, 2003.

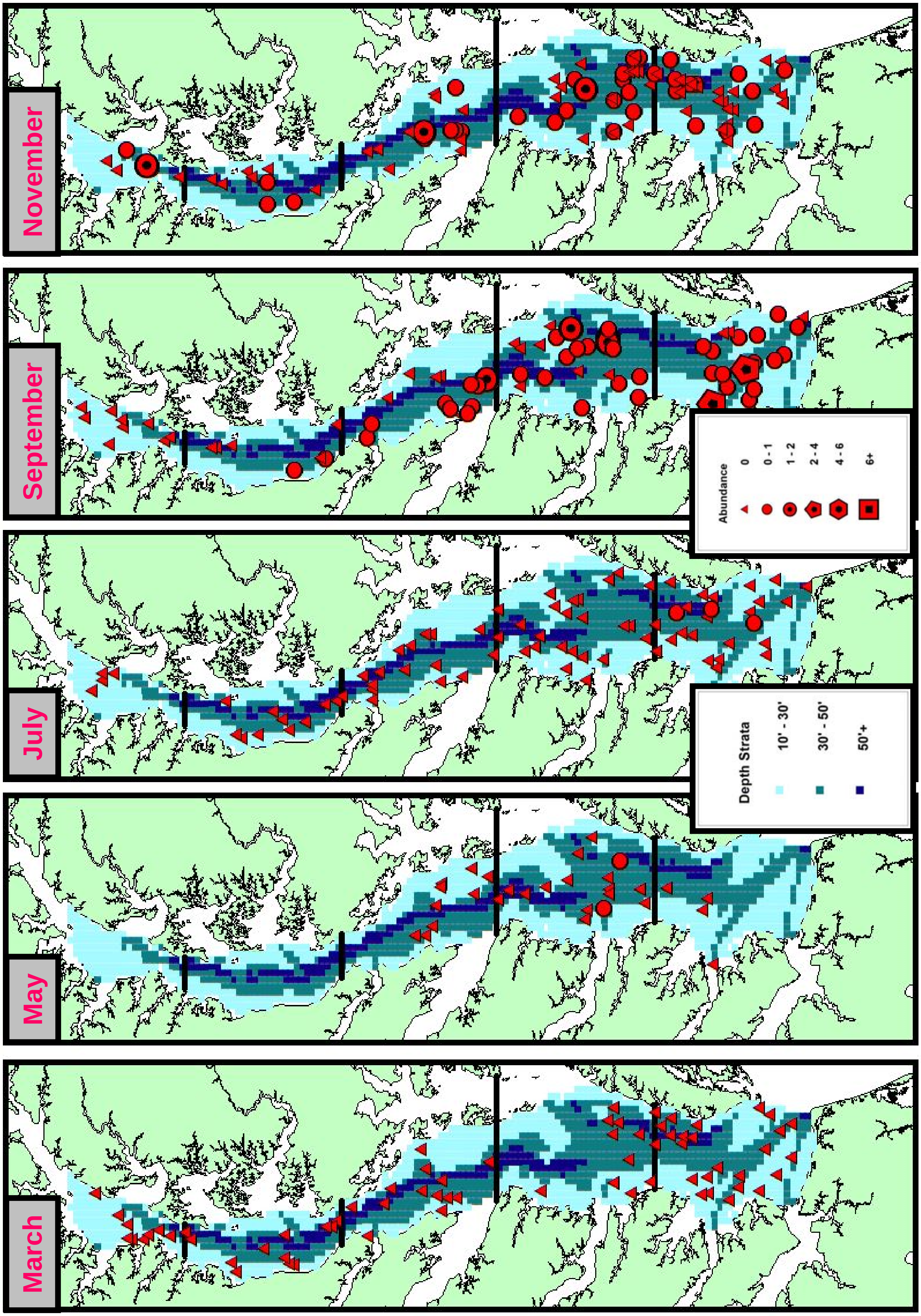


Figure 35. Abundance (number per hectare swept) of butterfish in Chesapeake Bay, 2004.

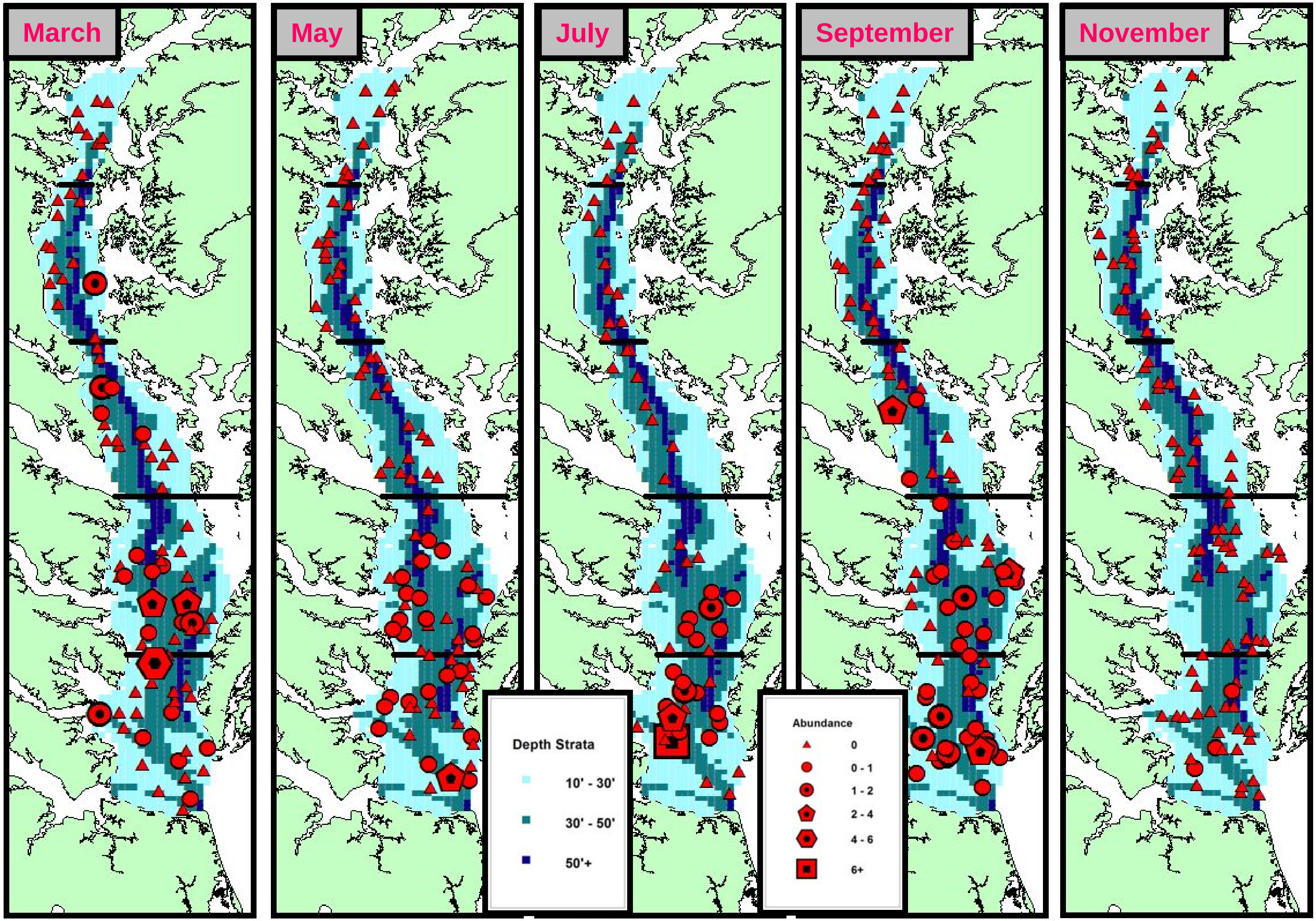


Figure 36. Abundance (number per hectare swept) of butterfish in Chesapeake Bay, 2005.

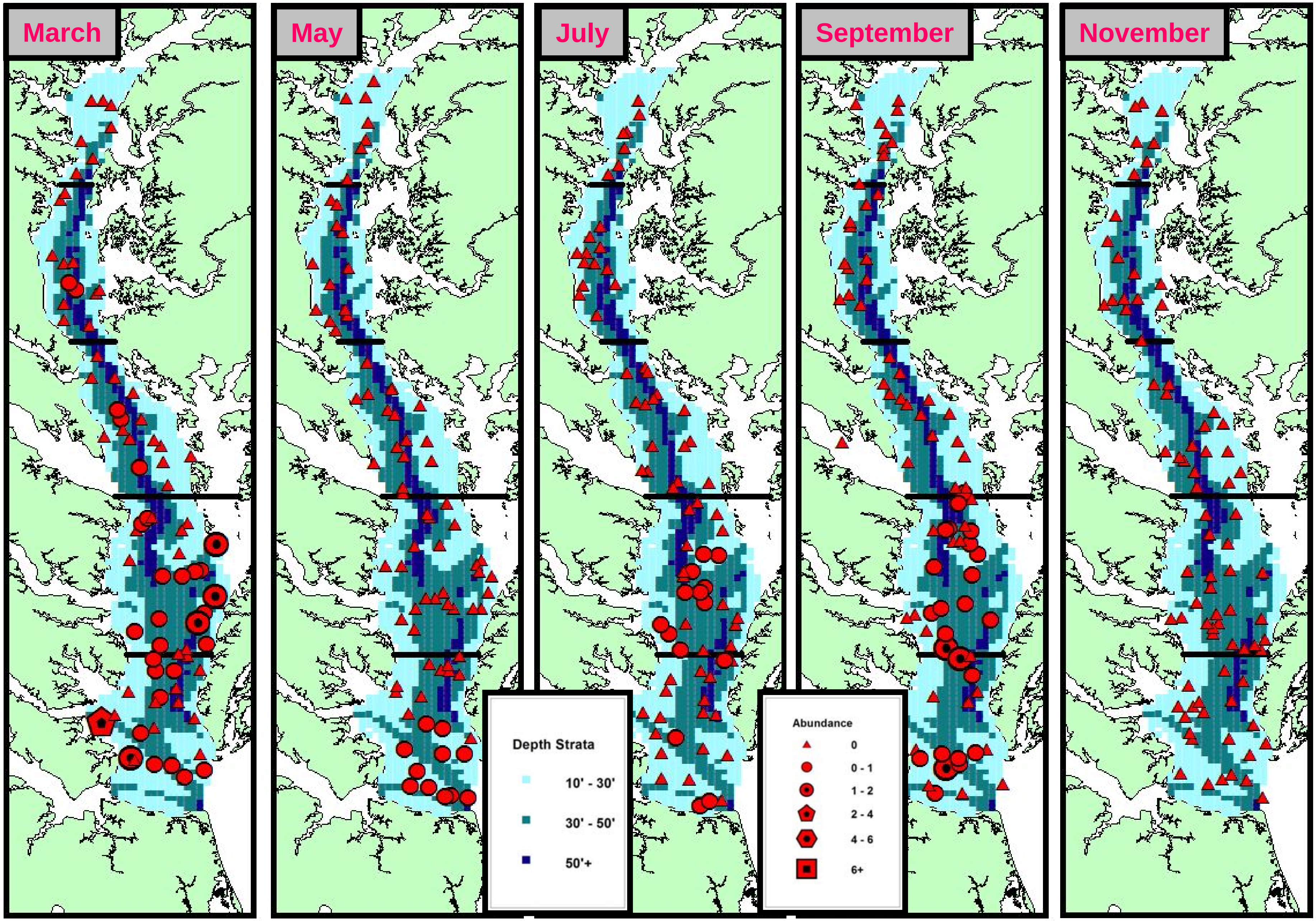


Figure 37. Abundance (number per hectare swept) of butterfish in Chesapeake Bay, 2006.

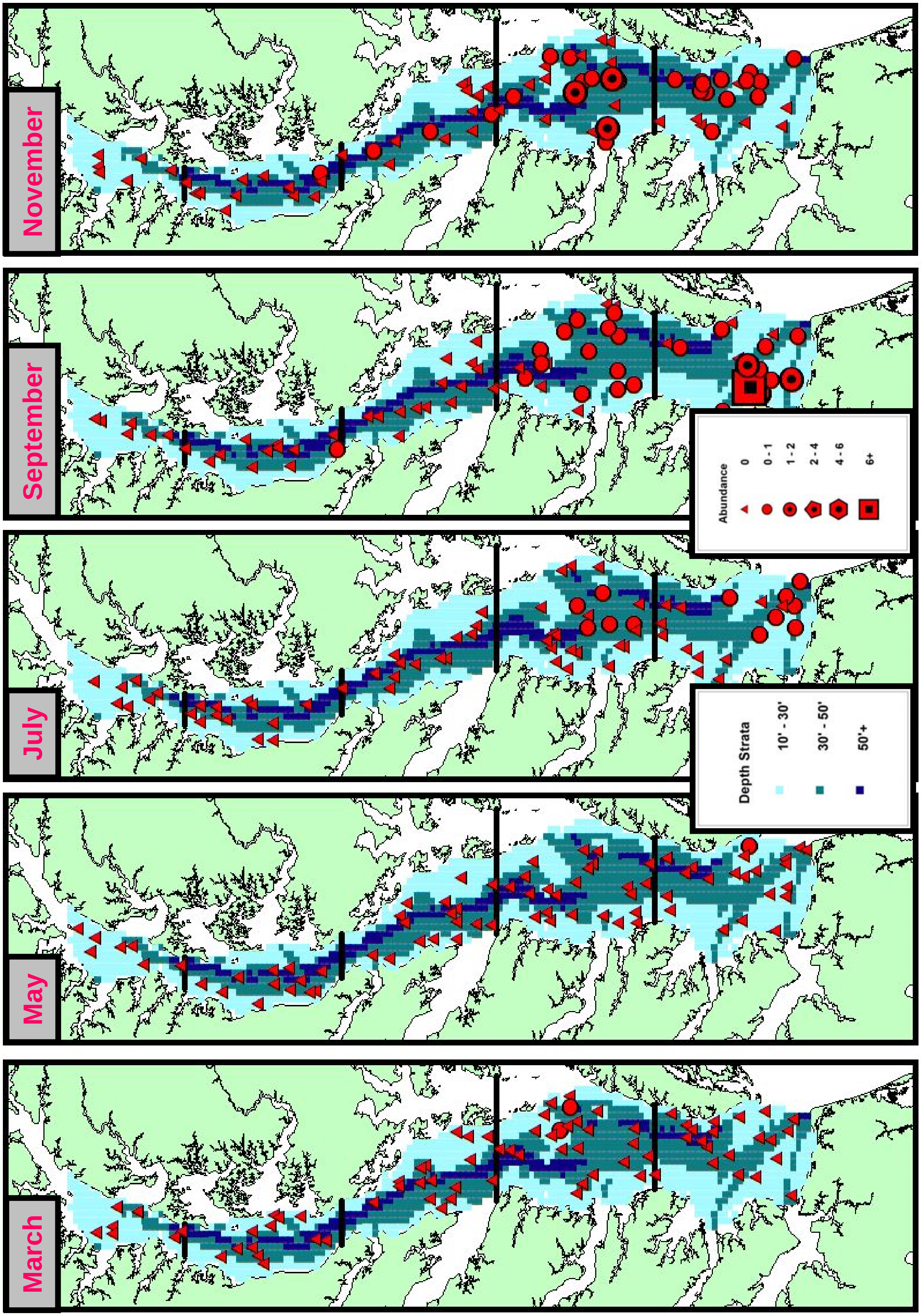


Figure 38. Butterfish length-frequency in Chesapeake Bay 2002-2006.

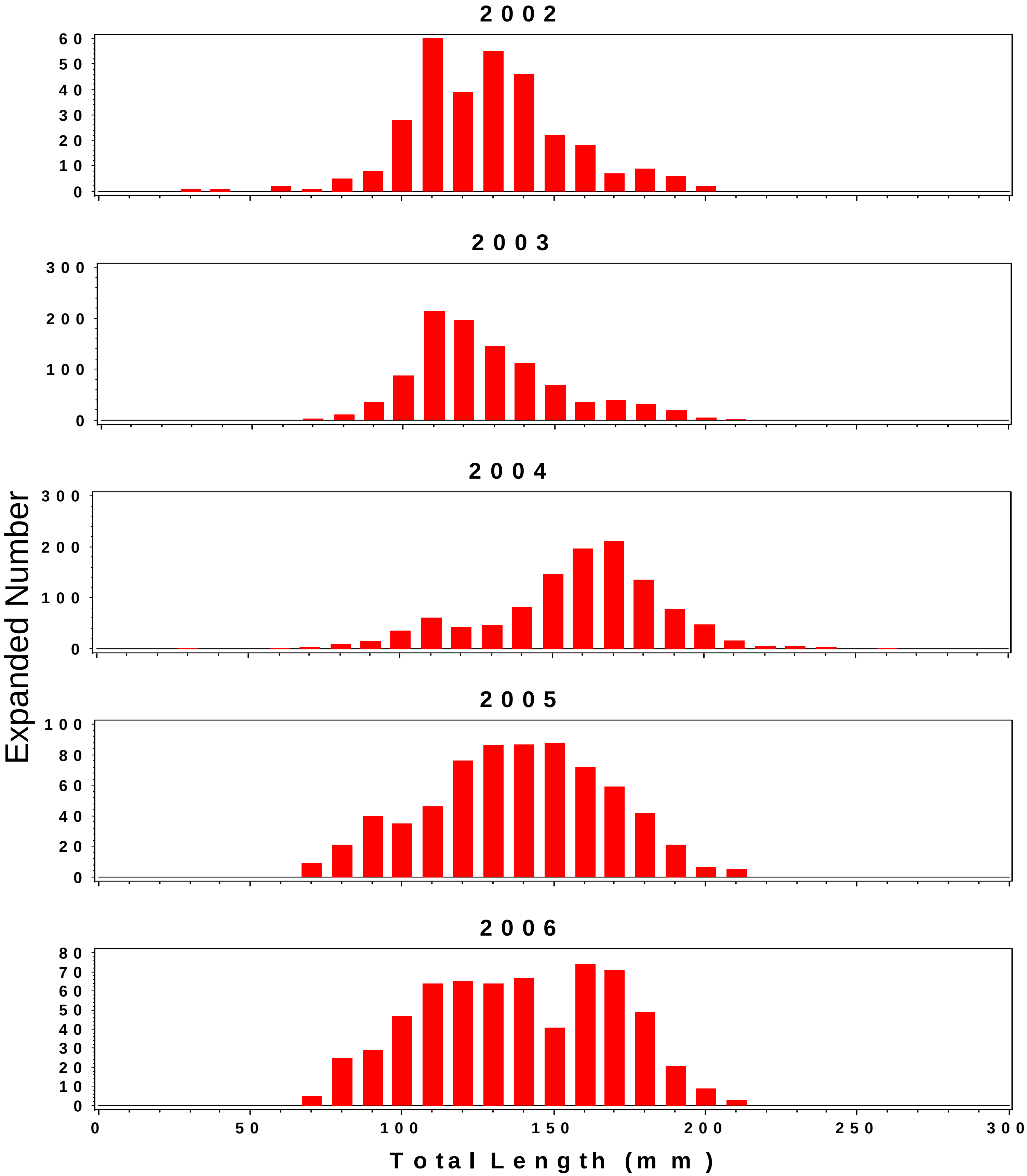


Figure 39. Butterfish length-weight relationship in Chesapeake Bay 2002-2006 as calculated by power regression.

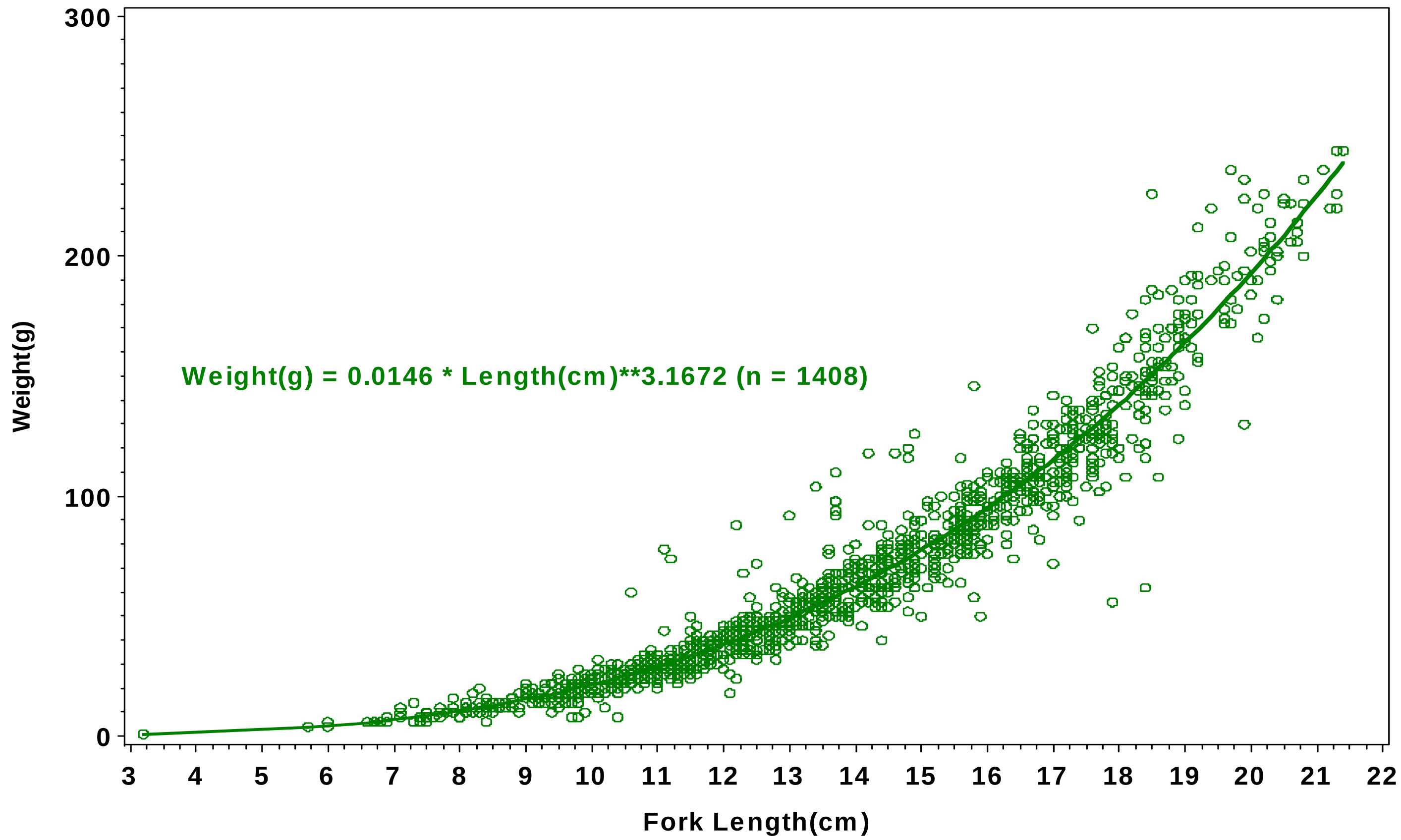


Figure 40. Butterfish diet in Chesapeake Bay 2002-2006 combined (Note: nearly all samples from 2002).

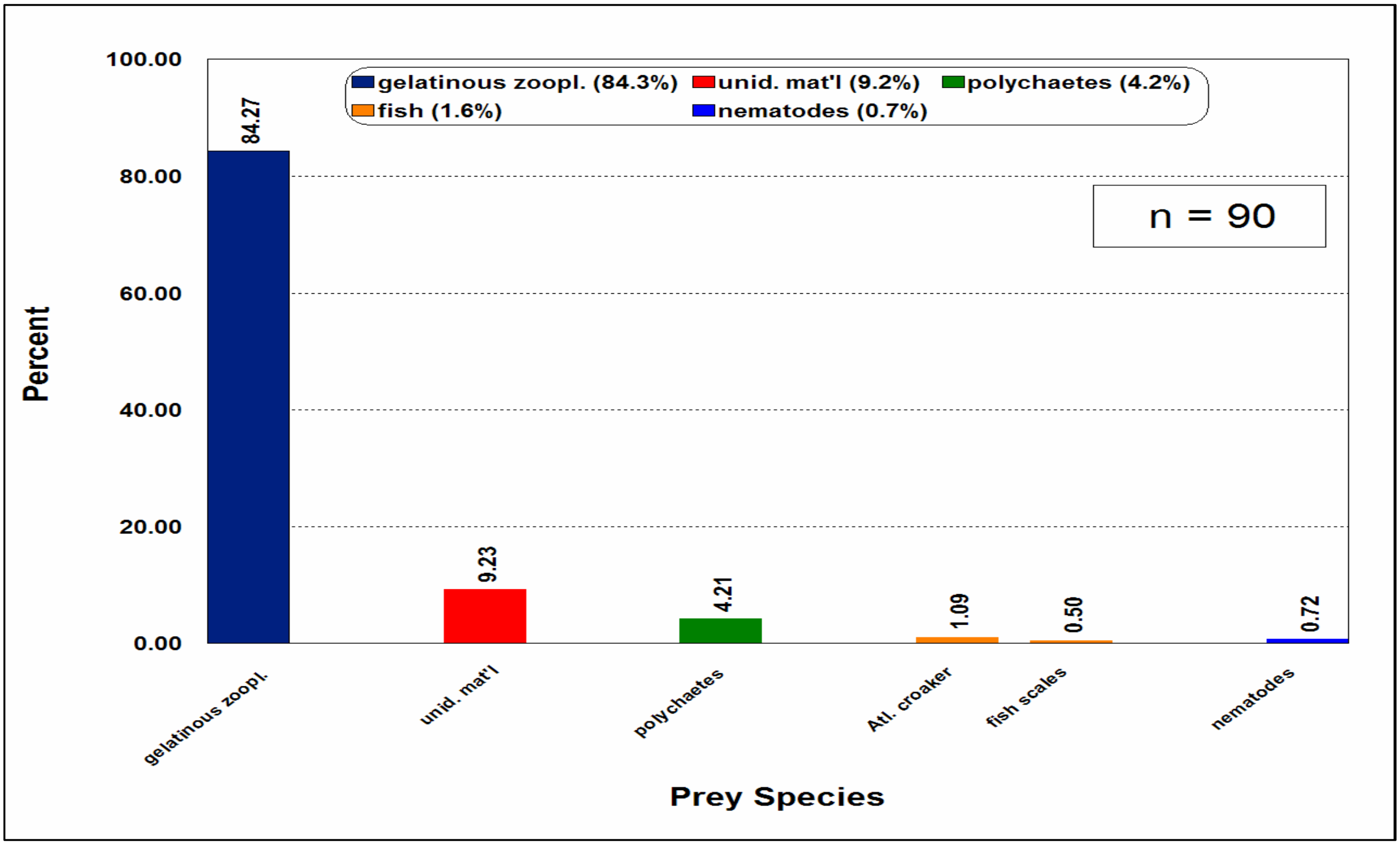
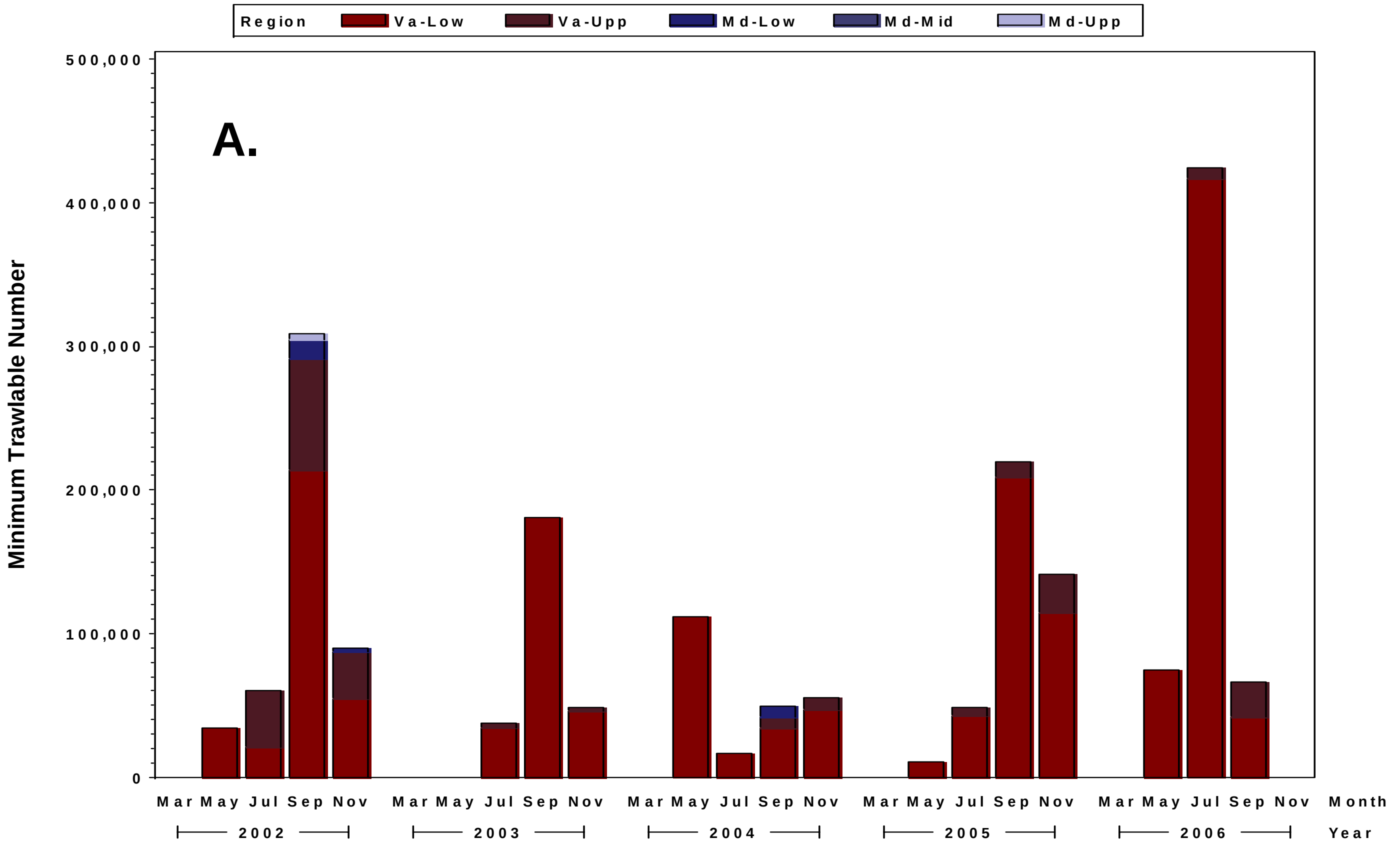


Figure 41. Northern kingfish minimum trawlable abundance estimates in numbers (A) and biomass (B) in Chesapeake Bay 2002-2006.



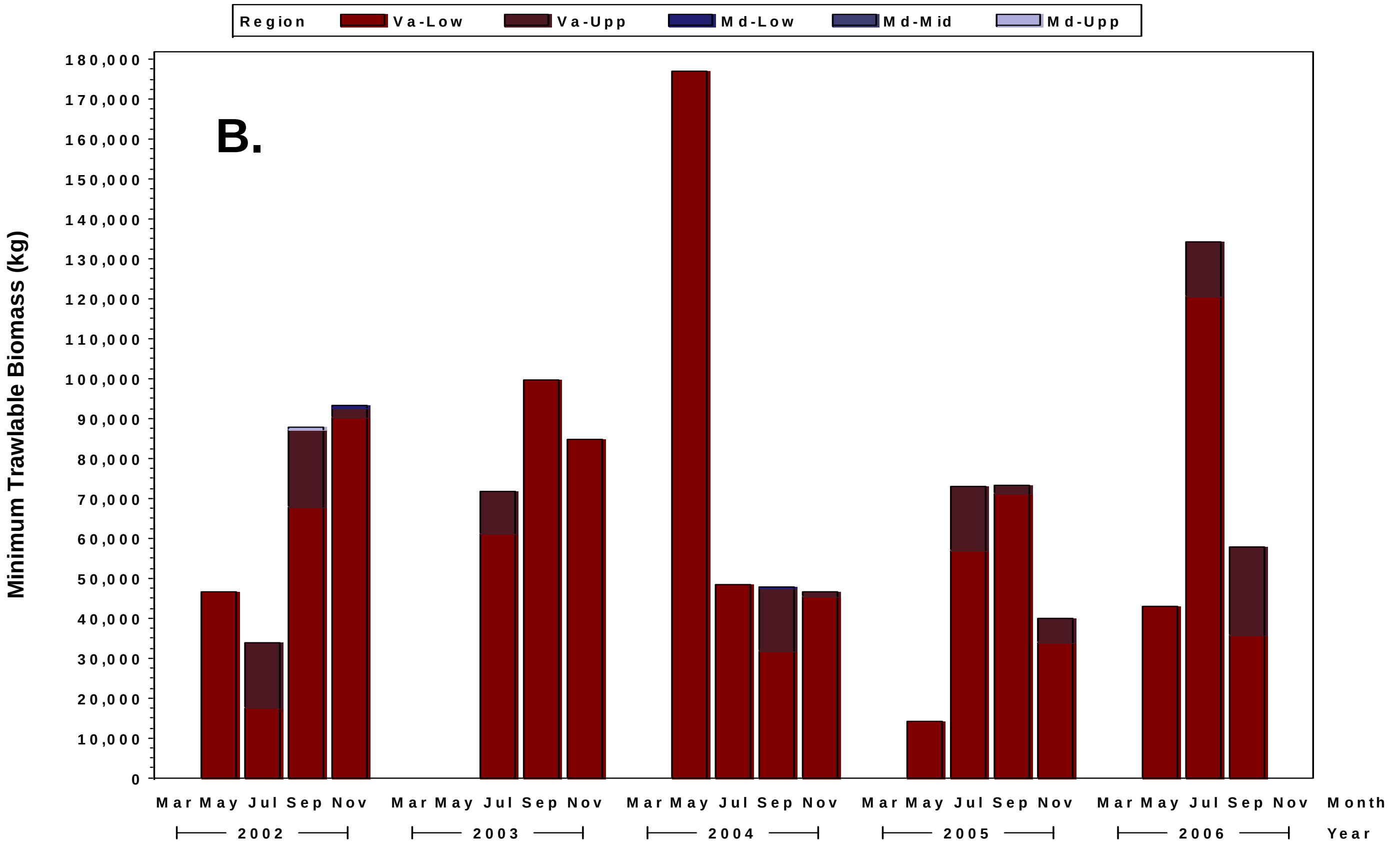


Figure 42. Abundance (number per hectare swept) of northern kingfish in Chesapeake Bay, 2002.

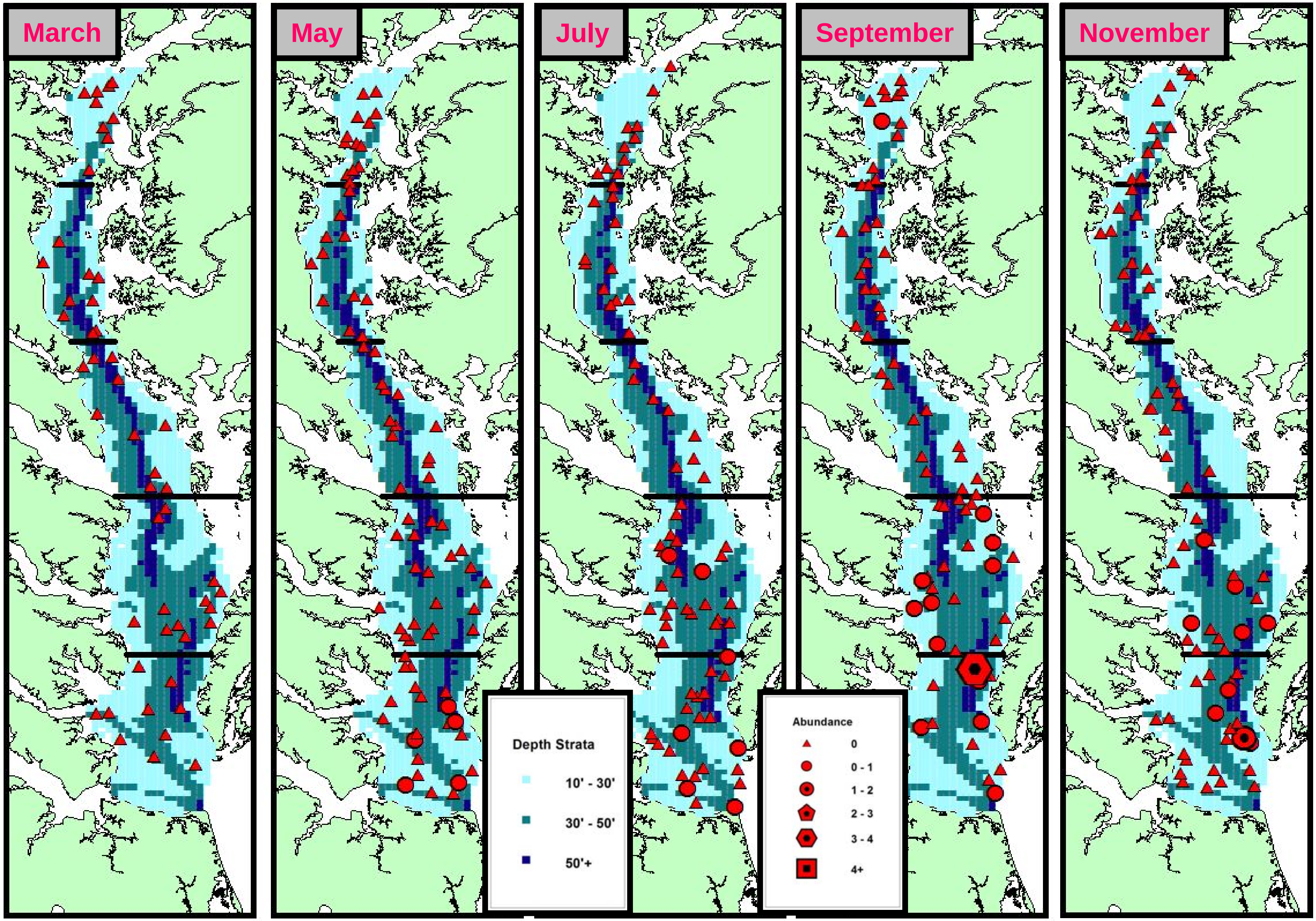
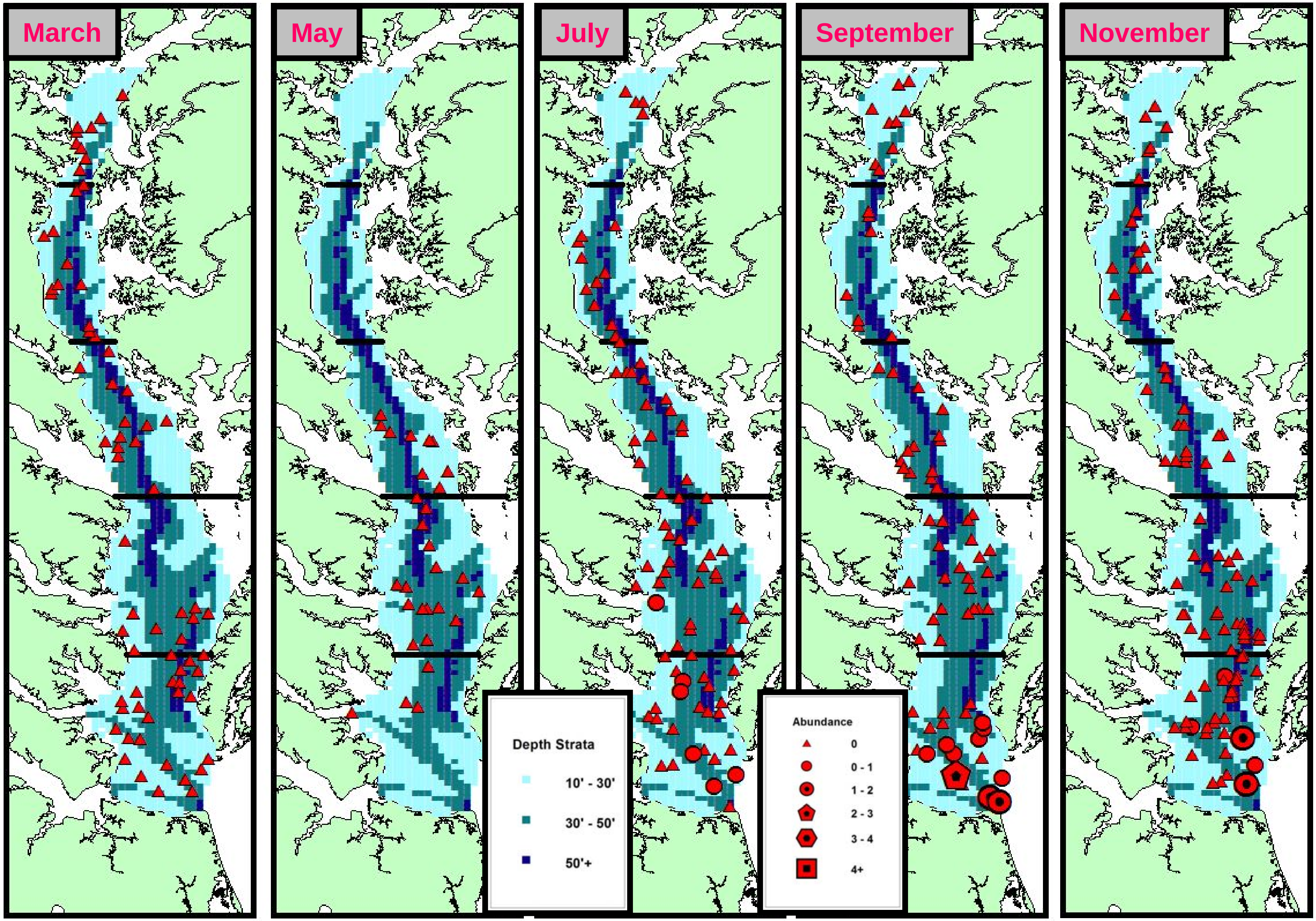


Figure 43. Abundance (number per hectare swept) of northern kingfish in Chesapeake Bay, 2003.



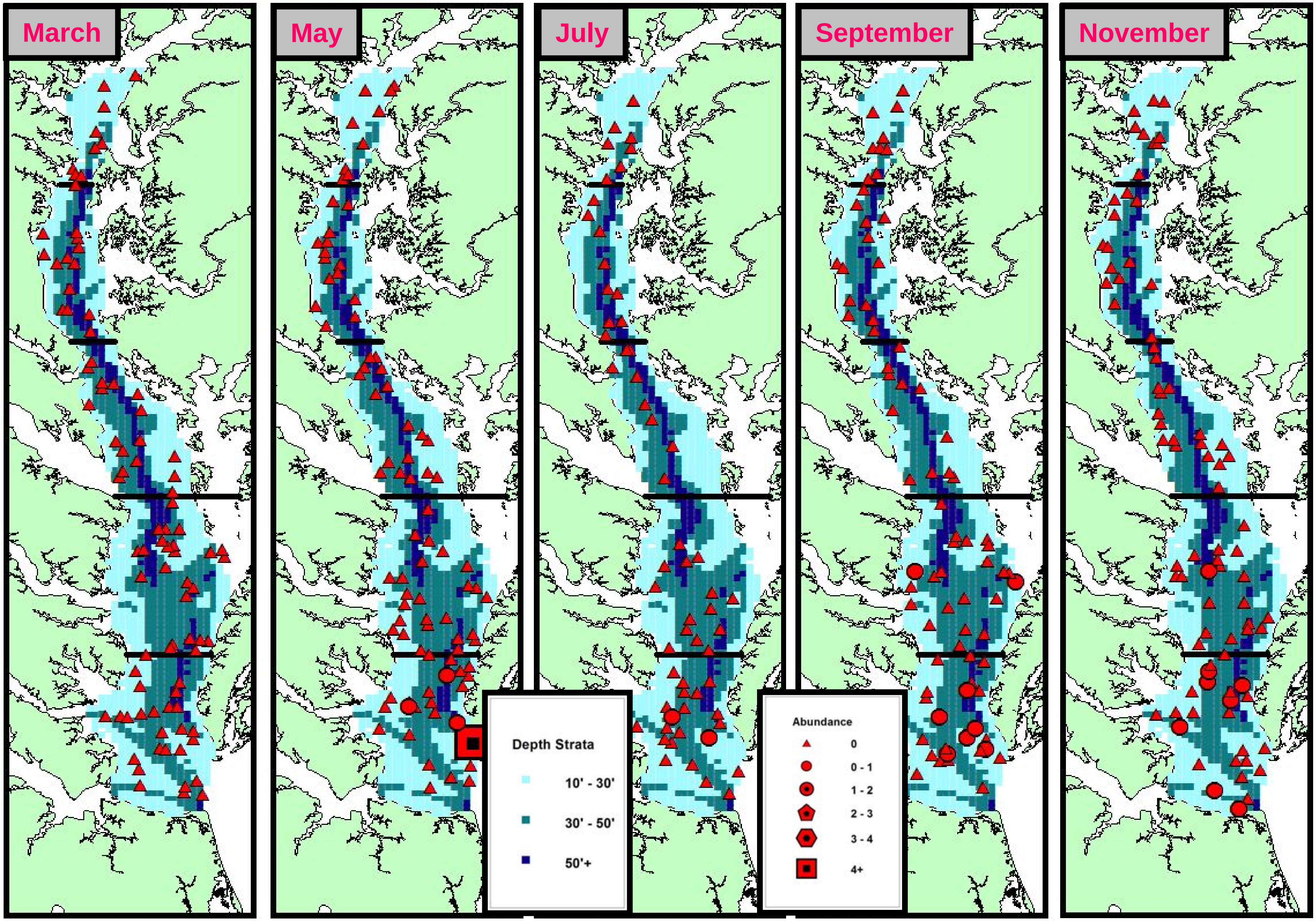


Figure 44. Abundance (number per hectare swept) of northern kingfish in Chesapeake Bay, 2004.

Figure 45. Abundance (number per hectare swept) of northern kingfish in Chesapeake Bay, 2005.

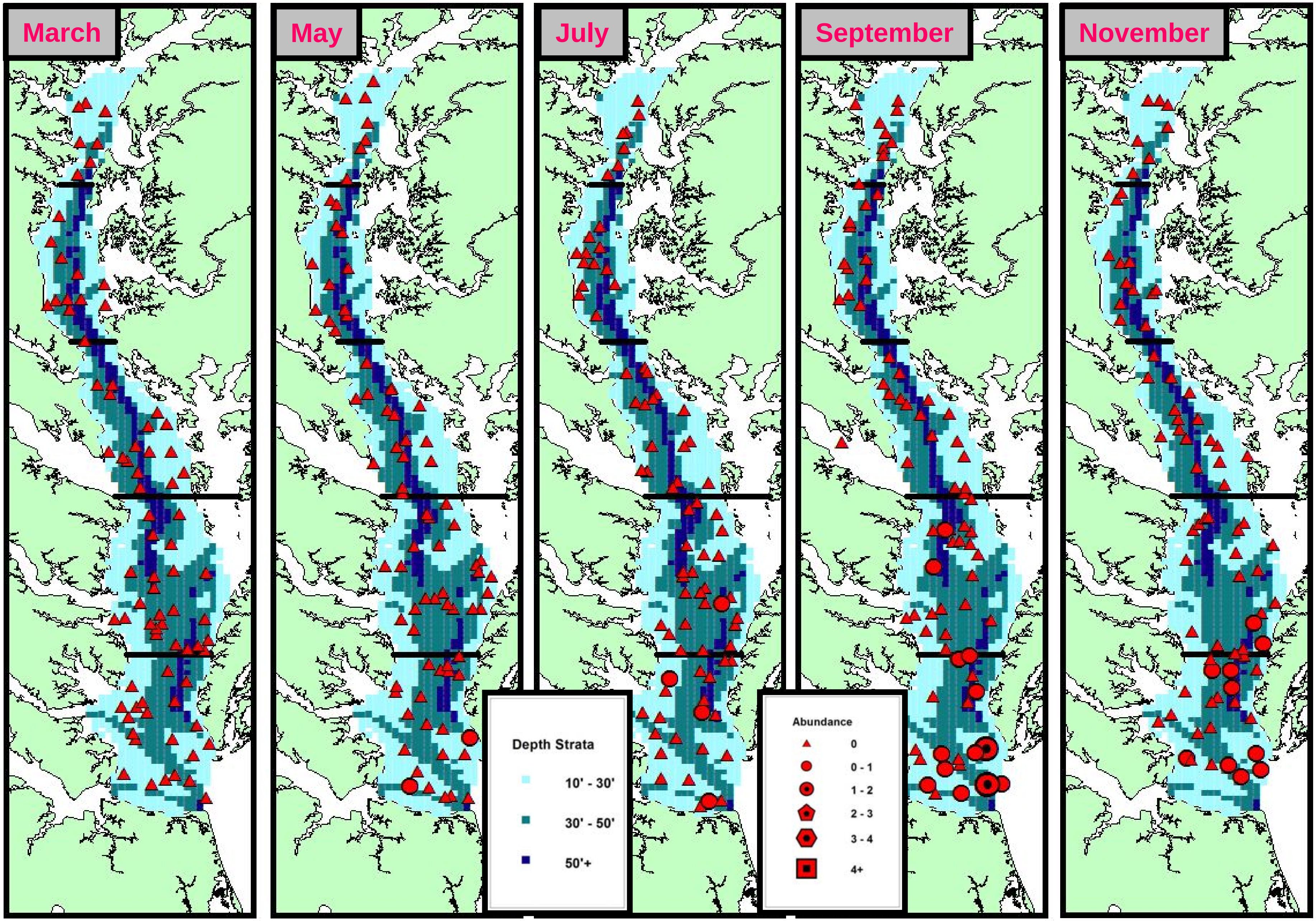


Figure 46. Abundance (number per hectare swept) of northern kingfish in Chesapeake Bay, 2006.

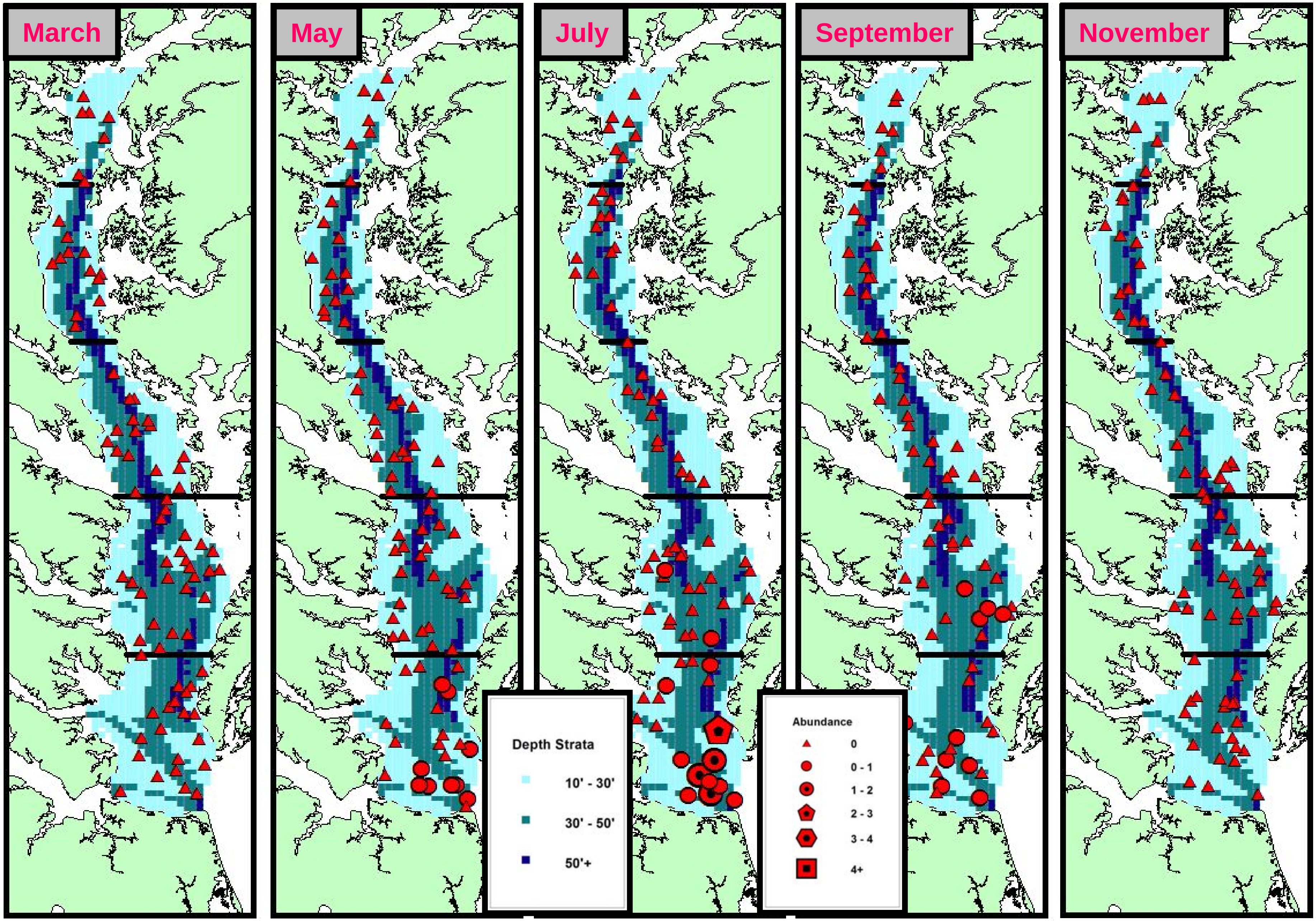


Figure 47. Northern kingfish length-frequency in Chesapeake Bay 2002-2006.

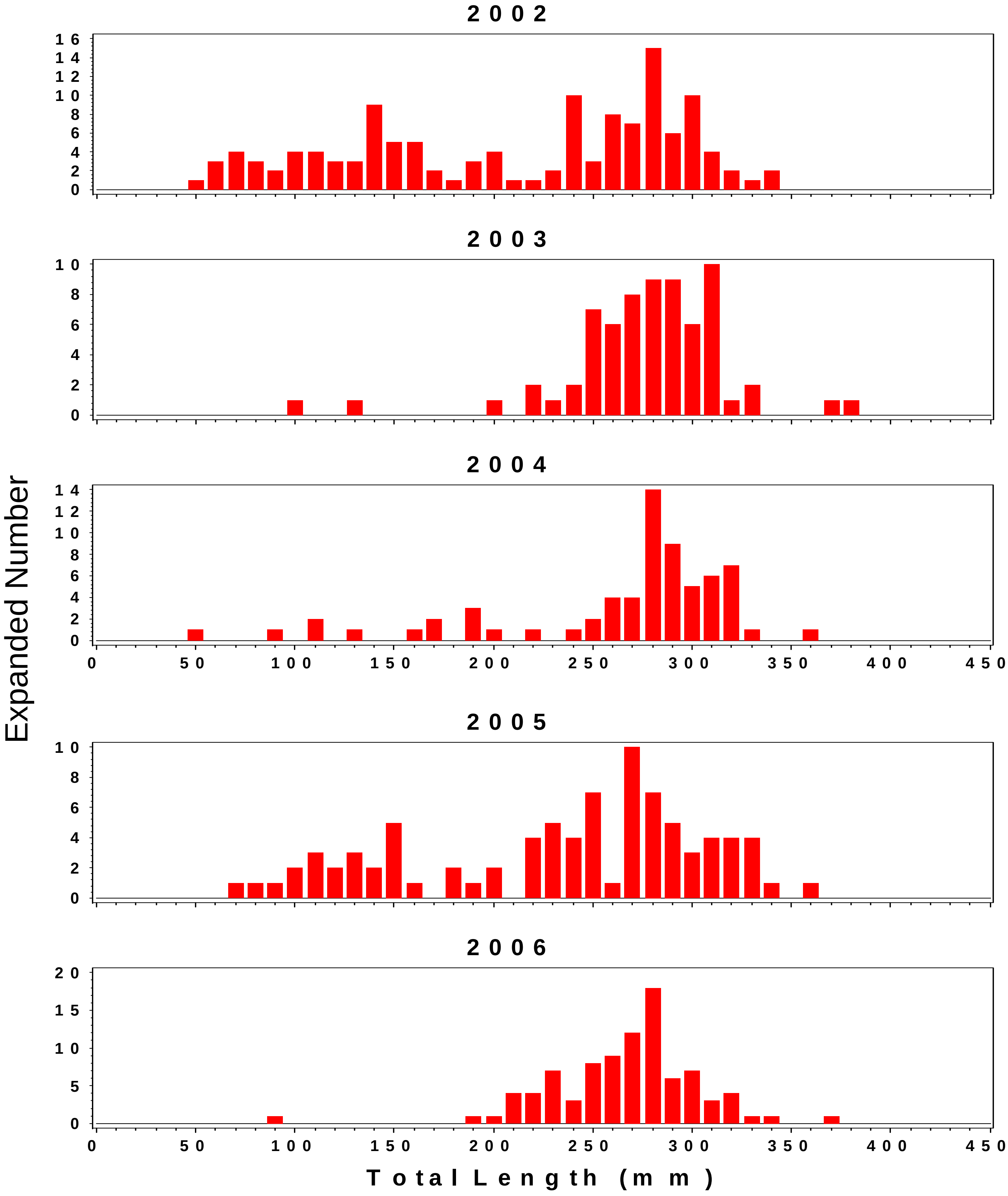


Figure 48. Northern kingfish sex-ratios in Chesapeake Bay 2002-2006, by year (A), month (B).

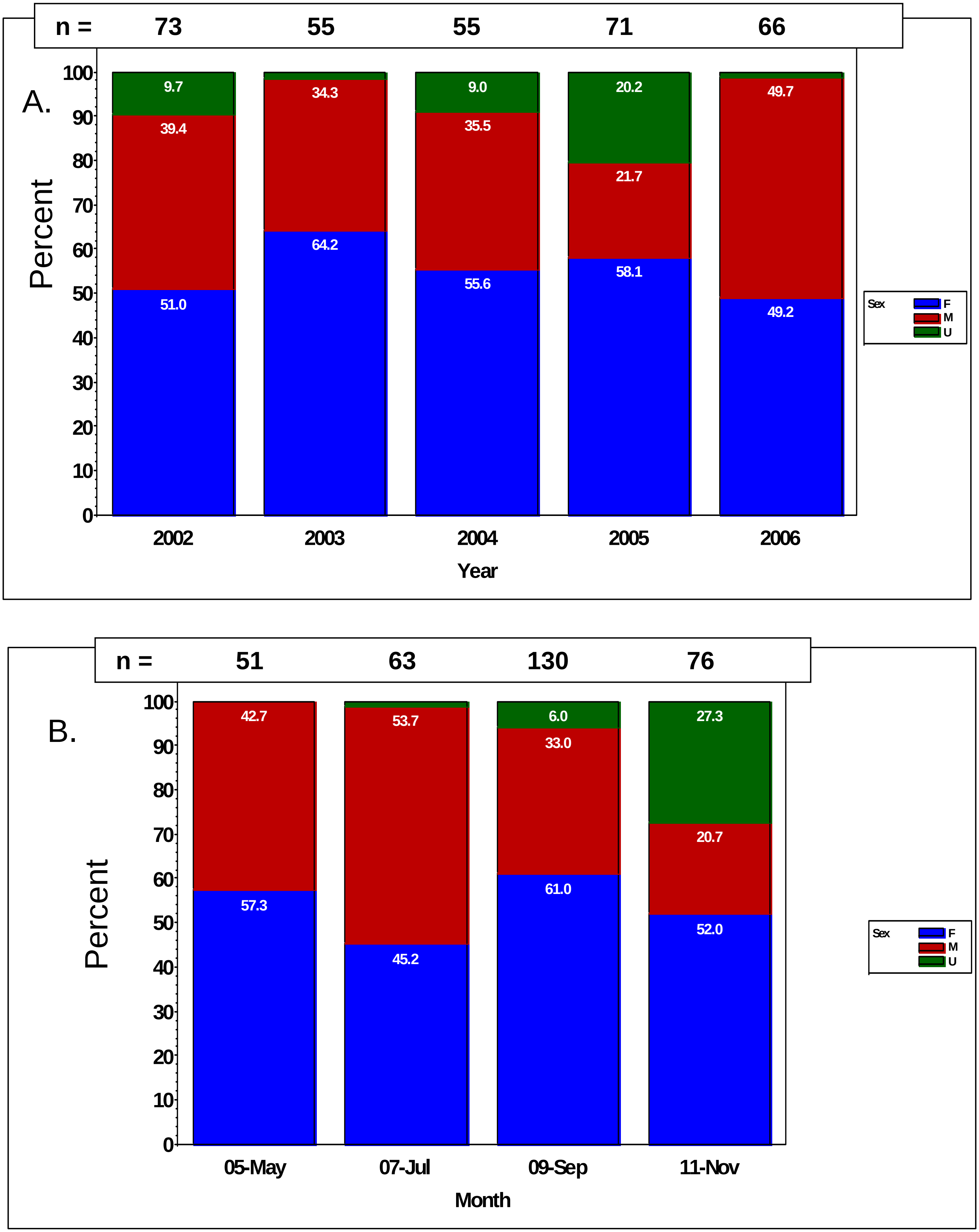
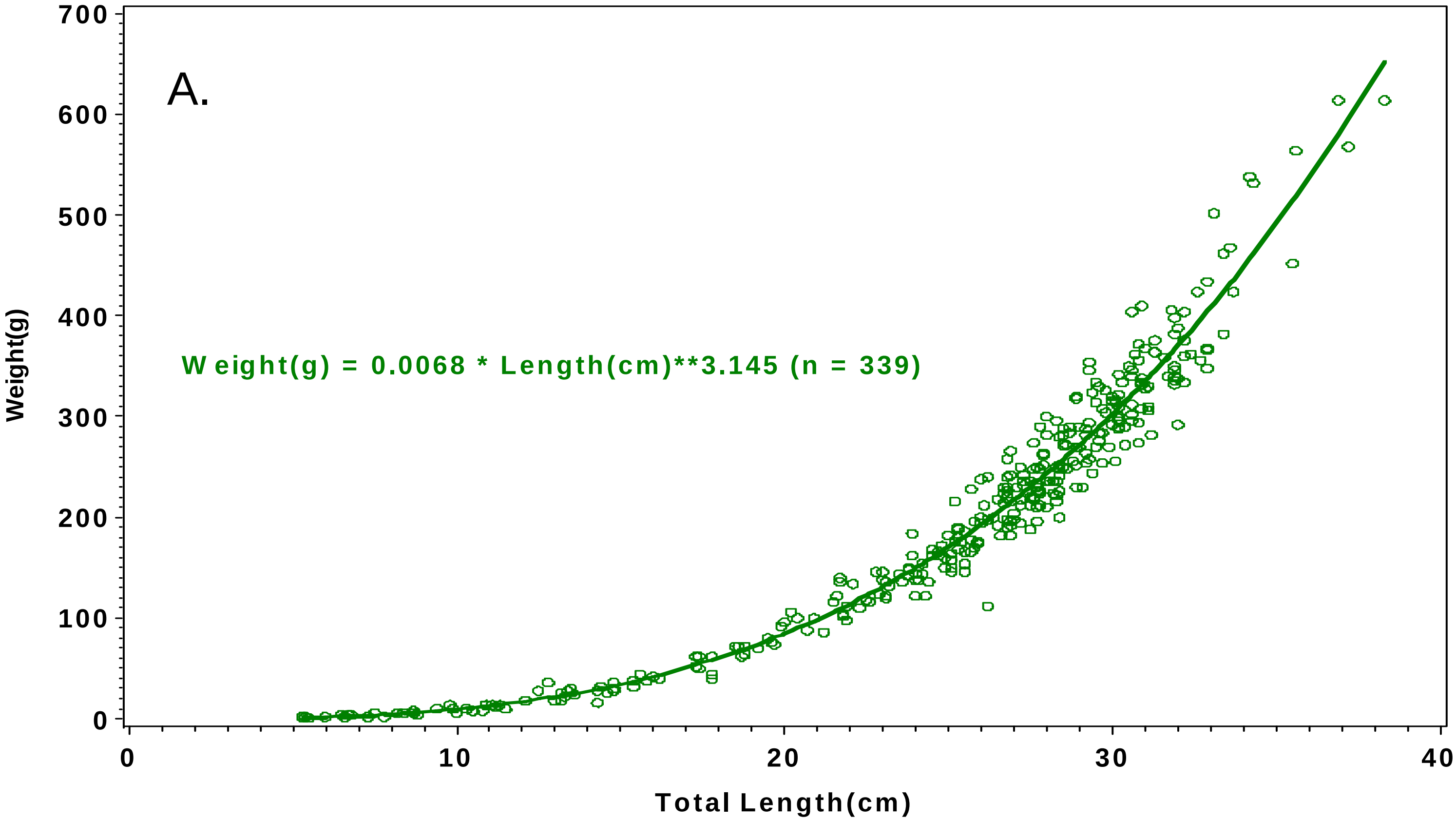


Figure 49. Northern kingfish length-weight relationships in Chesapeake Bay 2002-2006 as calculated by power regression for sexes combined (A) and separately (B).



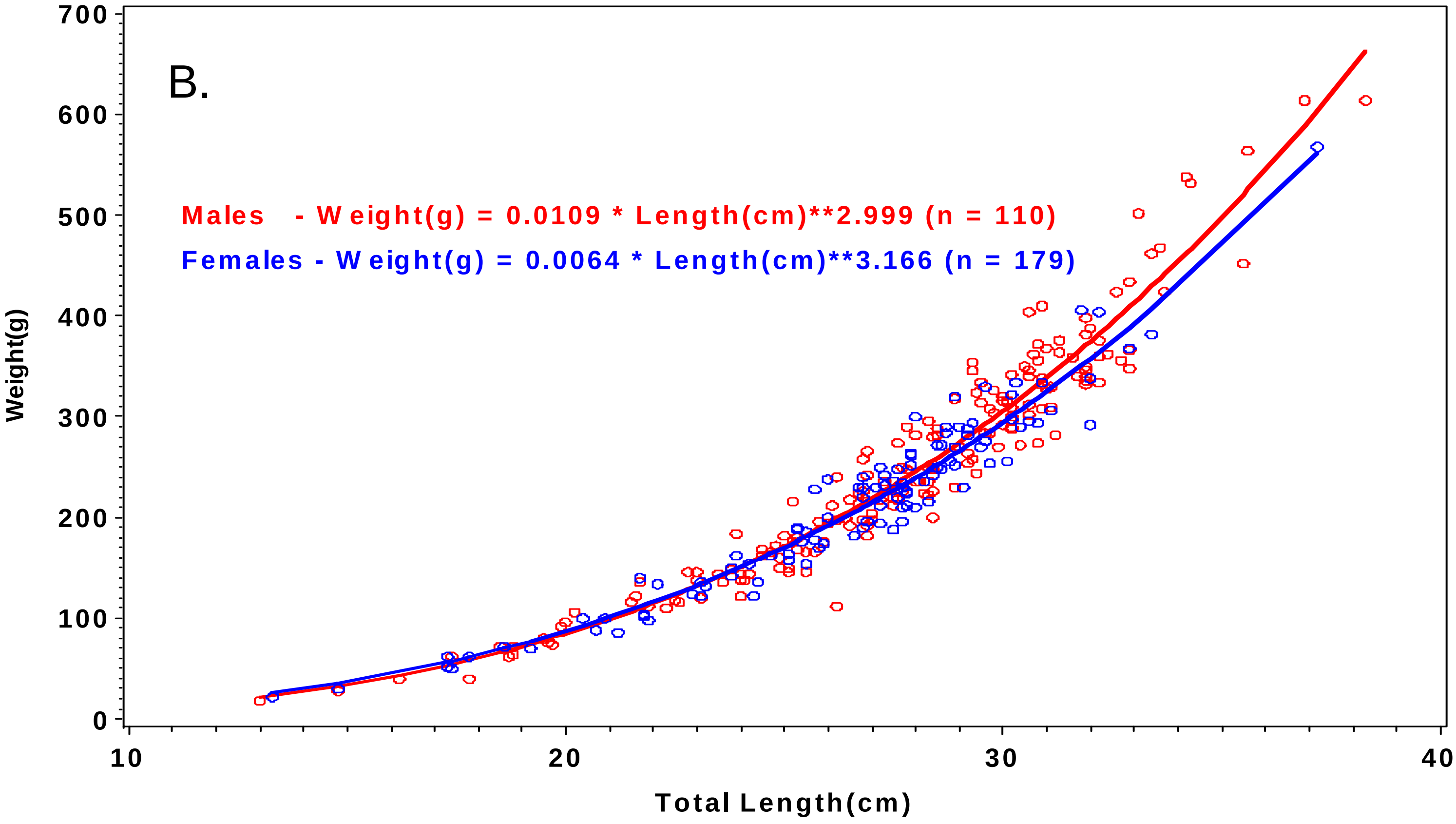


Figure 50. Northern kingfish maturity schedule in Chesapeake Bay 2002-2006 combined, by sex.

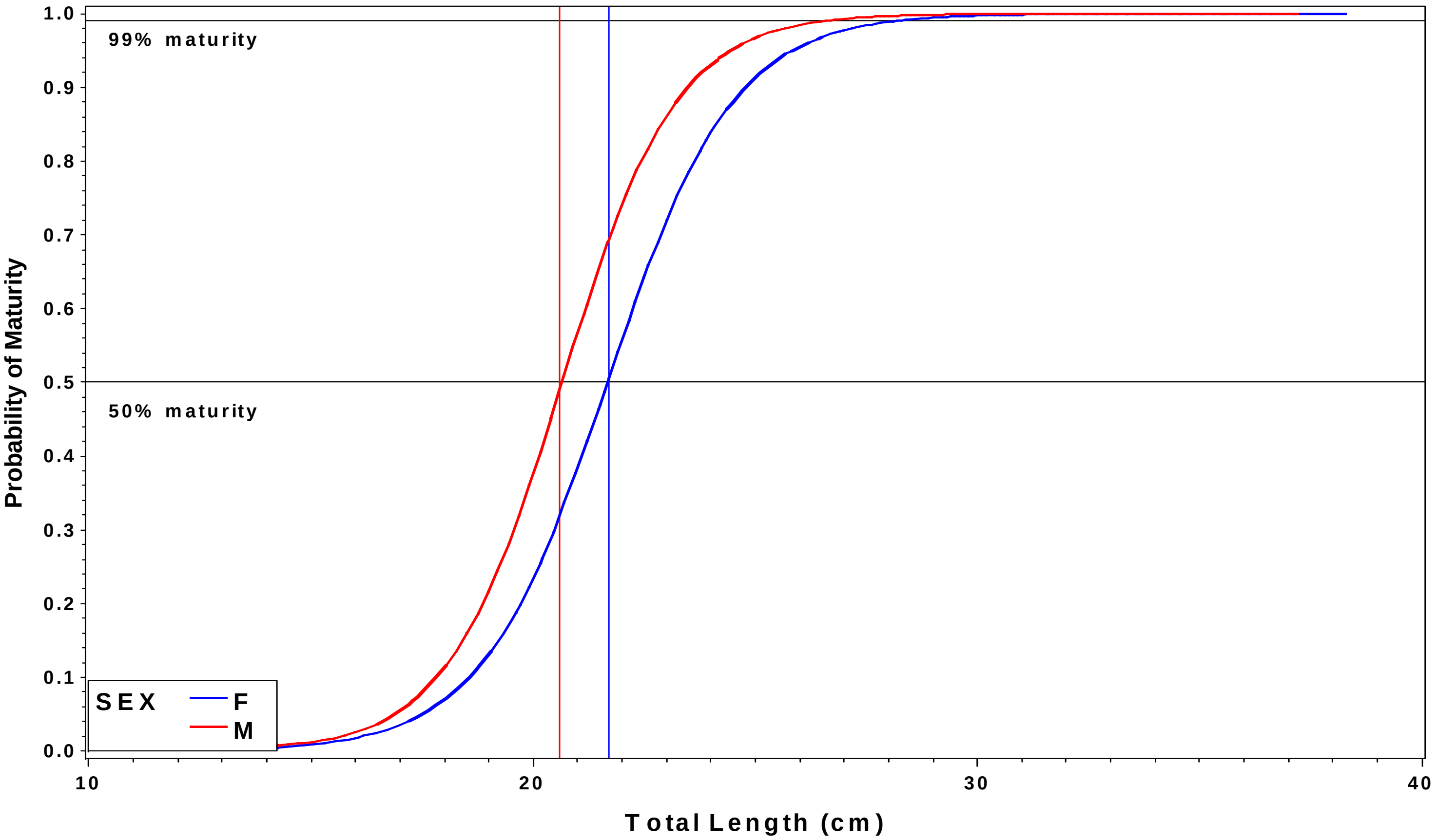


Figure 51. Northern kingfish diet in Chesapeake Bay 2002-2006 combined.

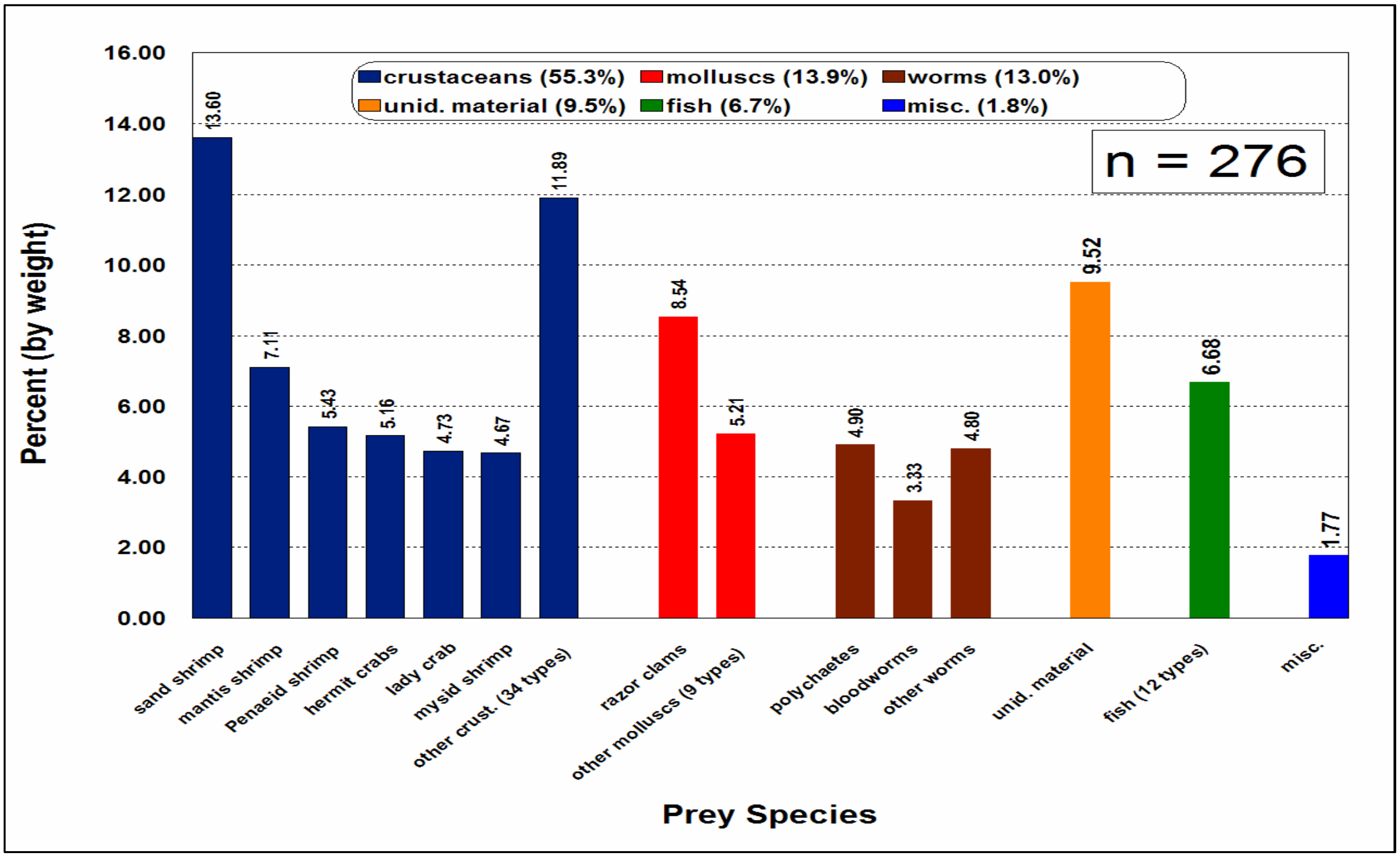
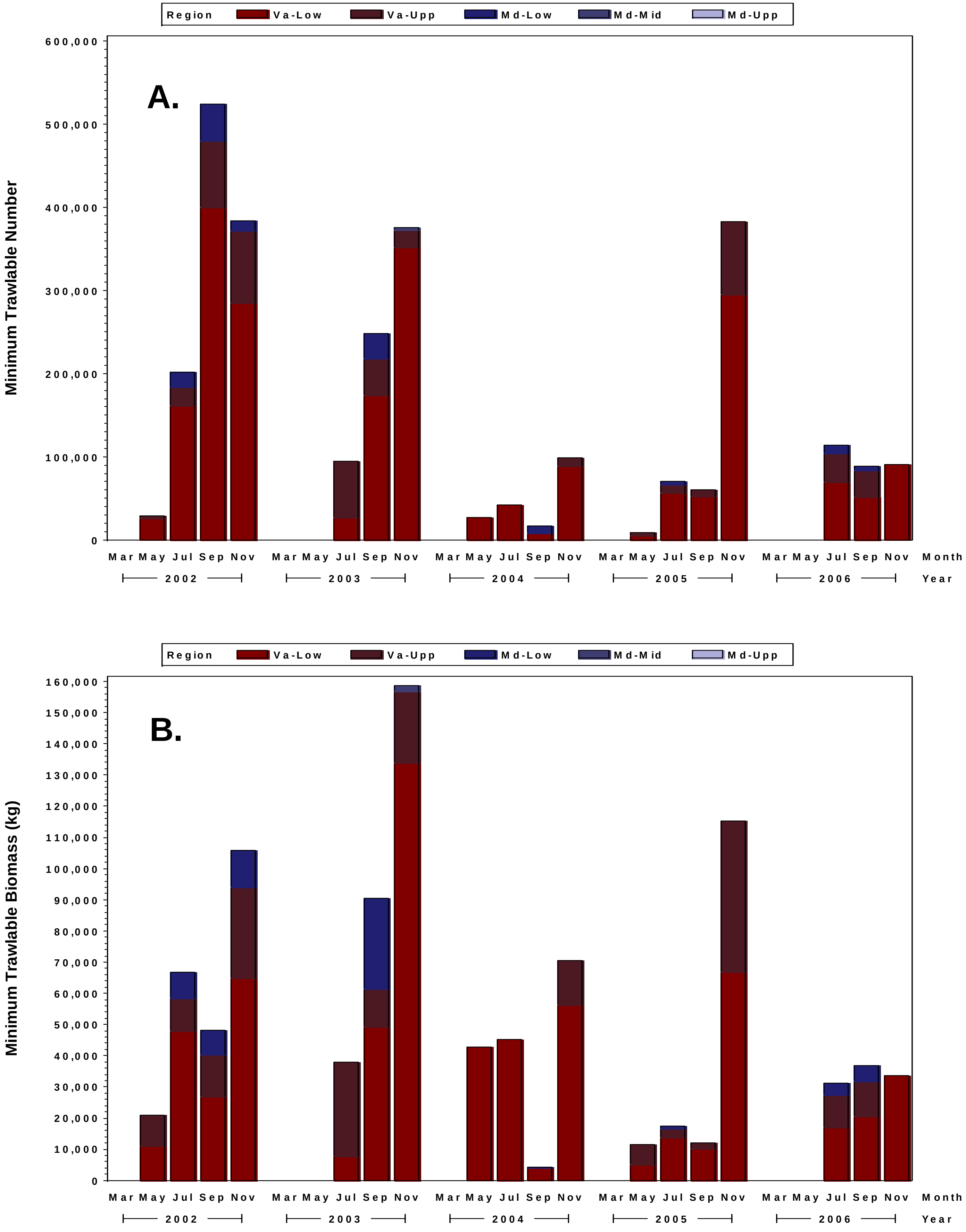


Figure 52. Northern puffer minimum trawlable abundance estimates in numbers (A) and biomass (B) in Chesapeake Bay 2002-2006.



Note: This species is not captured in enough abundance to create meaningful abundance maps.

Figure 53. Northern puffer length-frequency in Chesapeake Bay 2002-2006.

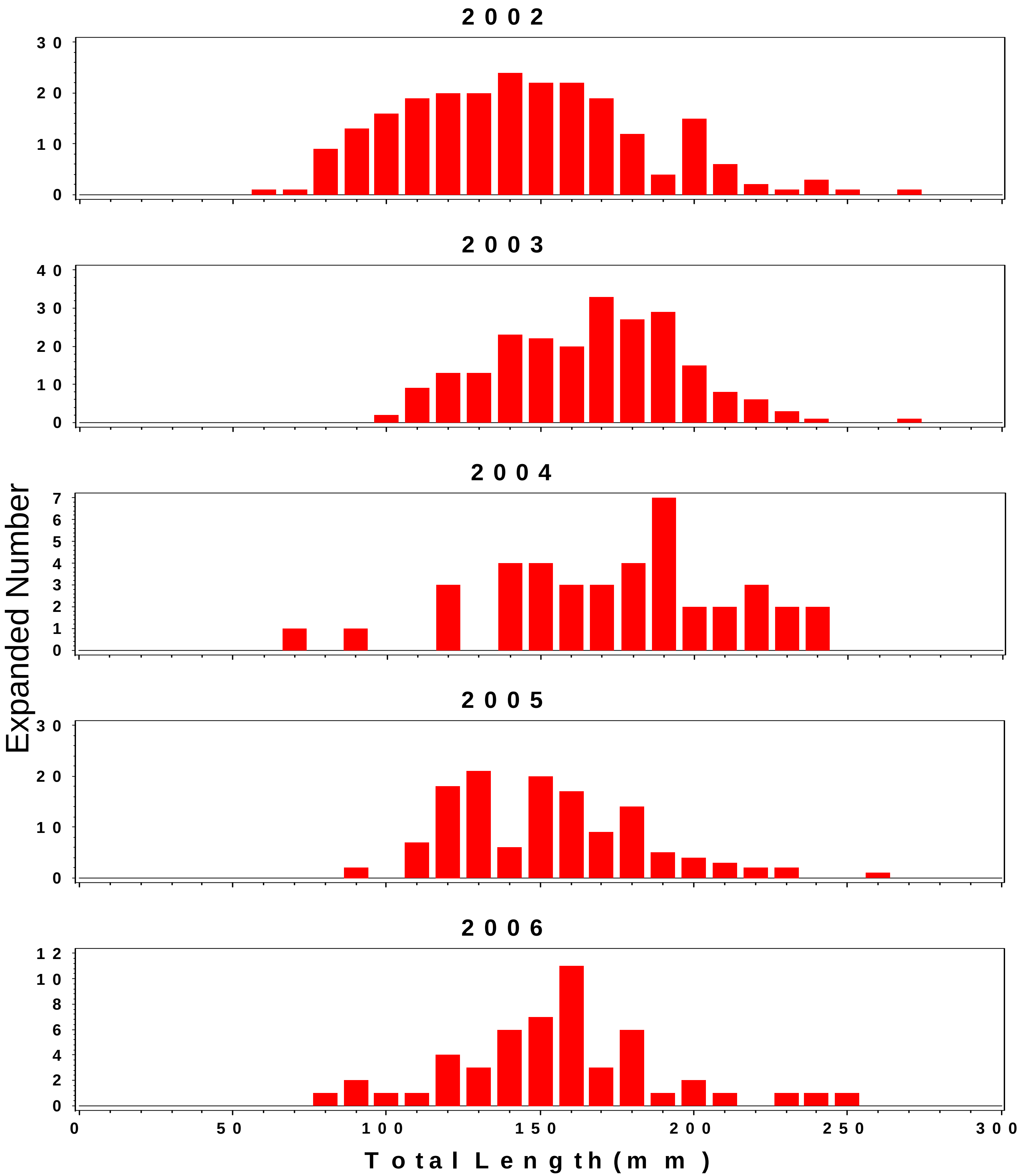


Figure 54. Northern puffer sex-ratios in Chesapeake Bay 2002-2006, by year (A), month (B).

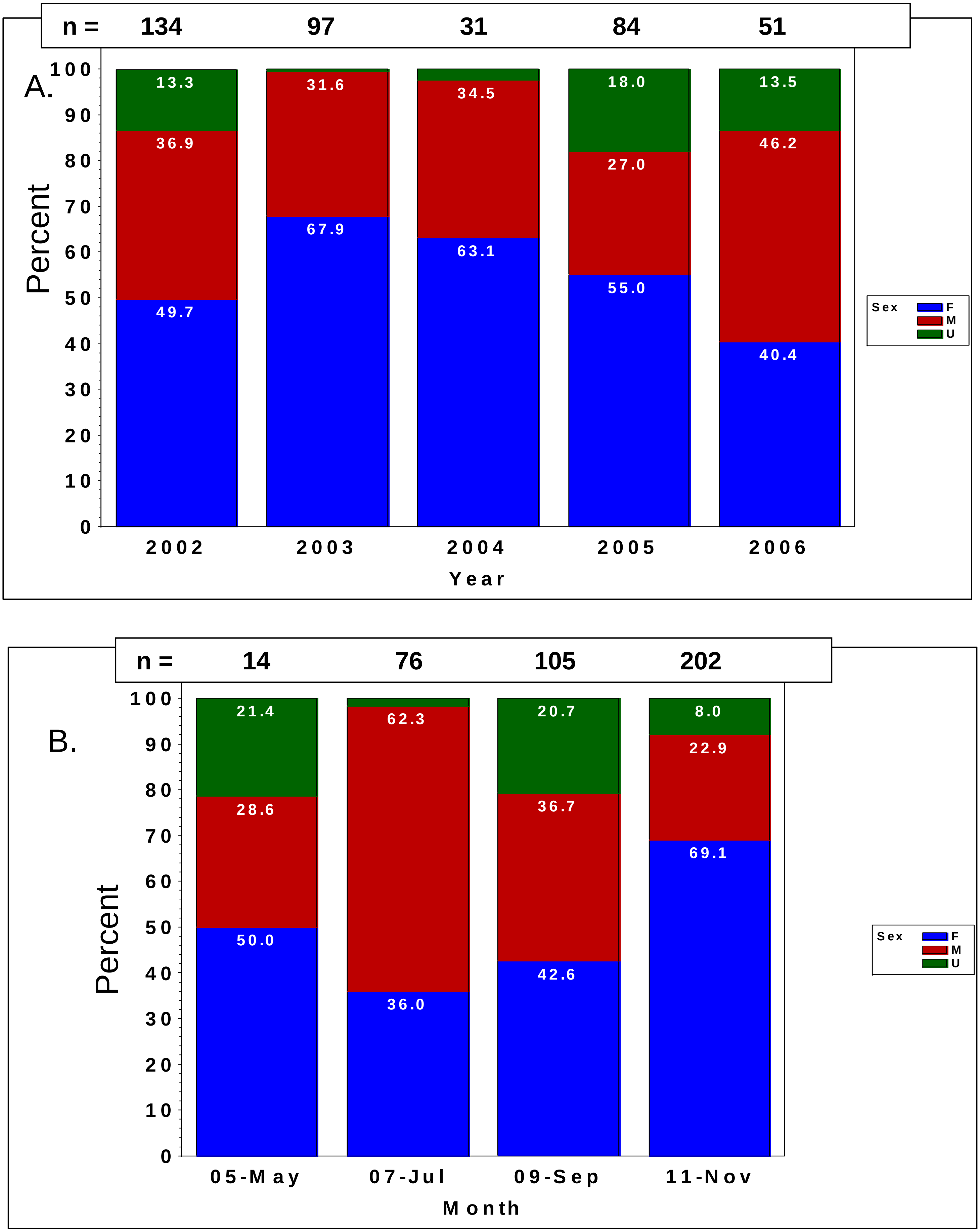
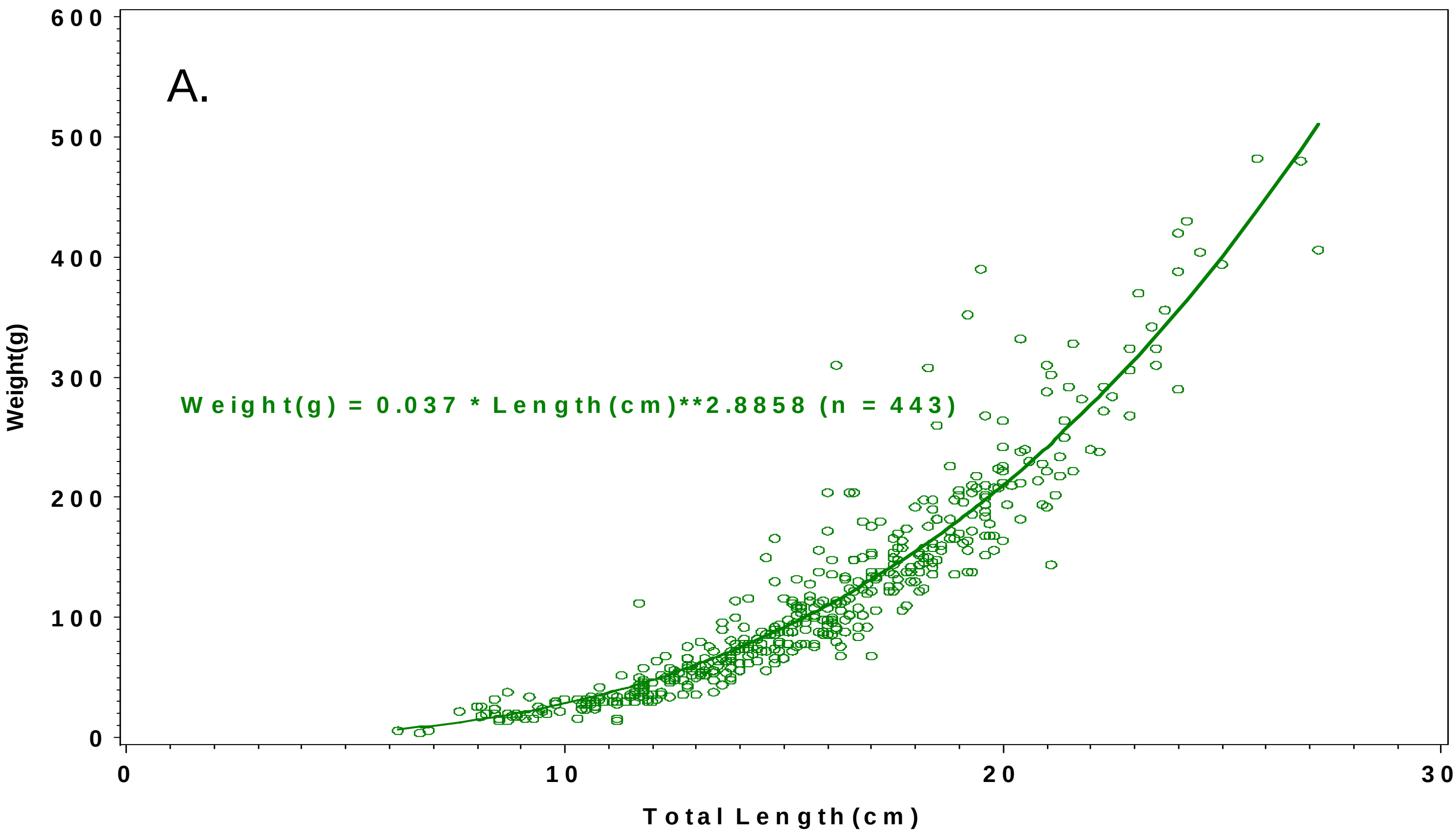


Figure 55. Northern puffer length-weight relationships in Chesapeake Bay 2002-2006 as calculated by power regression for sexes combined (A) and separately (B).



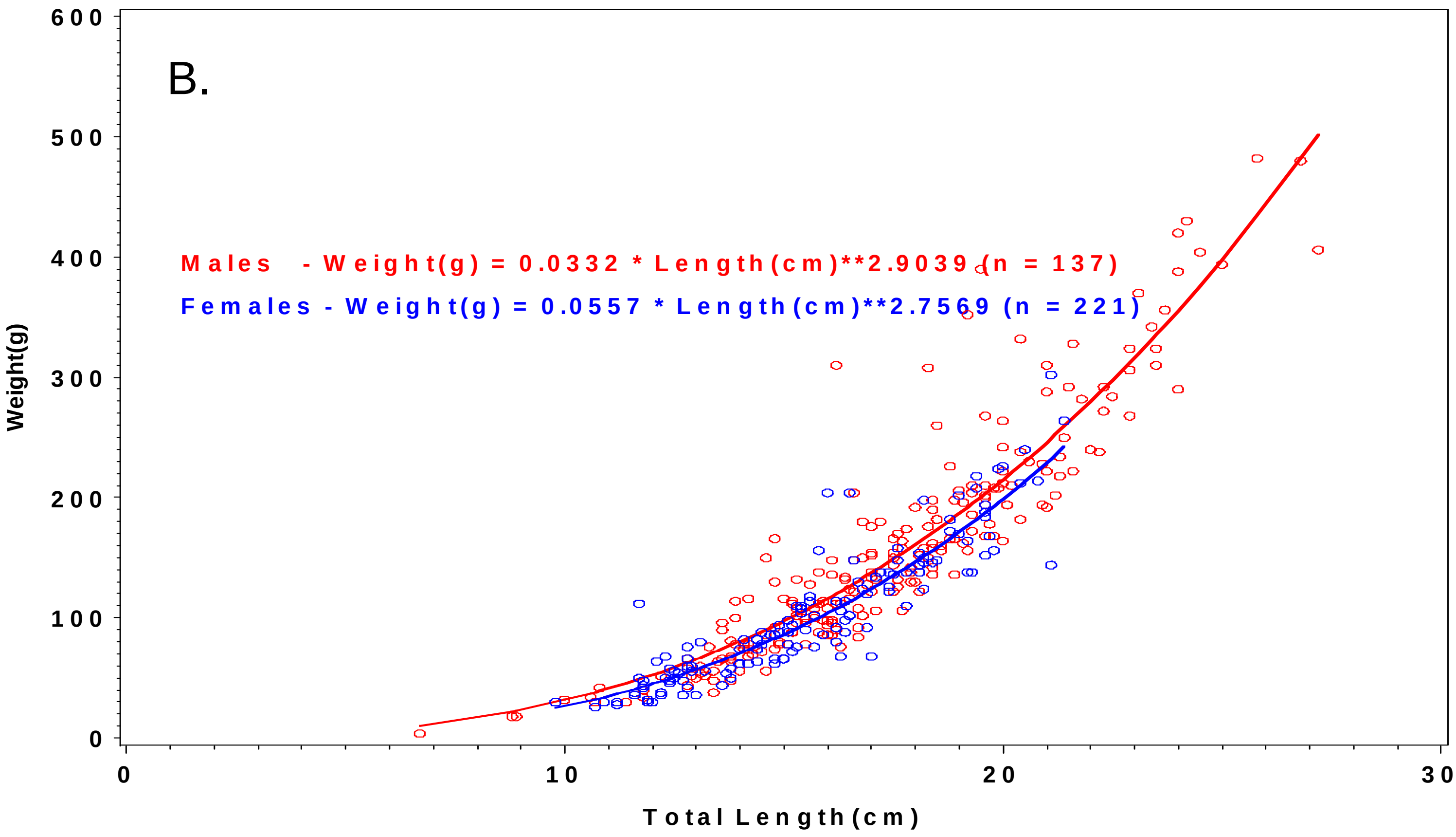


Figure 56. Northern puffer maturity schedule in Chesapeake Bay 2002-2006 combined, by sex.

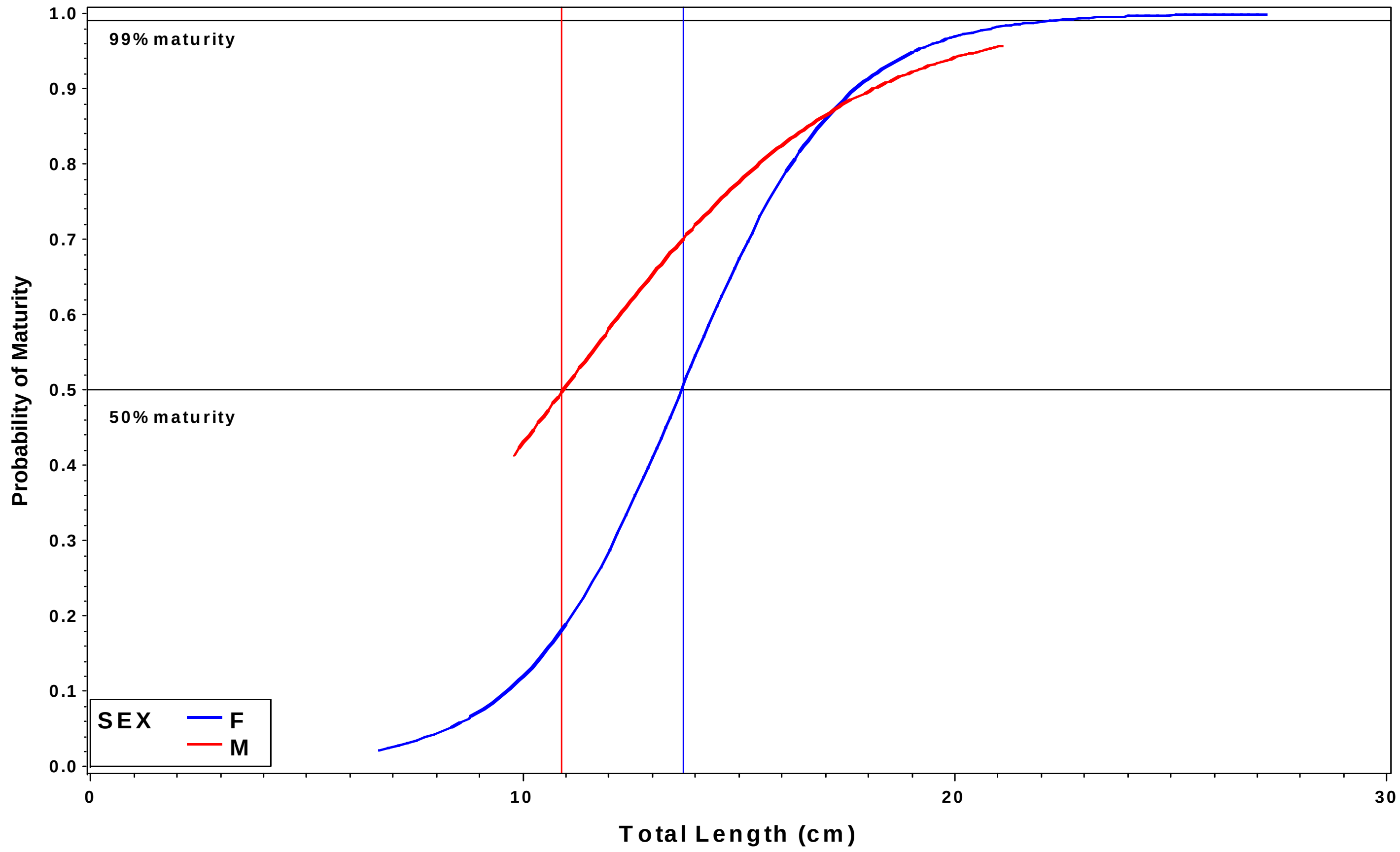


Figure 57. Northern puffer diet in Chesapeake Bay 2002-2006 combined.

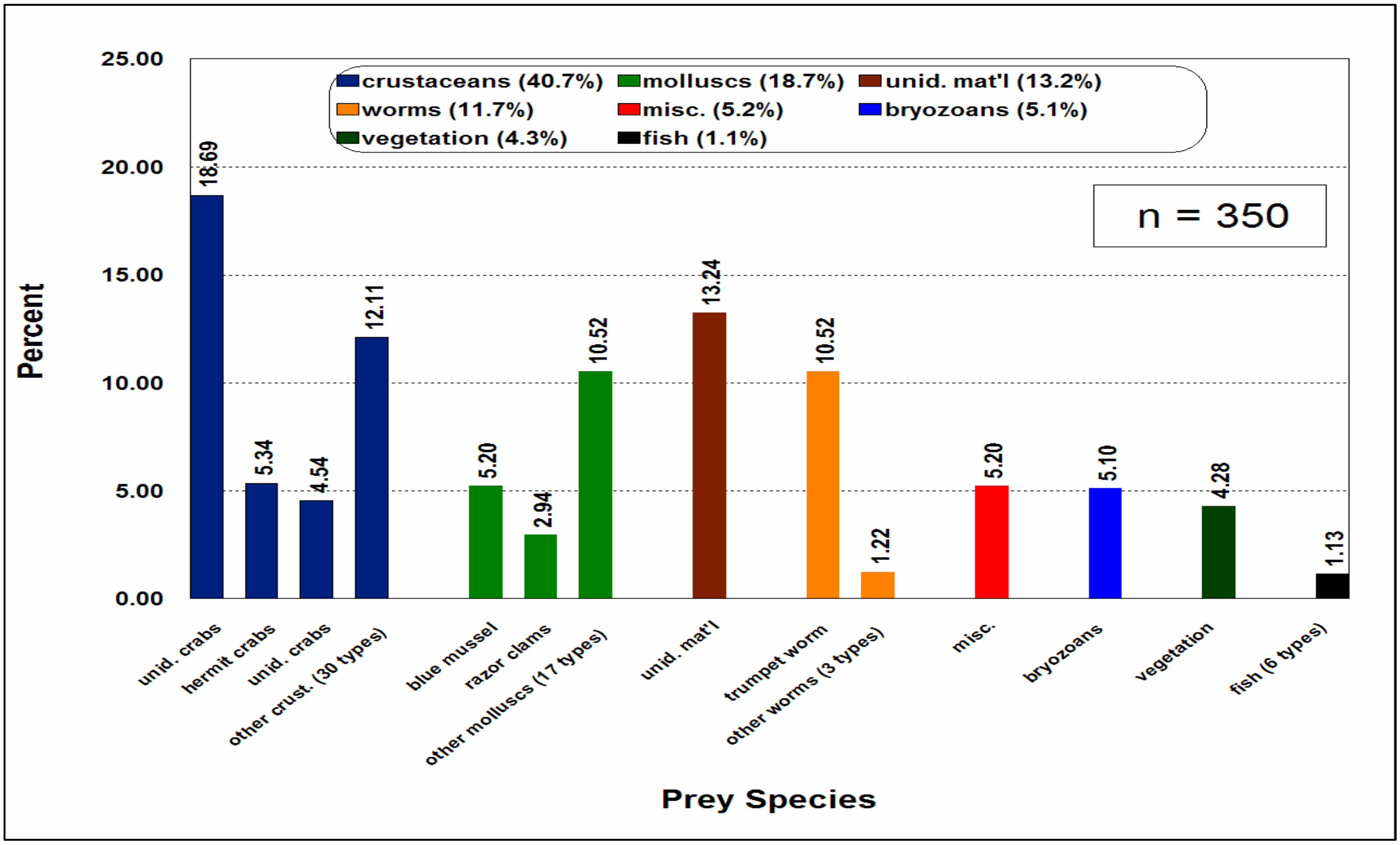
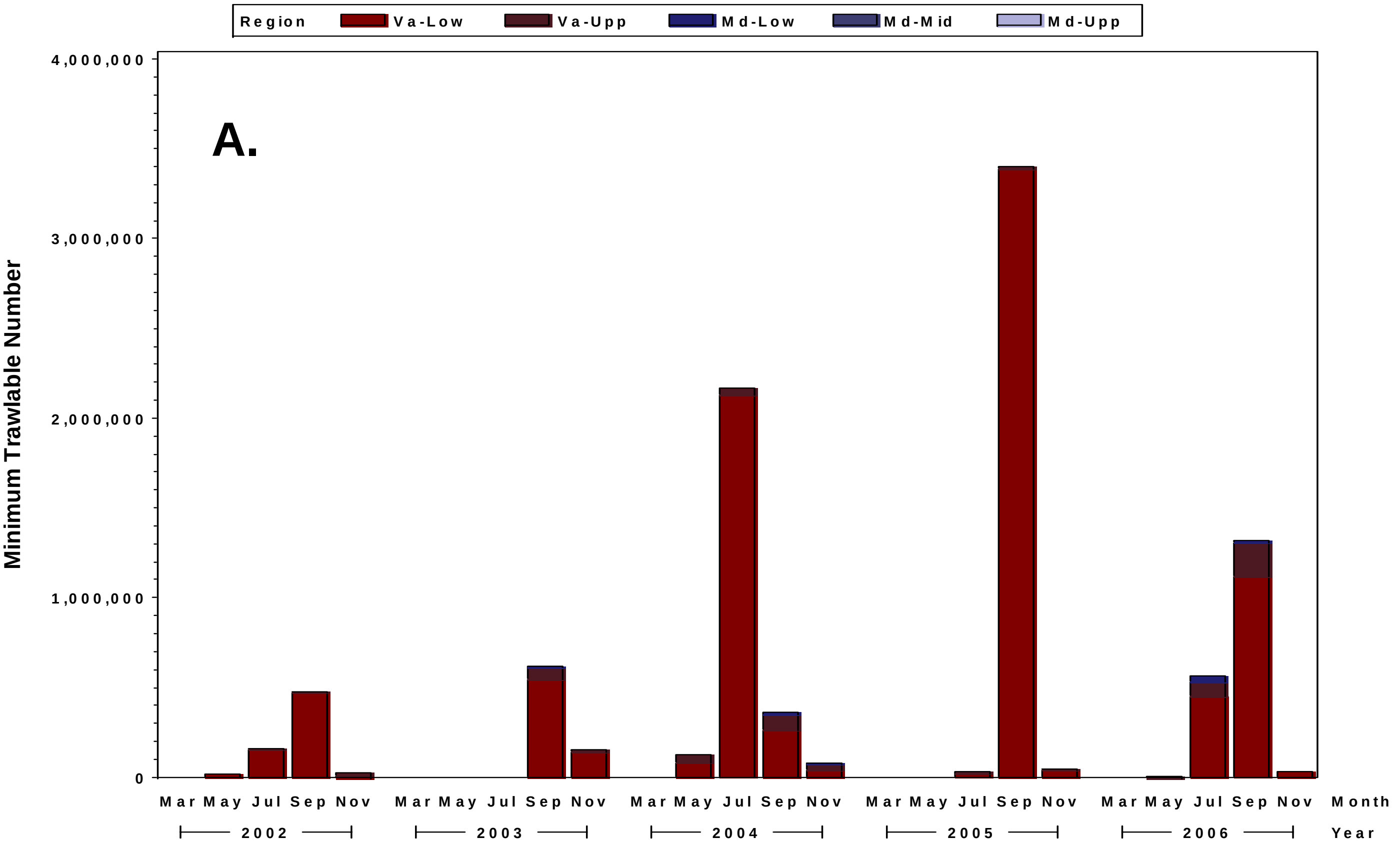


Figure 58. Scup minimum trawlable abundance estimates in numbers (A) and biomass (B) in Chesapeake Bay 2002-2006.



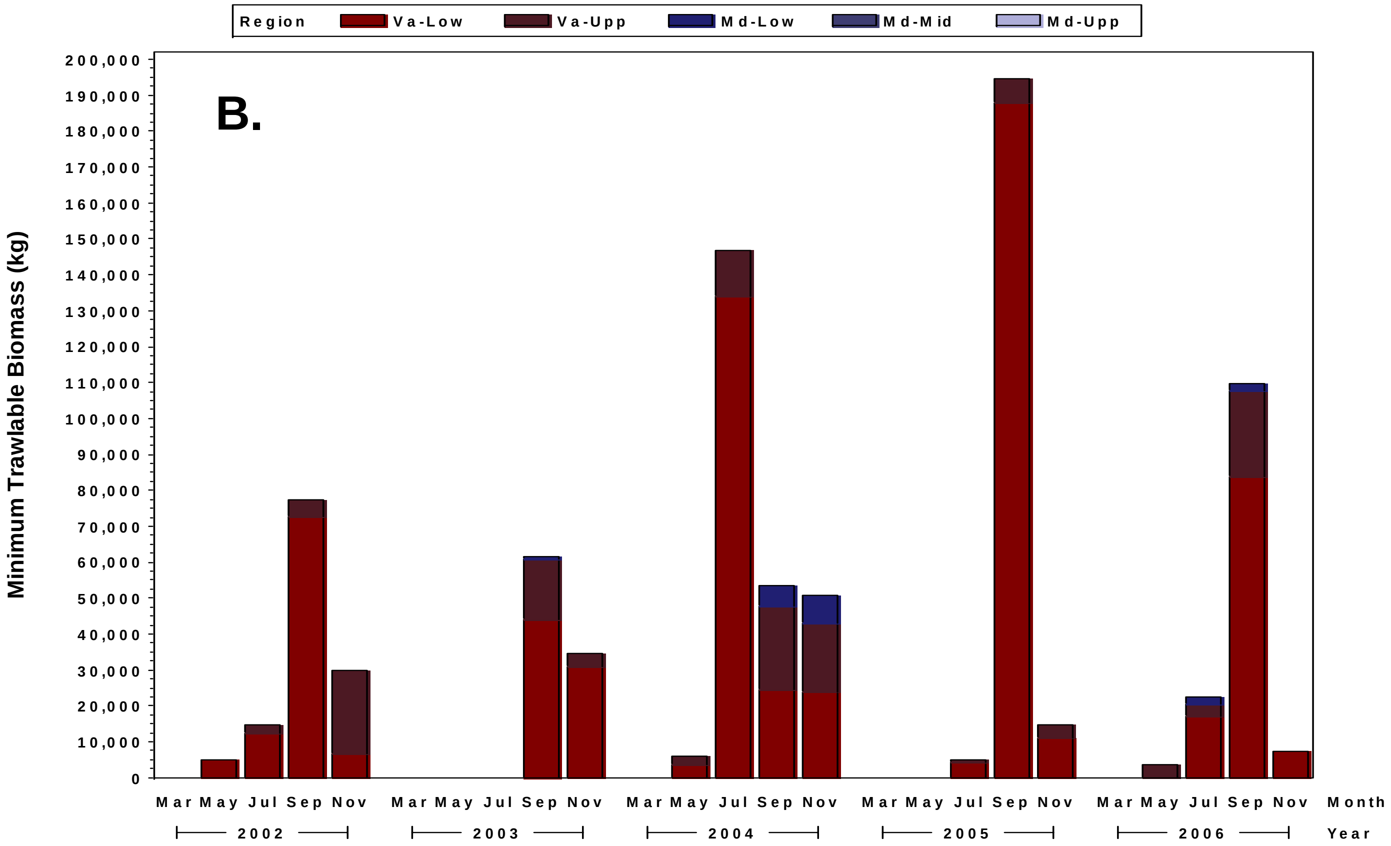


Figure 59. Abundance (number per hectare swept) of scup in Chesapeake Bay, 2002.

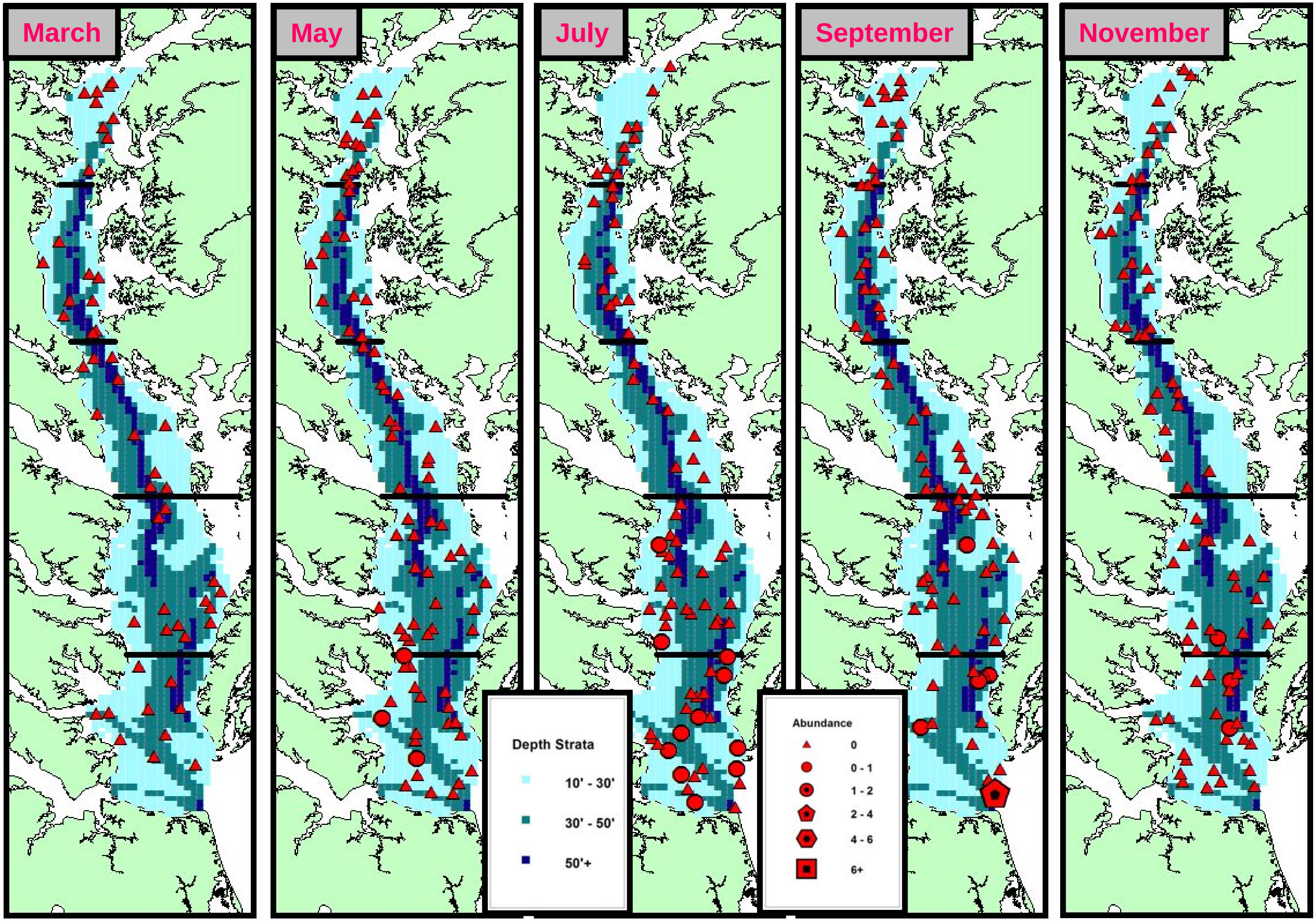


Figure 60. Abundance (number per hectare swept) of scup in Chesapeake Bay, 2003.

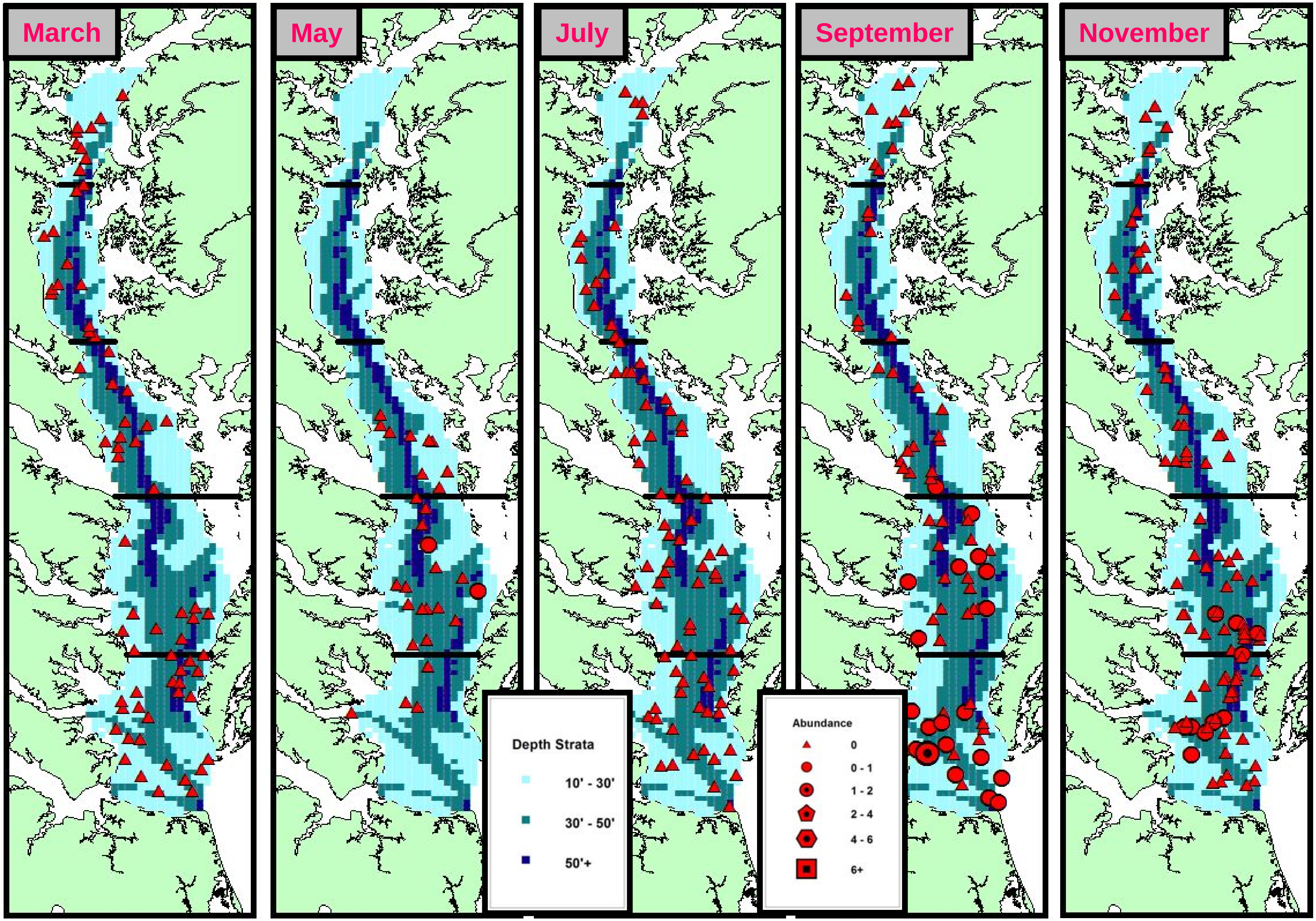


Figure 61. Abundance (number per hectare swept) of scup in Chesapeake Bay, 2004.

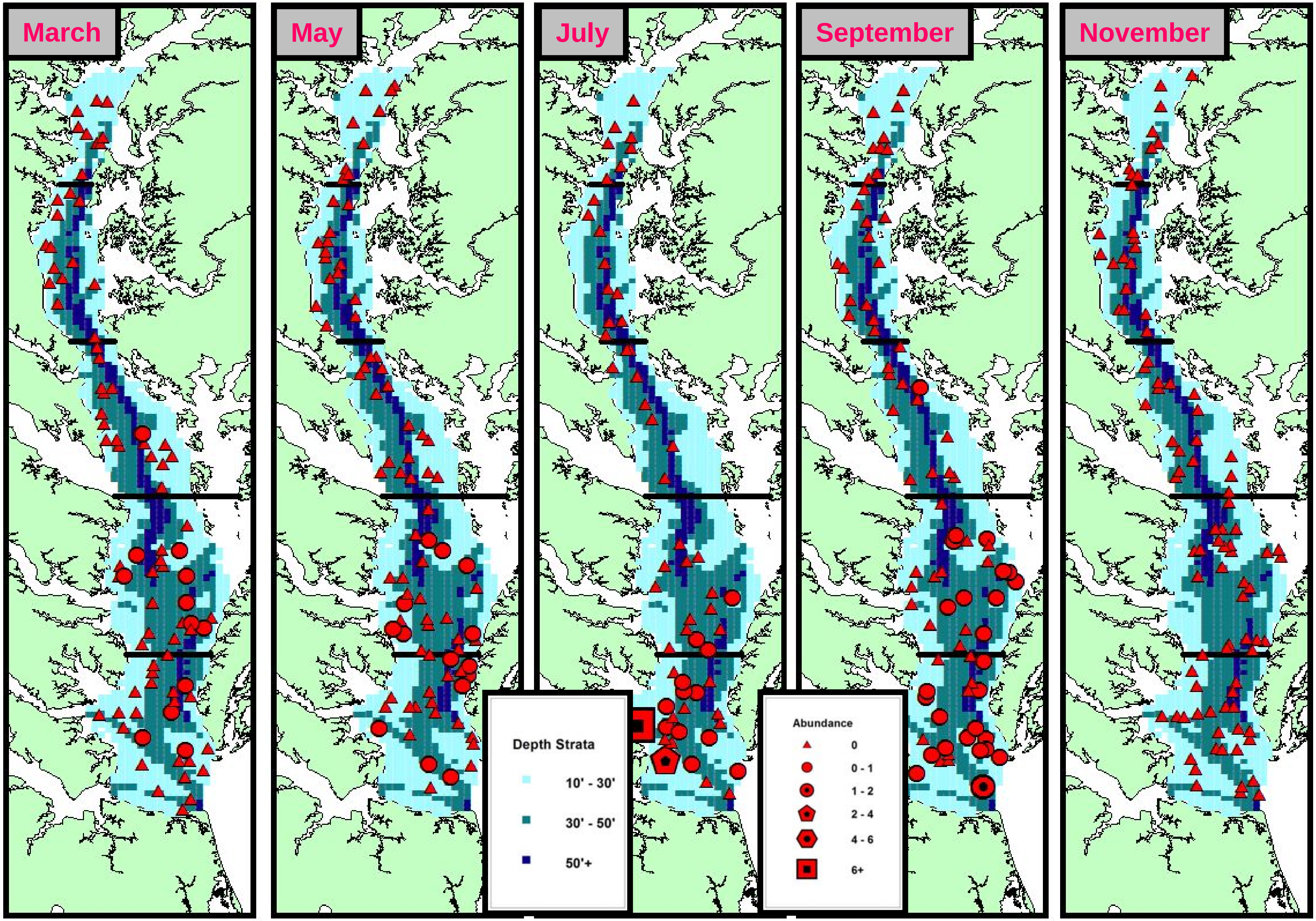


Figure 62. Abundance (number per hectare swept) of scup in Chesapeake Bay, 2005.

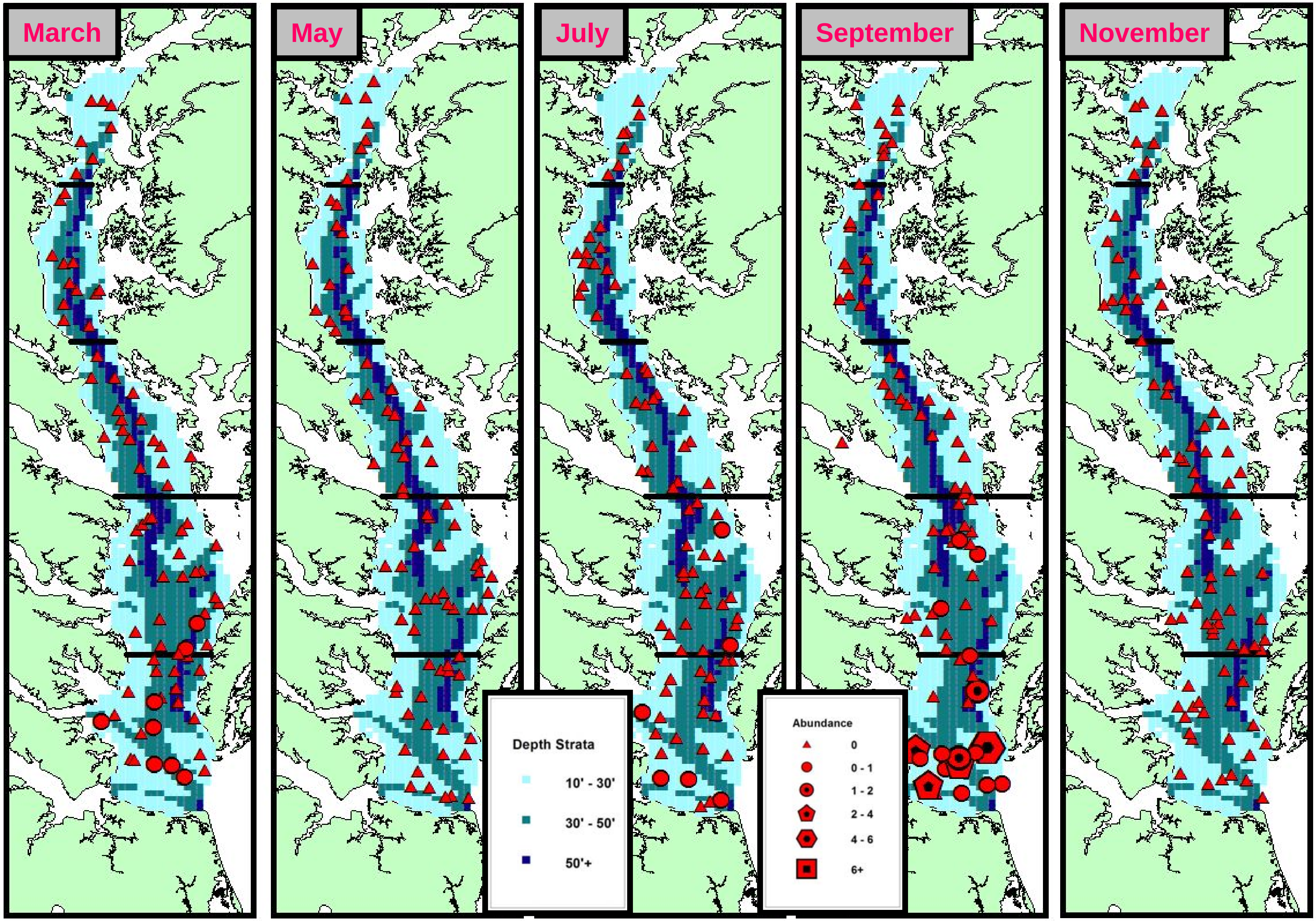


Figure 63. Abundance (number per hectare swept) of scup in Chesapeake Bay, 2006.

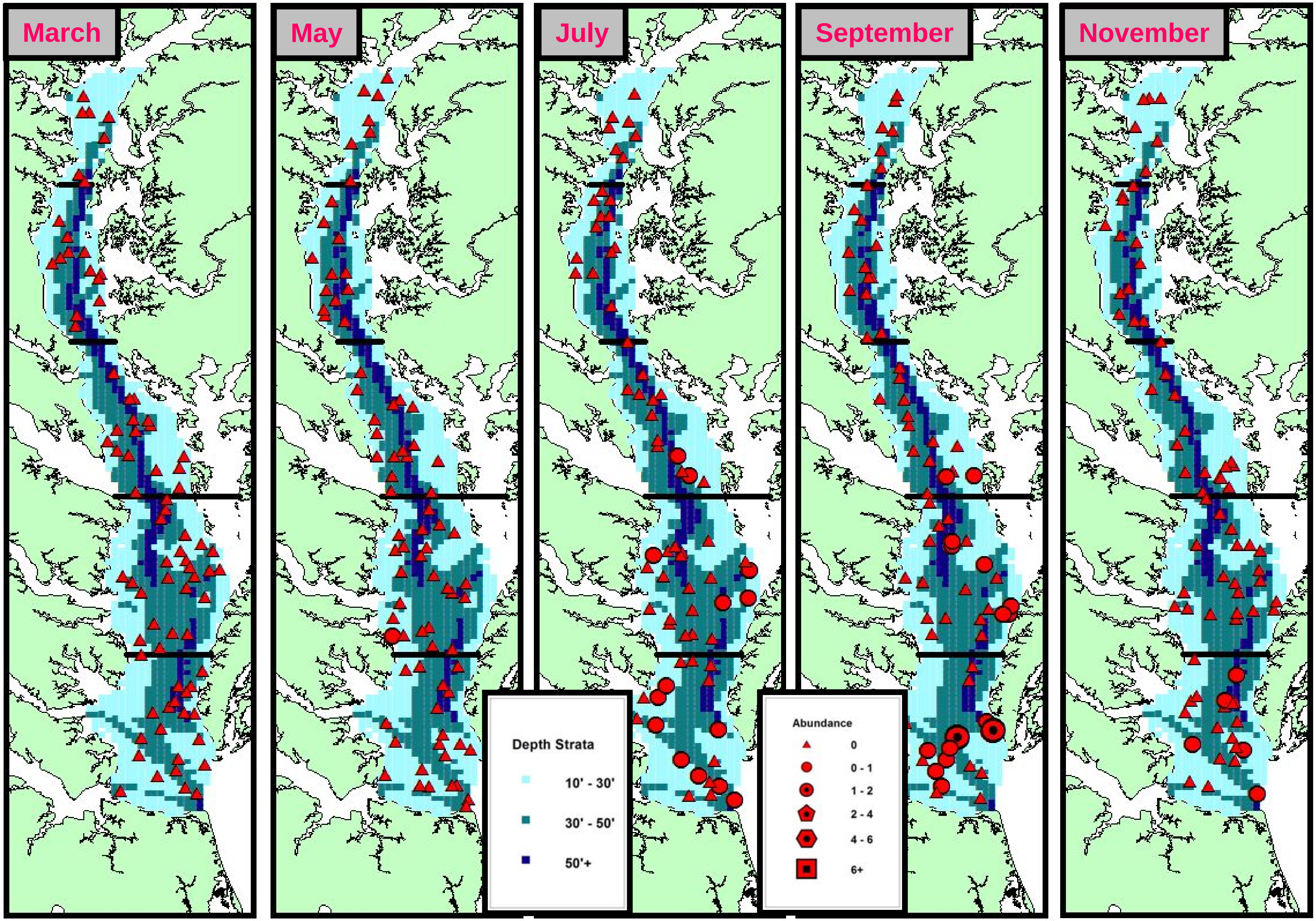


Figure 64. Scup length-frequency in Chesapeake Bay 2002-2006.

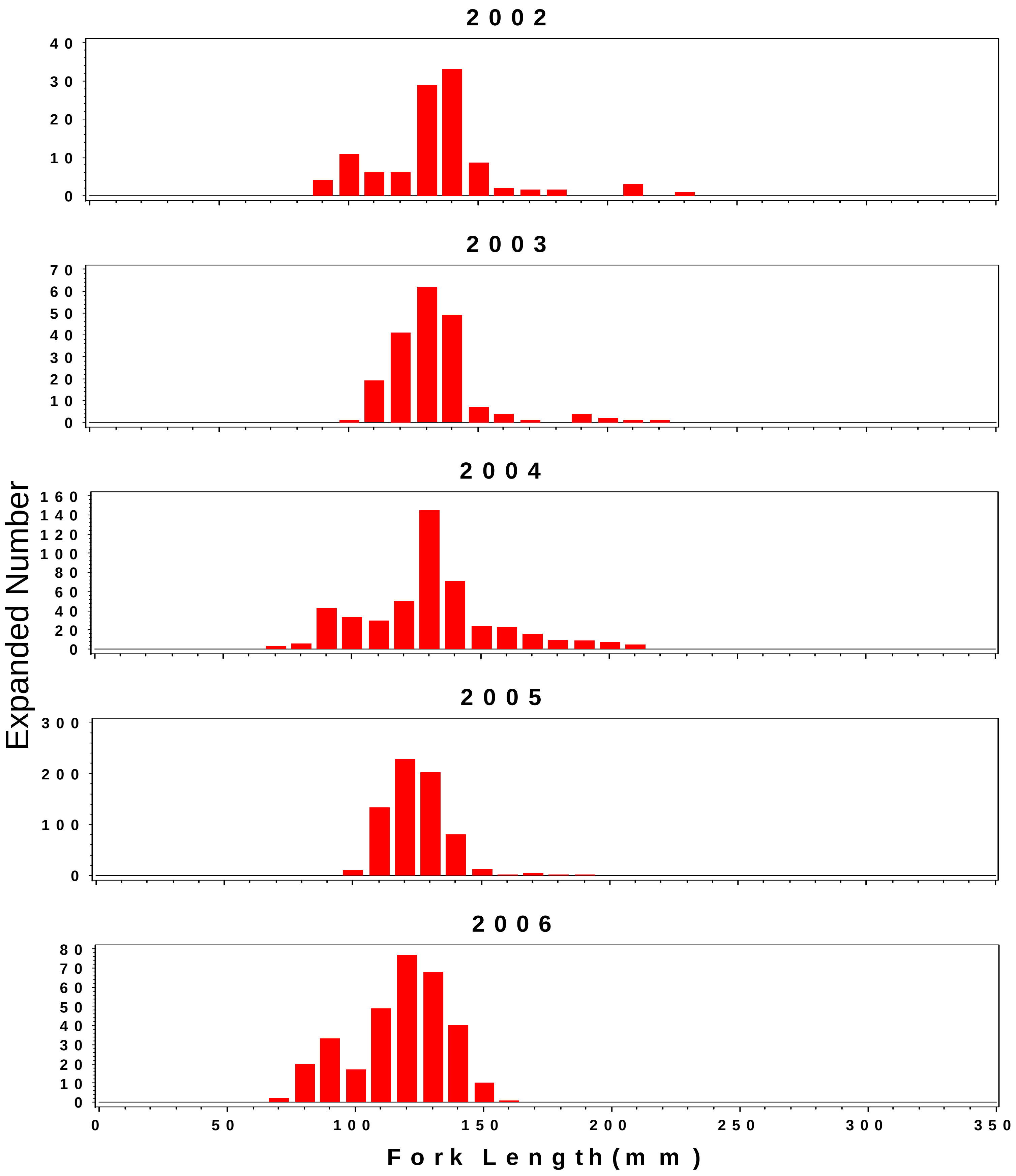


Figure 65. Scup sex-ratios in Chesapeake Bay 2002-2005, by year (A) and month (B).

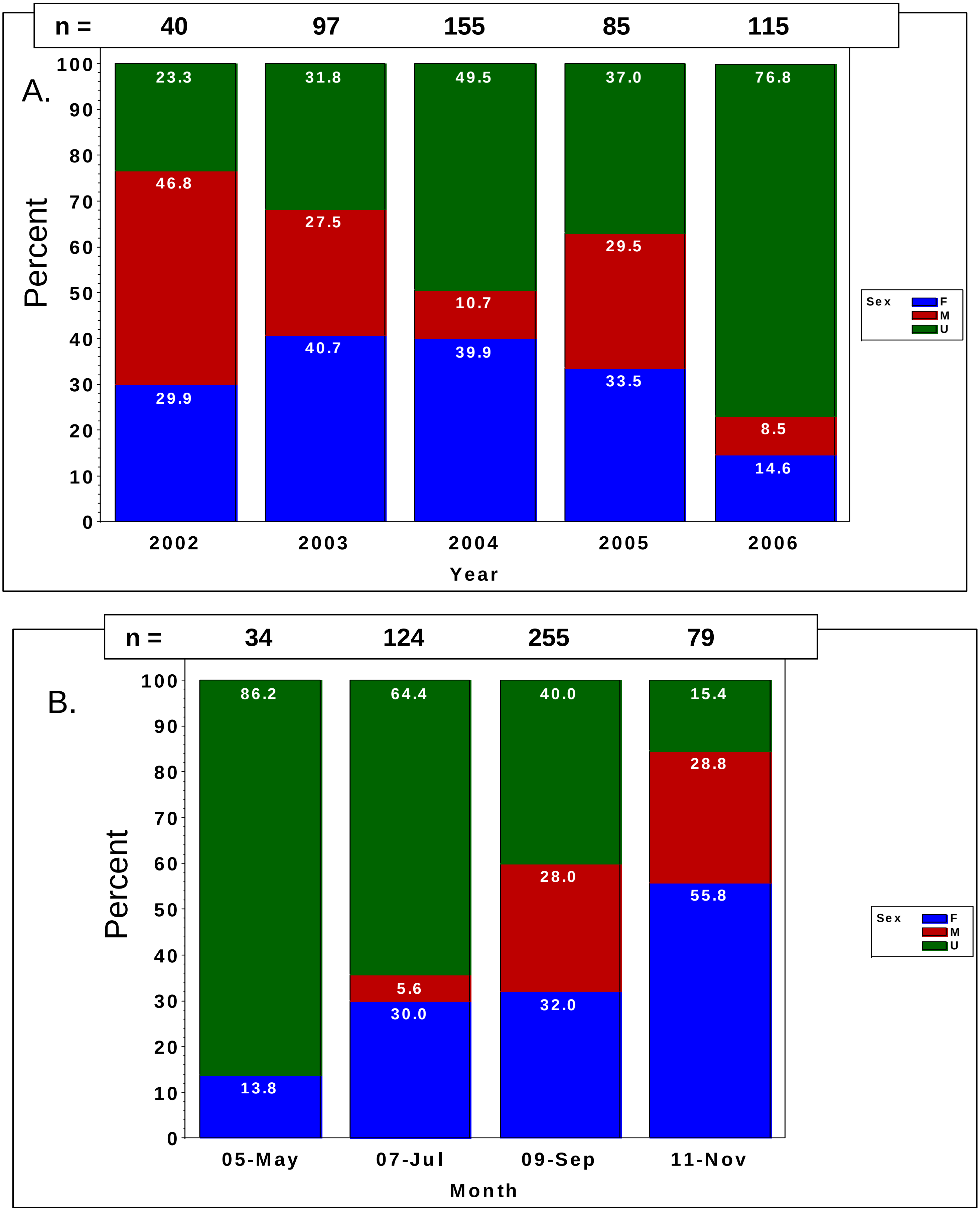
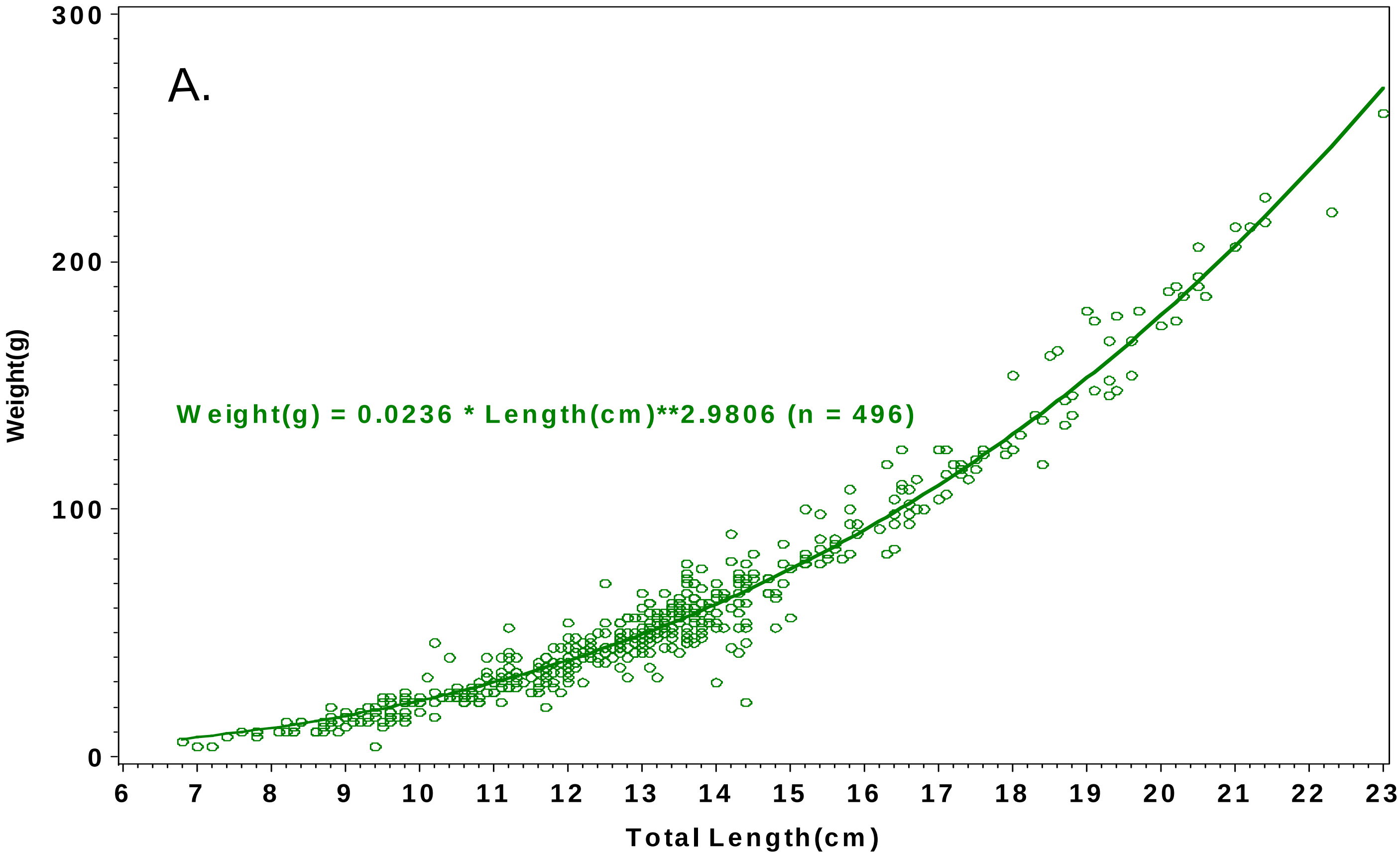


Figure 66. Scup length-weight relationships in Chesapeake Bay 2002-2006 as calculated by power regression for sexes combined (A) and separately (B).



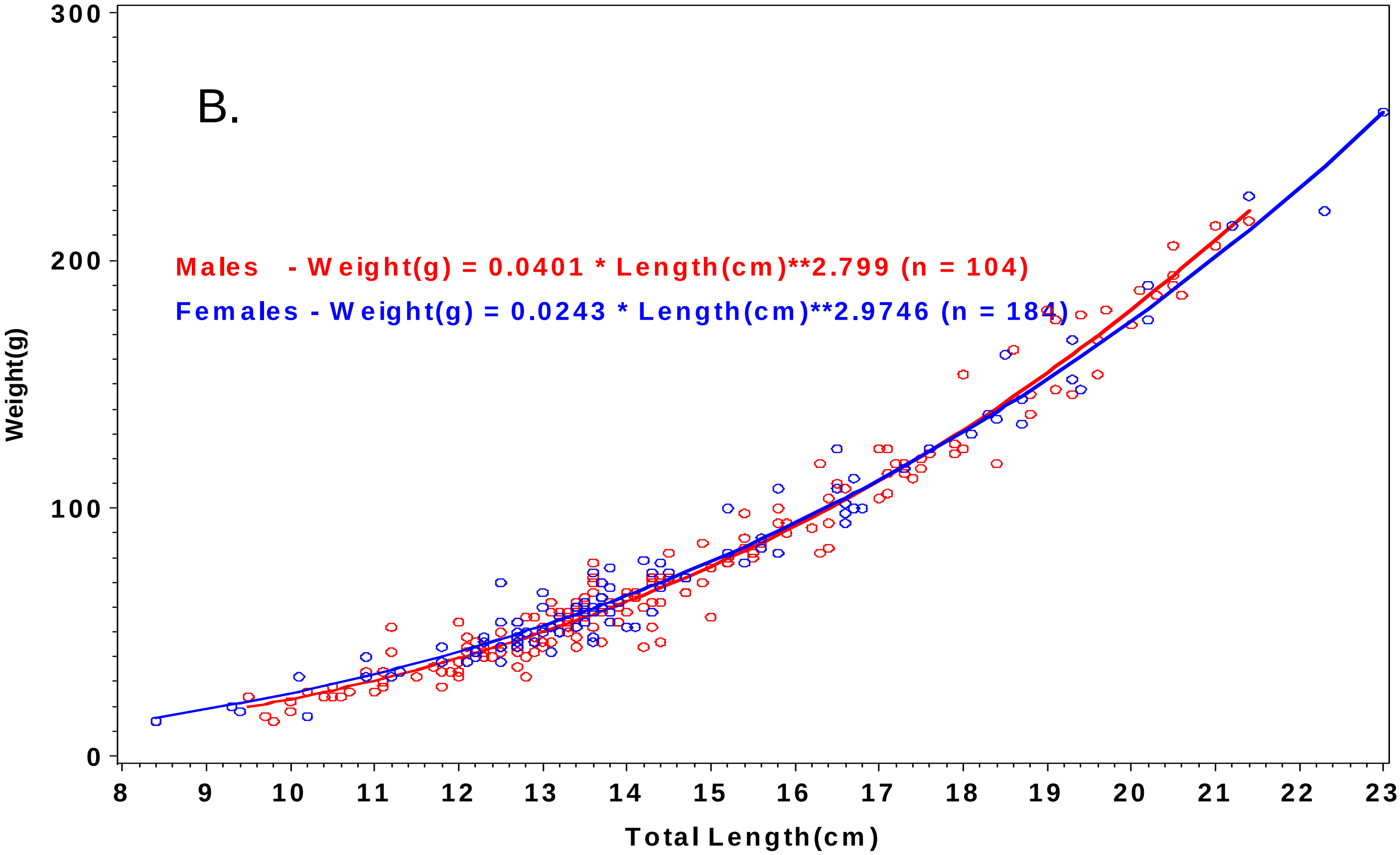


Figure 67. Scup maturity schedule in Chesapeake Bay 2002-2006 combined, by sex.

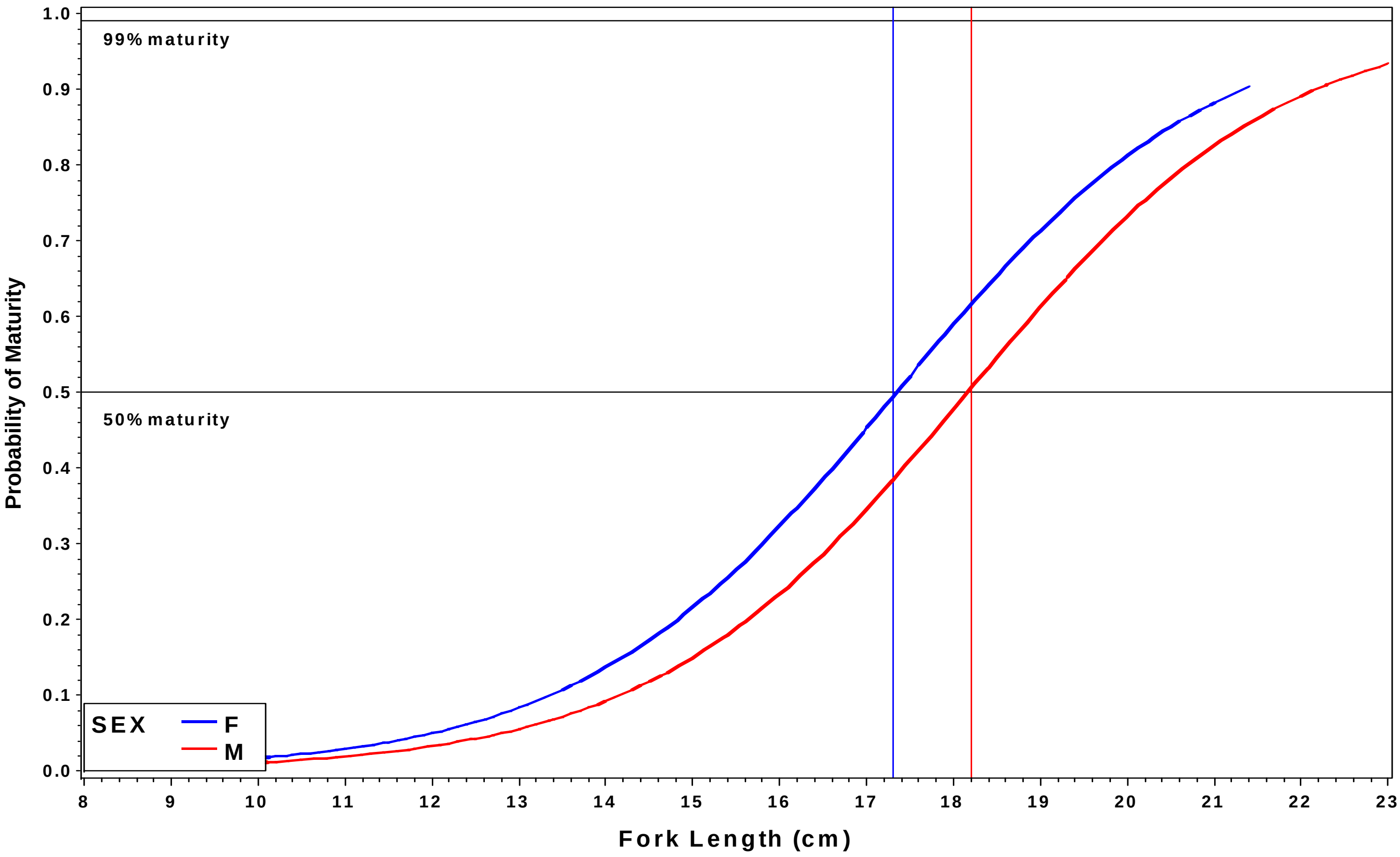


Figure 68. Scup diet in Chesapeake Bay 2002-2006 combined.

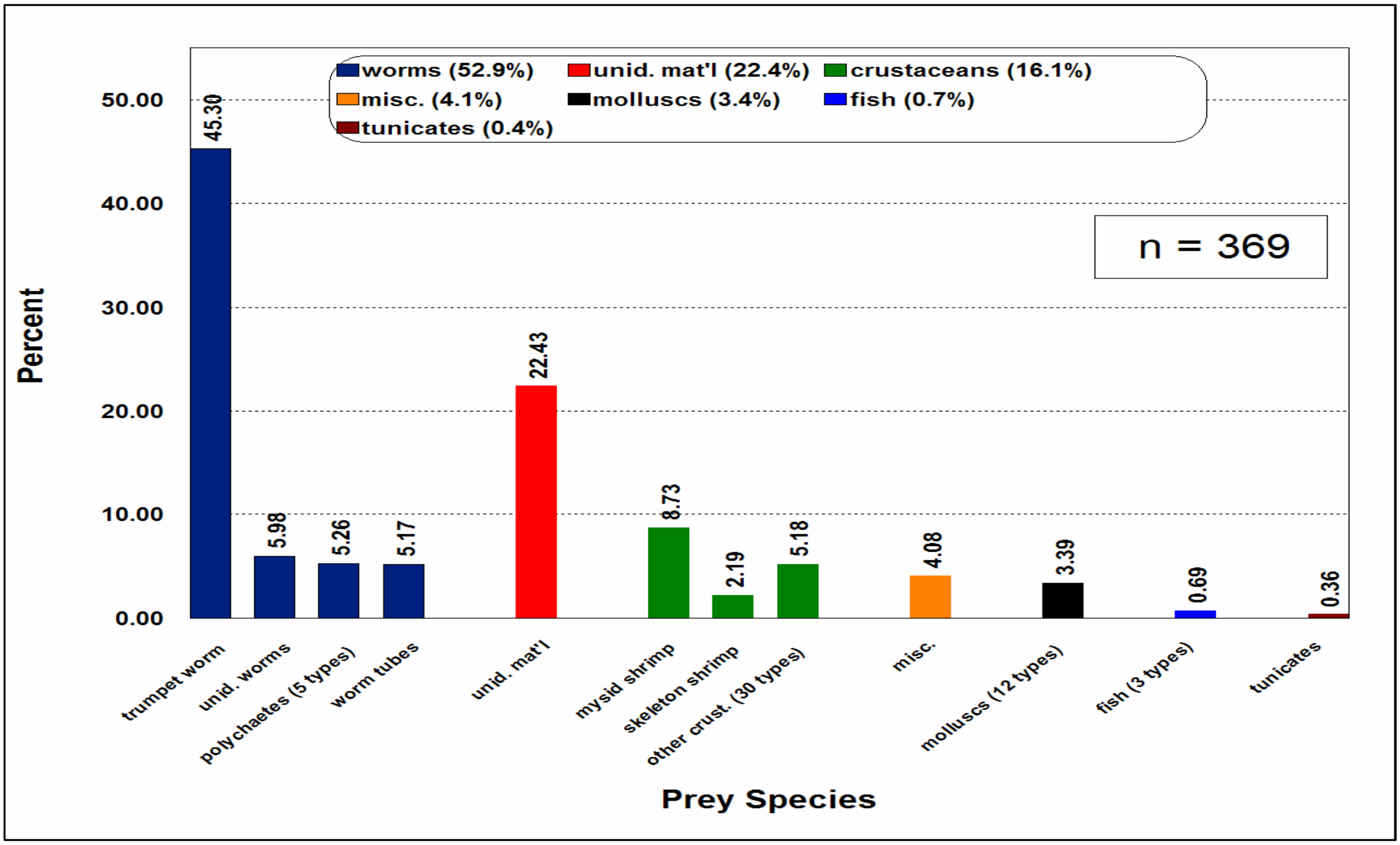
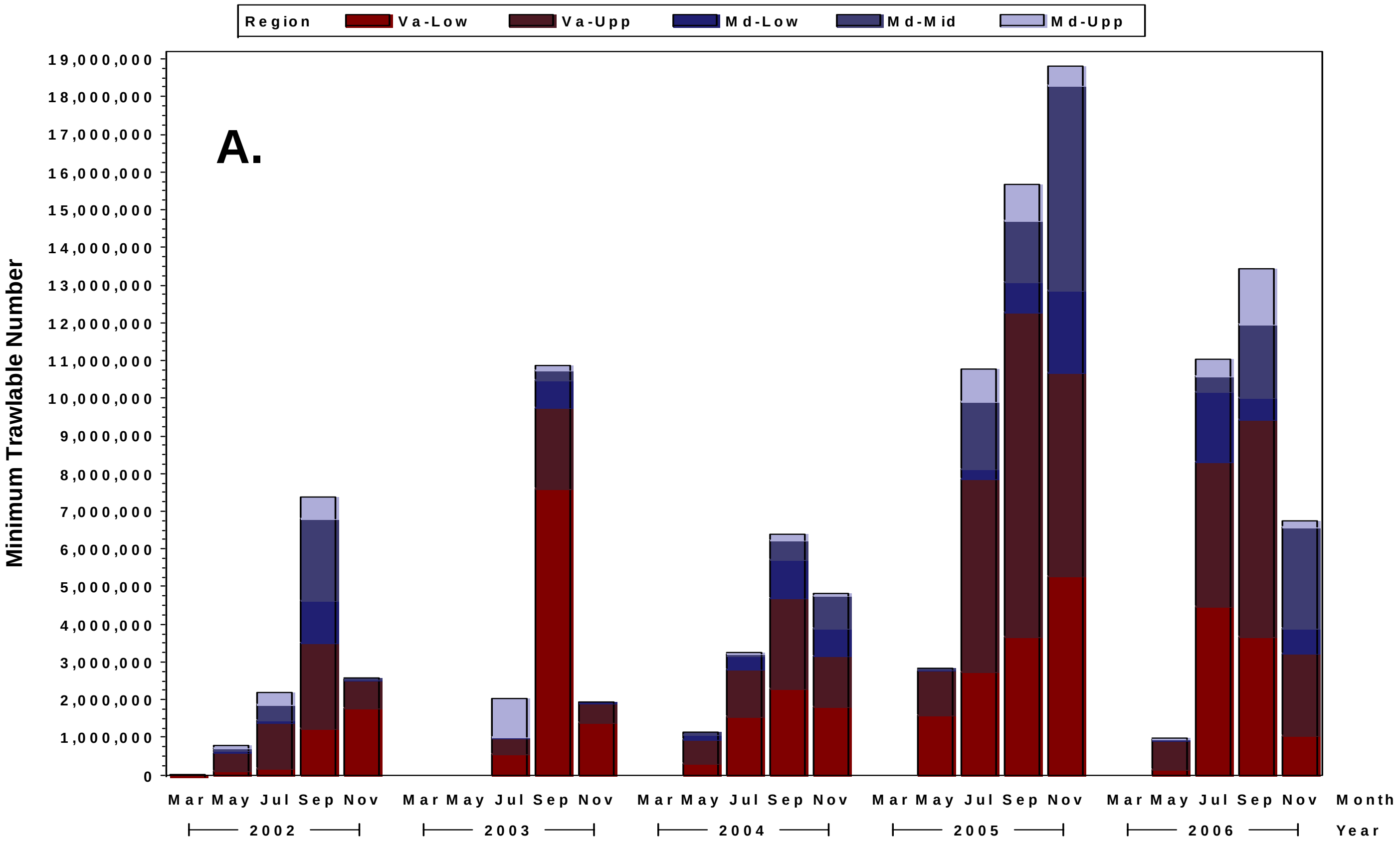


Figure 69. Spot minimum trawlable abundance estimates in numbers (A) and biomass (B) in Chesapeake Bay 2002-2006.



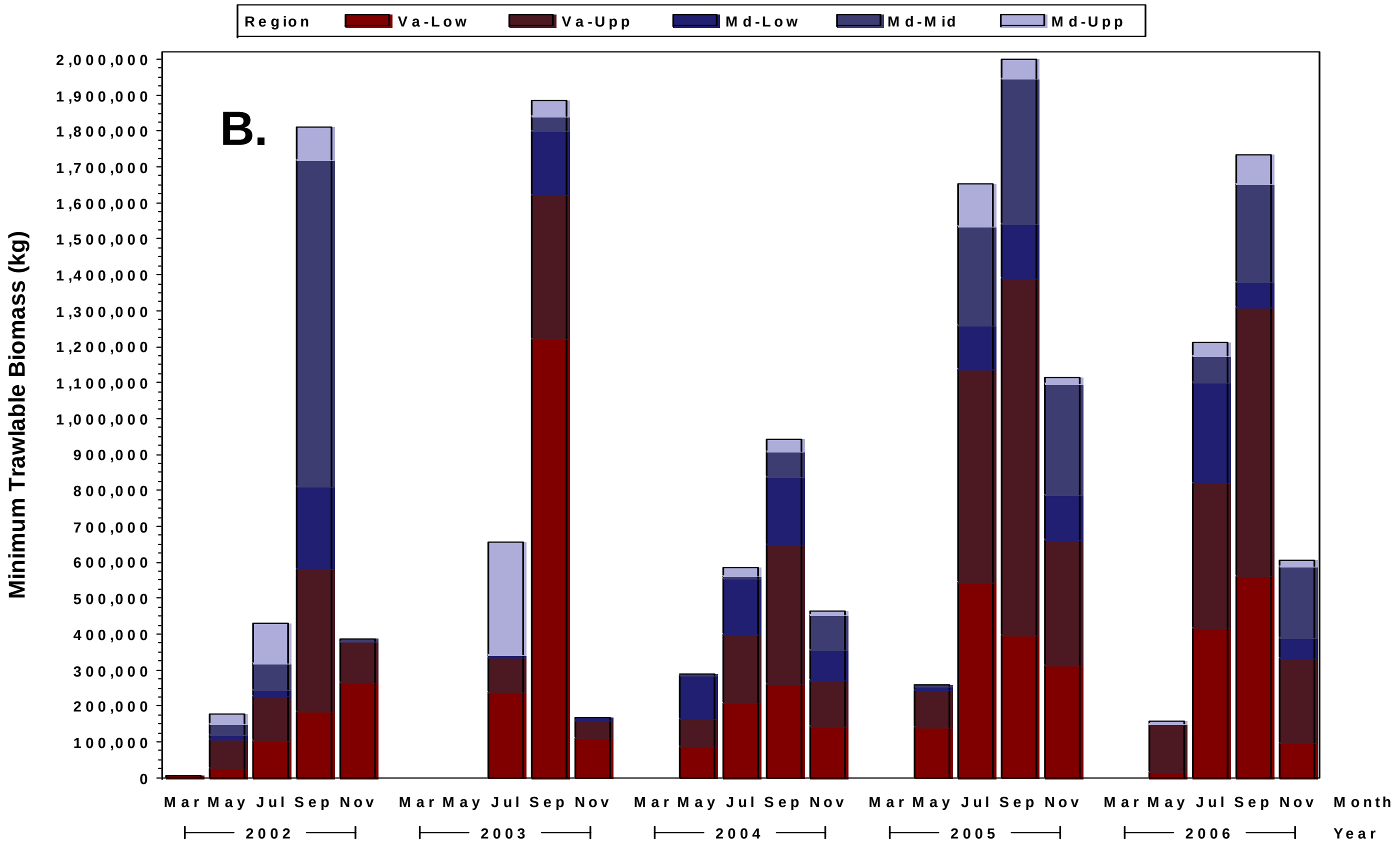


Figure 70. Abundance (number per hectare swept) of spot in Chesapeake Bay, 2002.

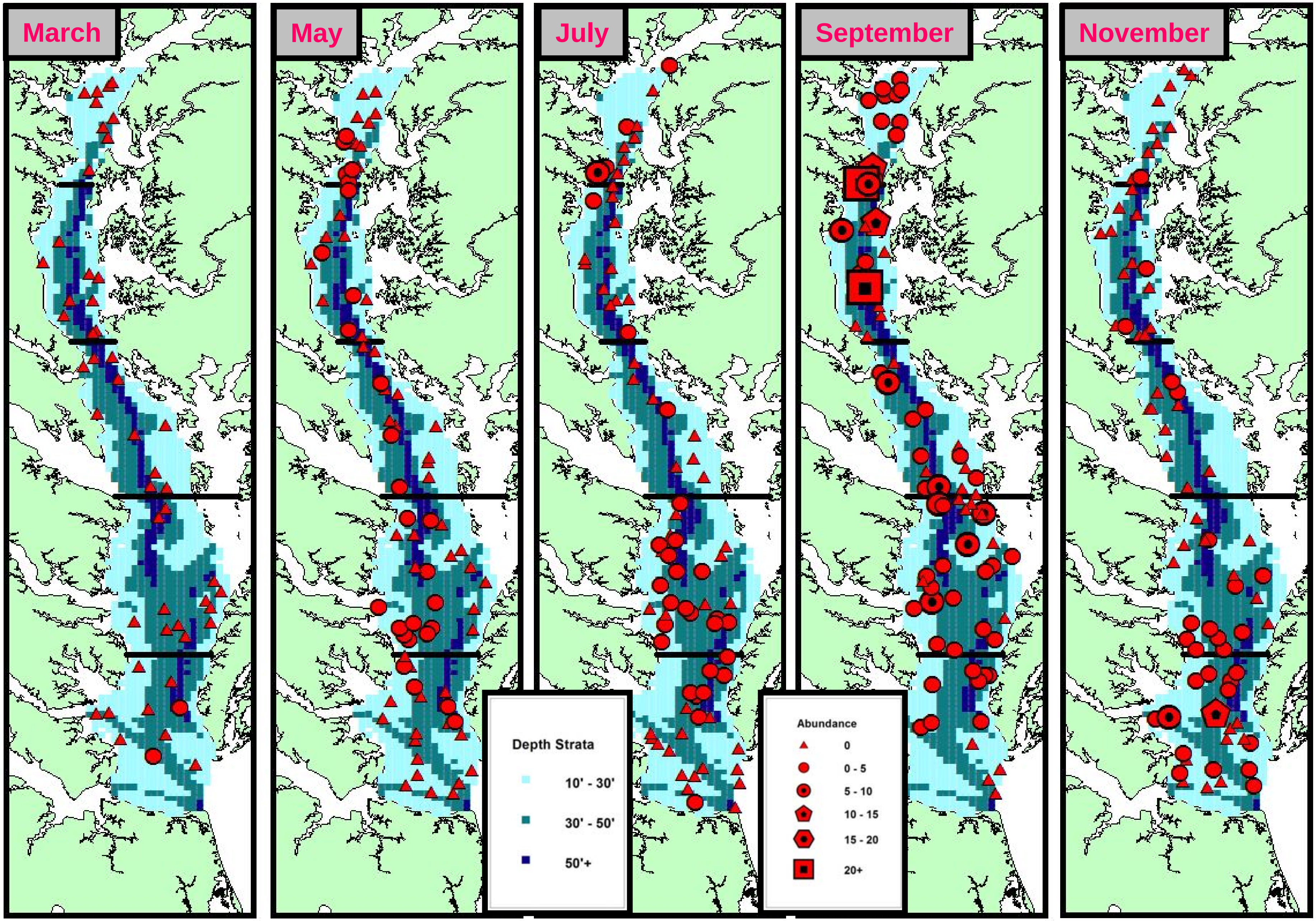


Figure 71. Abundance (number per hectare swept) of spot in Chesapeake Bay, 2003.

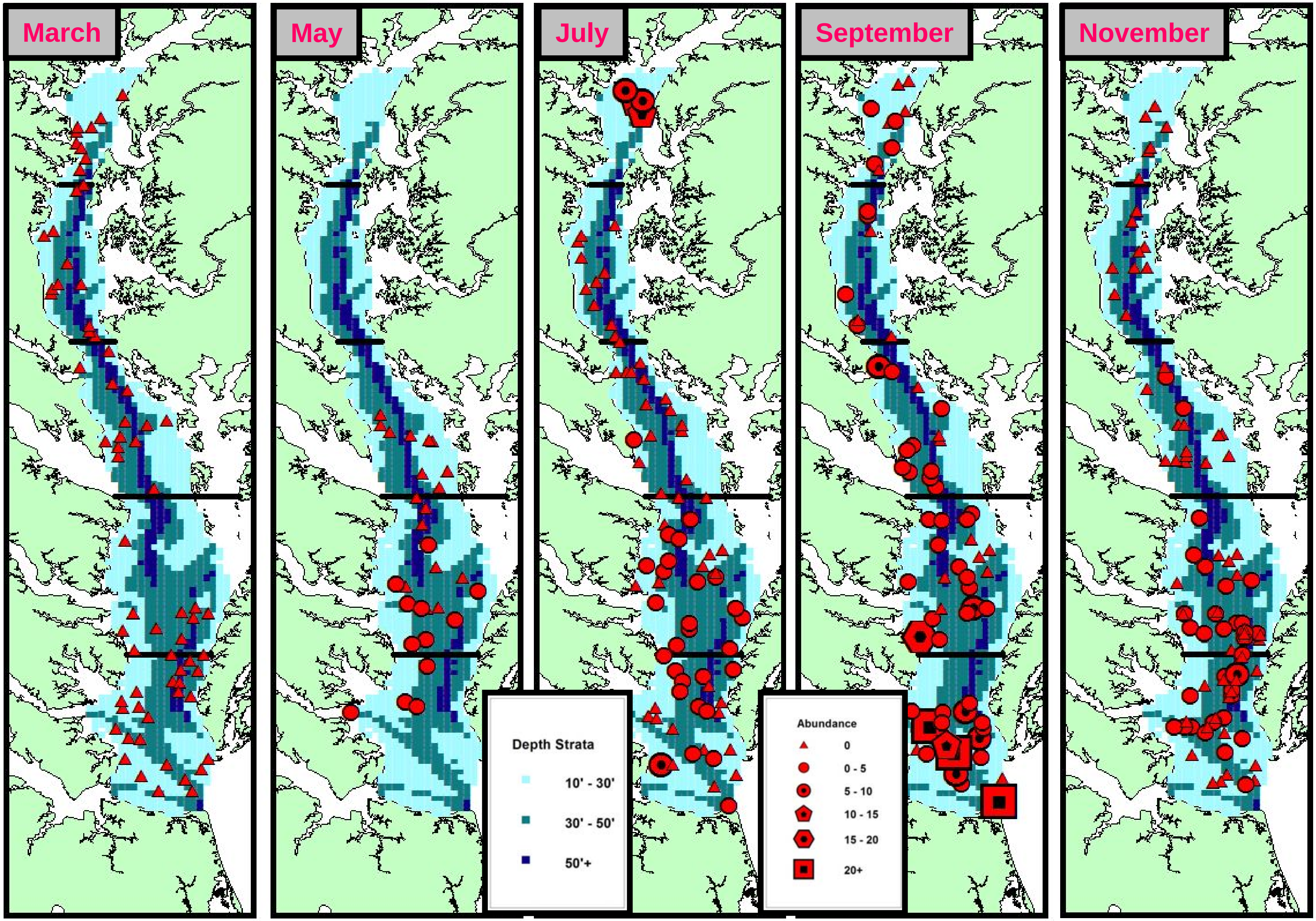


Figure 72. Abundance (number per hectare swept) of spot in Chesapeake Bay, 2004.

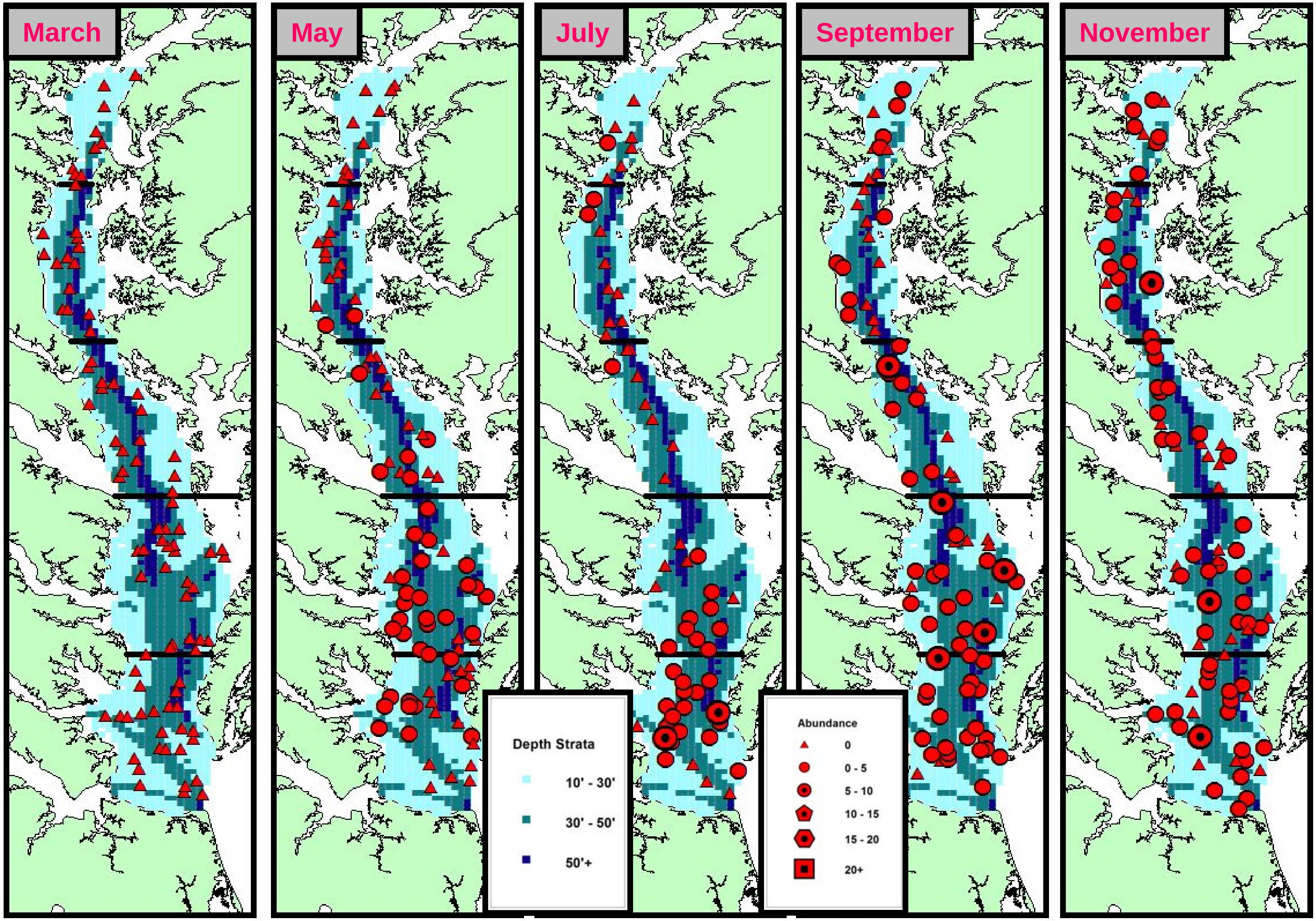


Figure 73. Abundance (number per hectare swept) of spot in Chesapeake Bay, 2005.

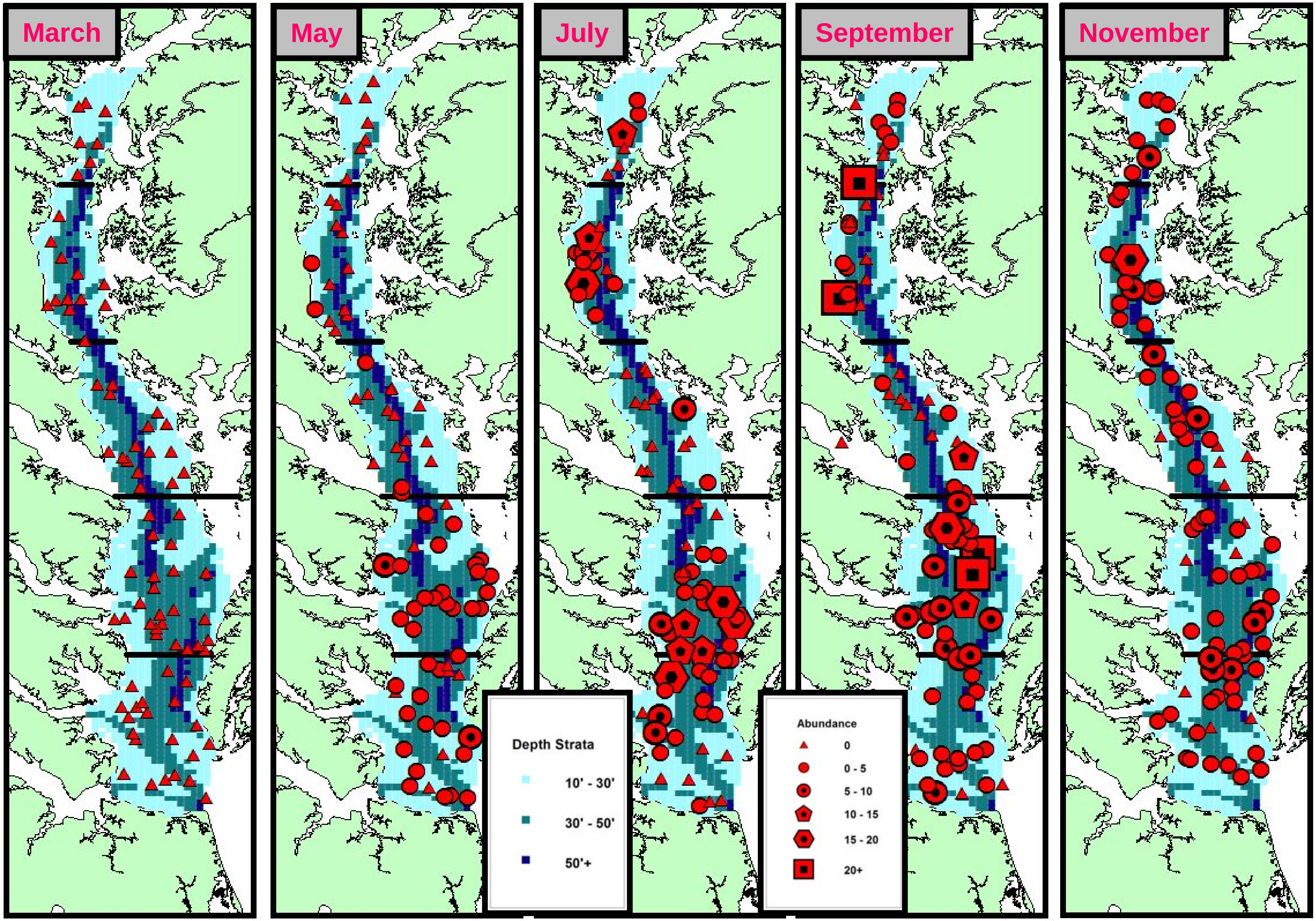


Figure 74. Abundance (number per hectare swept) of spot in Chesapeake Bay, 2006.

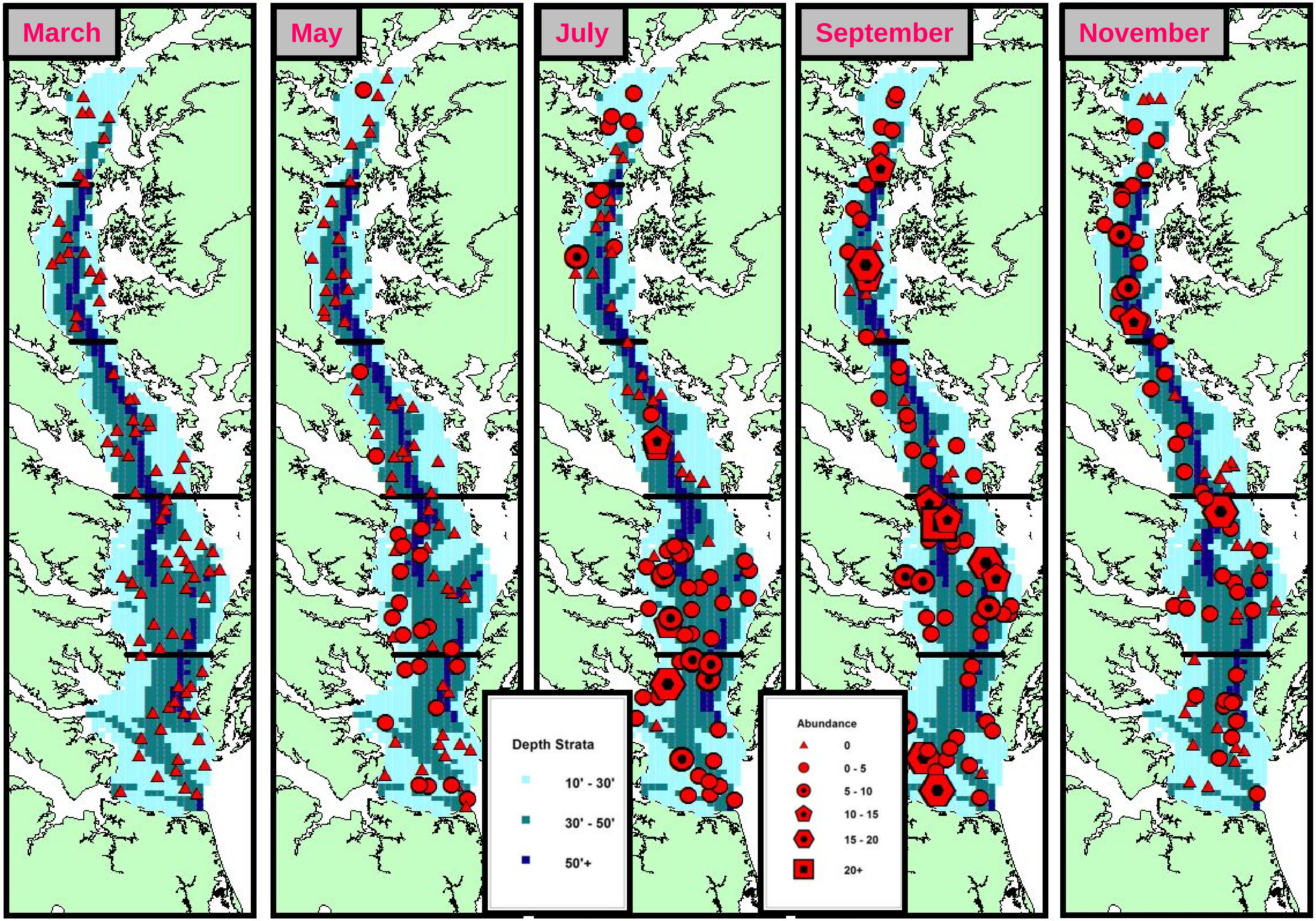


Figure 75. Spot length-frequency in Chesapeake Bay 2002-2006.

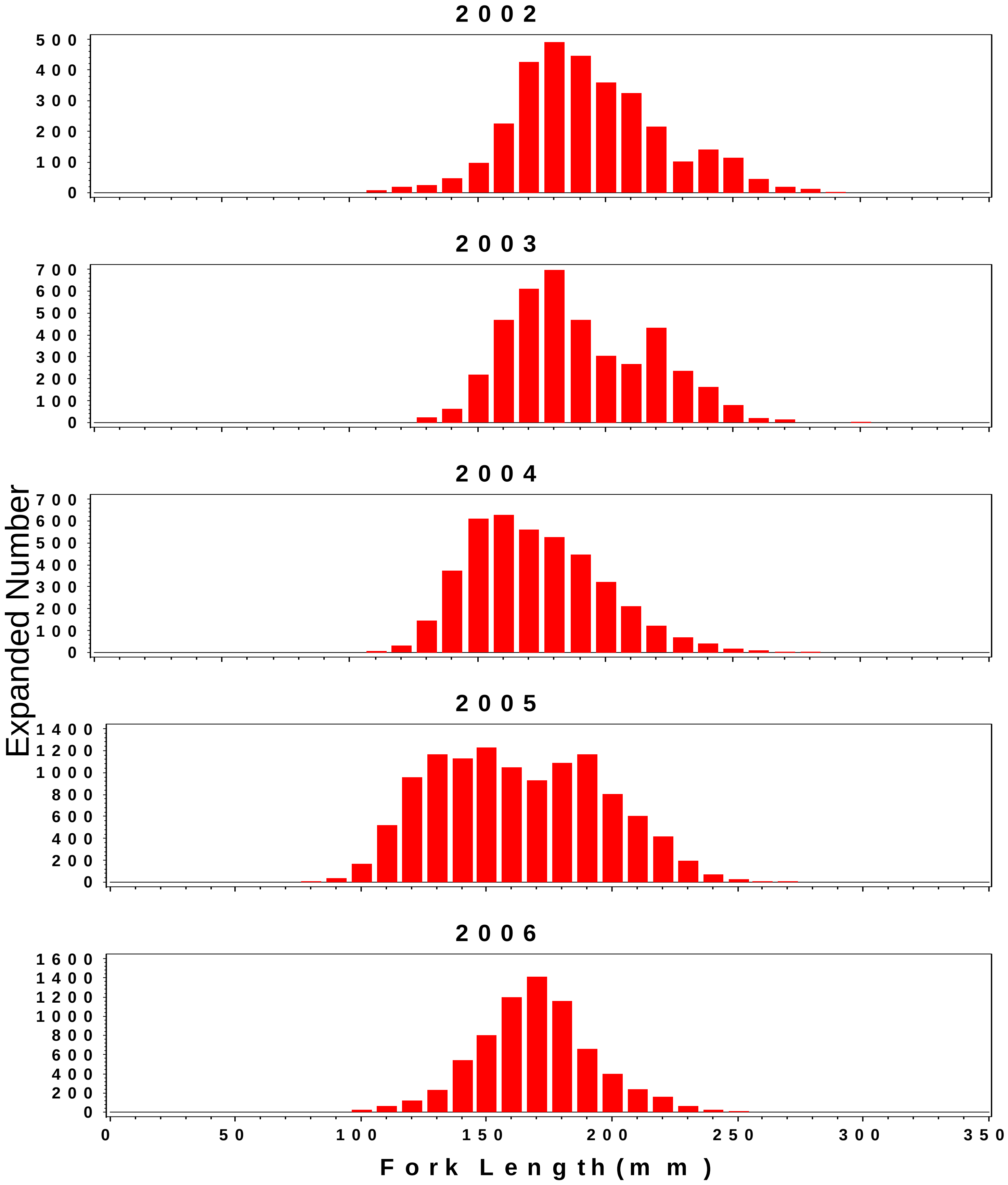


Figure 76. Spot age-structure in Chesapeake Bay 2002-2006.

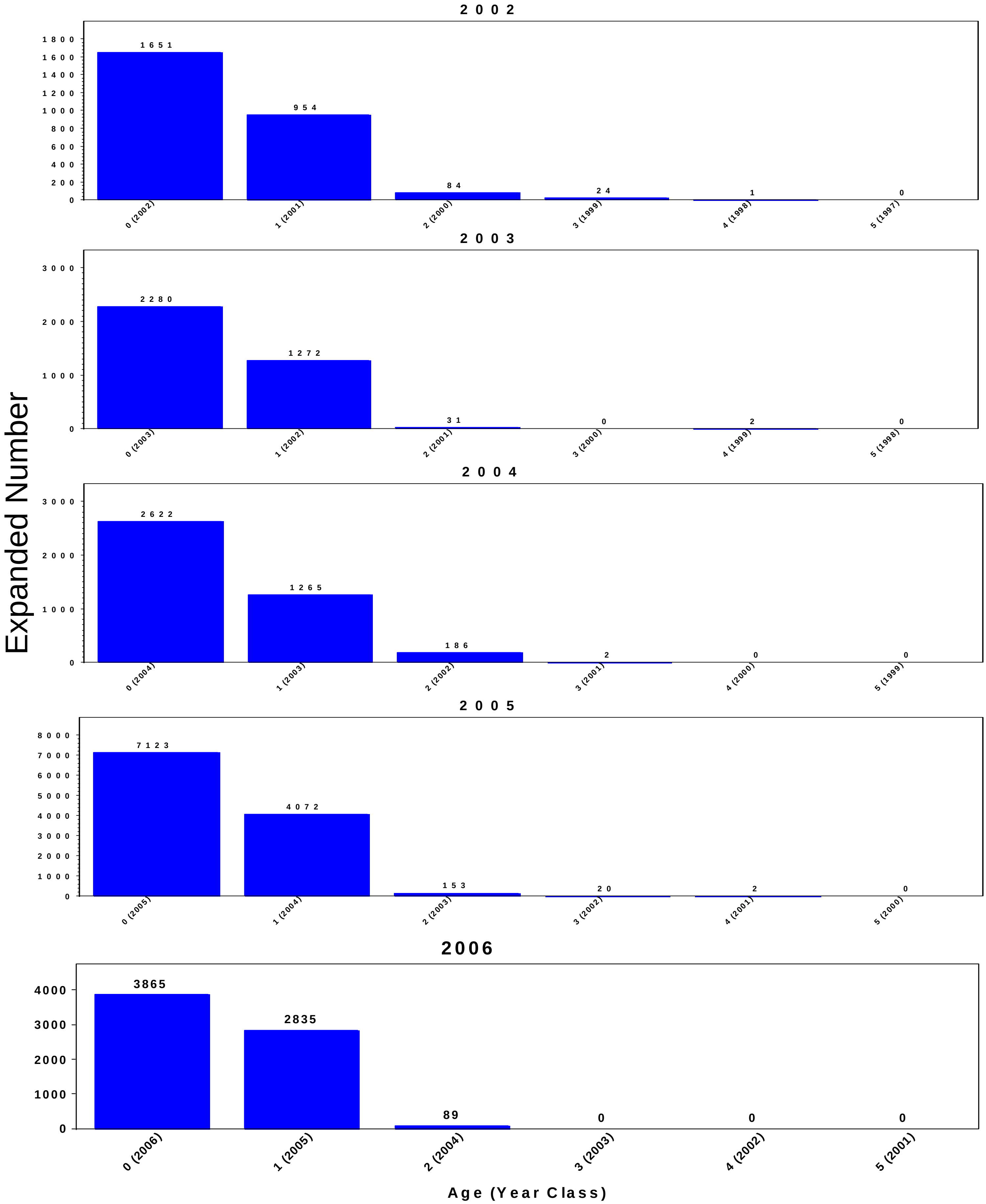
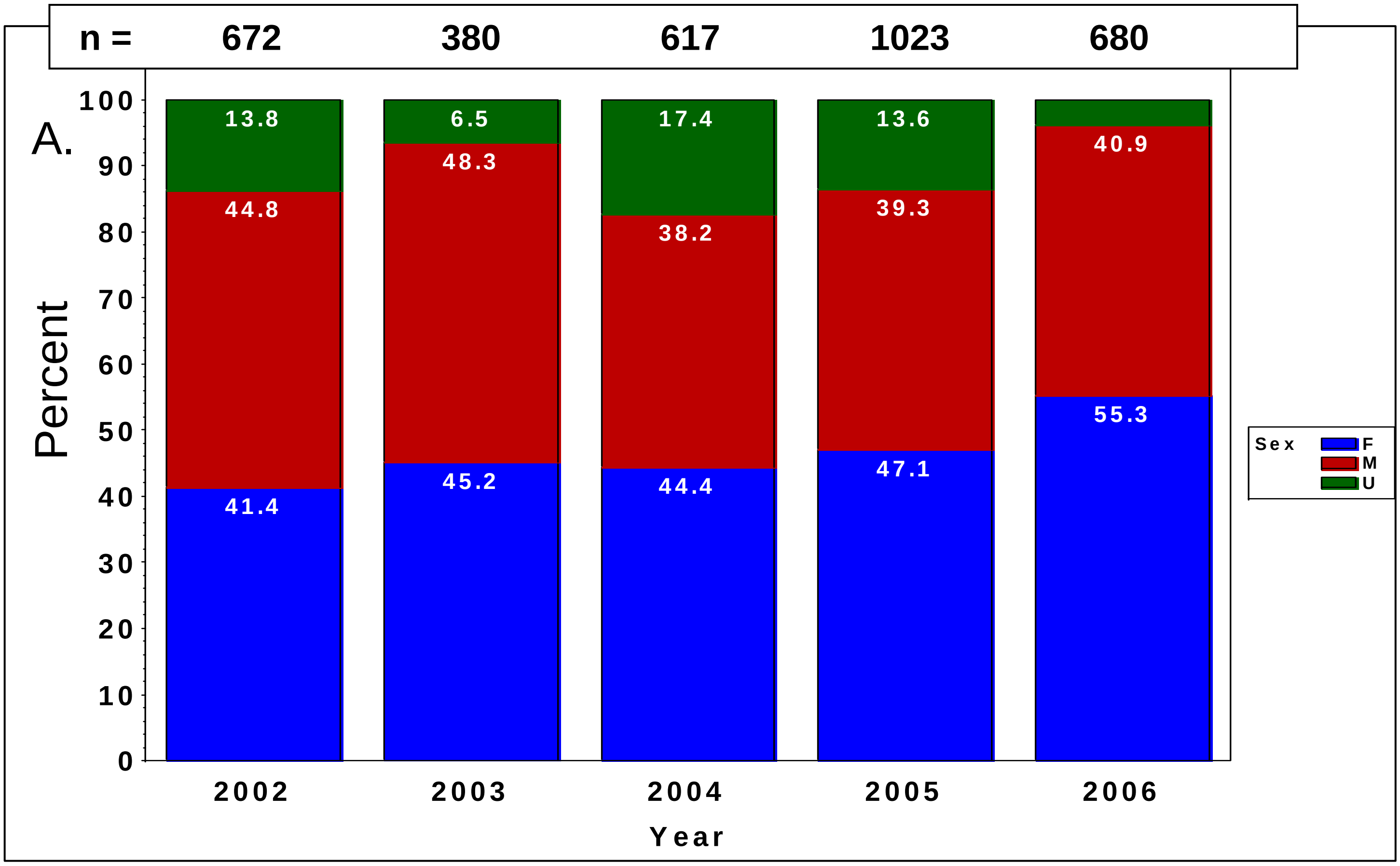


Figure 77. Spot sex-ratios in Chesapeake Bay 2002-2005, by year (A), month (B).



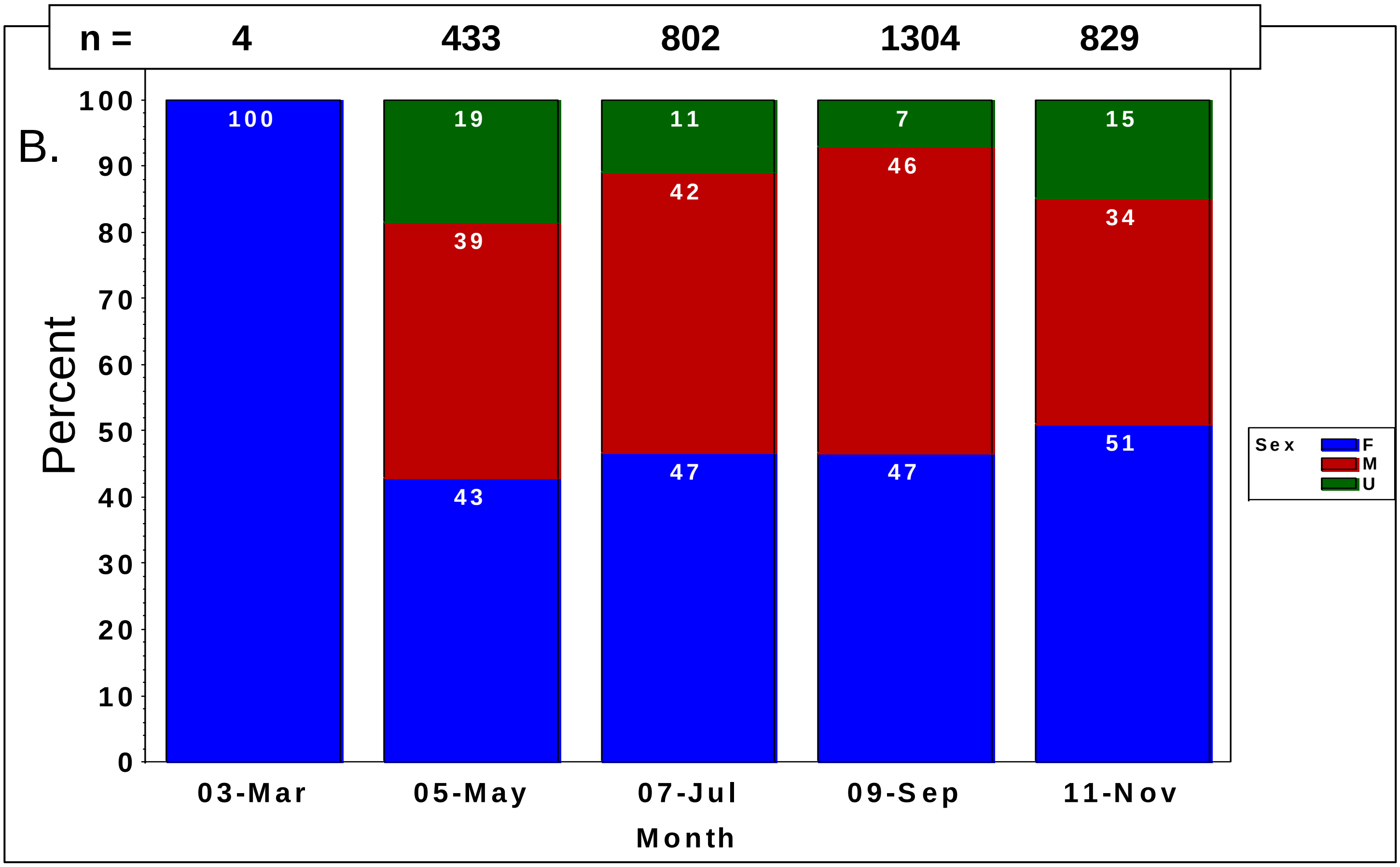


Figure 78. Spot length-weight relationships in Chesapeake Bay 2002-2006 as calculated by power regression for sexes combined (A) and separately (B).

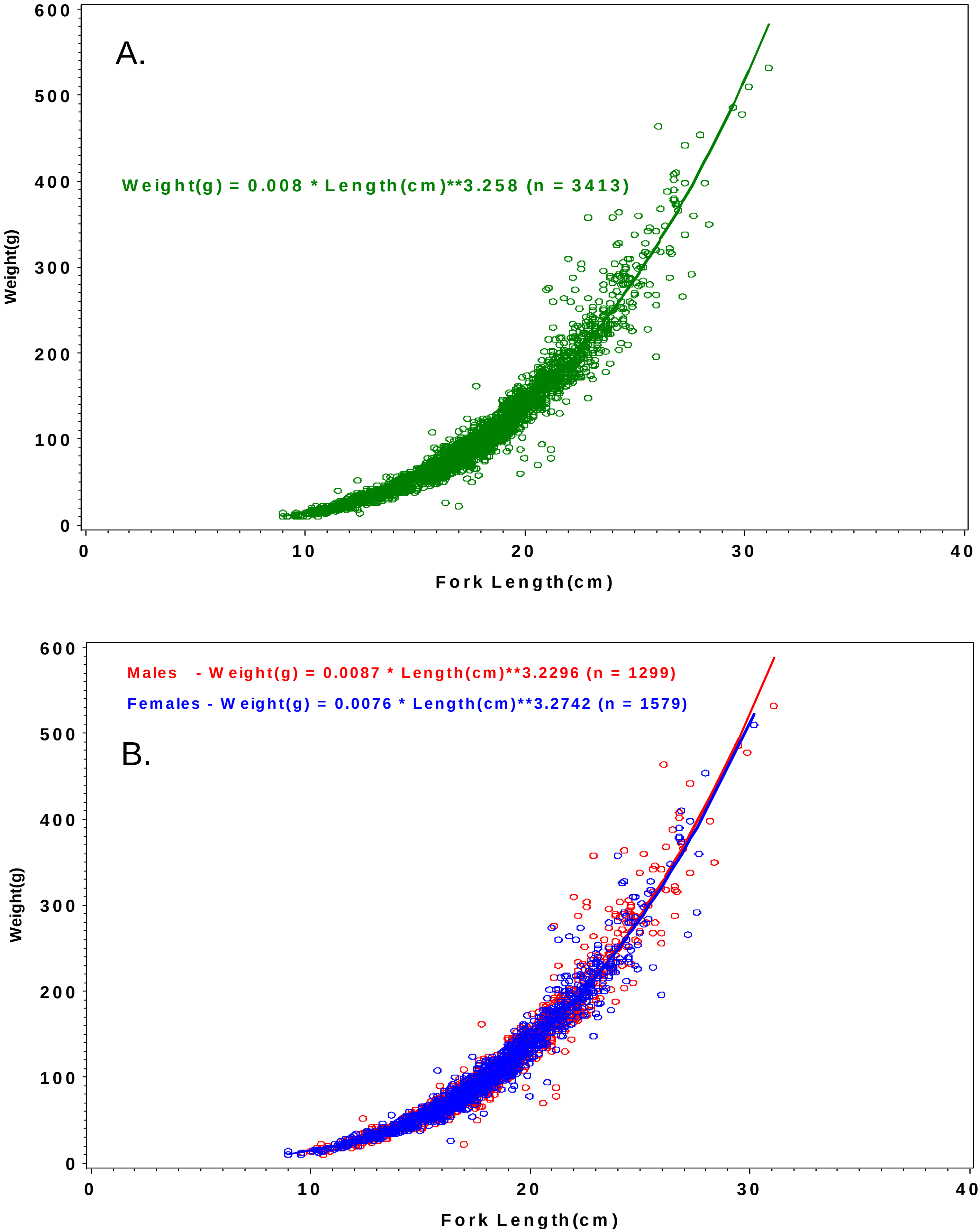


Figure 79. Spot maturity schedule in Chesapeake Bay 2002-2006 combined, by sex.

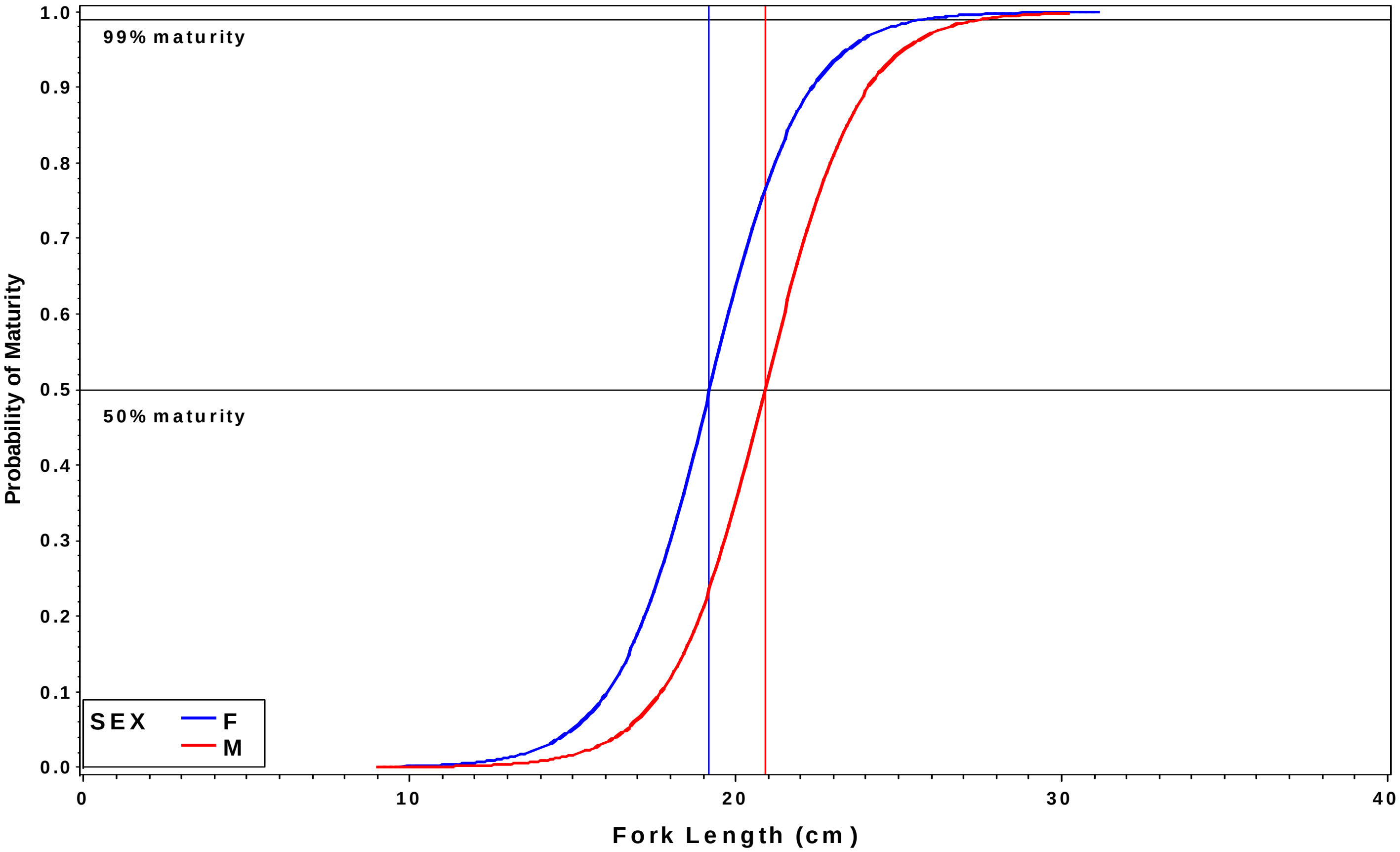
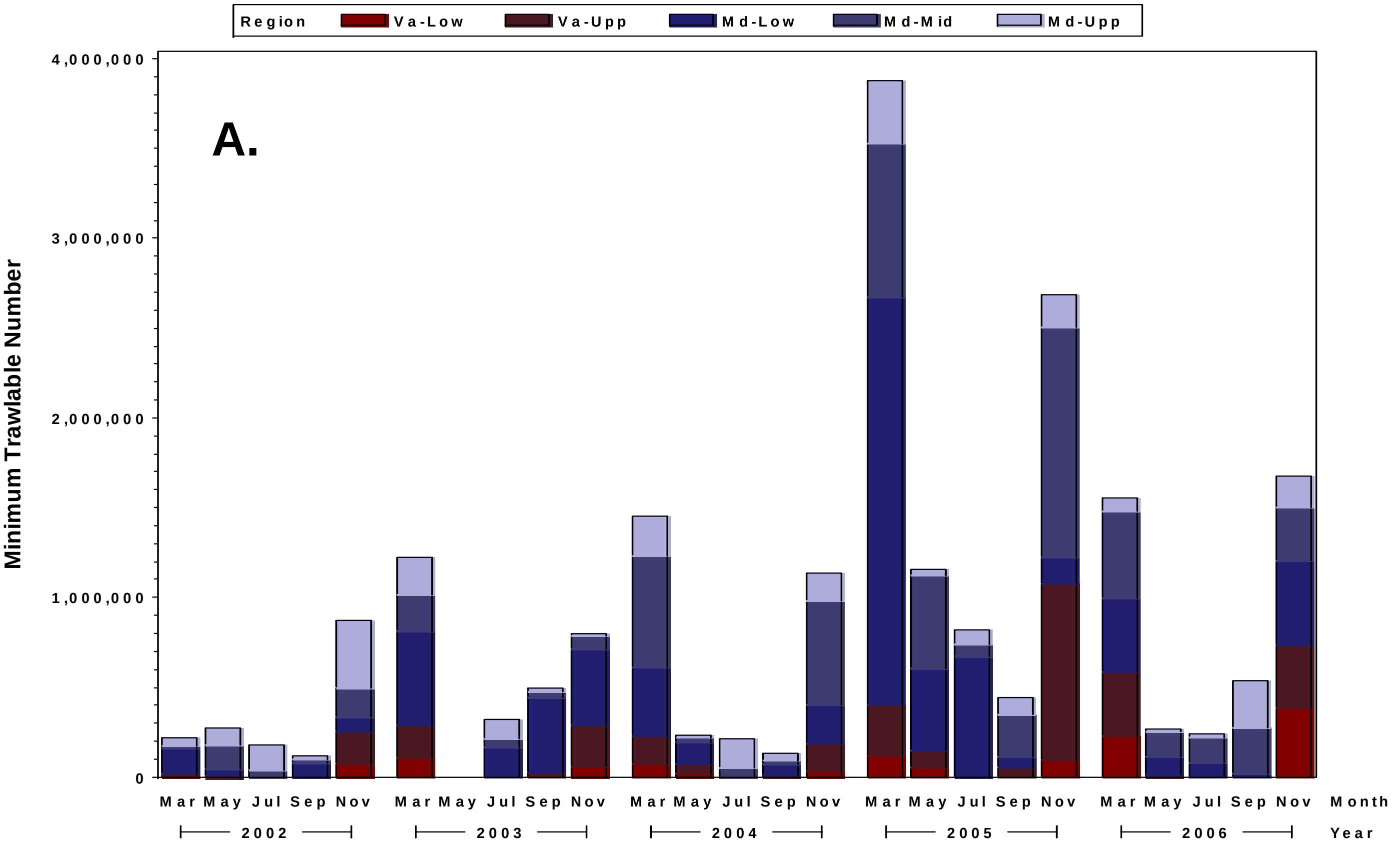


Figure 80. Striped bass minimum trawlable abundance estimates in numbers (A) and biomass (B) in Chesapeake Bay 2002-2006.



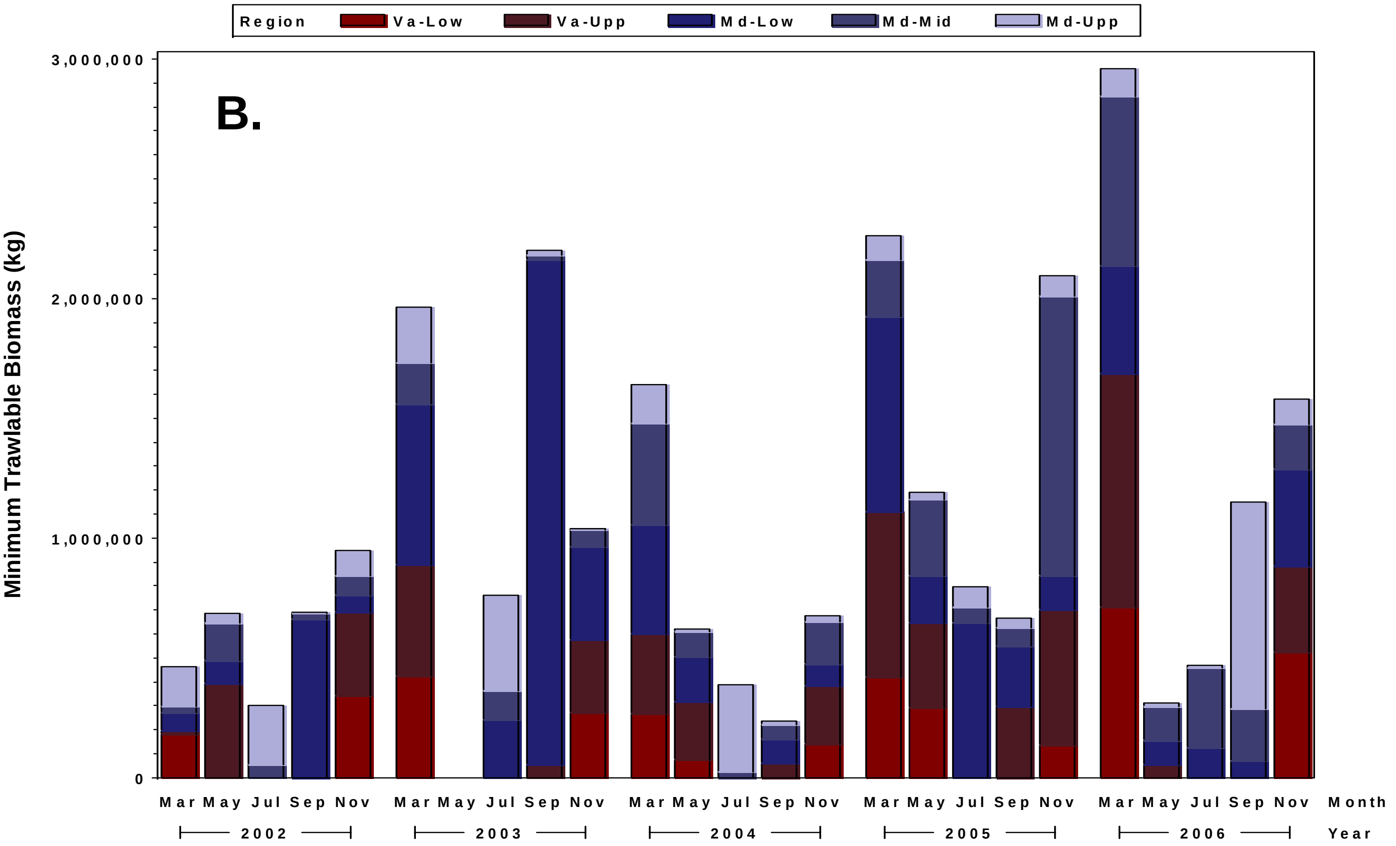


Figure 81. Abundance (number per hectare swept) of striped bass in Chesapeake Bay, 2002.

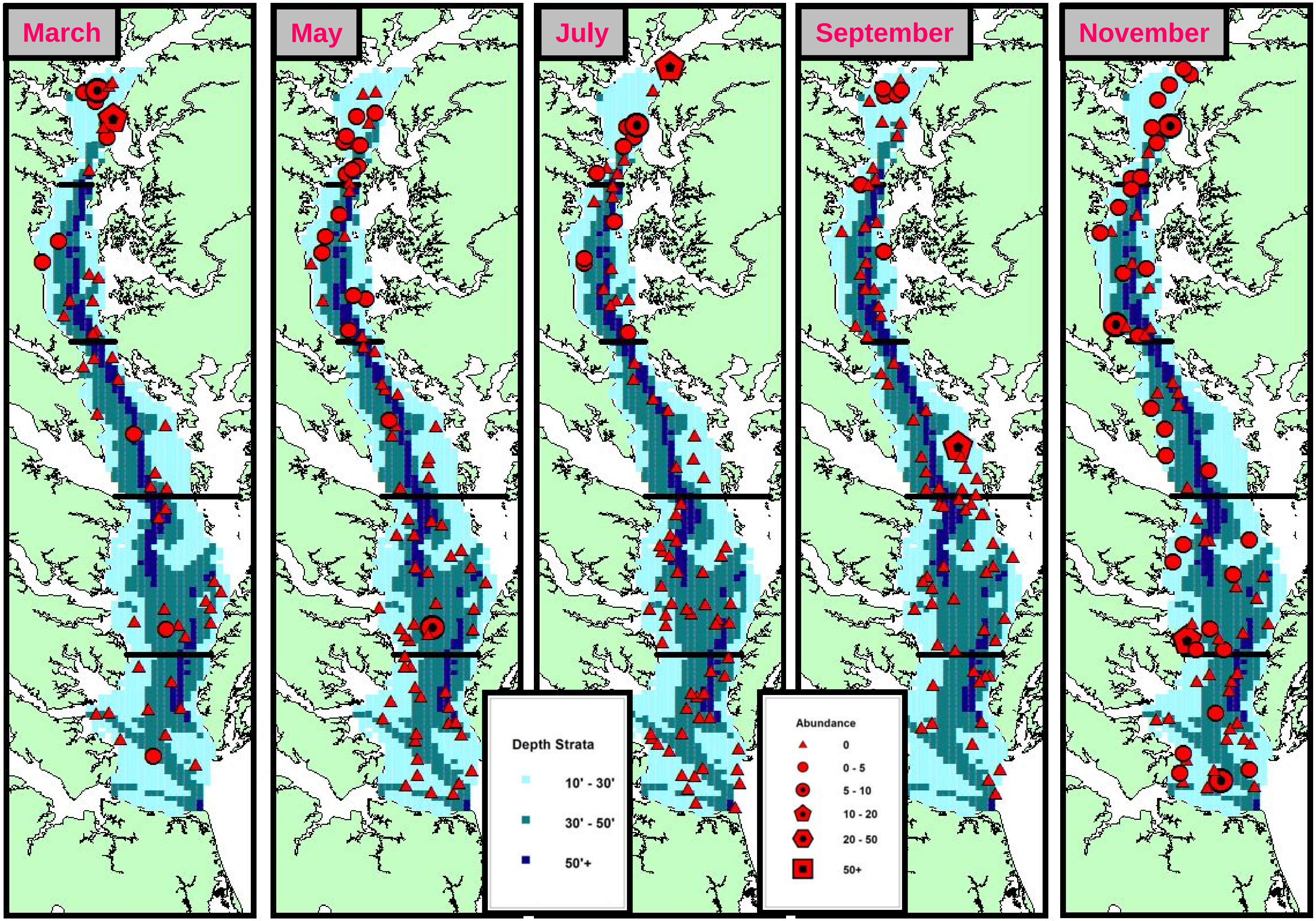
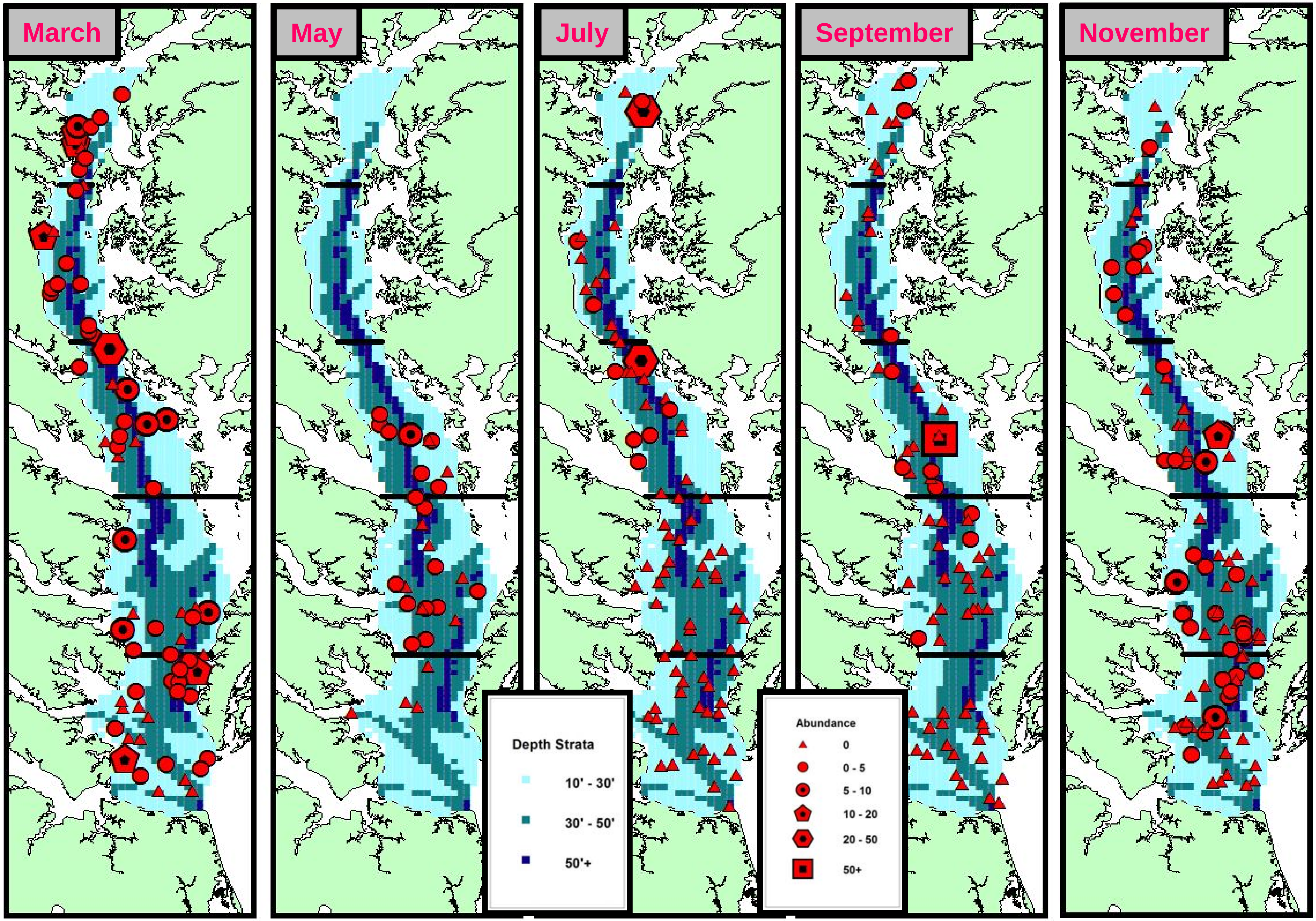


Figure 82. Abundance (number per hectare swept) of striped bass in Chesapeake Bay, 2003.



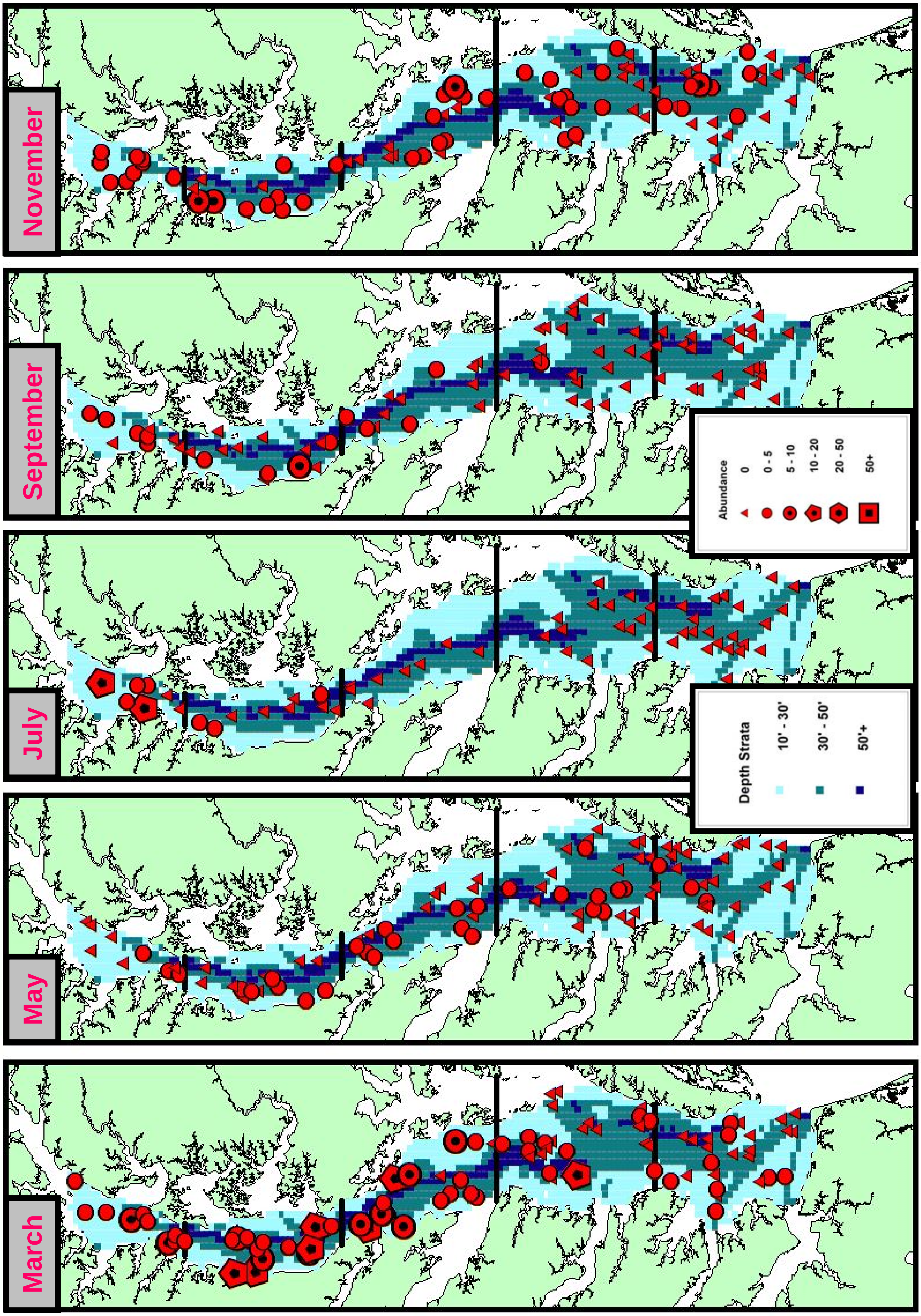


Figure 83. Abundance (number per hectare swept) of striped bass in Chesapeake Bay, 2004.

Figure 84. Abundance (number per hectare swept) of striped bass in Chesapeake Bay, 2005.

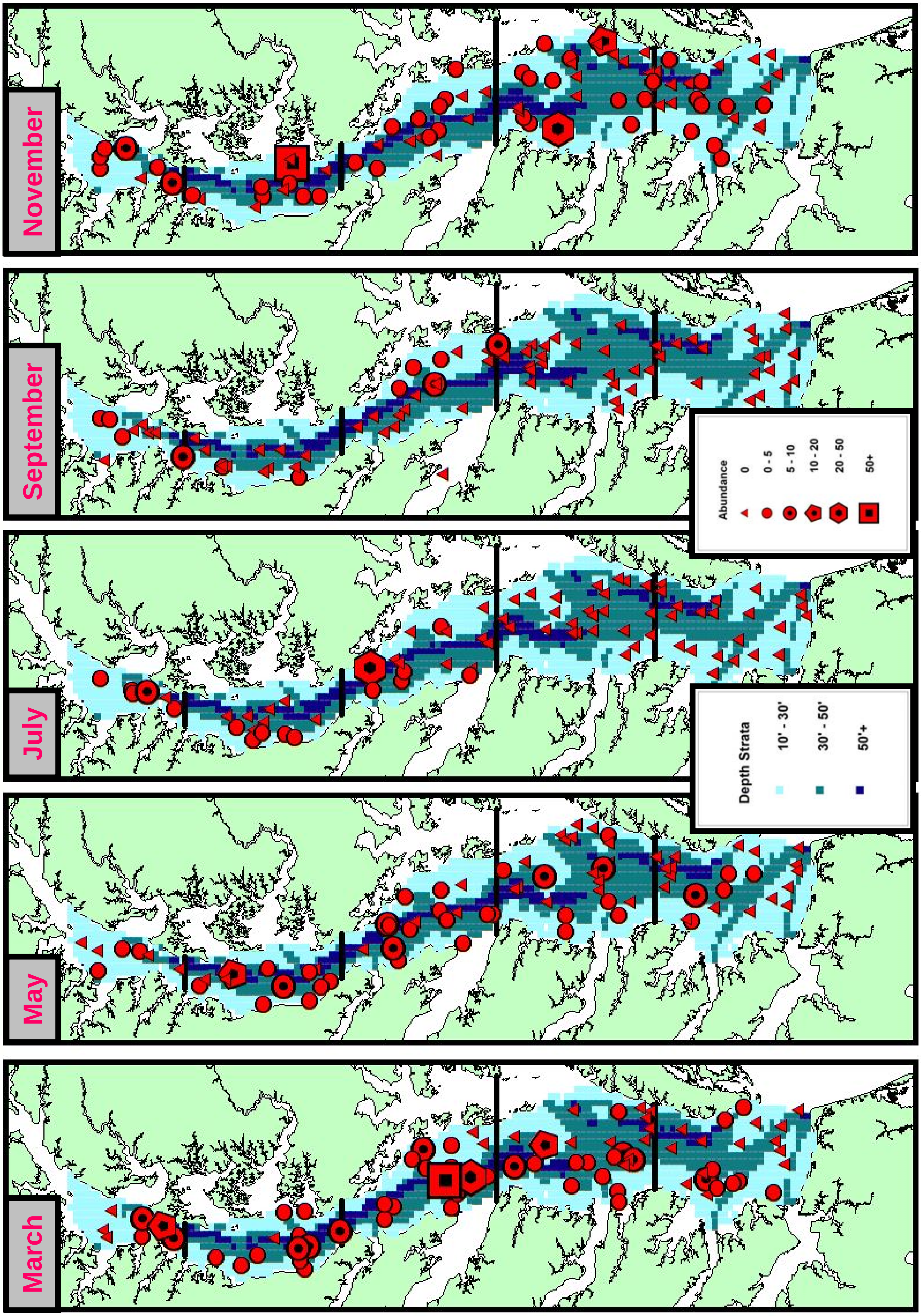


Figure 85. Abundance (number per hectare swept) of striped bass in Chesapeake Bay, 2006.

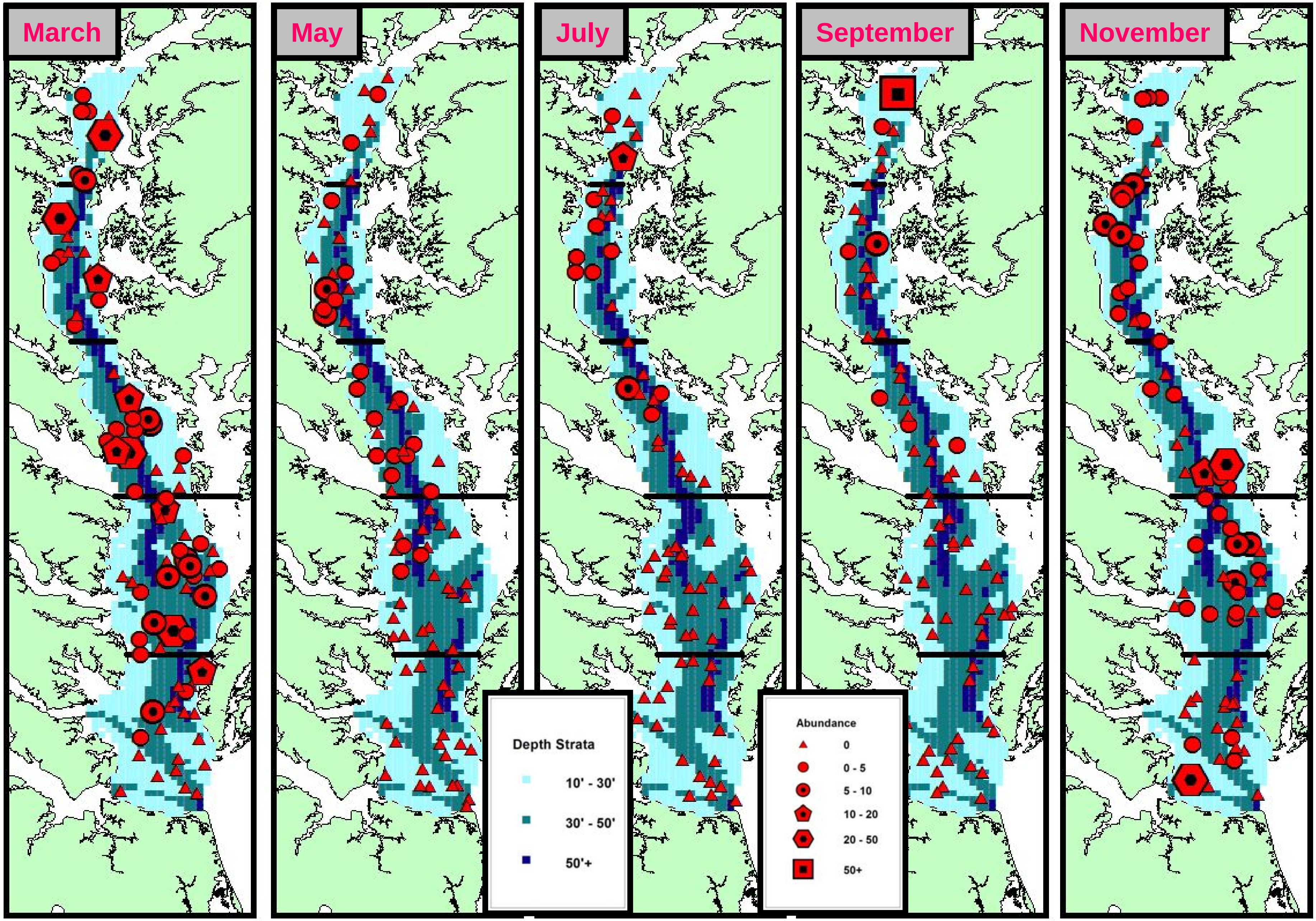


Figure 86. Striped bass length-frequency in Chesapeake Bay 2002-2006.

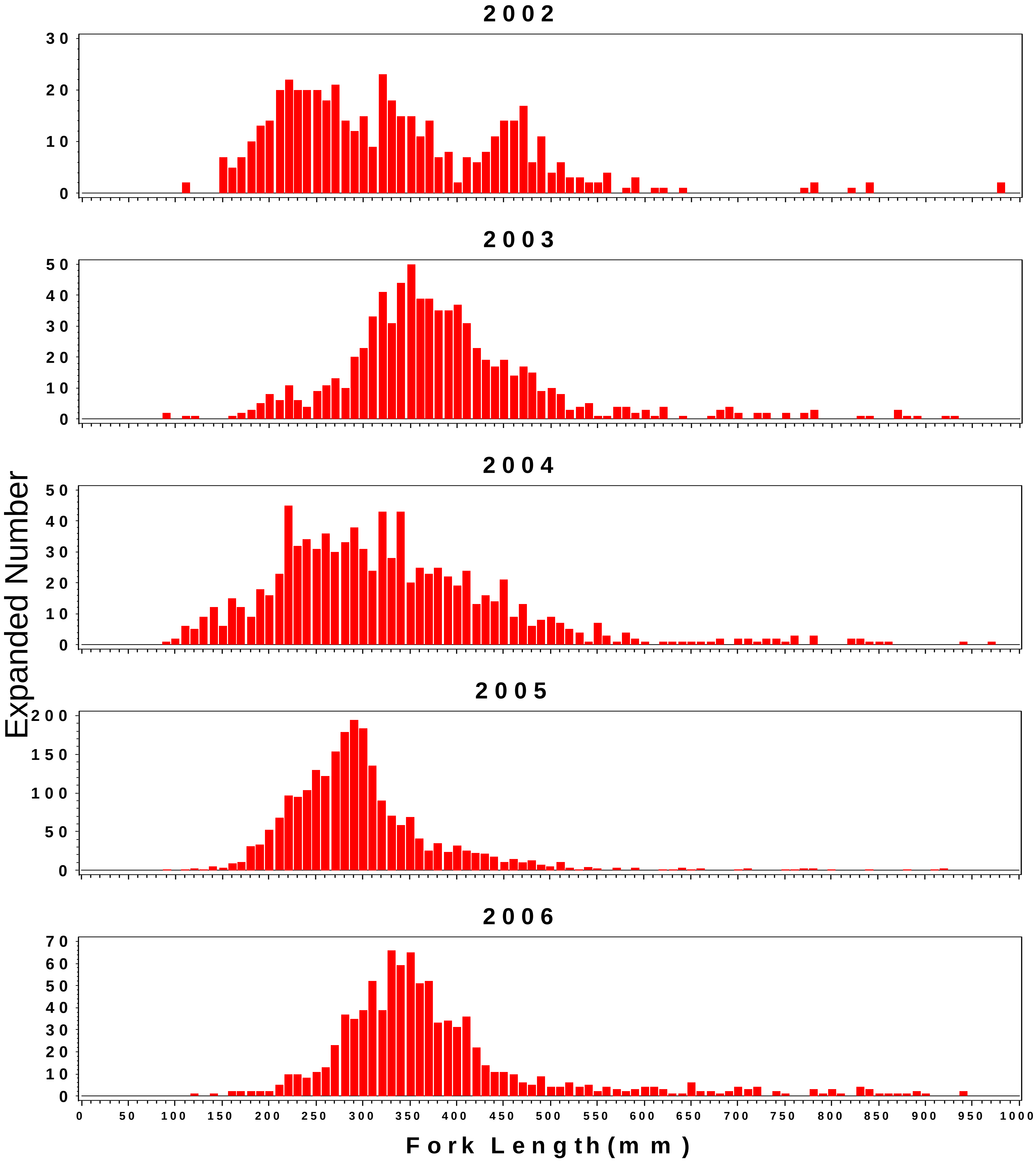
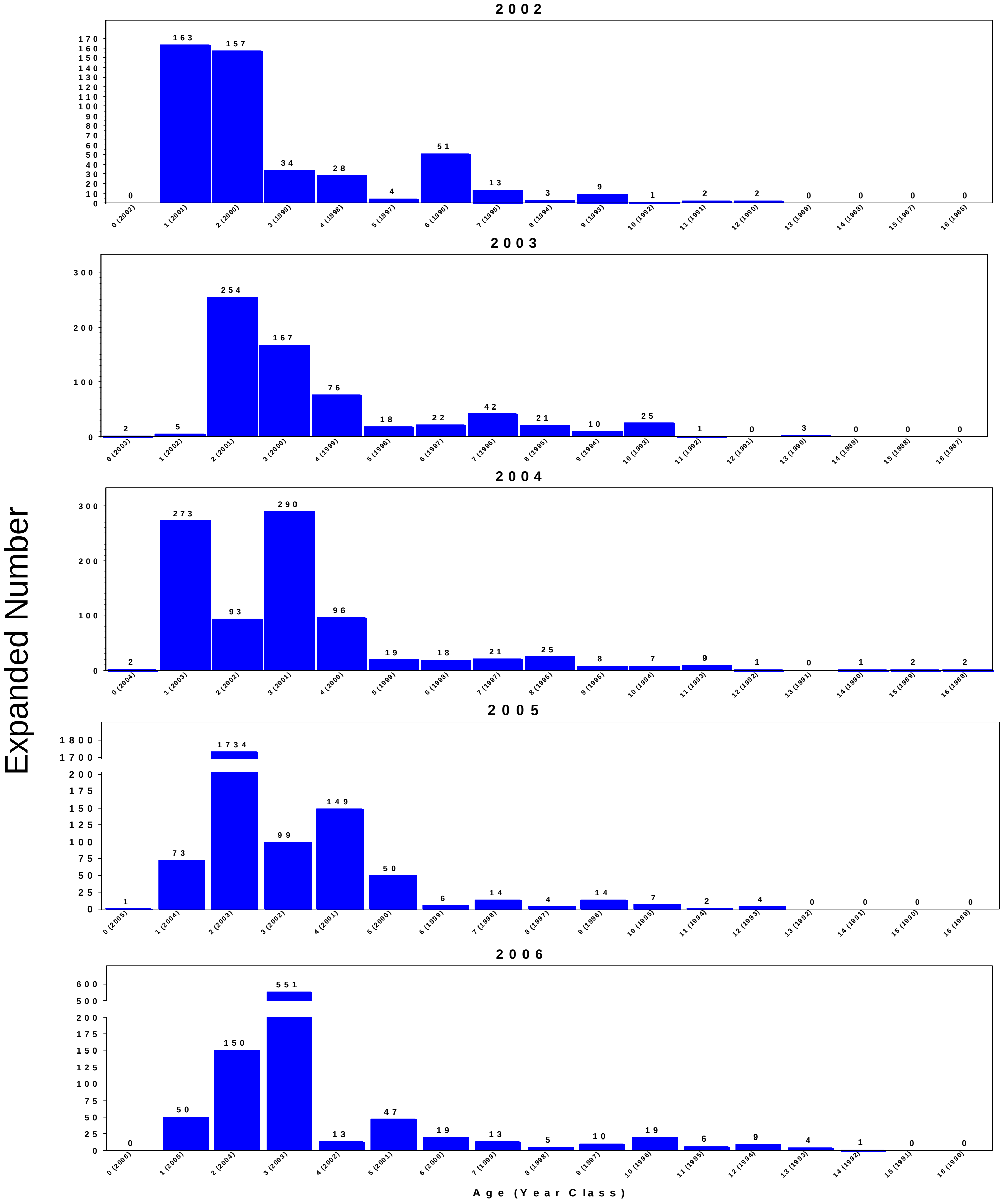


Figure 87. Striped bass age-structure in Chesapeake Bay 2002-2006.


2002

2003

2004

2005

2006

Figure 88. Striped bass sex-ratios in Chesapeake Bay 2002-2006, by year (A), month (B), age (C).

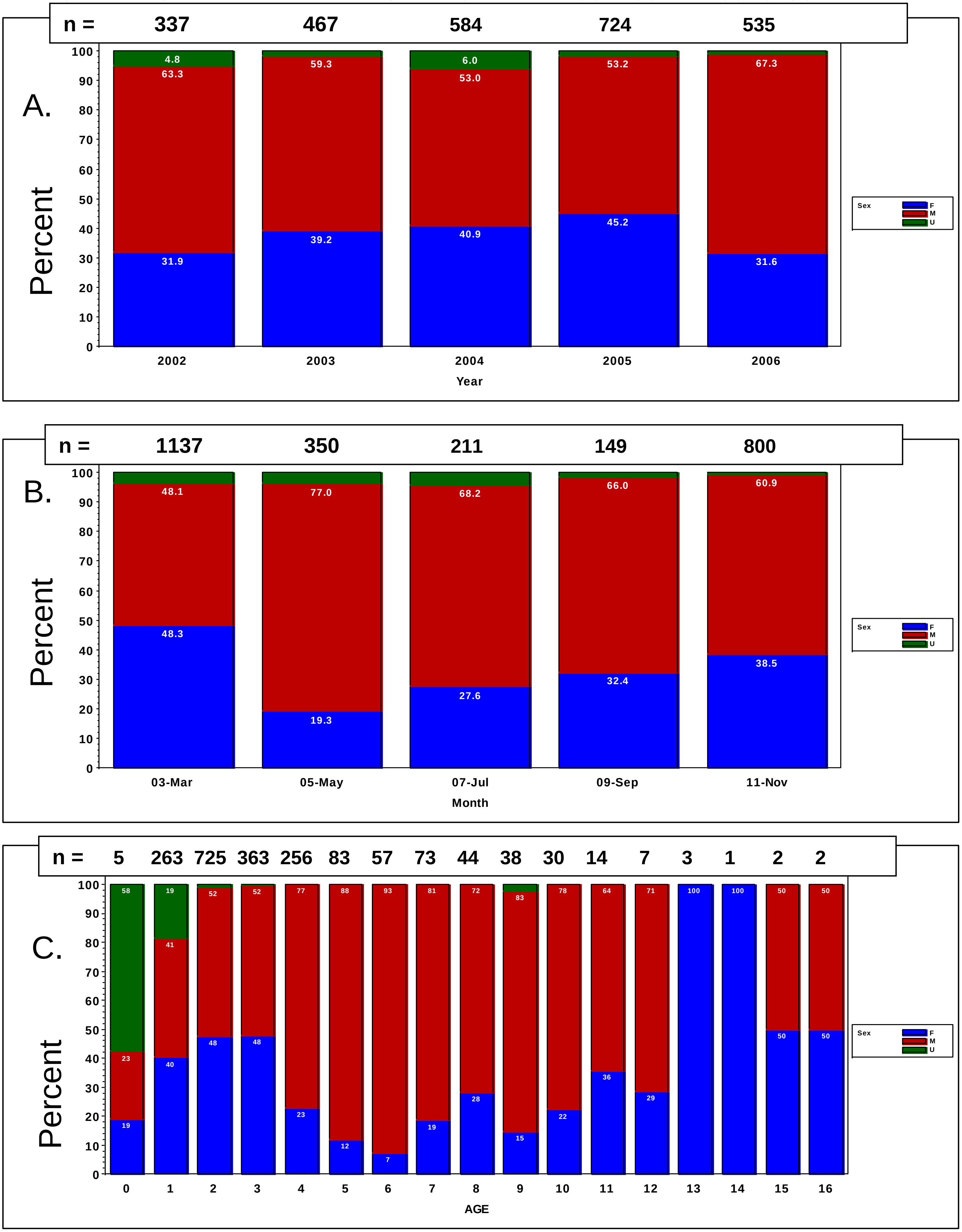
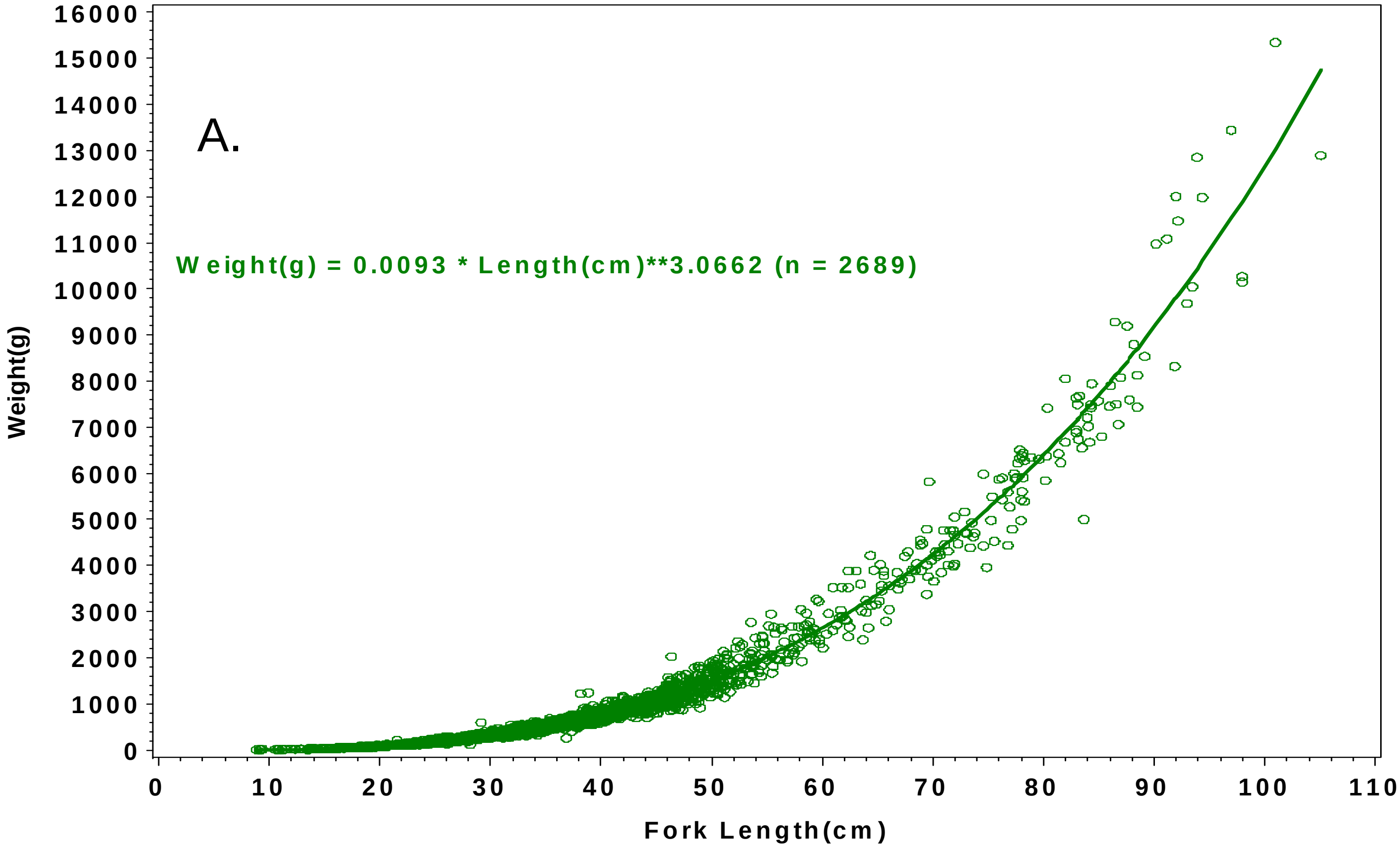


Figure 89. Striped bass length-weight relationships in Chesapeake Bay 2002-2006 as calculated by power regression for sexes combined (A) and separately (B).



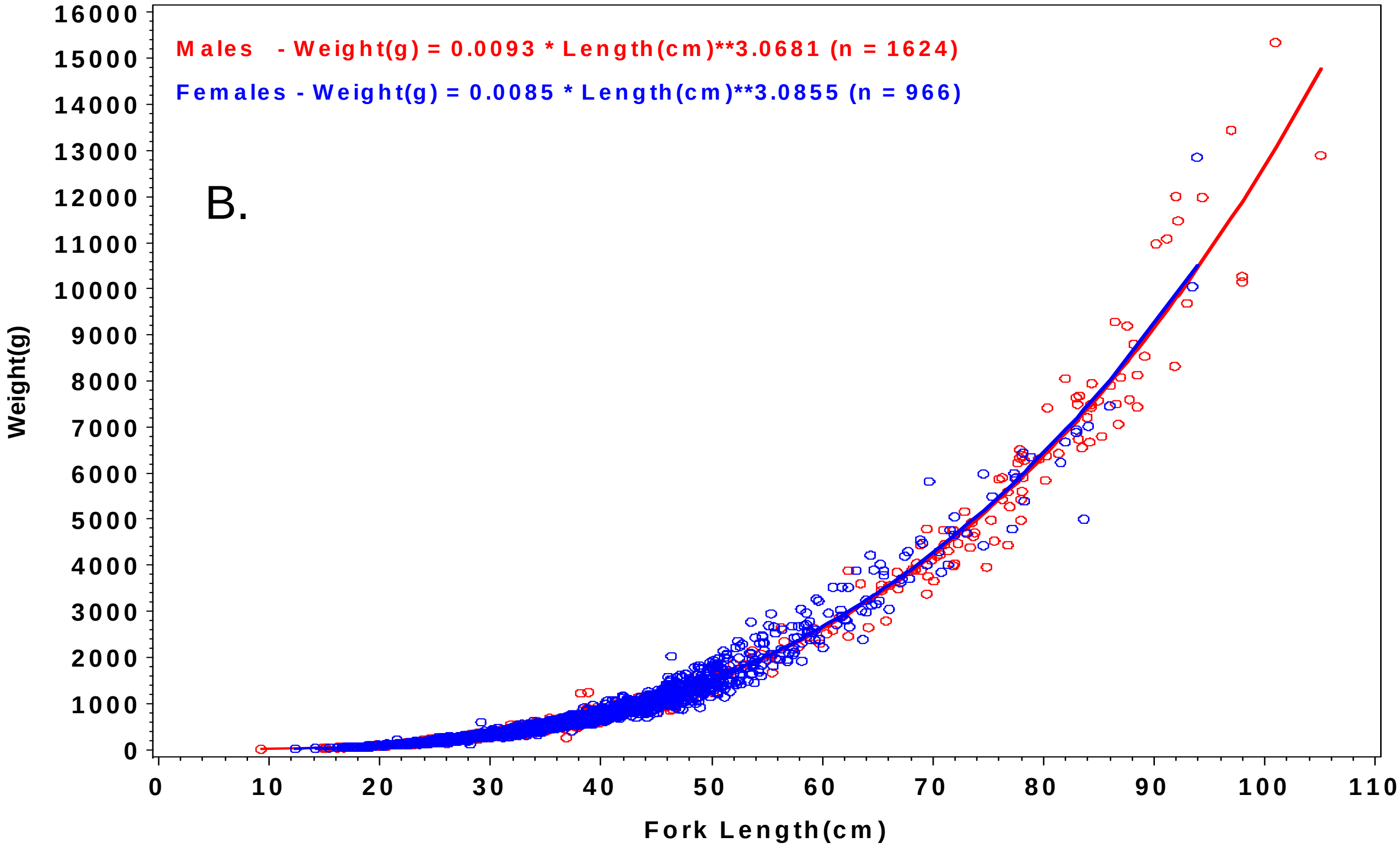


Figure 90. Striped bass maturity schedule in Chesapeake Bay 2002-2006 combined, by sex.

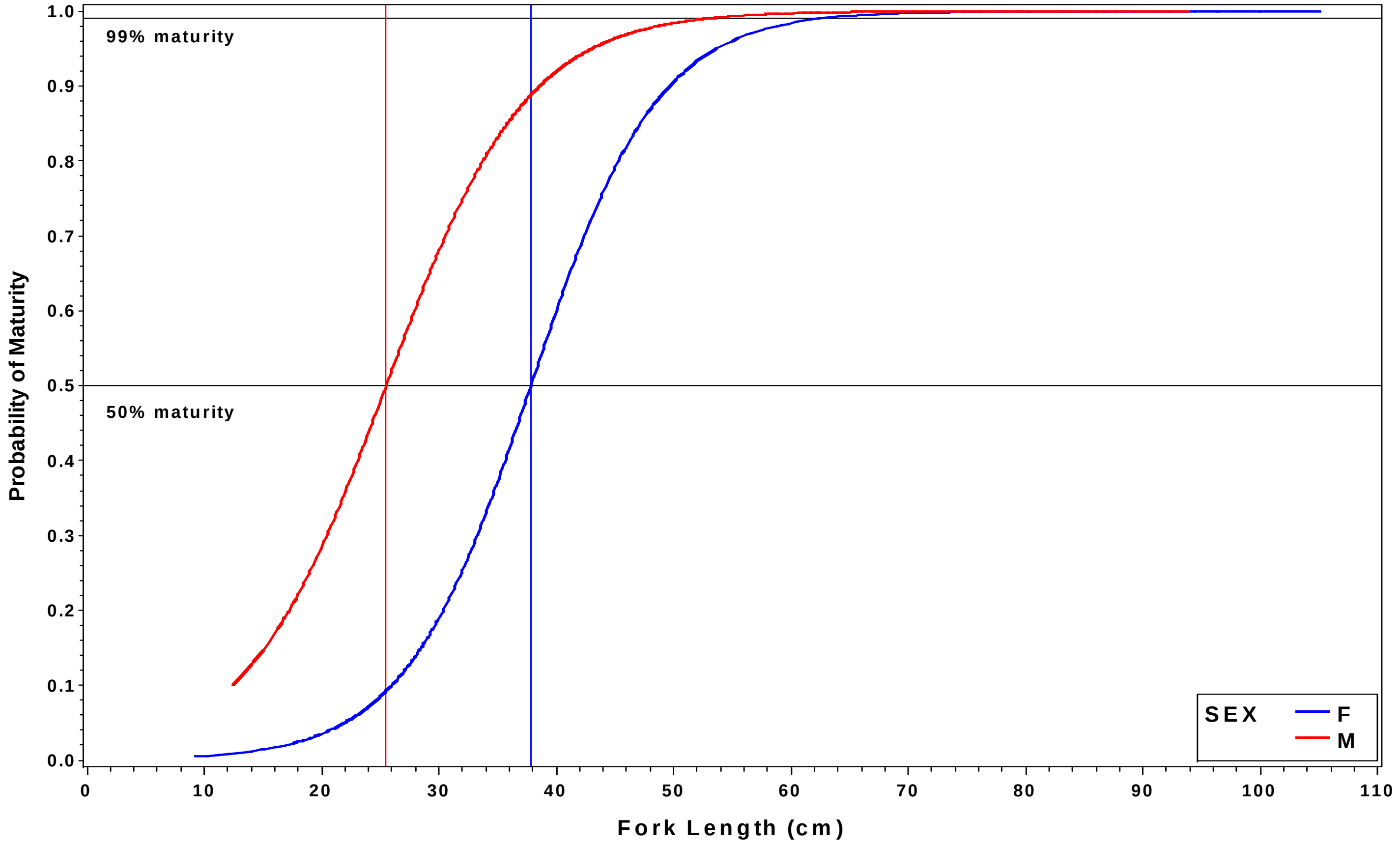


Figure 91. Striped bass diet in Chesapeake Bay 2002-2006 combined.

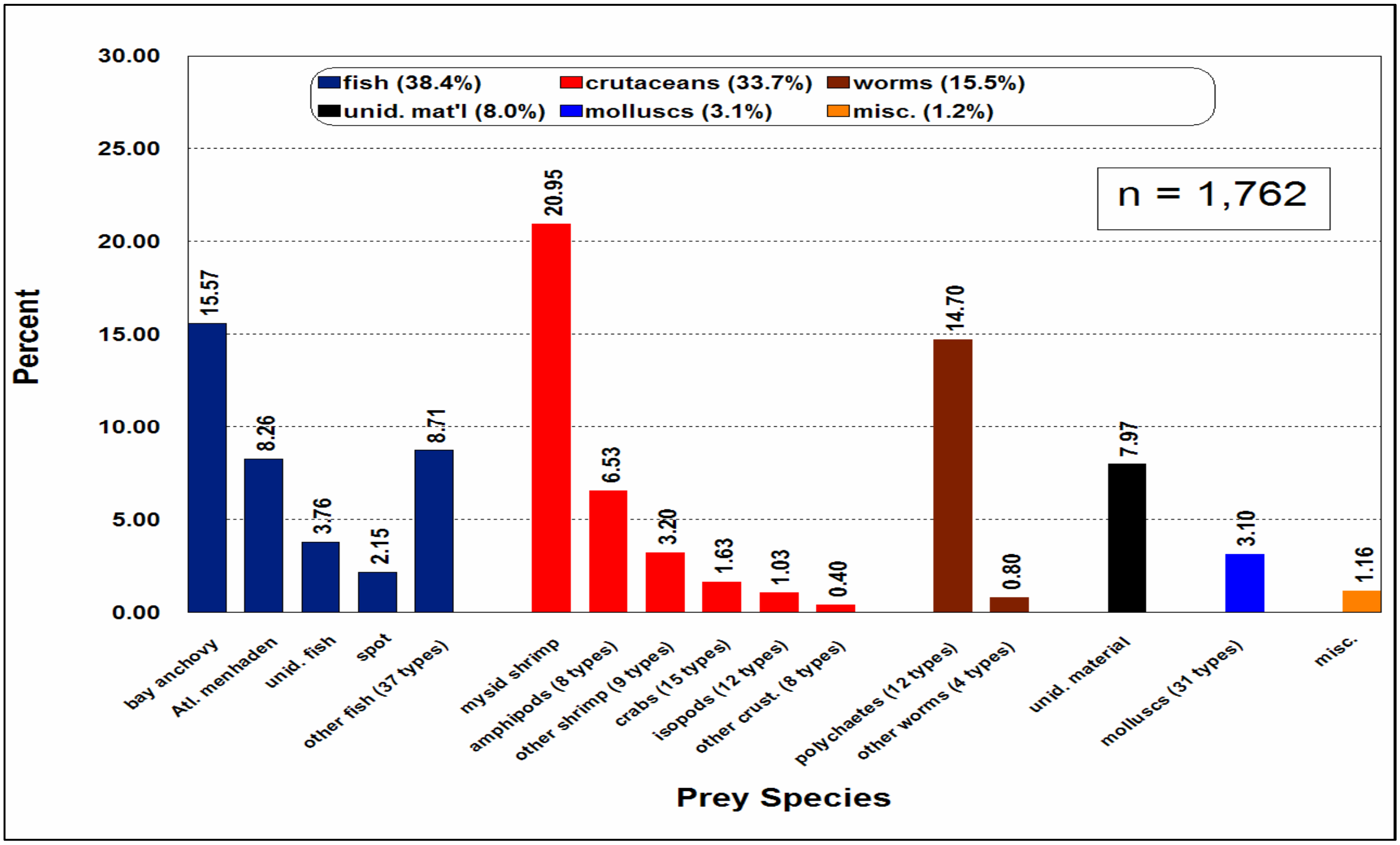


Figure 92. Summer flounder minimum trawlable abundance estimates in numbers (A) and biomass (B) in Chesapeake Bay 2002-2006.

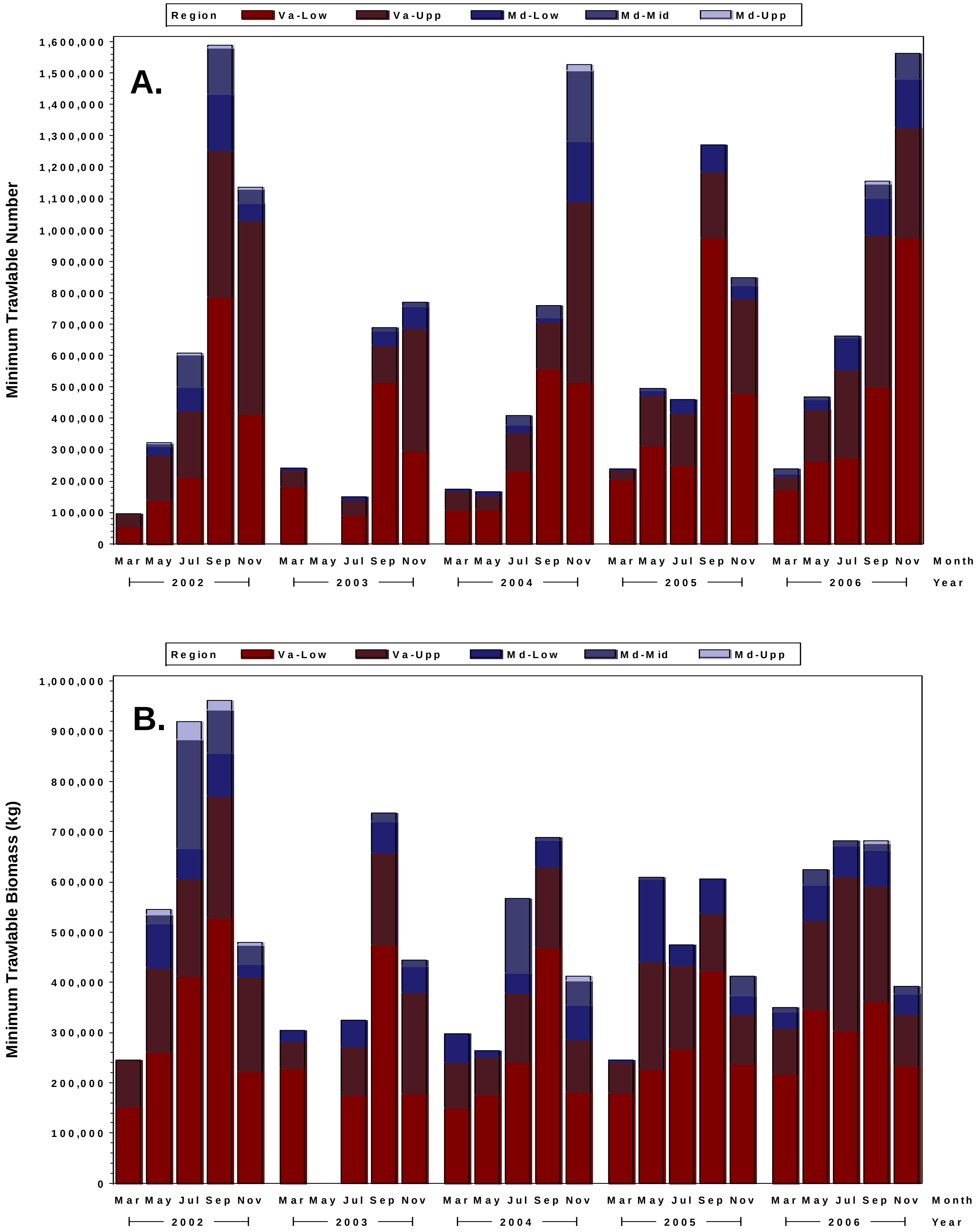


Figure 93. Site-specific summer flounder abundance (number per hectare swept), 2002.

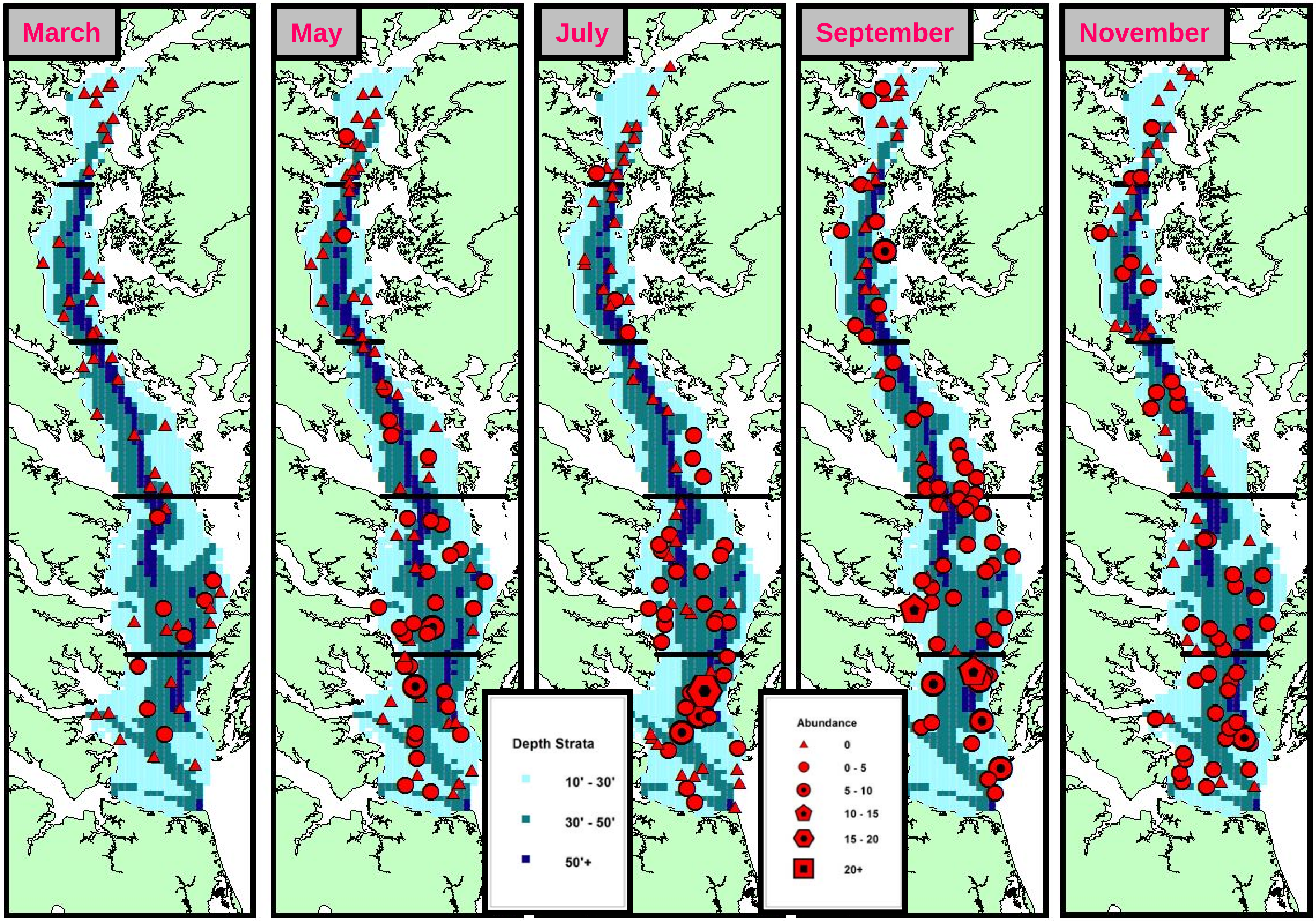


Figure 94. Site-specific summer flounder abundance (number per hectare swept), 2003.

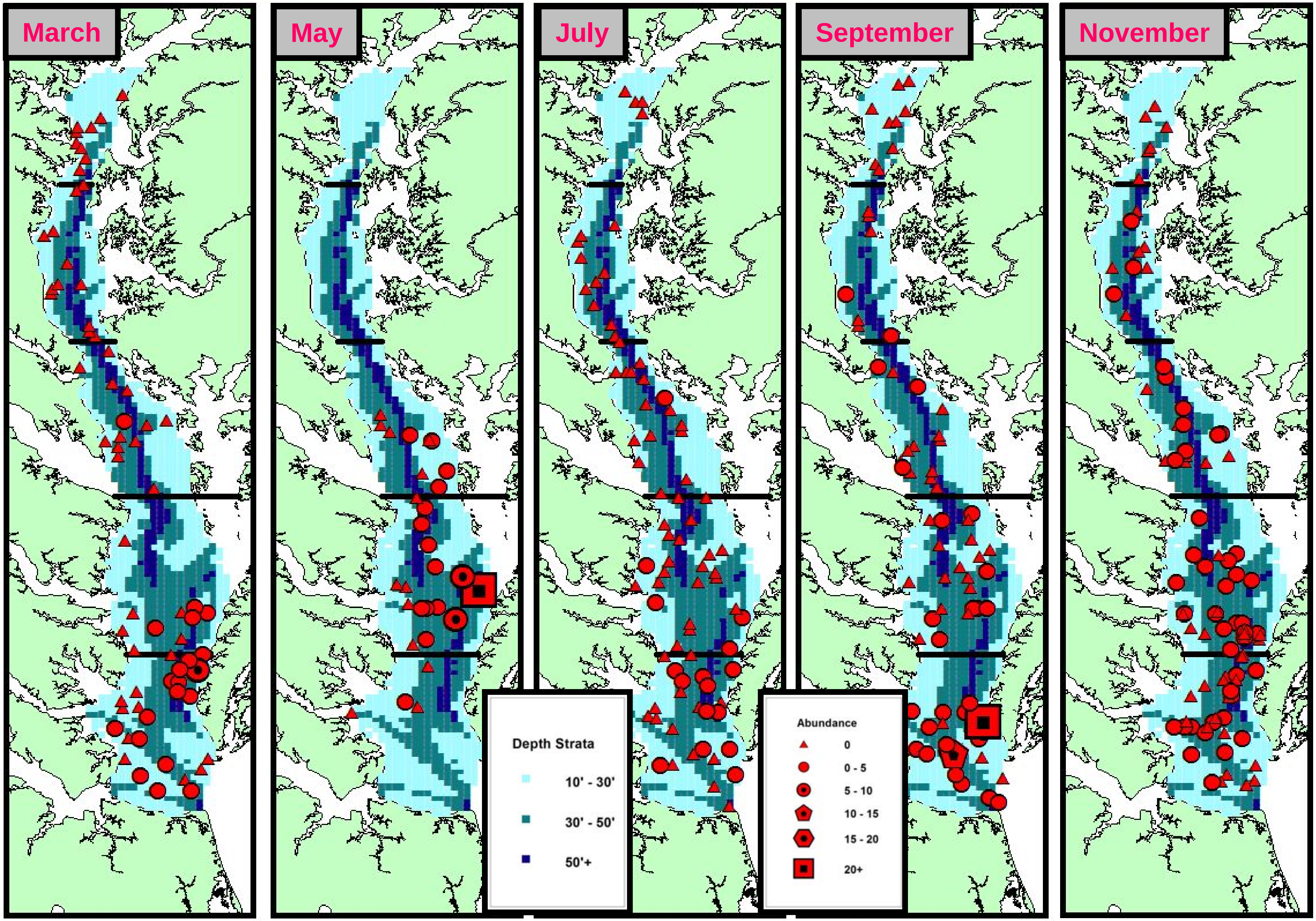


Figure 95. Site-specific summer flounder abundance (number per hectare swept), 2004.

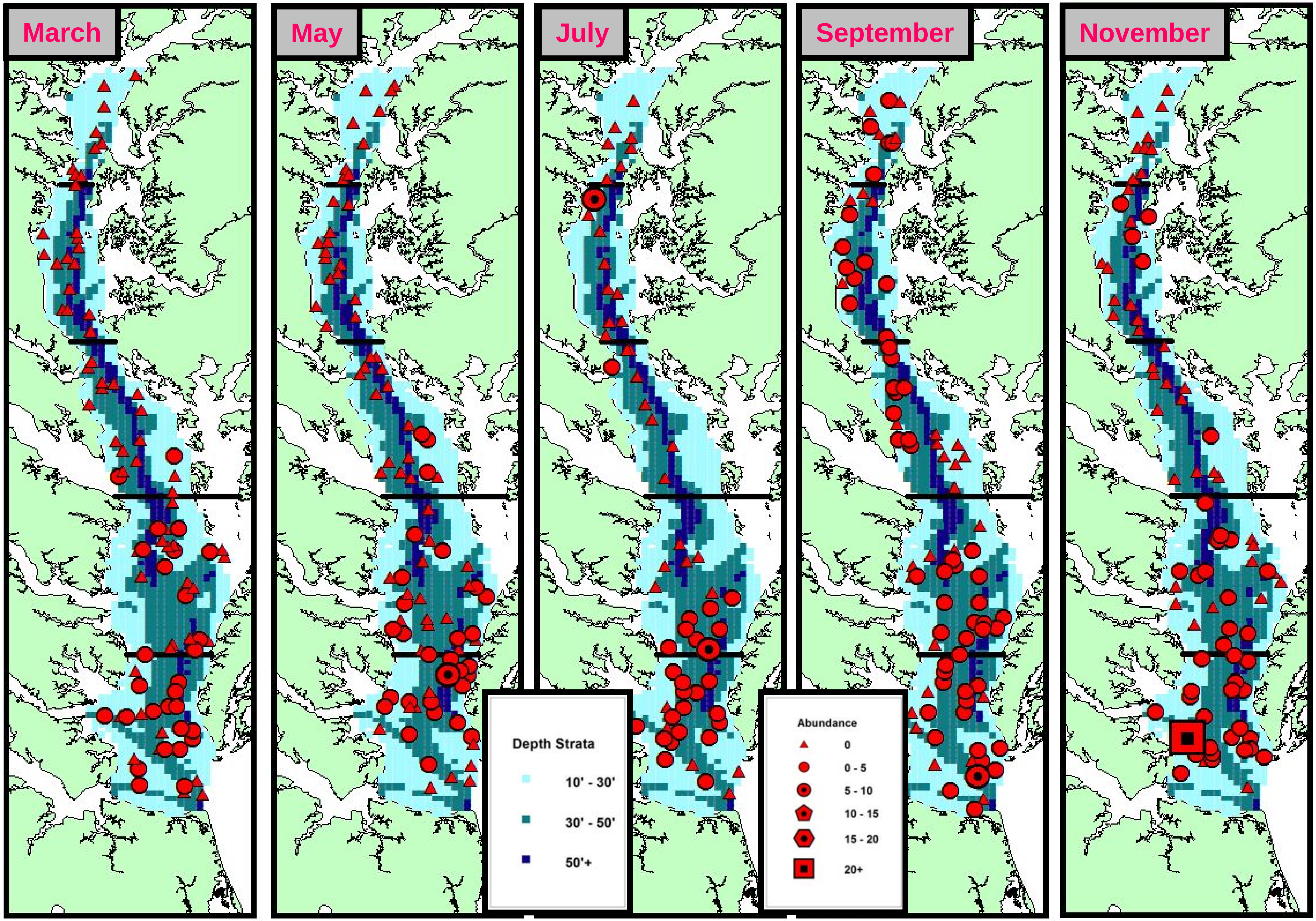


Figure 96. Site-specific summer flounder abundance (number per hectare swept), 2005.

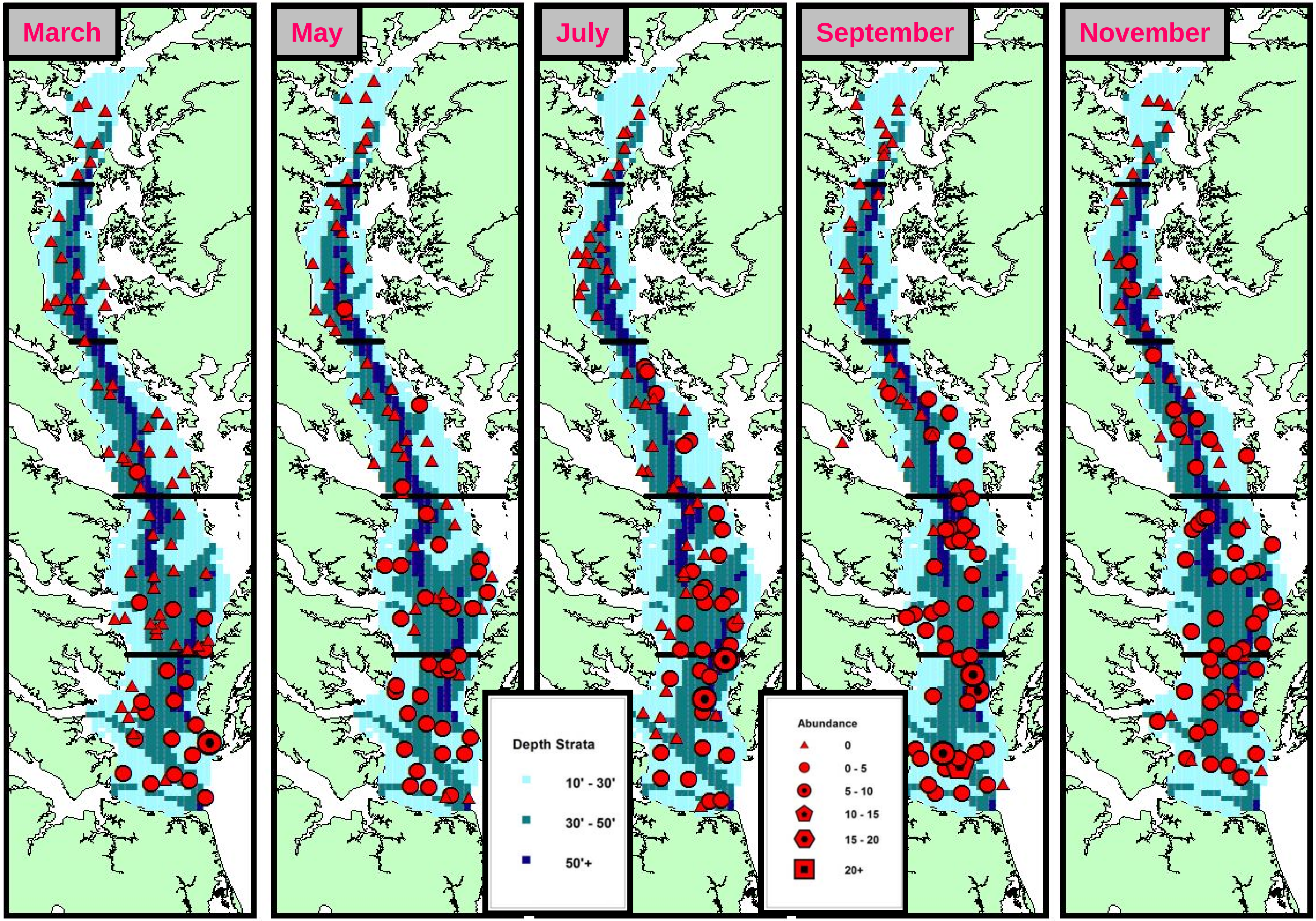


Figure 97. Site-specific summer flounder abundance (number per hectare swept), 2007.

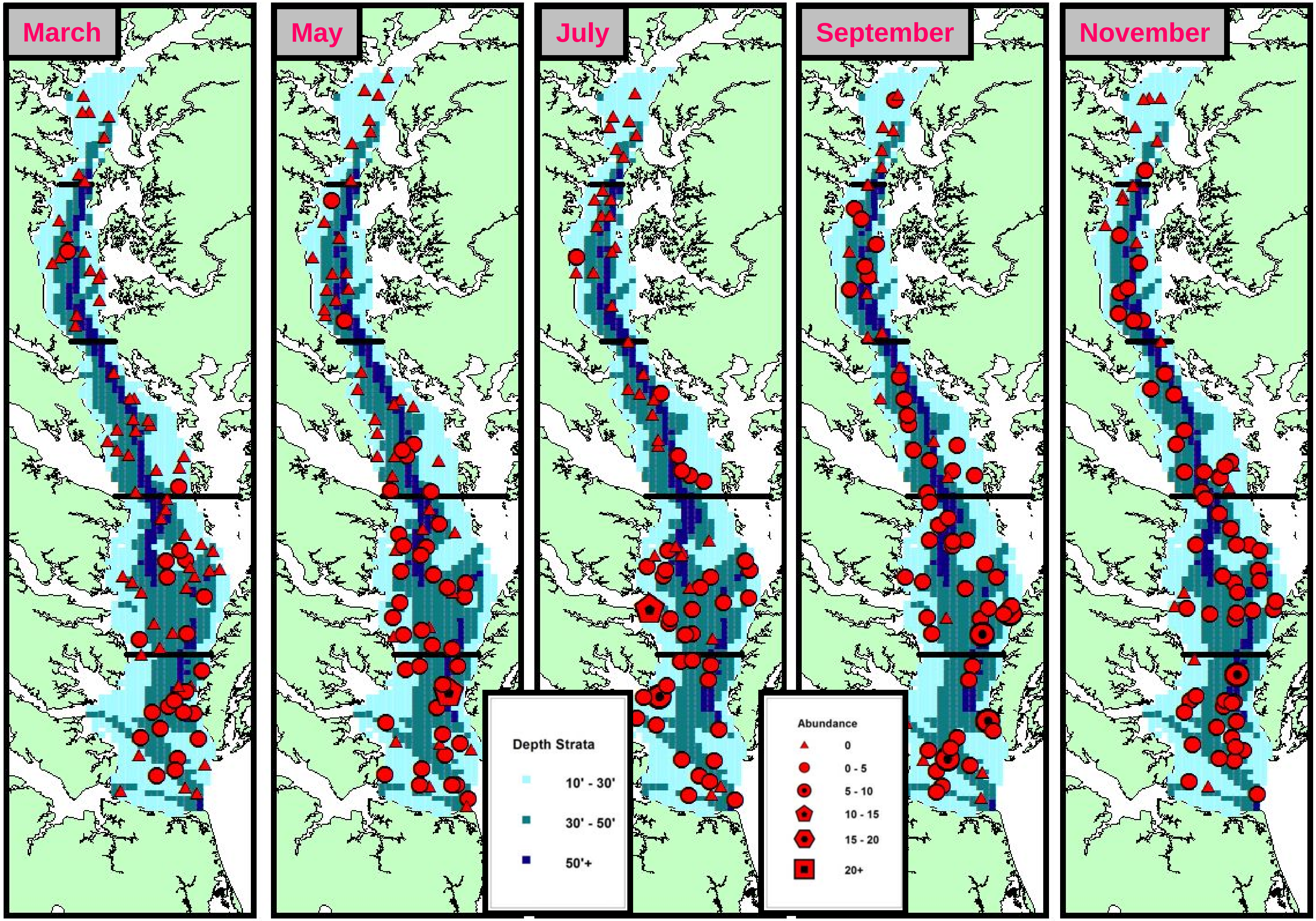


Figure 98. Summer flounder length-frequency in Chesapeake Bay 2002-2006.

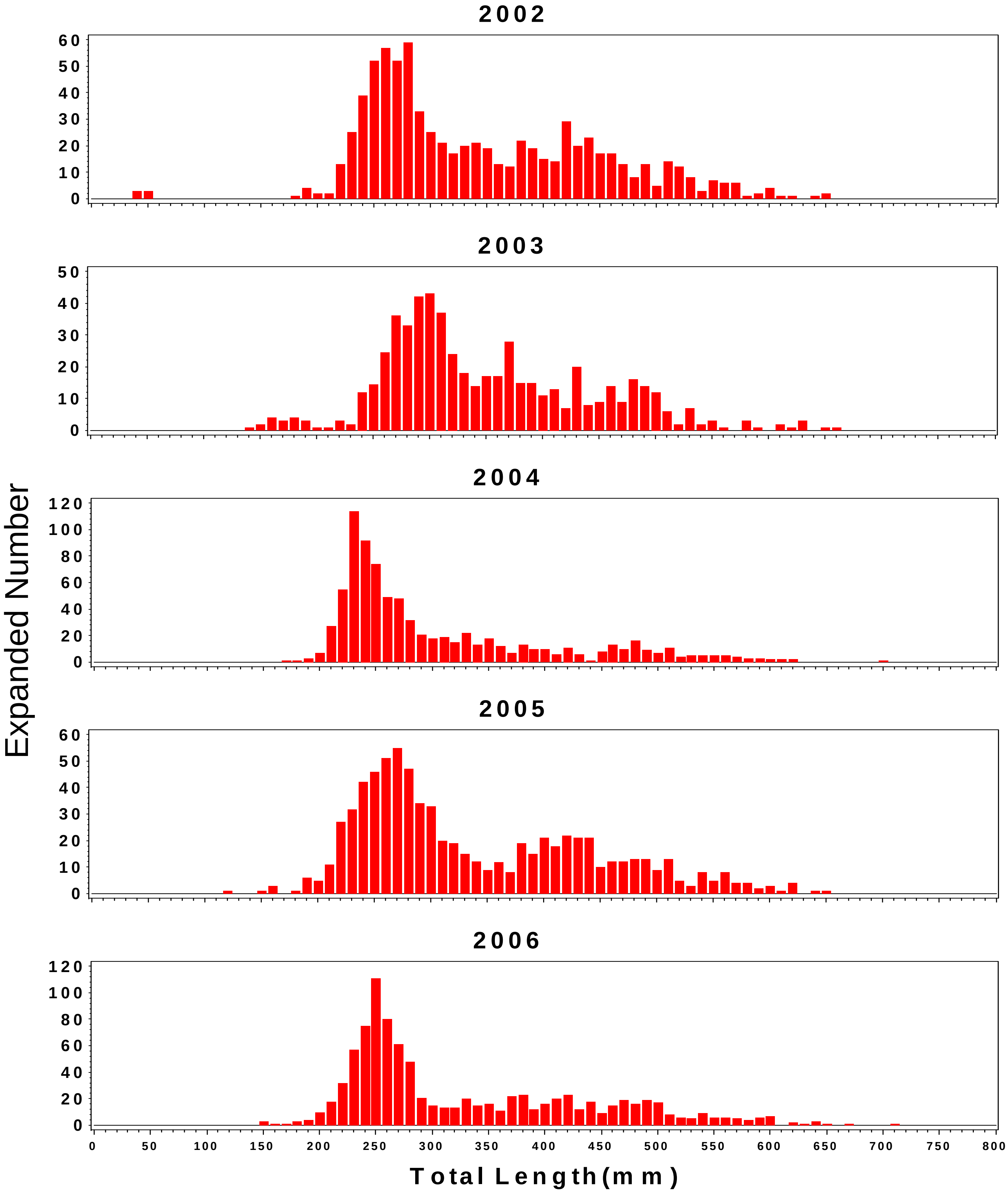


Figure 99. Summer flounder age-structure in Chesapeake Bay 2002-2006.

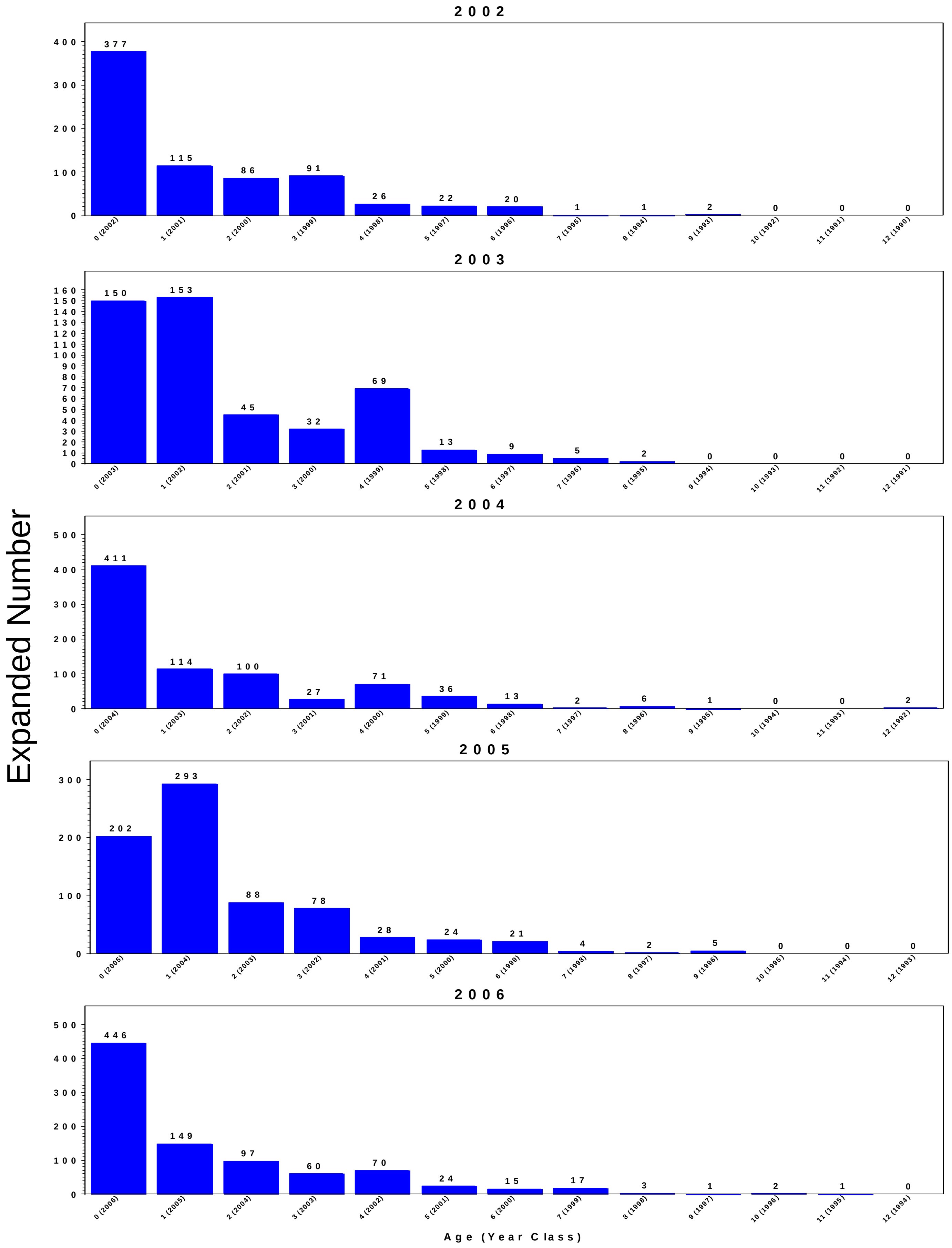


Figure 100. Summer flounder sex-ratios in Chesapeake Bay 2002-2006, by month (A), region (B), age (C).

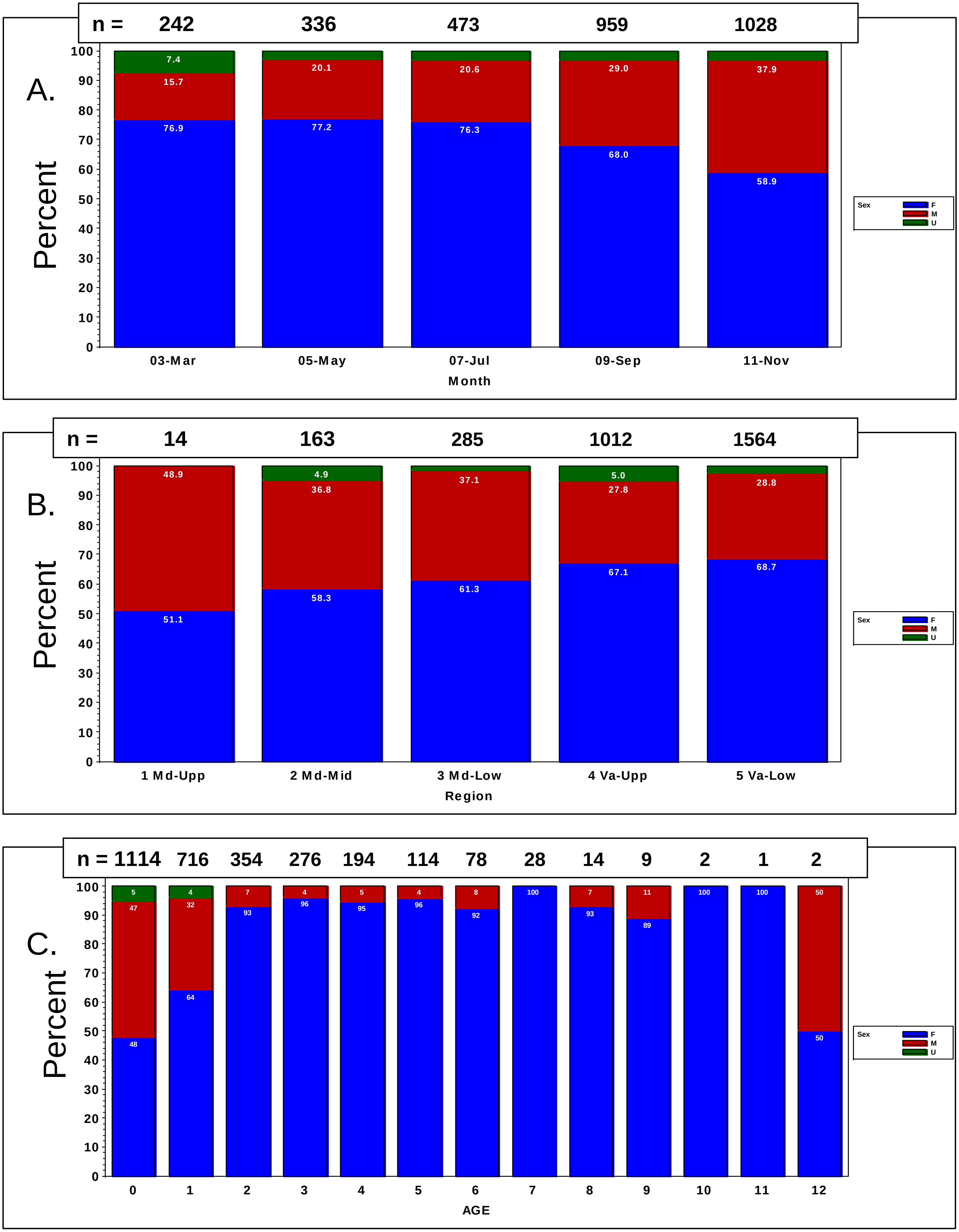
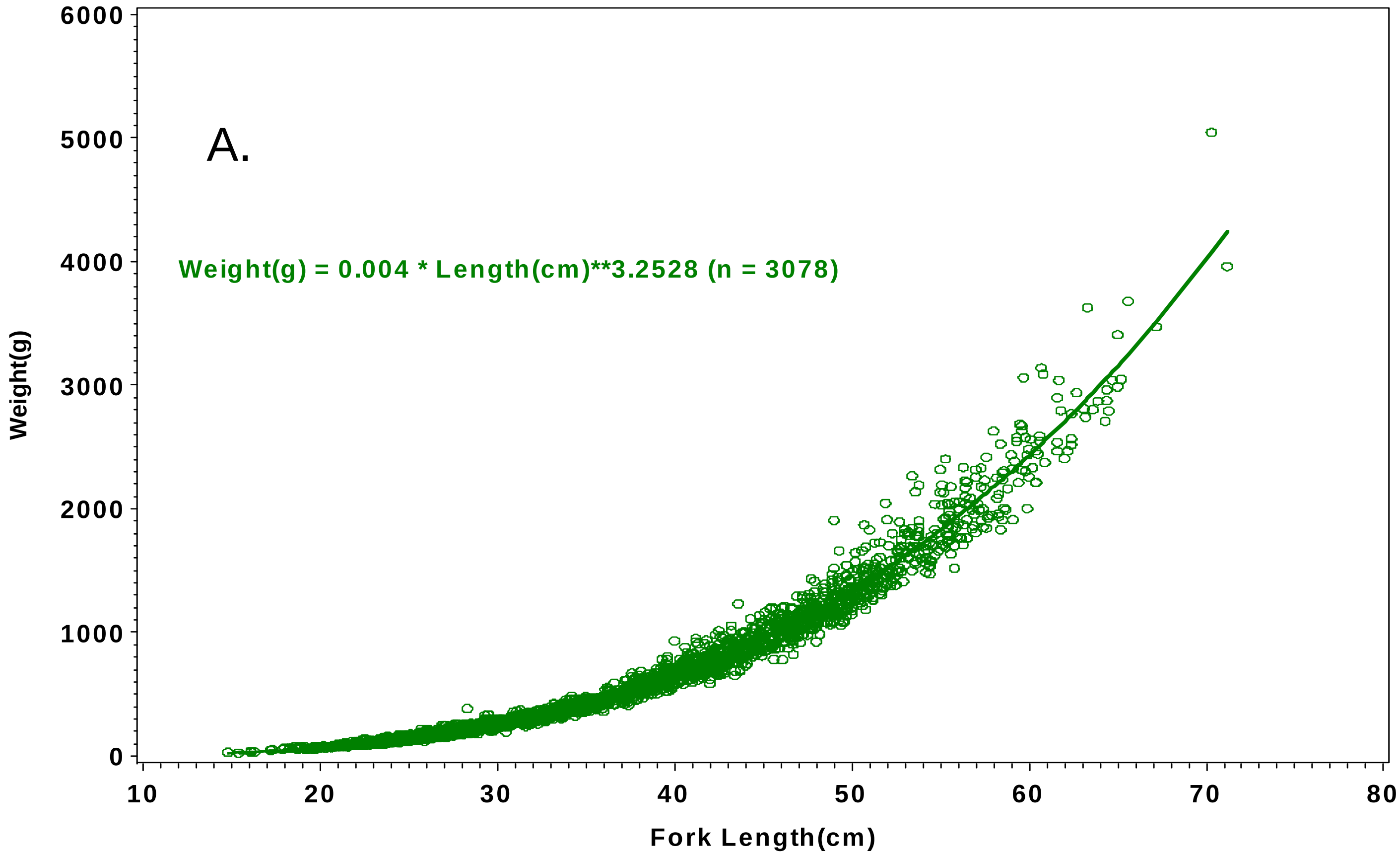


Figure 101. Summer flounder length-weight relationships in Chesapeake Bay 2002-2005 as calculated by power regression for sexes combined (A) and separately (B).



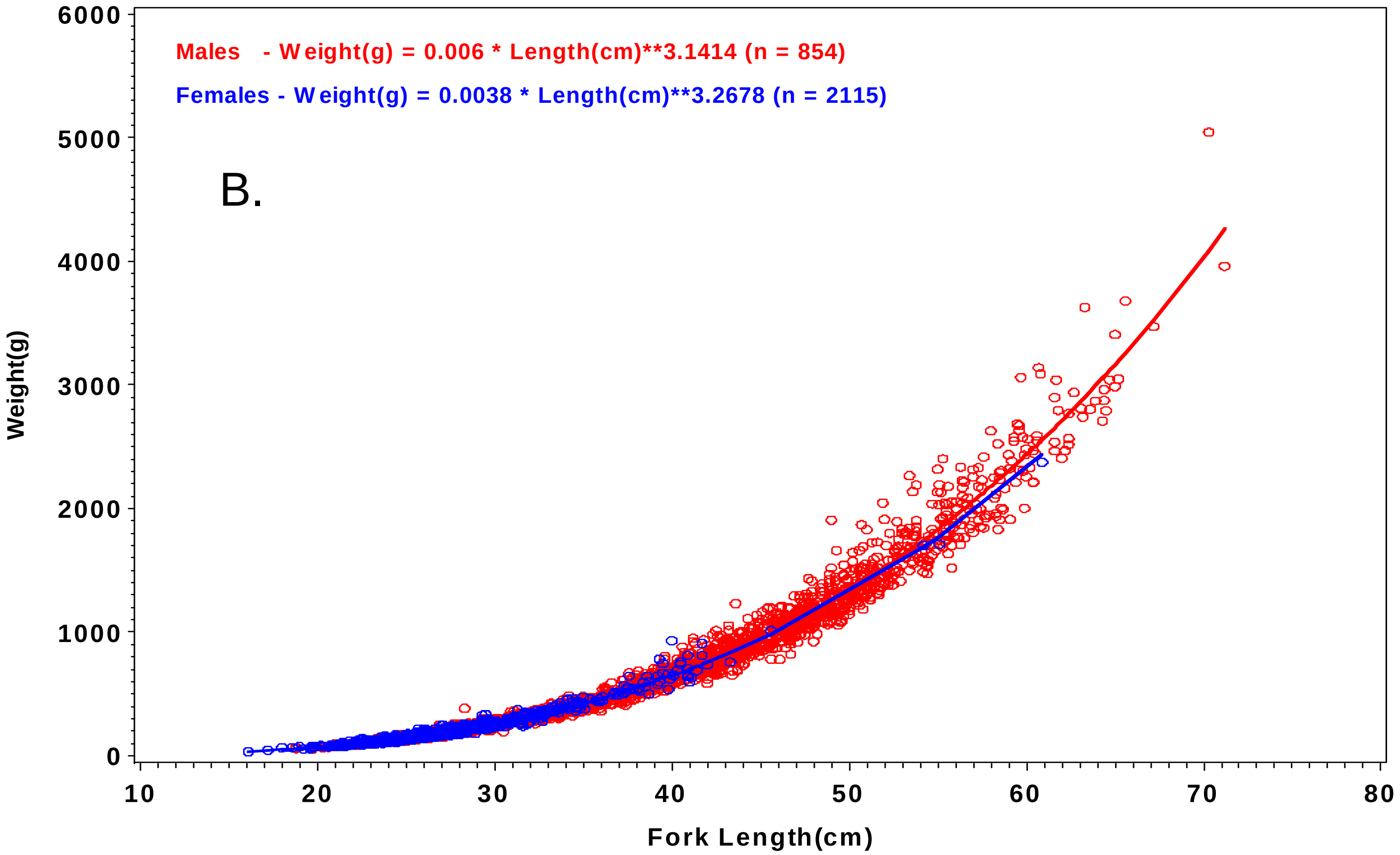


Figure 102. Summer flounder maturity schedule in Chesapeake Bay 2002-2006 combined, by sex.

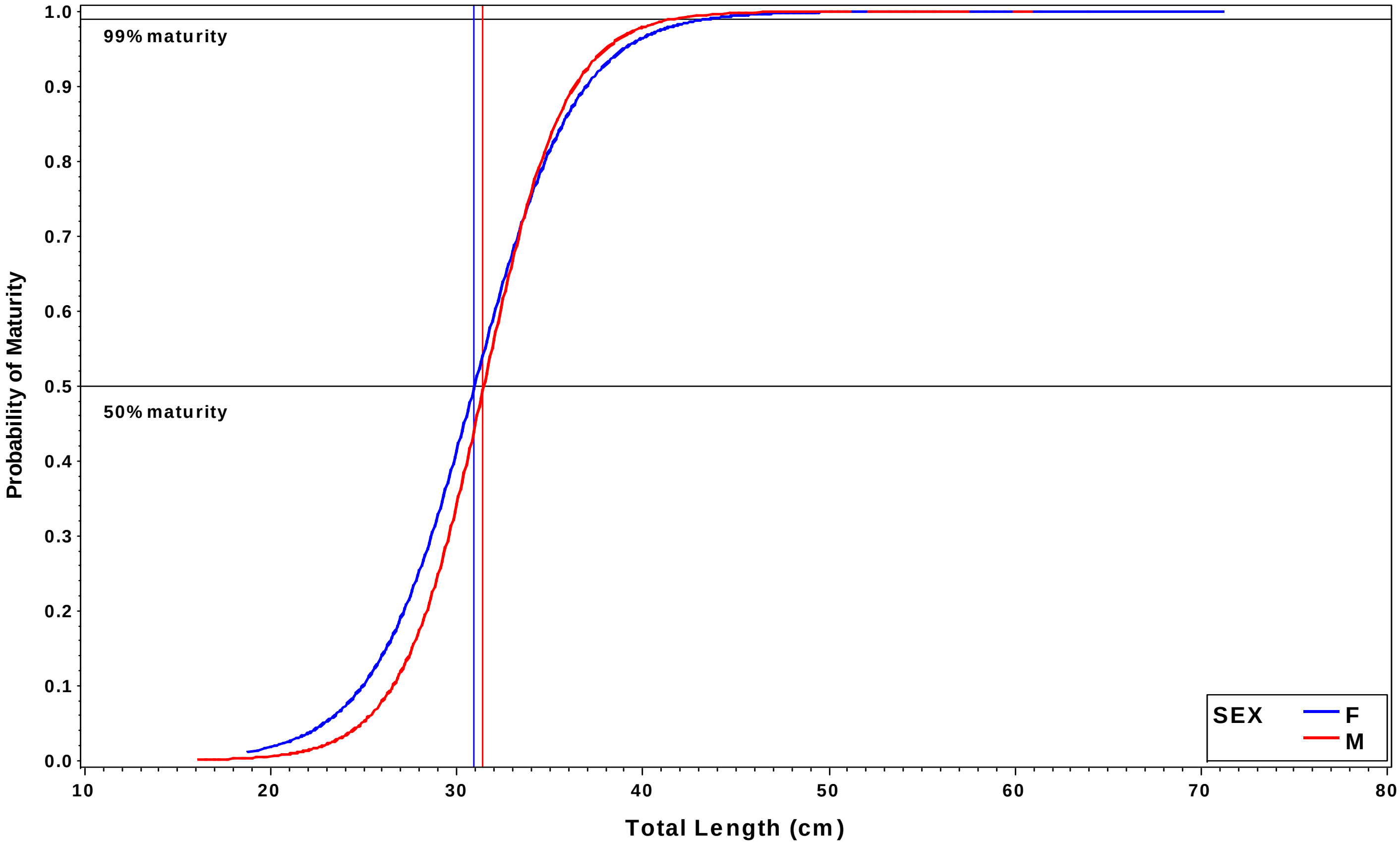


Figure 103. Summer flounder diet in Chesapeake Bay 2002-2006 combined.

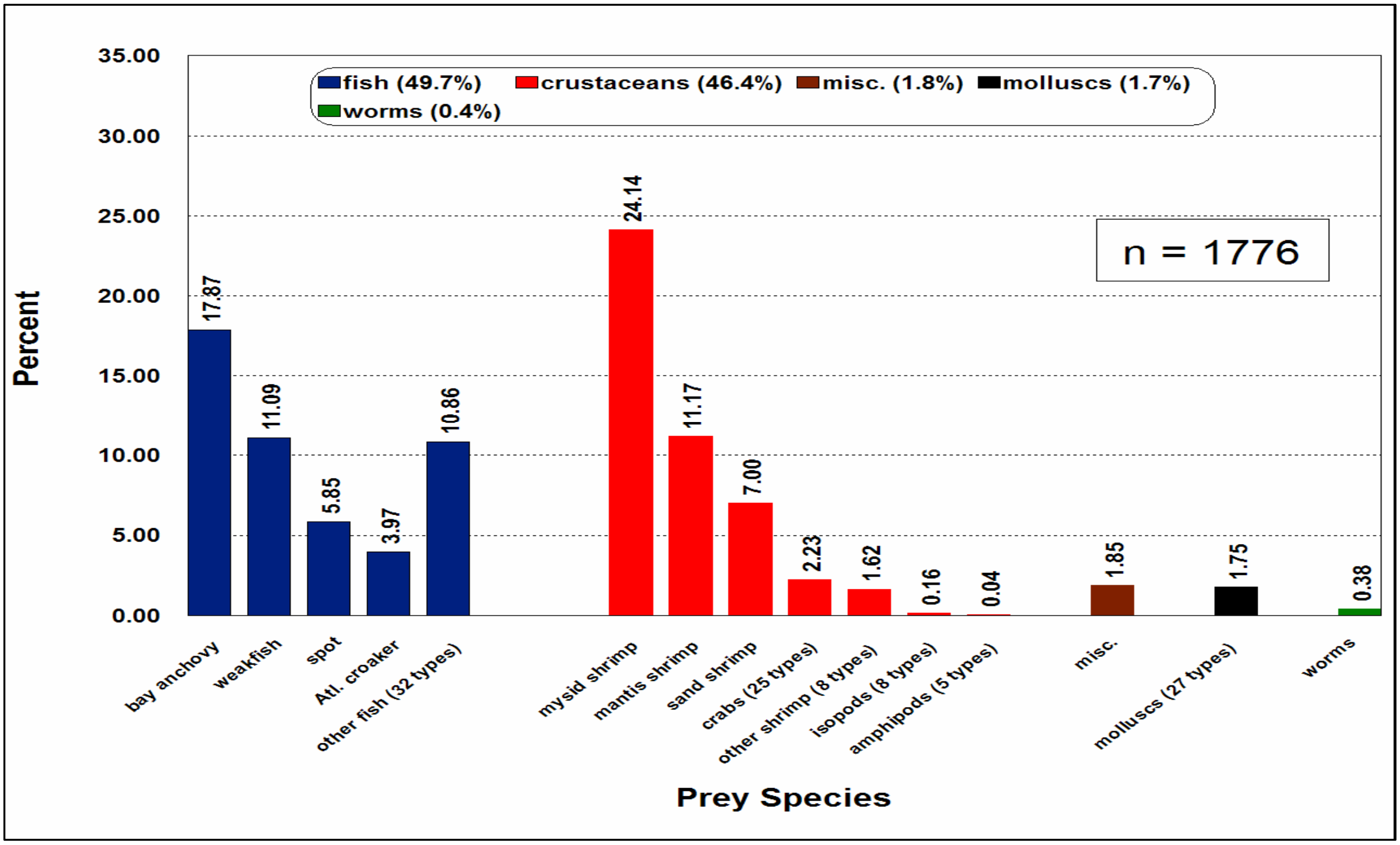
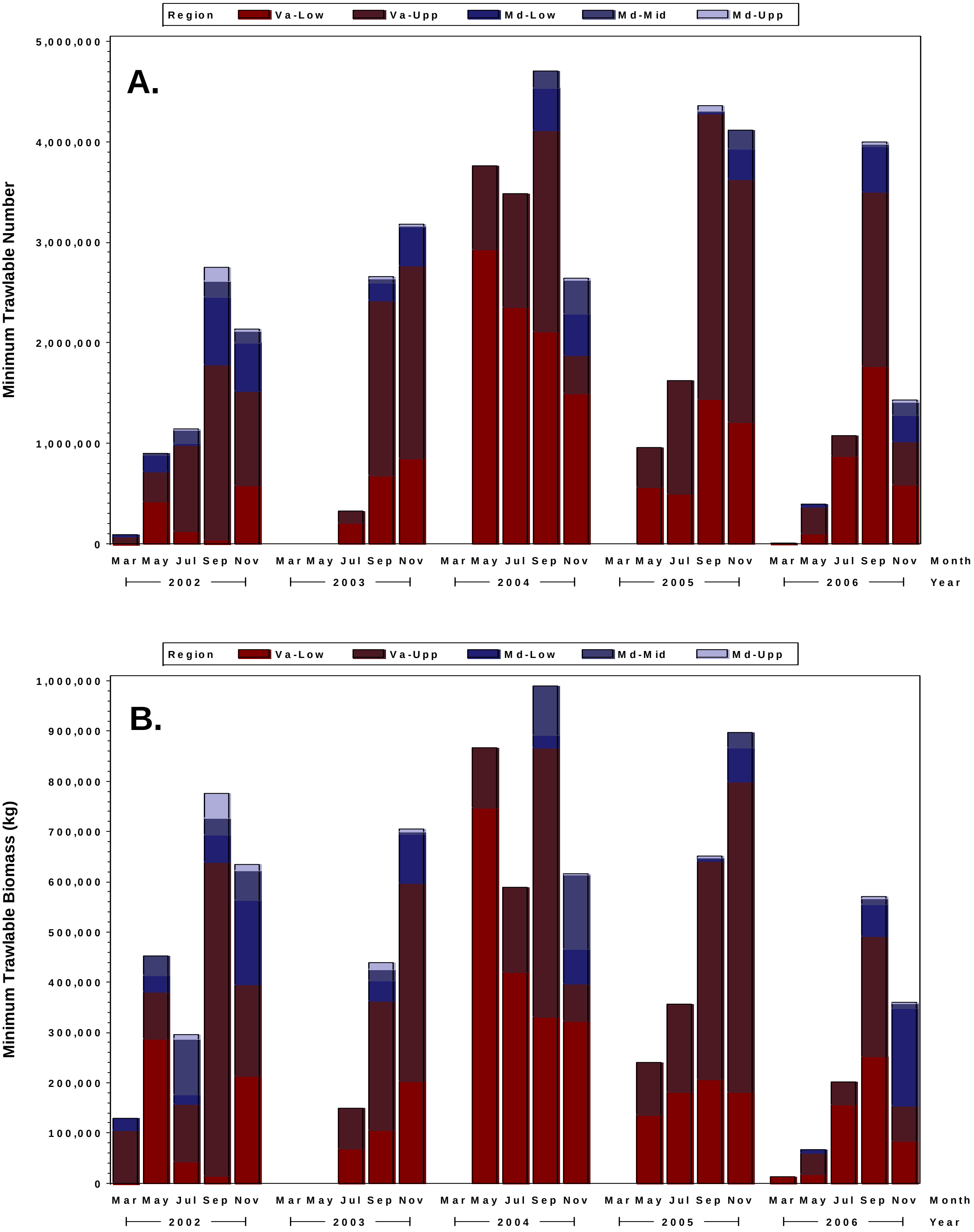


Figure 104. Weakfish minimum trawlable abundance estimates in numbers (A) and biomass (B) in Chesapeake Bay 2002-2006.



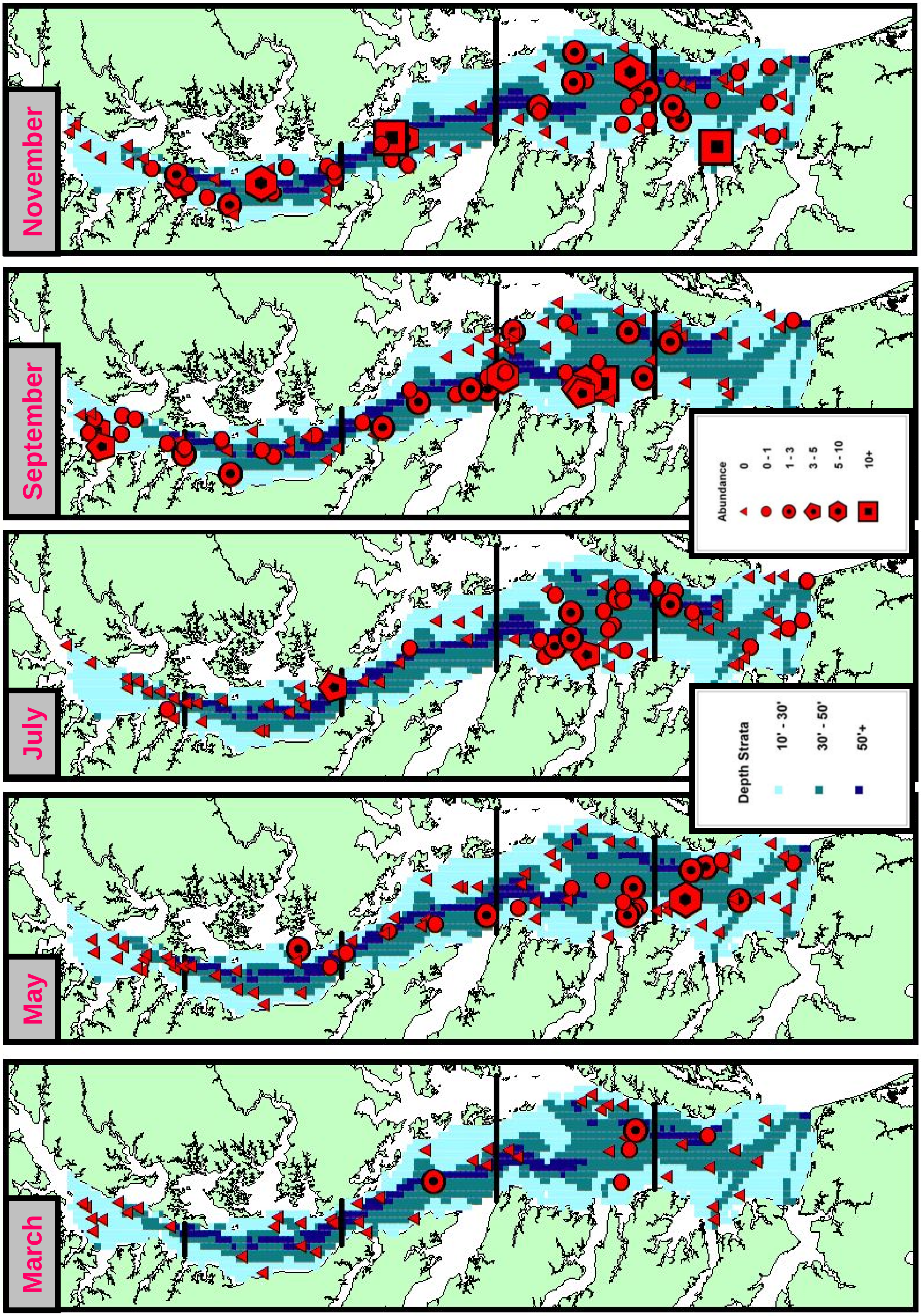


Figure 105. Site-specific weakfish abundance (number per hectare swept), 2002.

Figure 106. Site-specific weakfish abundance (number per hectare swept), 2003.

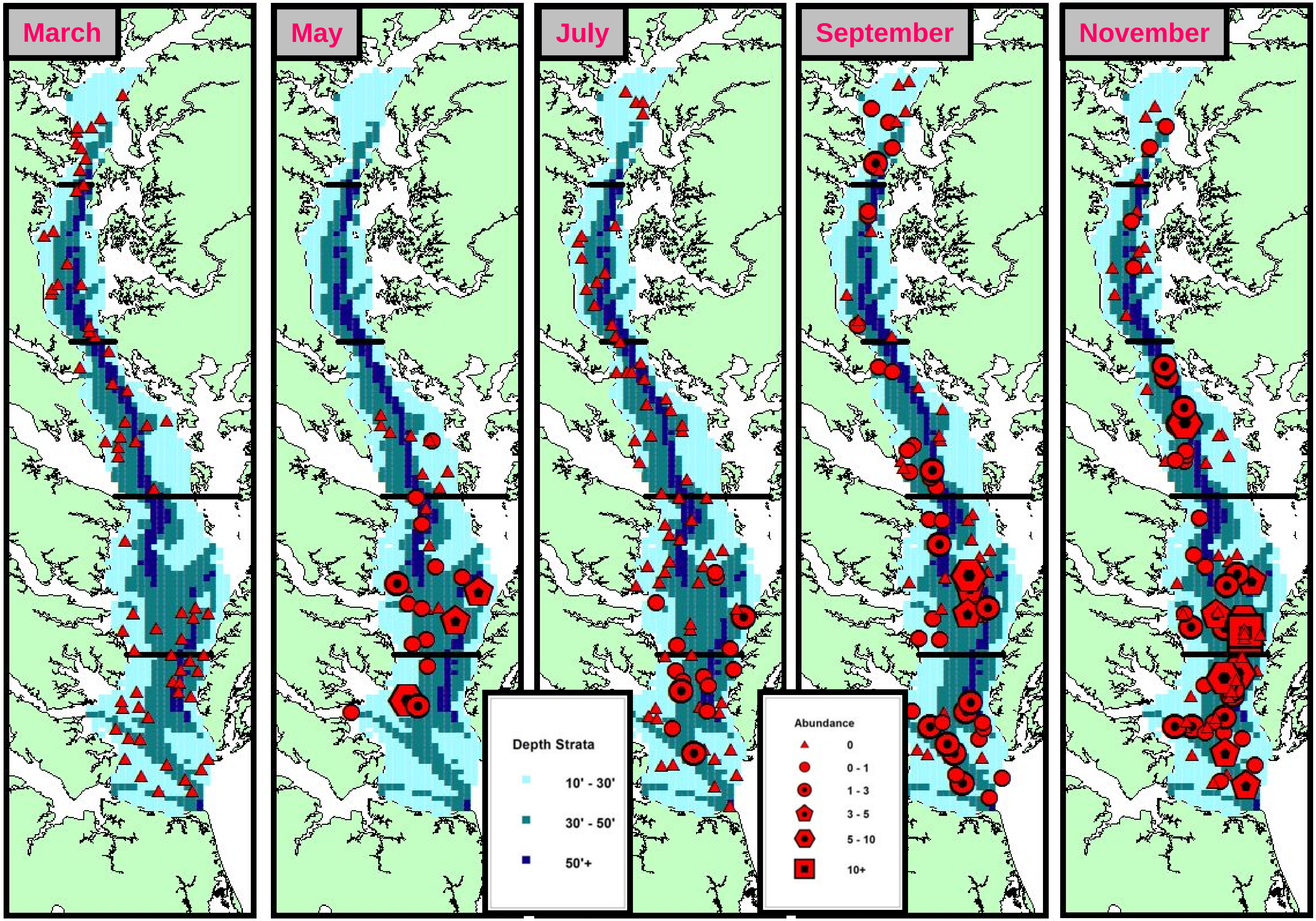


Figure 107. Site-specific weakfish abundance (number per hectare swept), 2004.

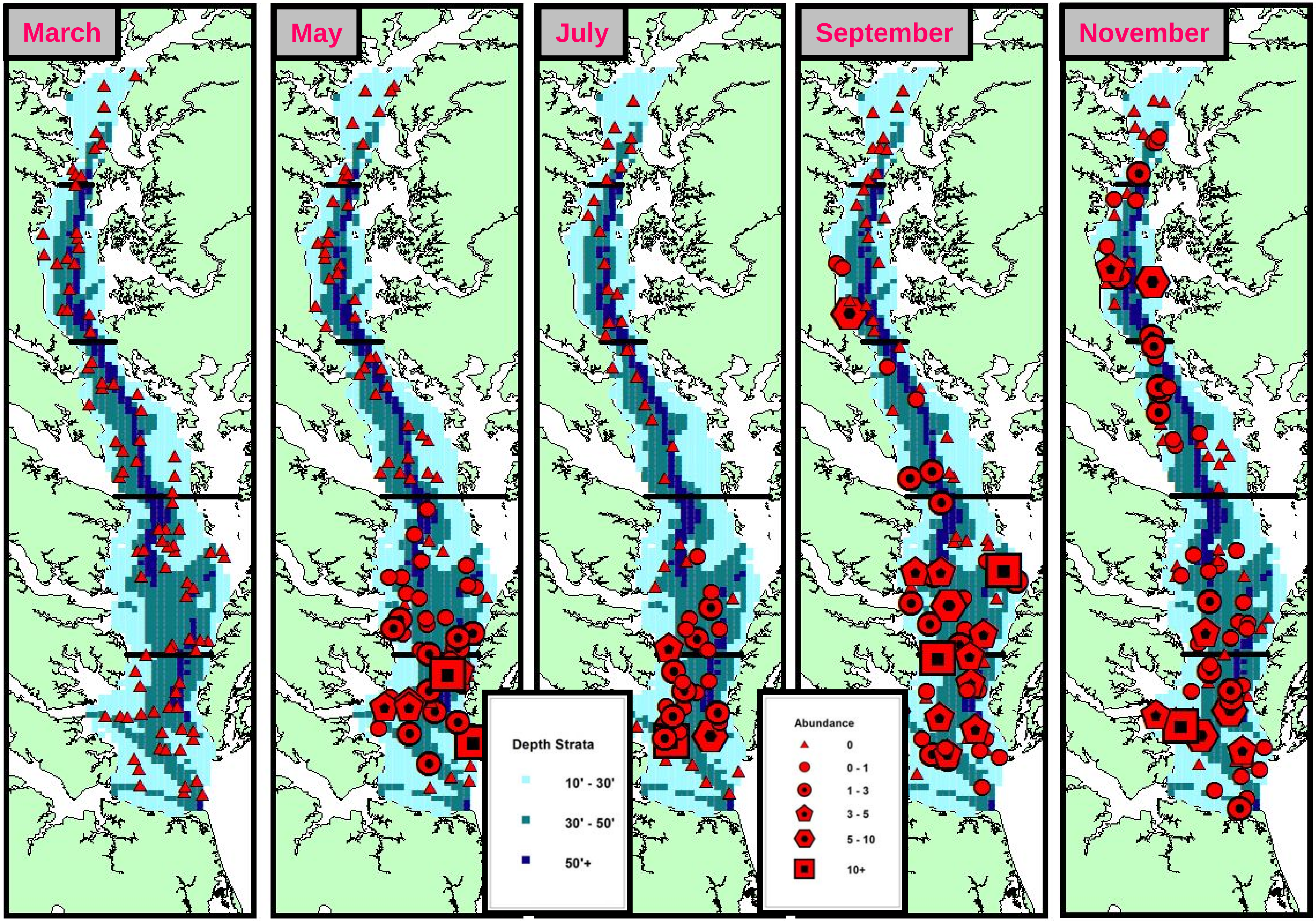


Figure 108. Site-specific weakfish abundance (number per hectare swept), 2005.

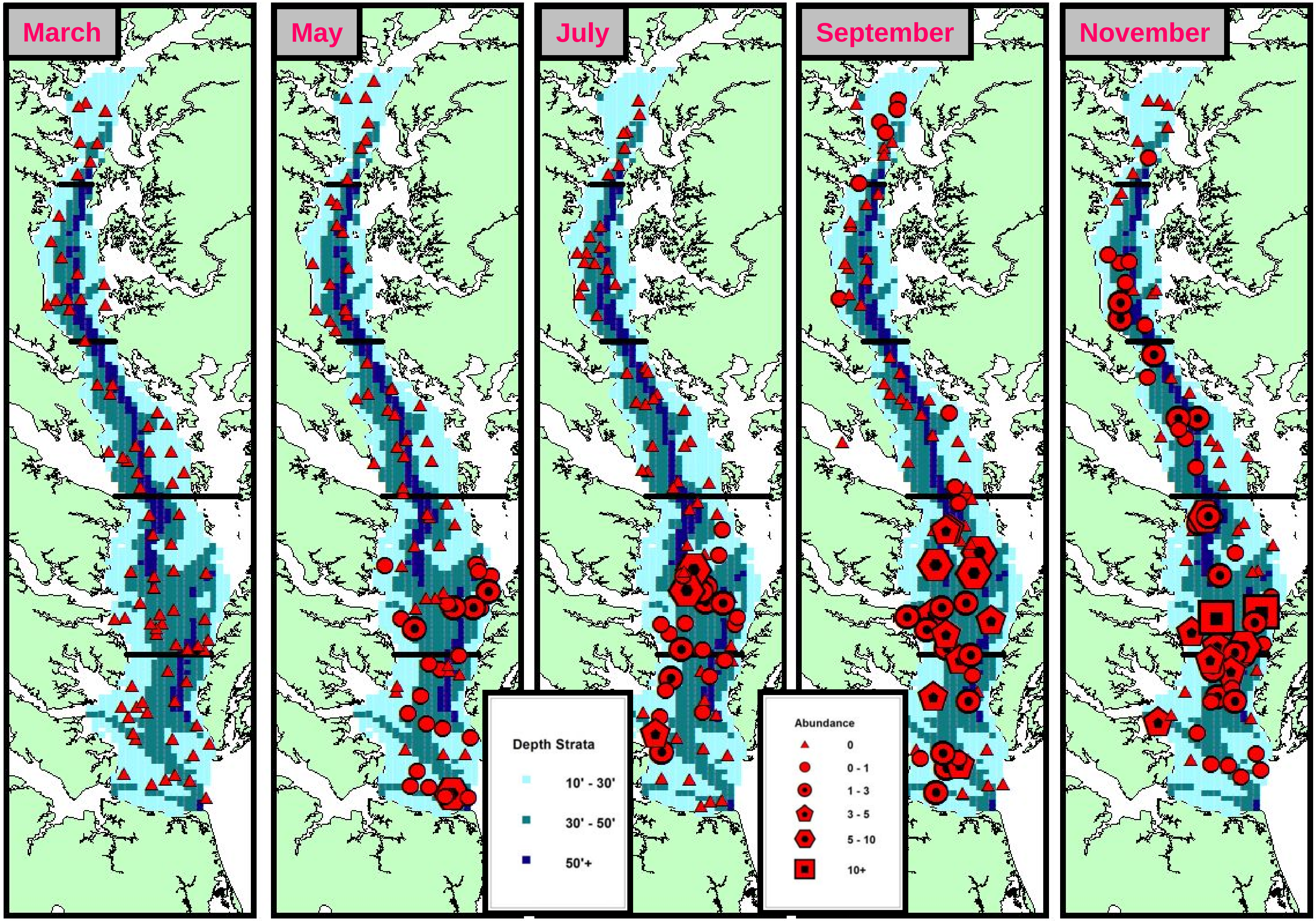


Figure 109. Site-specific weakfish abundance (number per hectare swept), 2006.

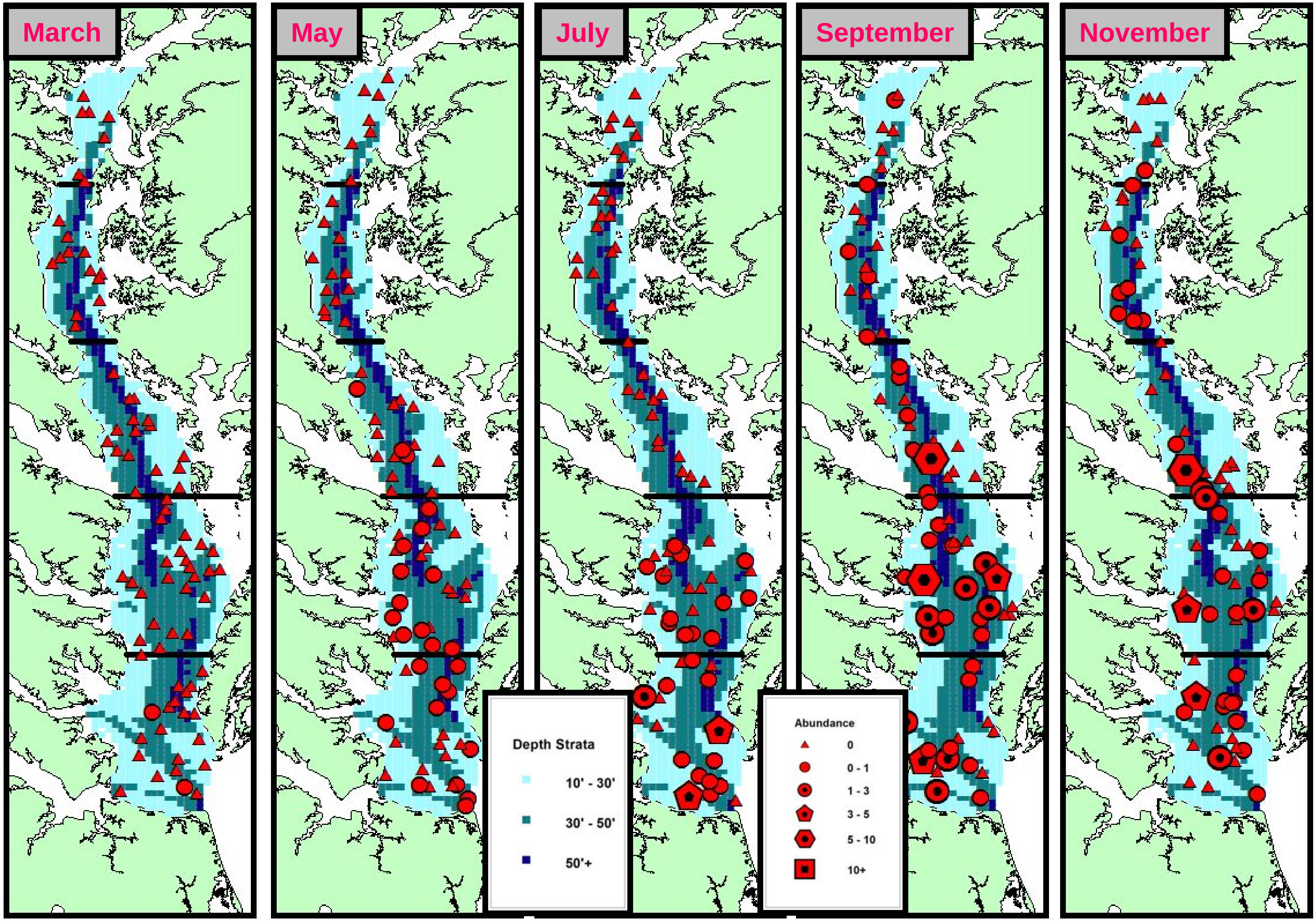


Figure 110. Weakfish length-frequency in Chesapeake Bay 2002-2006.

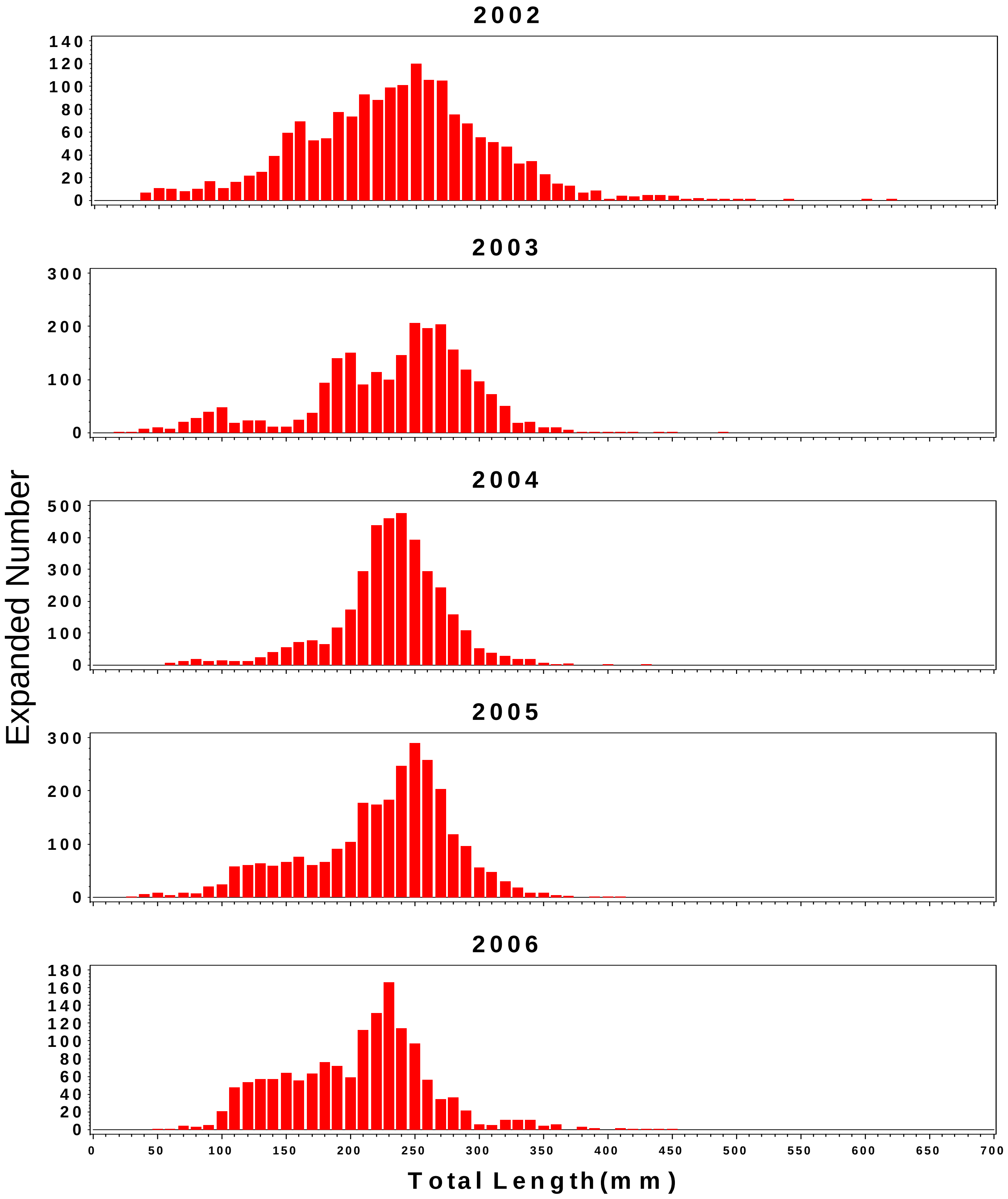


Figure 111. Weakfish age-structure in Chesapeake Bay 2002-2006.

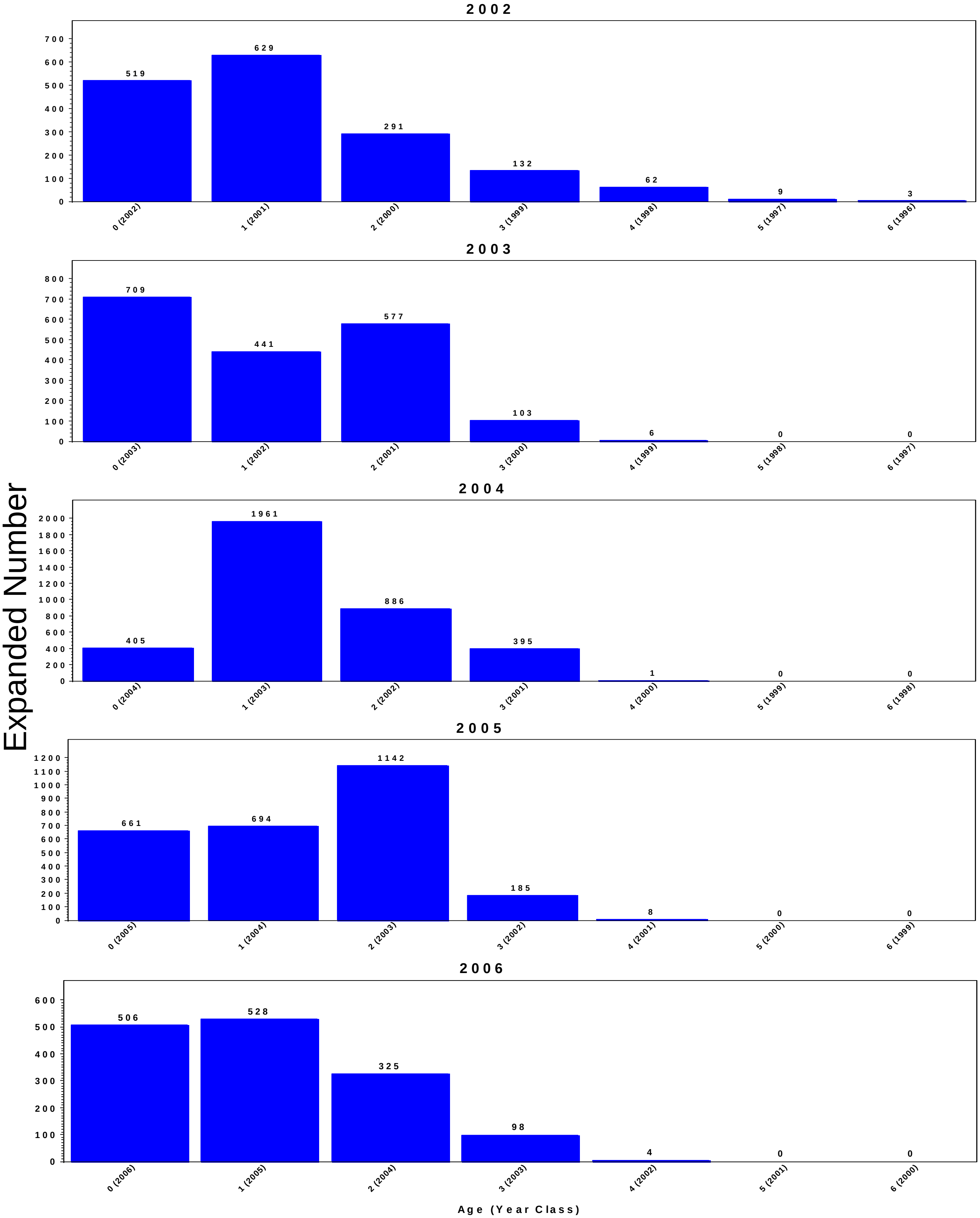


Figure 112. Weakfish sex-ratios in Chesapeake Bay 2002-2005, by year (A), region (B), age (C).

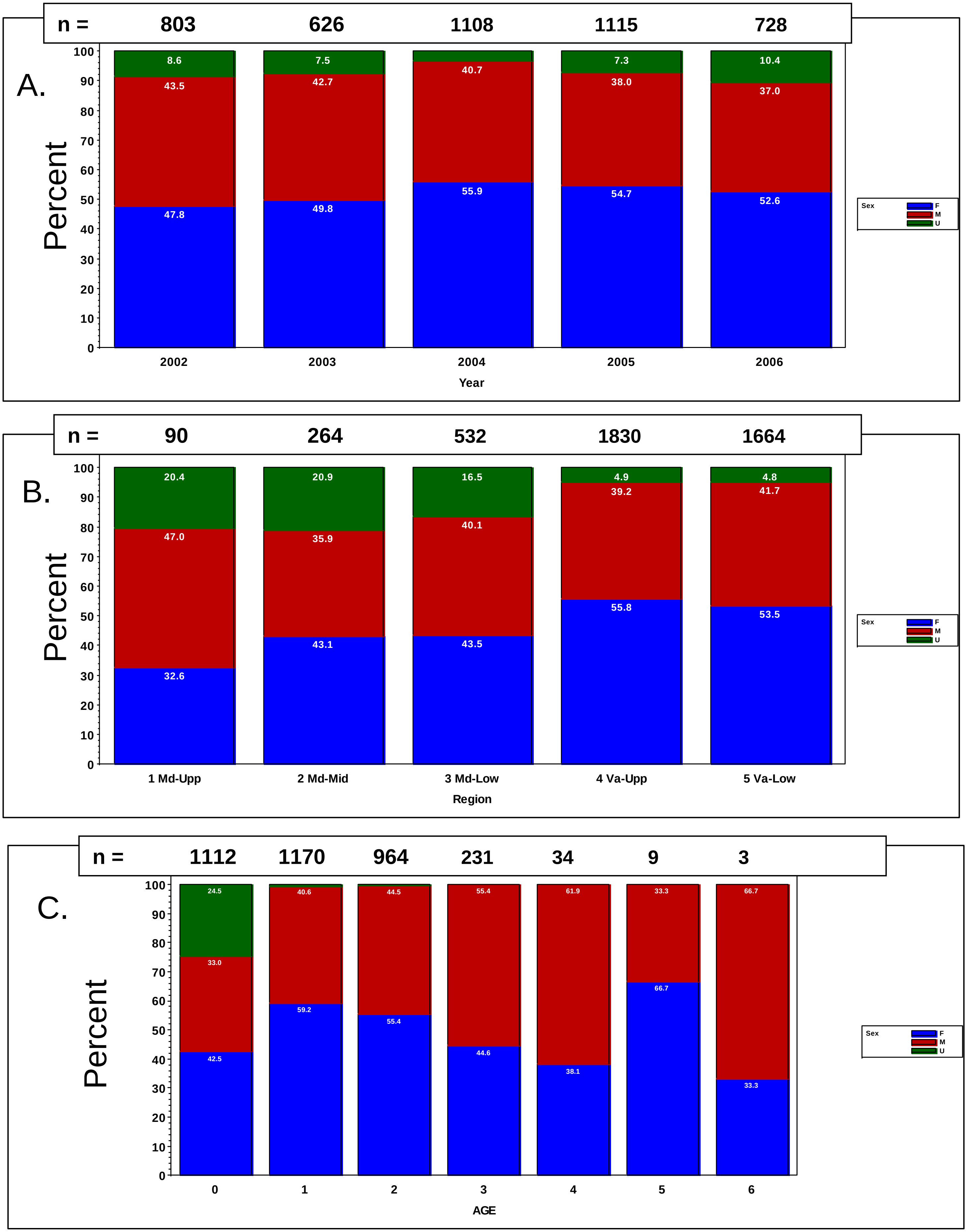


Figure 113. Weakfish length-weight relationships in Chesapeake Bay 2002-2006 as calculated by power regression for sexes combined (A) and separately (B).

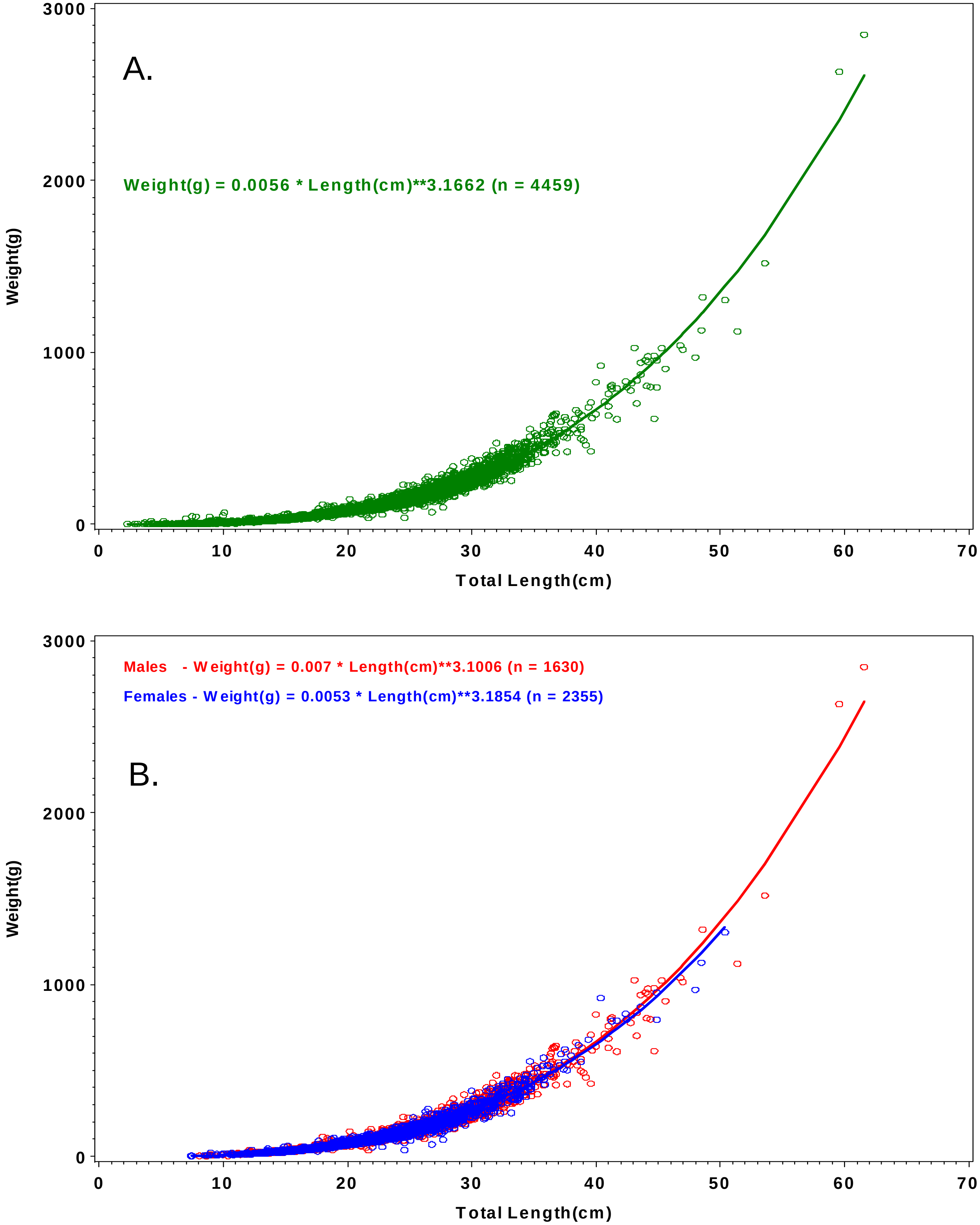


Figure 114. Weakfish maturity schedule in Chesapeake Bay 2002-2006 combined, by sex.

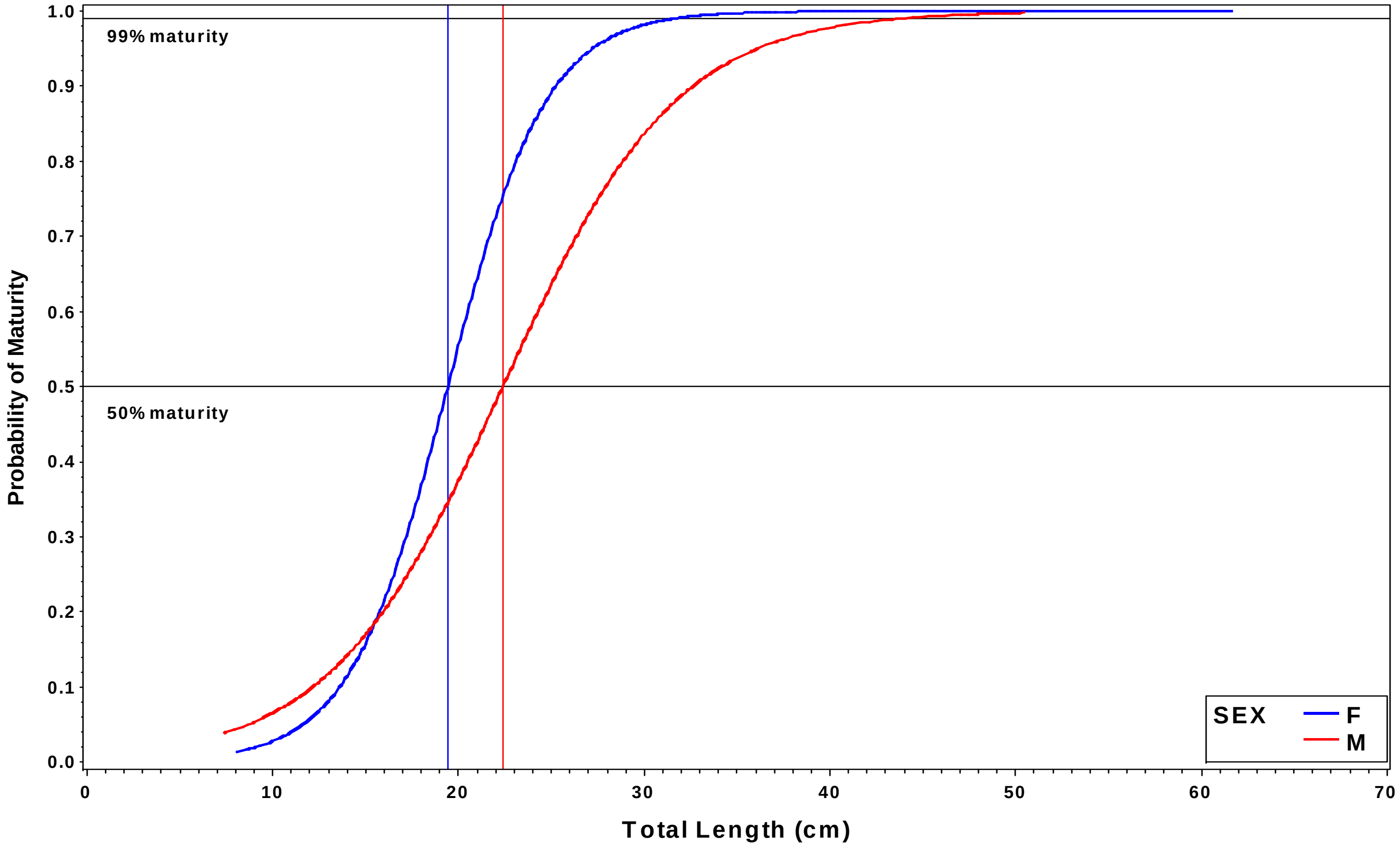


Figure 115. Weakfish diet in Chesapeake Bay 2002-2006 combined.

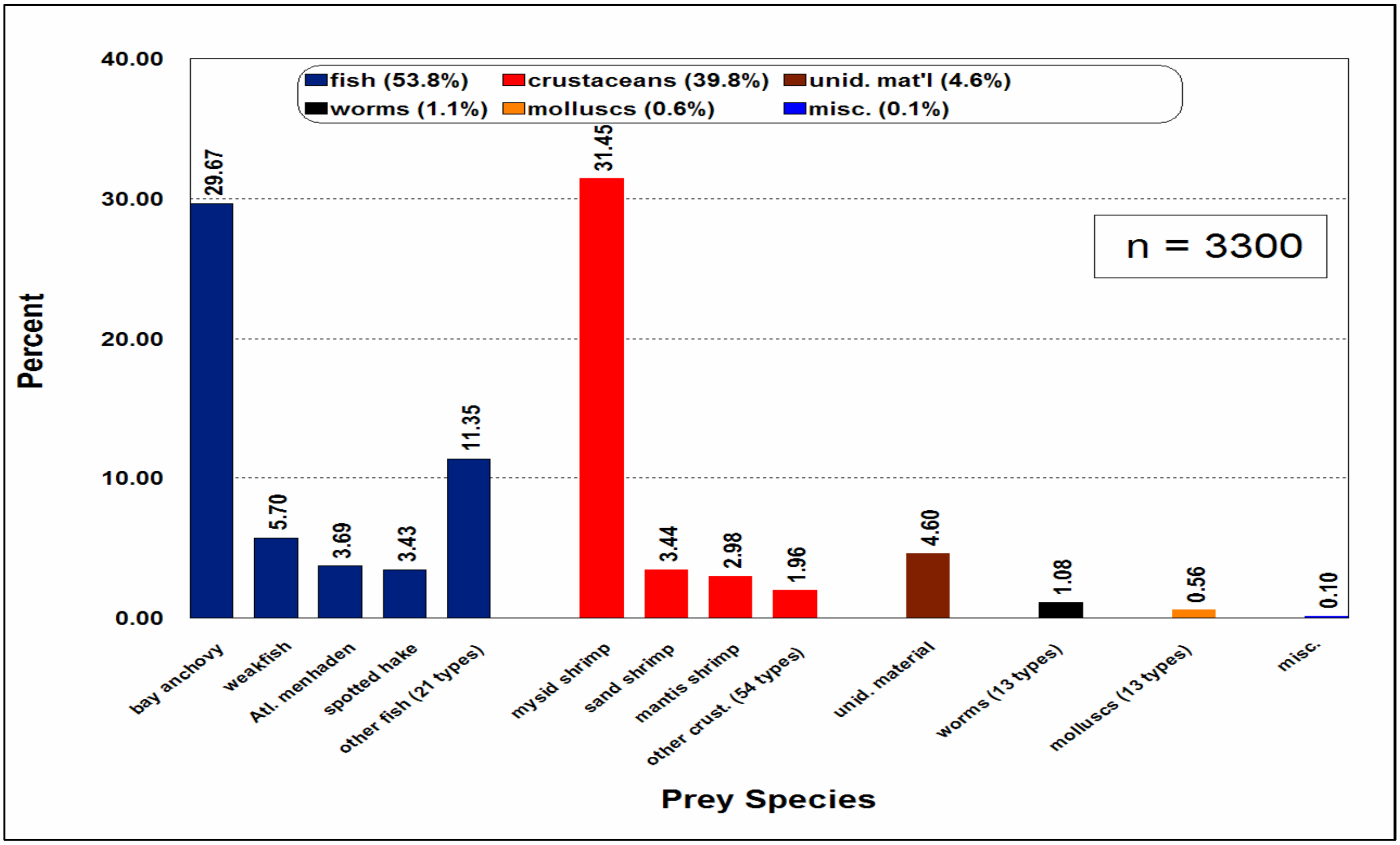


Figure 116. White perch minimum trawlable abundance estimates in numbers (A) and biomass (B) in Chesapeake Bay 2002-2006.

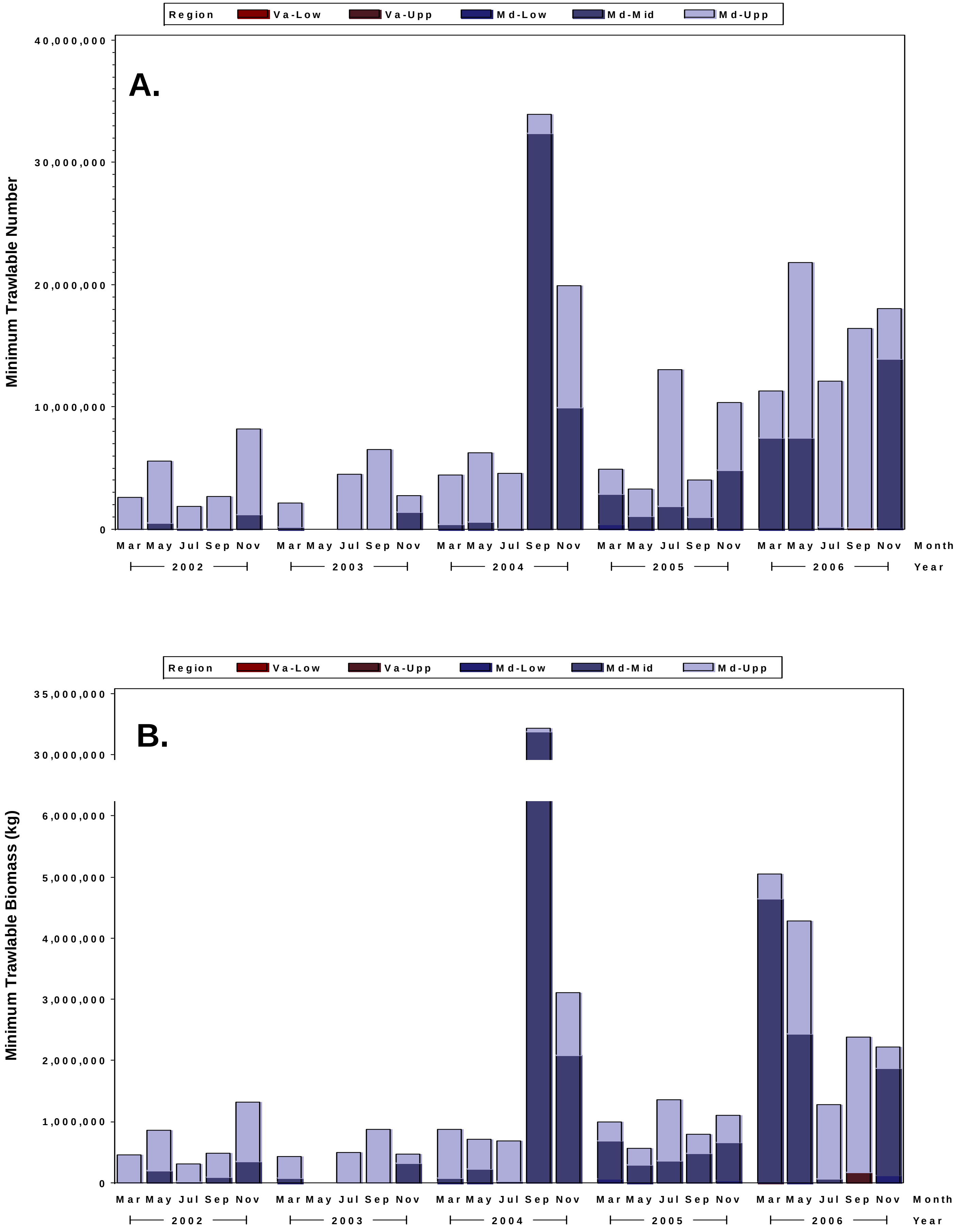


Figure 117. Figures 117. Site-specific white perch abundance (number per hectare swept), 2002.

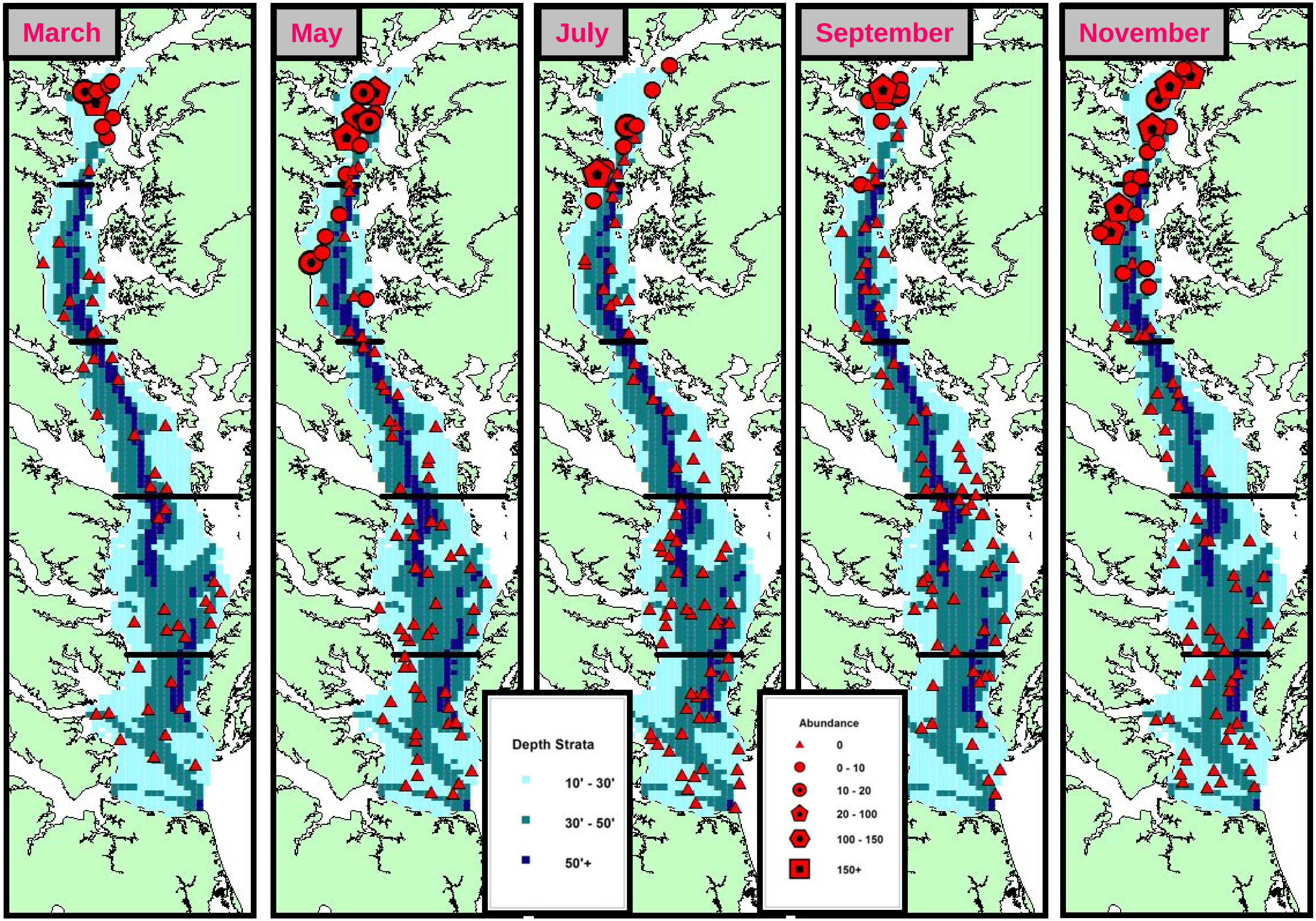


Figure 118. Site-specific white perch abundance (number per hectare swept), 2003.

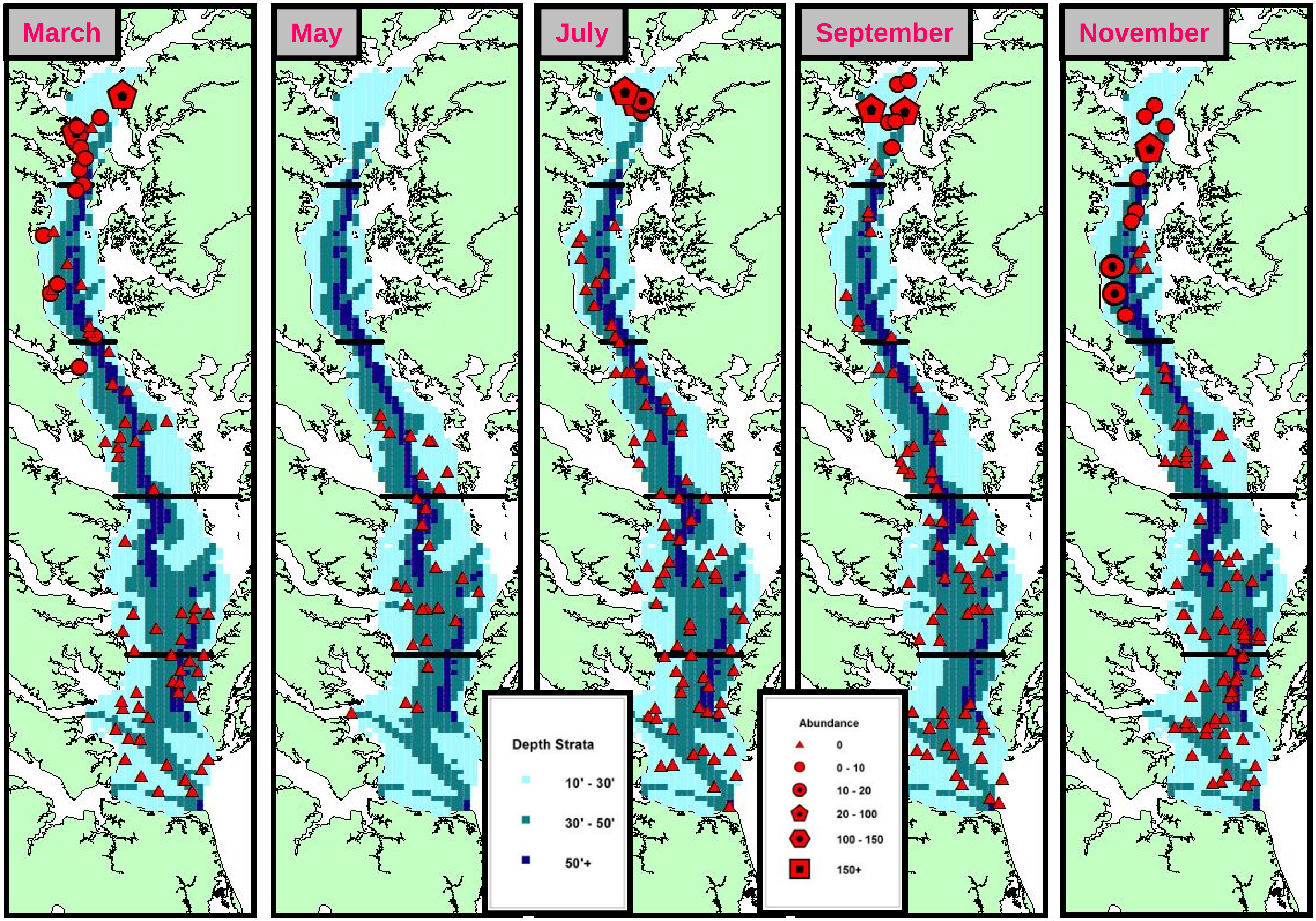


Figure 119. Site-specific white perch abundance (number per hectare swept), 2004.

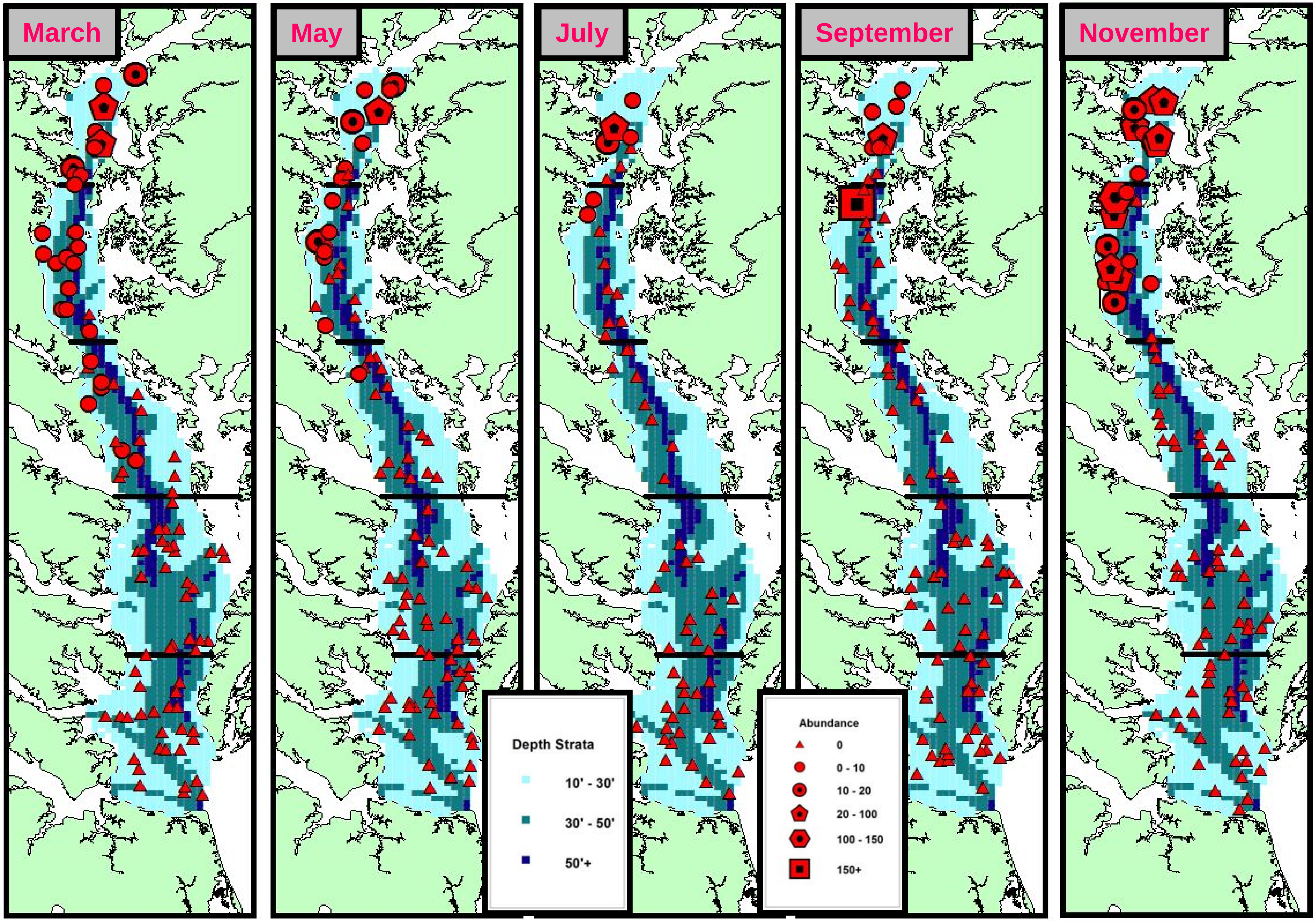


Figure 120. Site-specific white perch abundance (number per hectare swept), 2005.

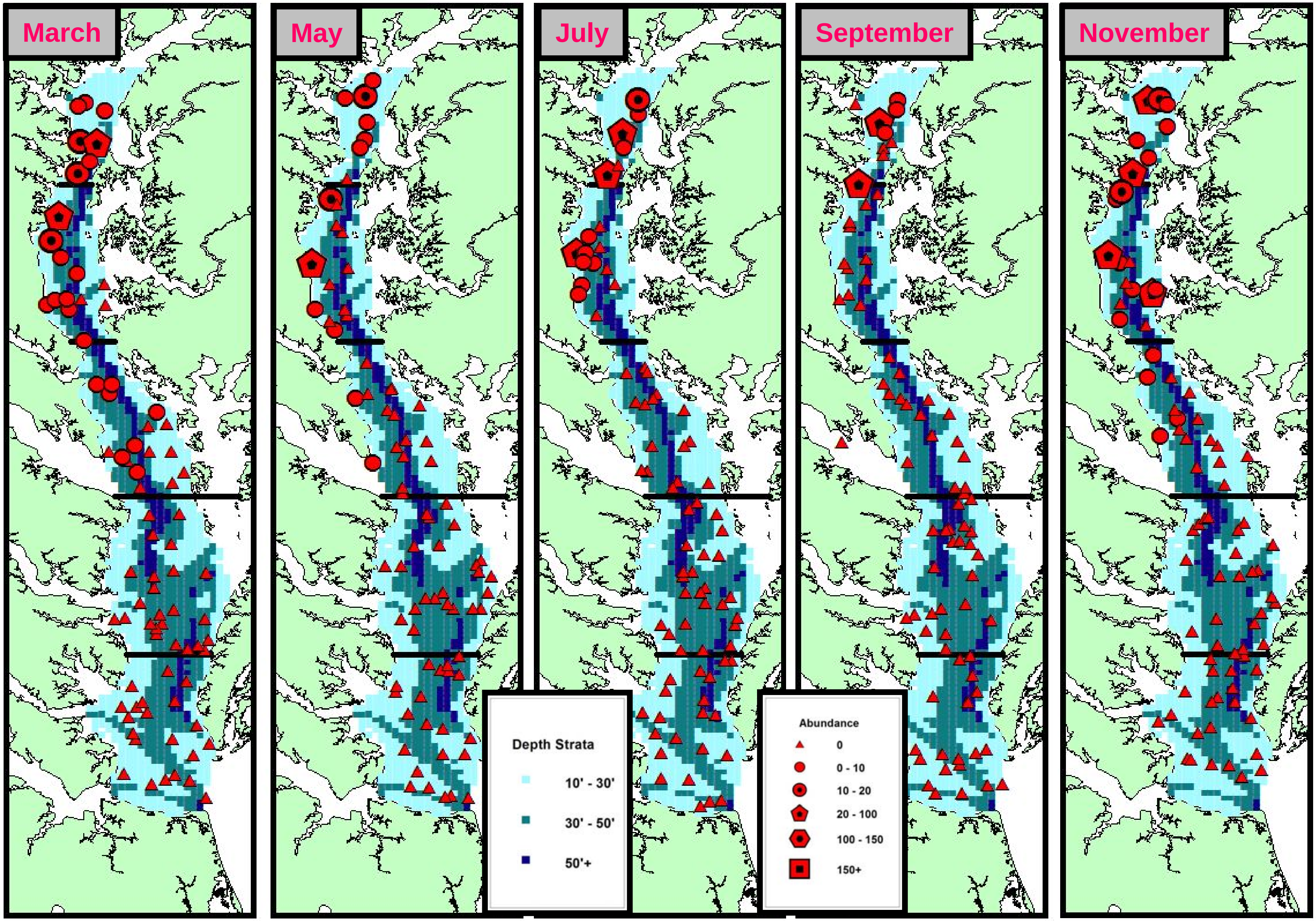


Figure 121. Site-specific white perch abundance (number per hectare swept), 2006.

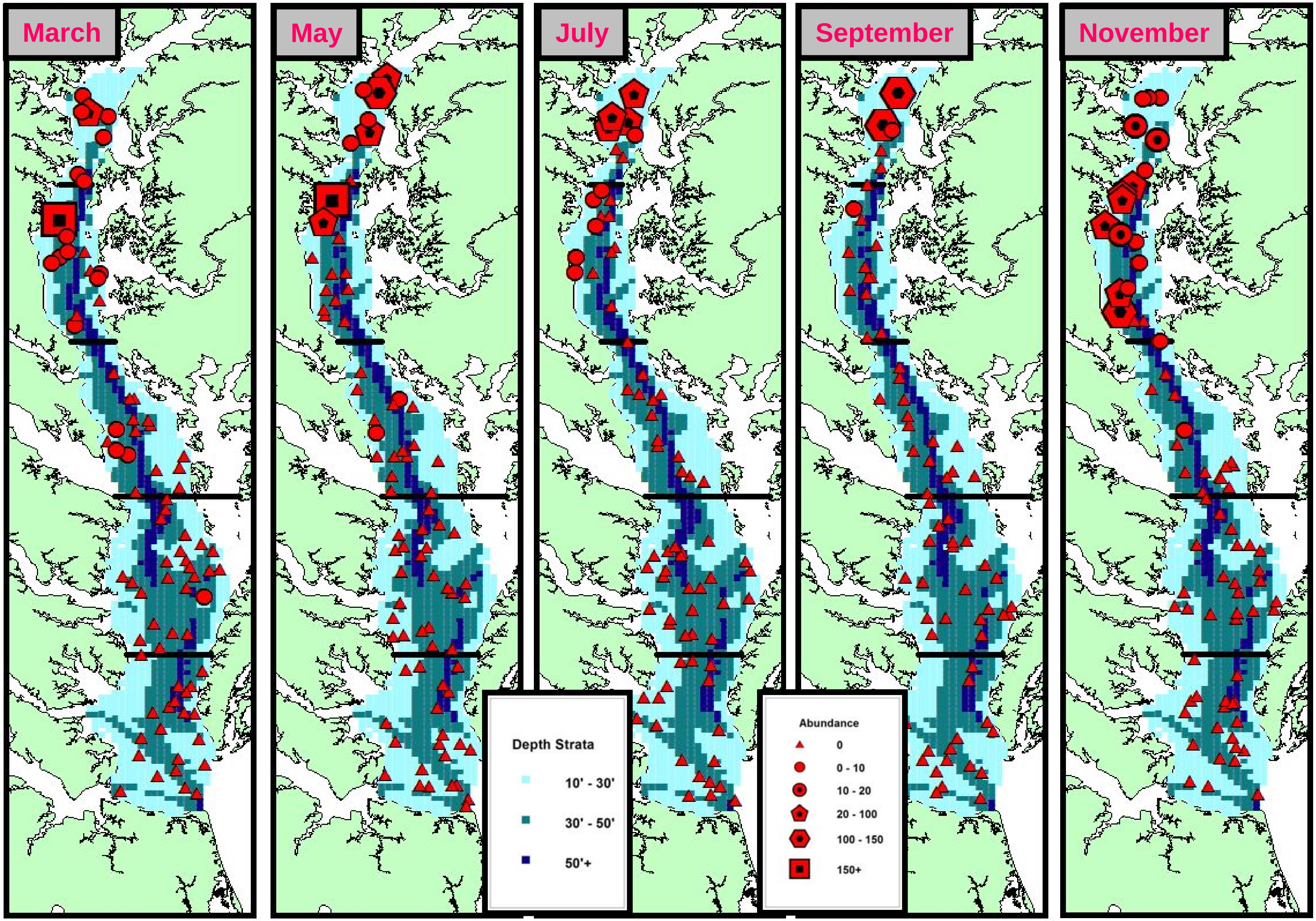


Figure 122. White perch length-frequency in Chesapeake Bay 2002-2006.

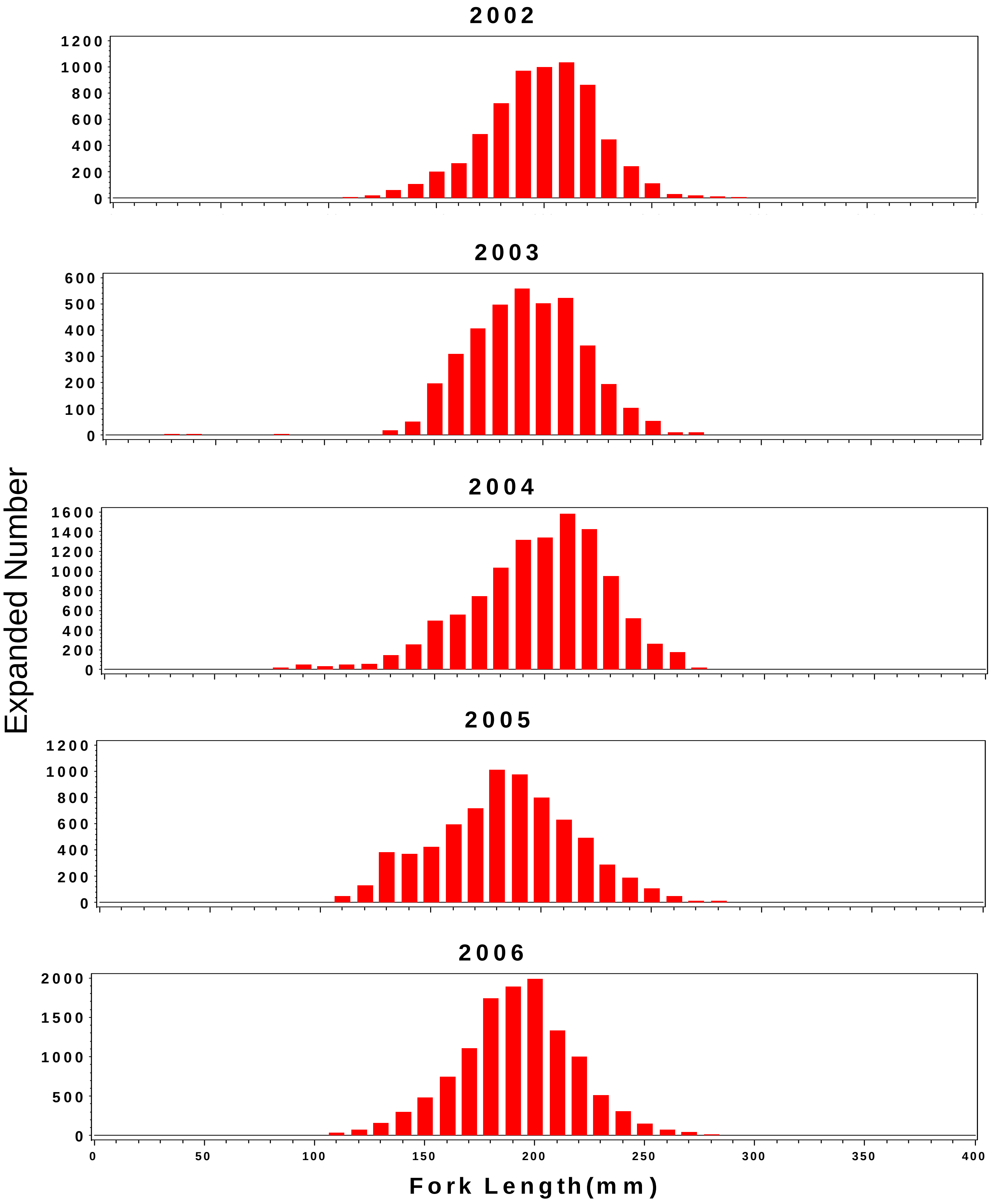


Figure 123. White perch age-structure in Chesapeake Bay 2002-2005 (2006 ages not yet assigned).

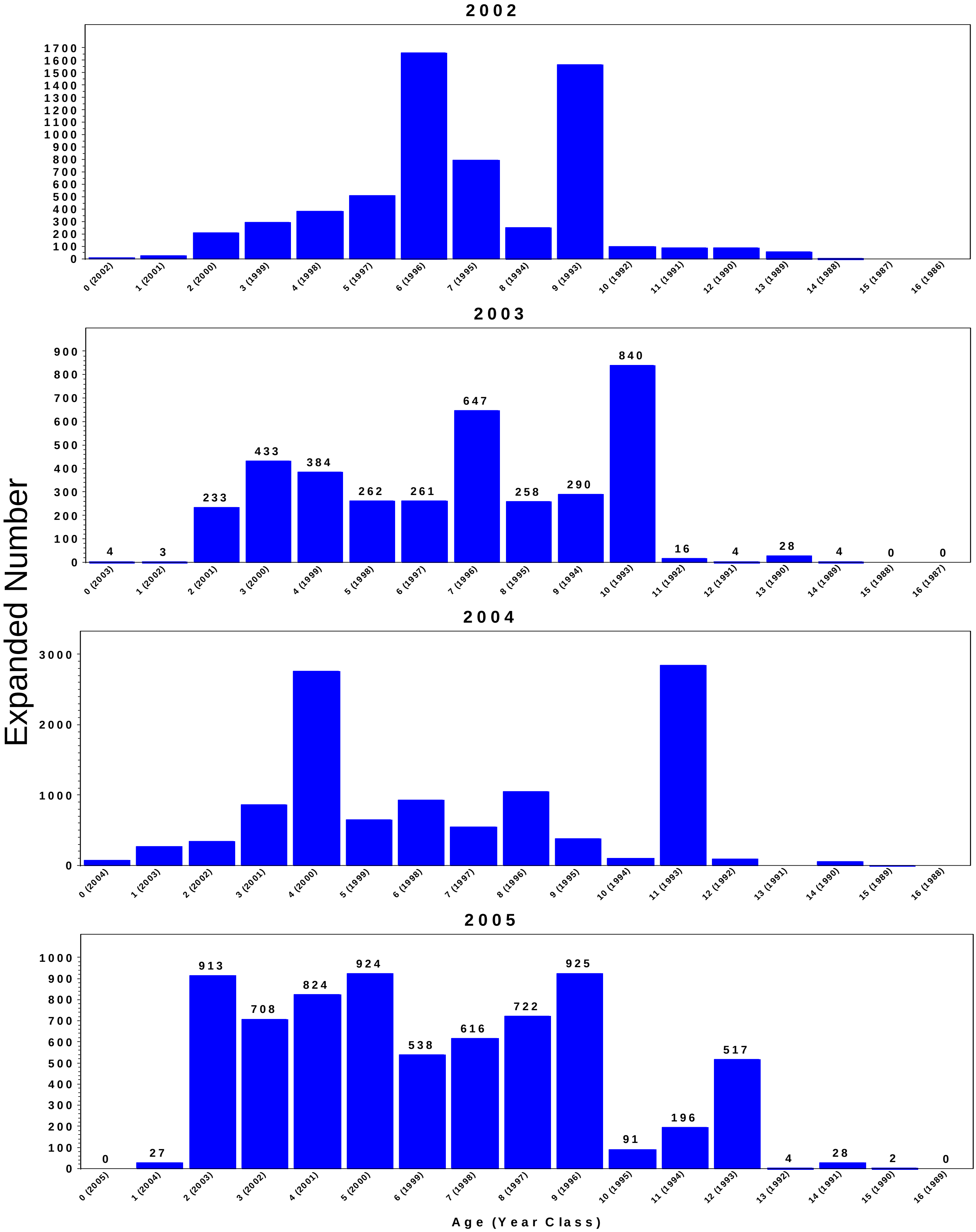


Figure 124. White perch sex-ratios in Chesapeake Bay 2002-2005, by year (A), age (B).

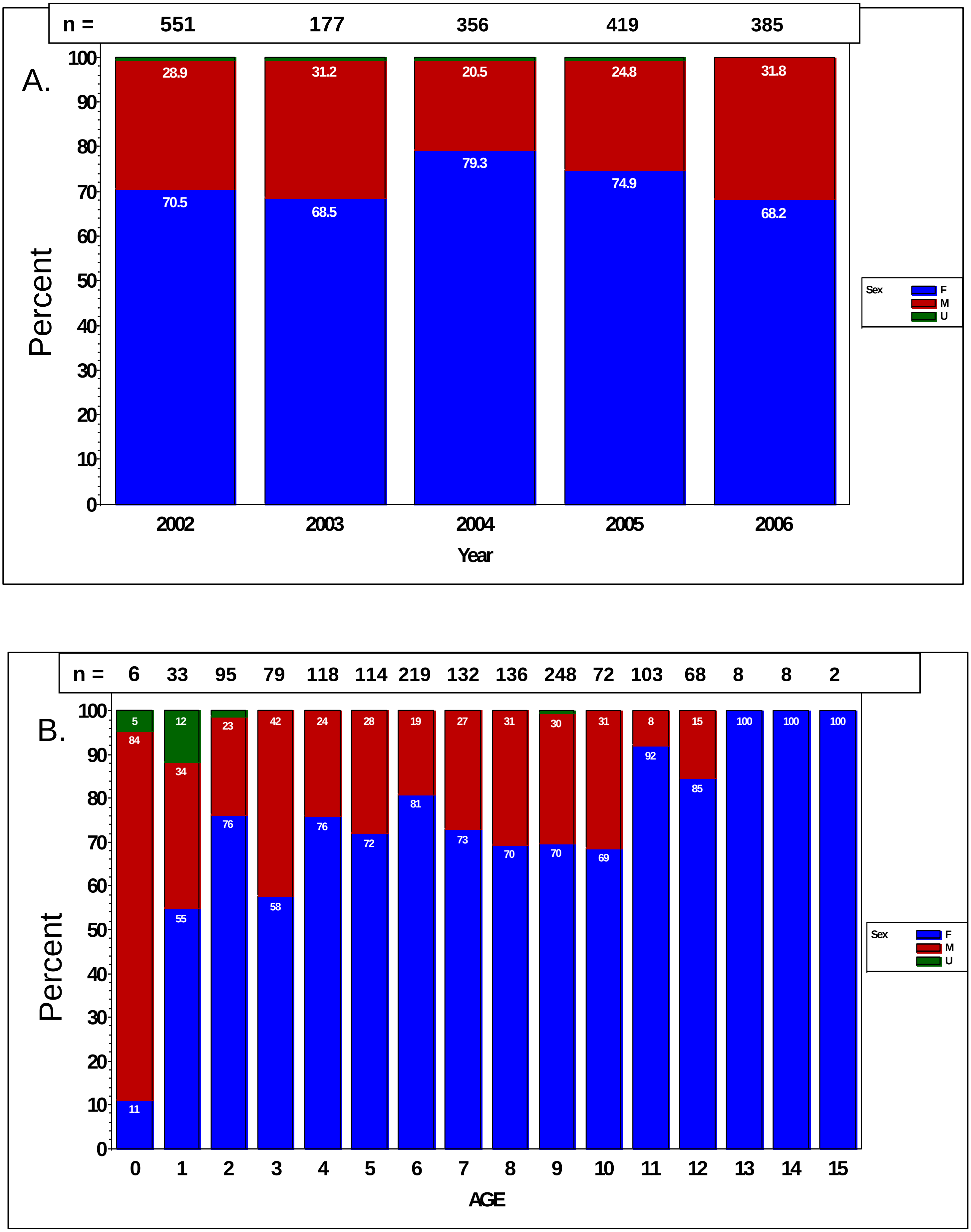


Figure 125. White perch length-weight relationships in Chesapeake Bay 2002-2006 as calculated by power regression for sexes combined (A) and separately (B).

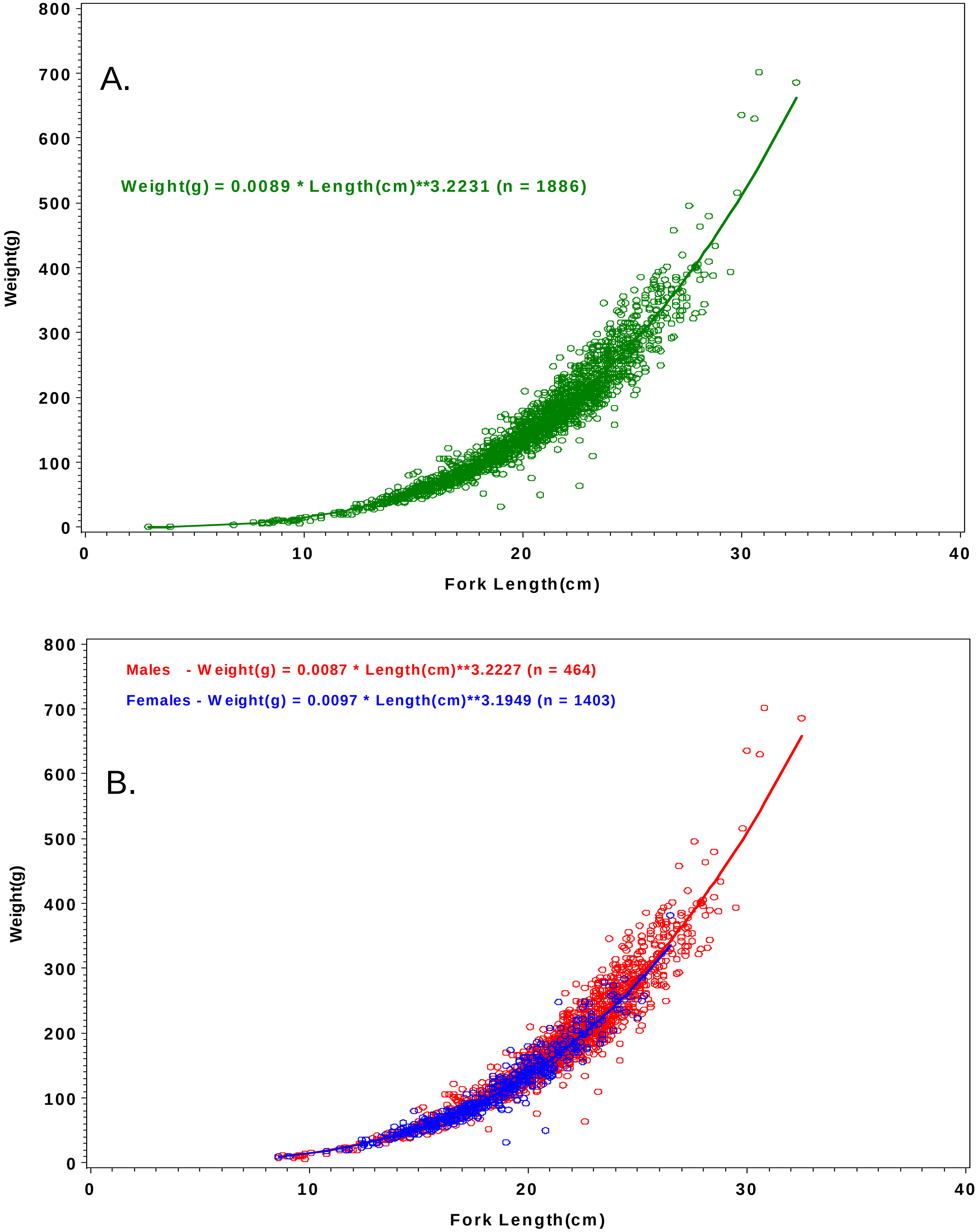


Figure 126. White perch maturity schedule in Chesapeake Bay 2002-2006 combined, by sex.

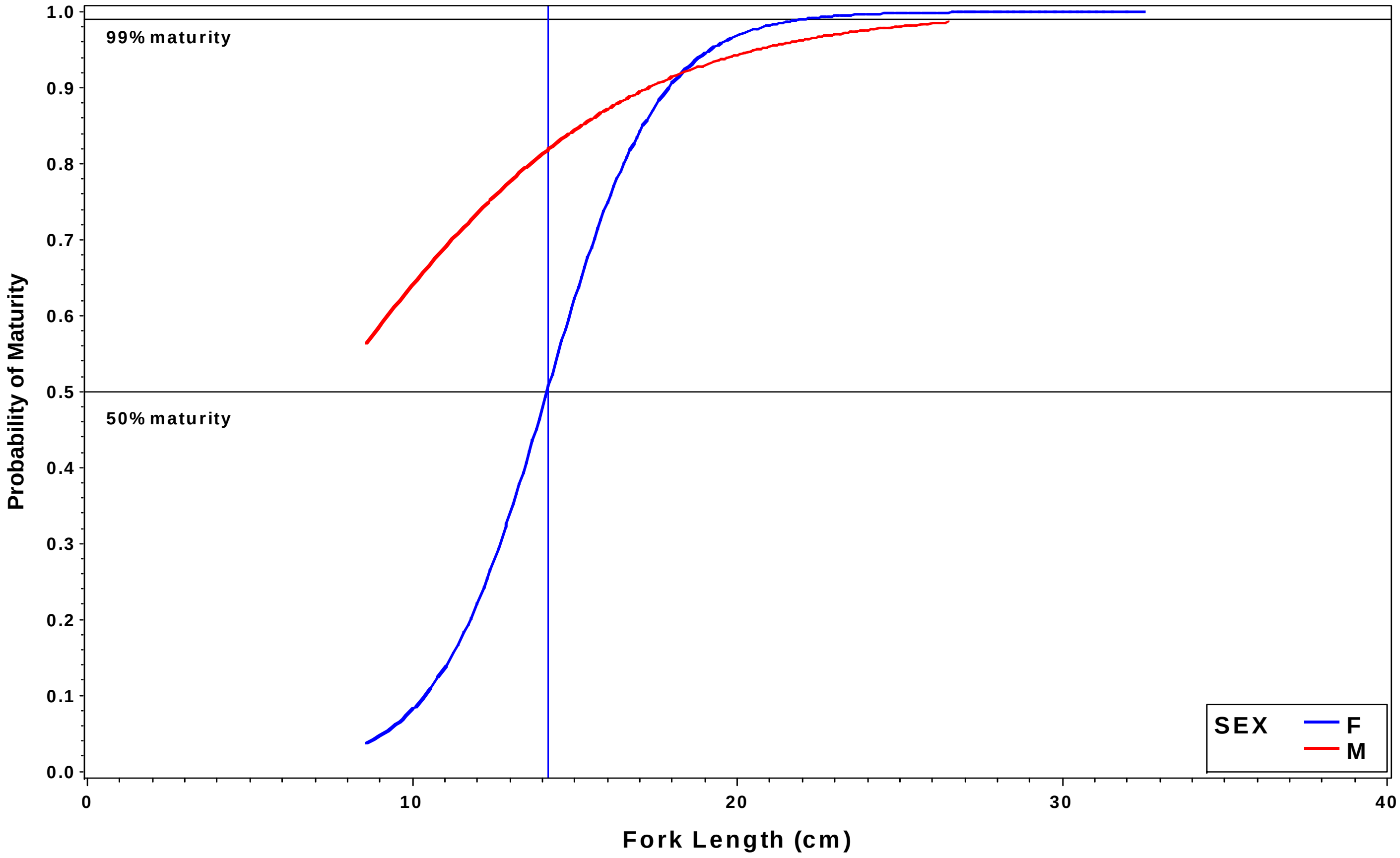


Figure 127. White perch diet in Chesapeake Bay 2002-2006 combined.

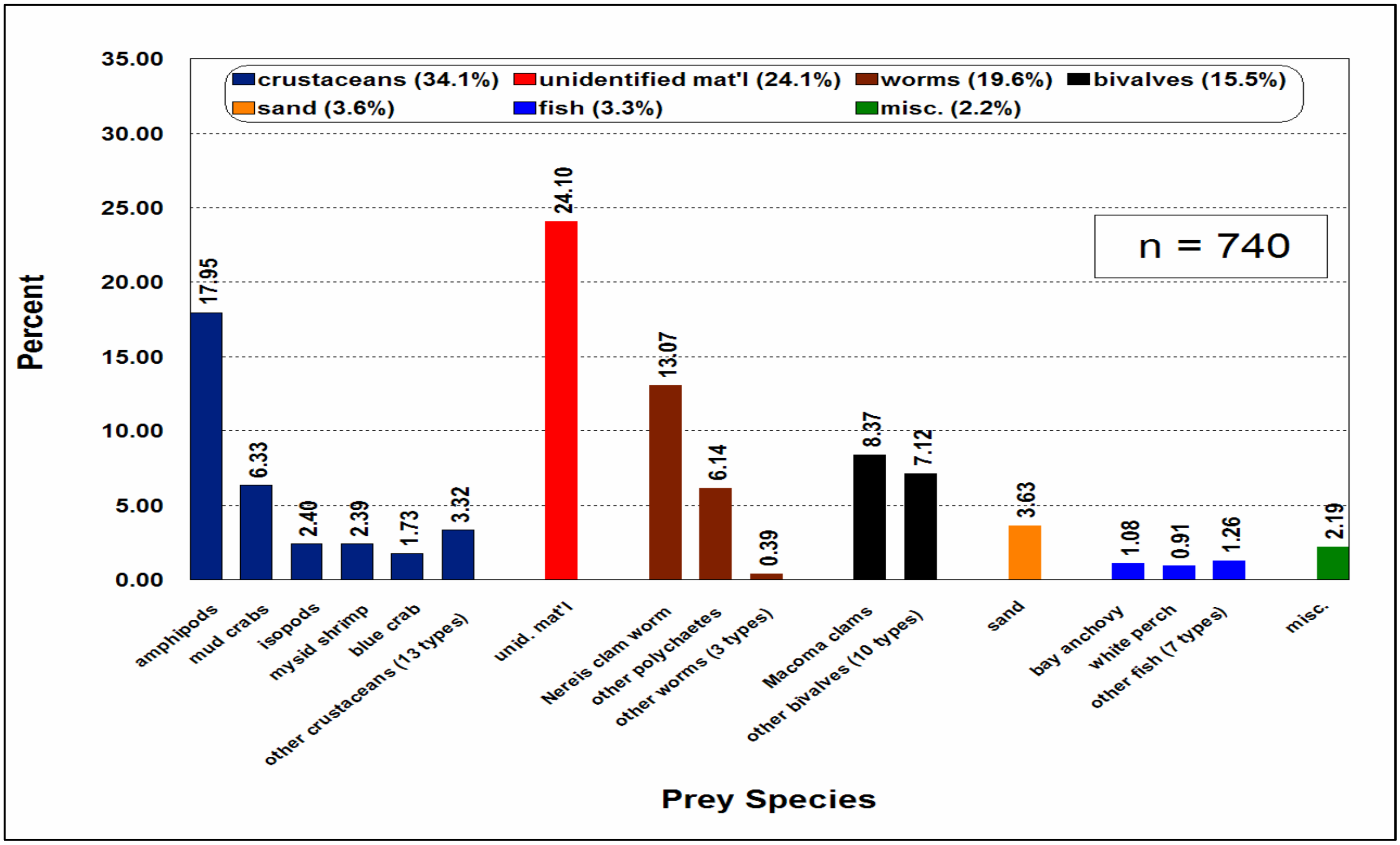


Figure 128. Surface temperature in Chesapeake Bay, 2002.

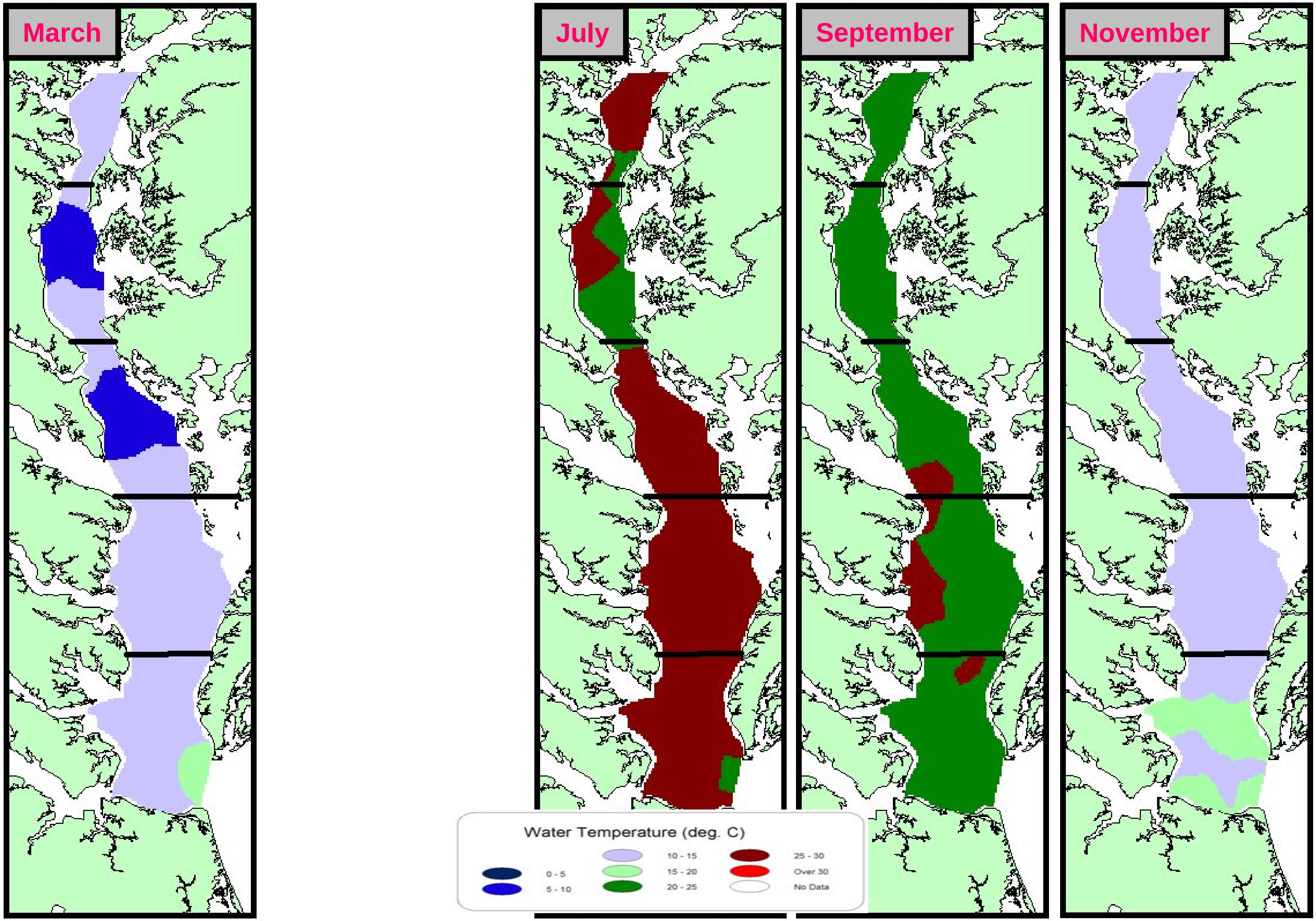


Figure 129. Bottom temperature in Chesapeake Bay, 2002.

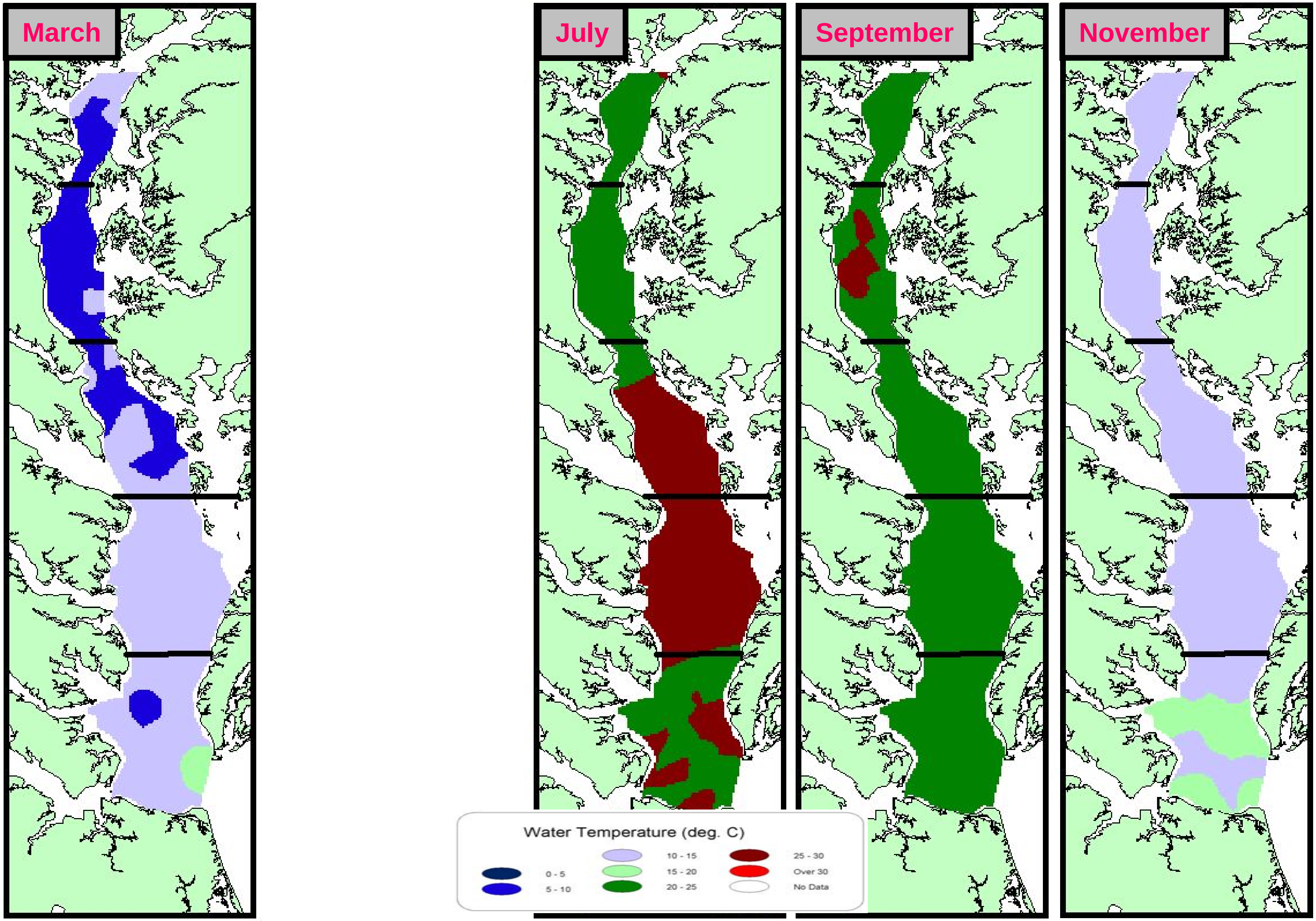


Figure 130. Surface temperature in Chesapeake Bay, 2003.

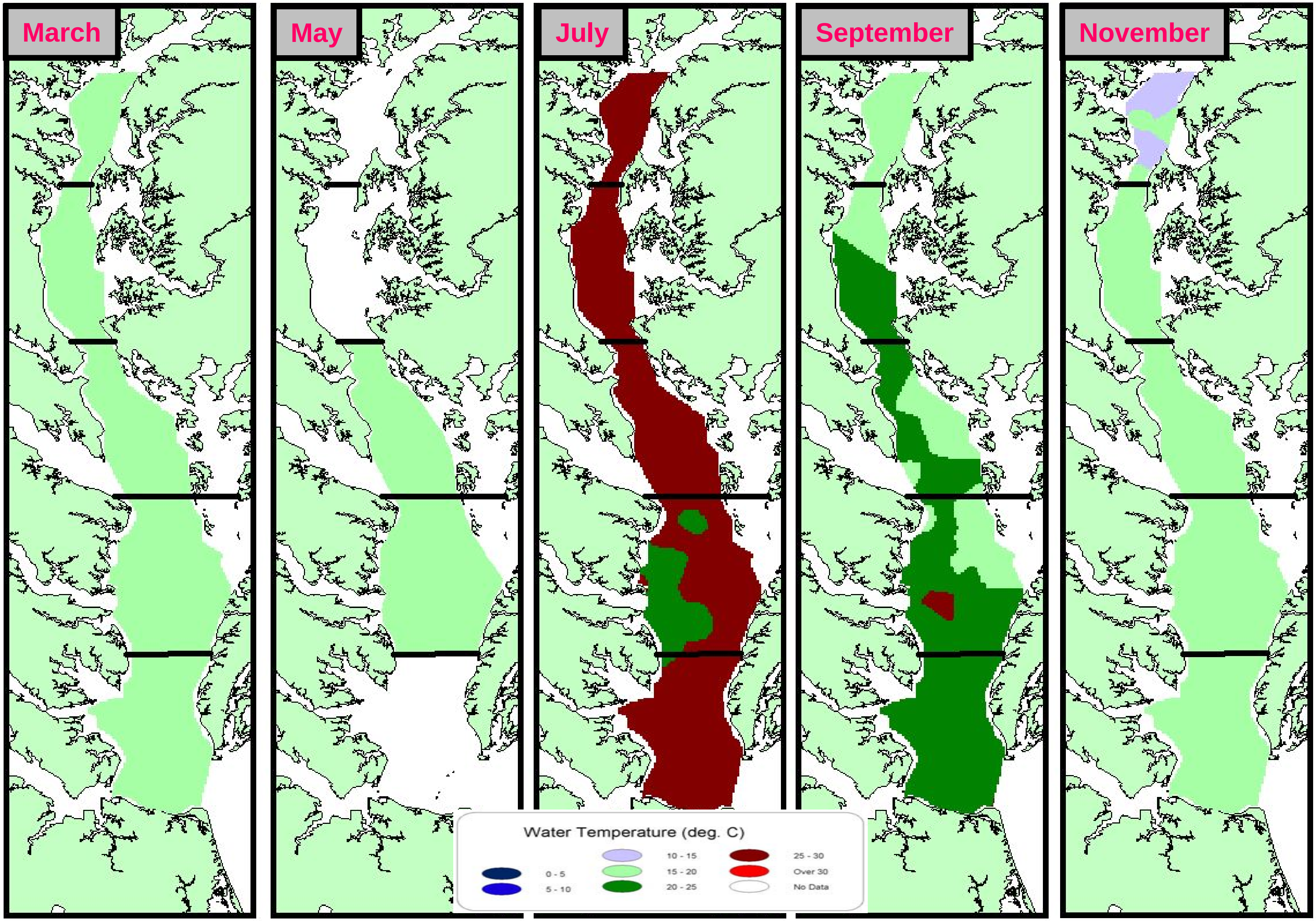


Figure 131. Bottom temperature in Chesapeake Bay, 2003.

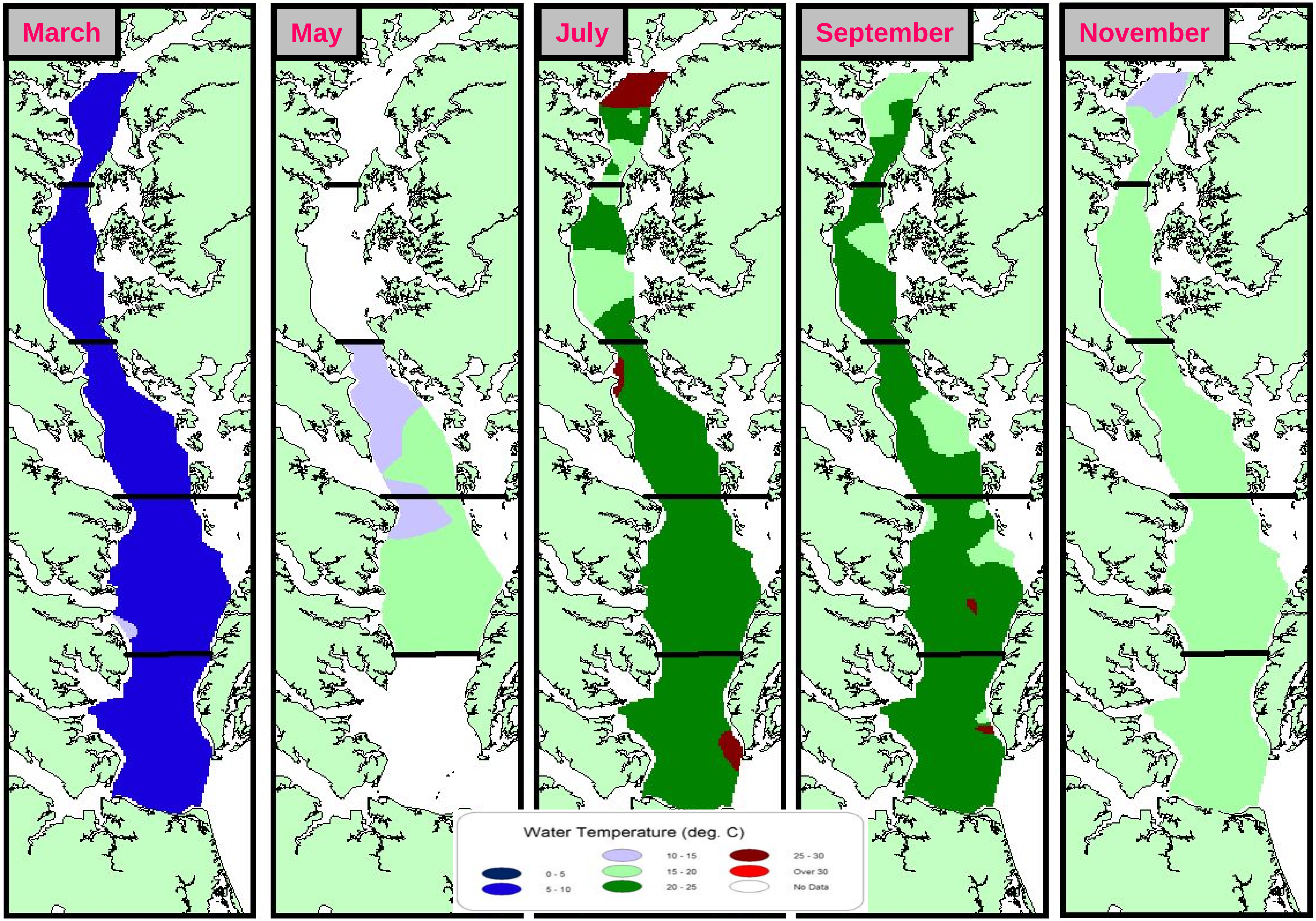


Figure 132. Surface temperature in Chesapeake Bay, 2004.

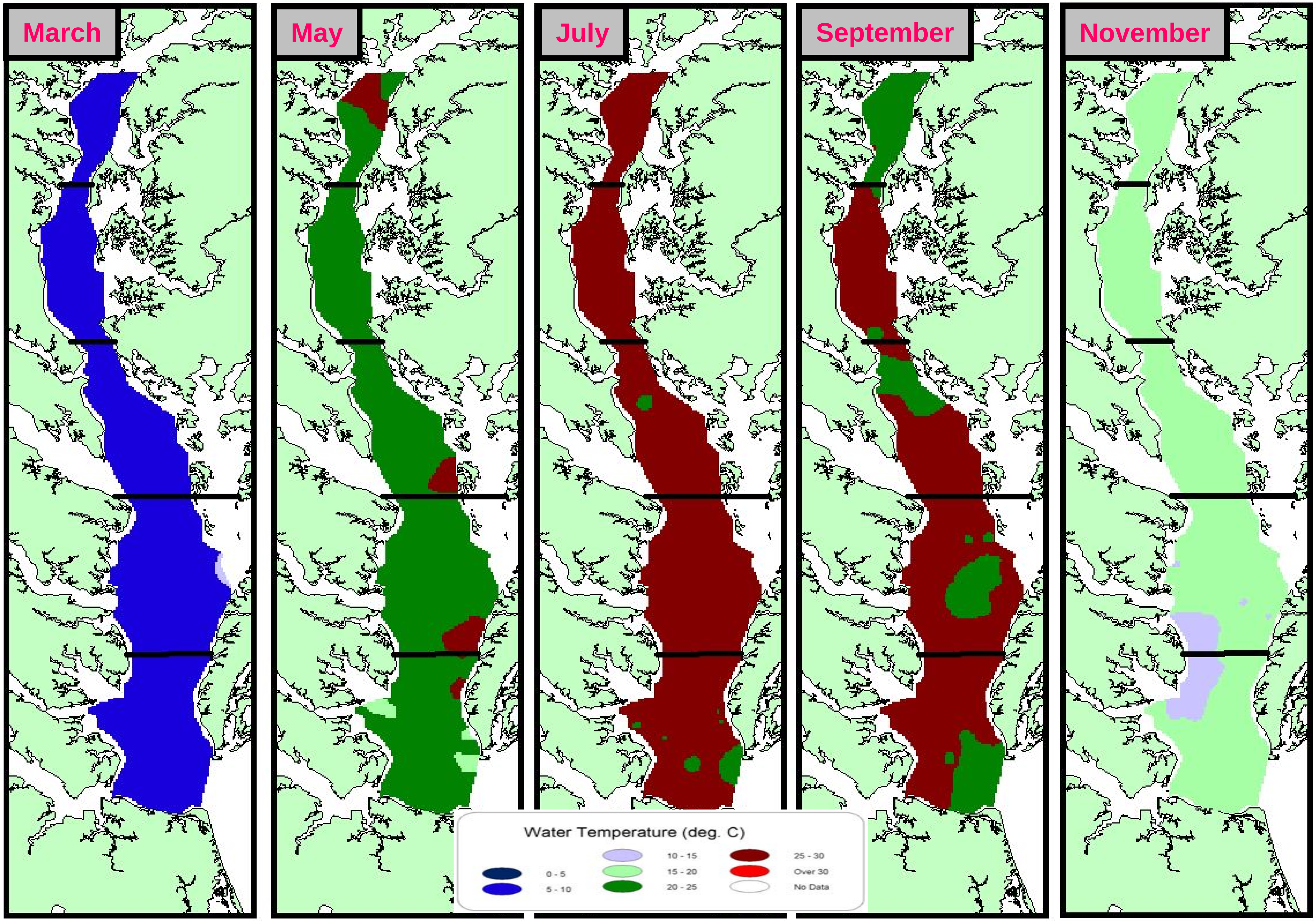


Figure 133. Bottom temperature in Chesapeake Bay, 2004.

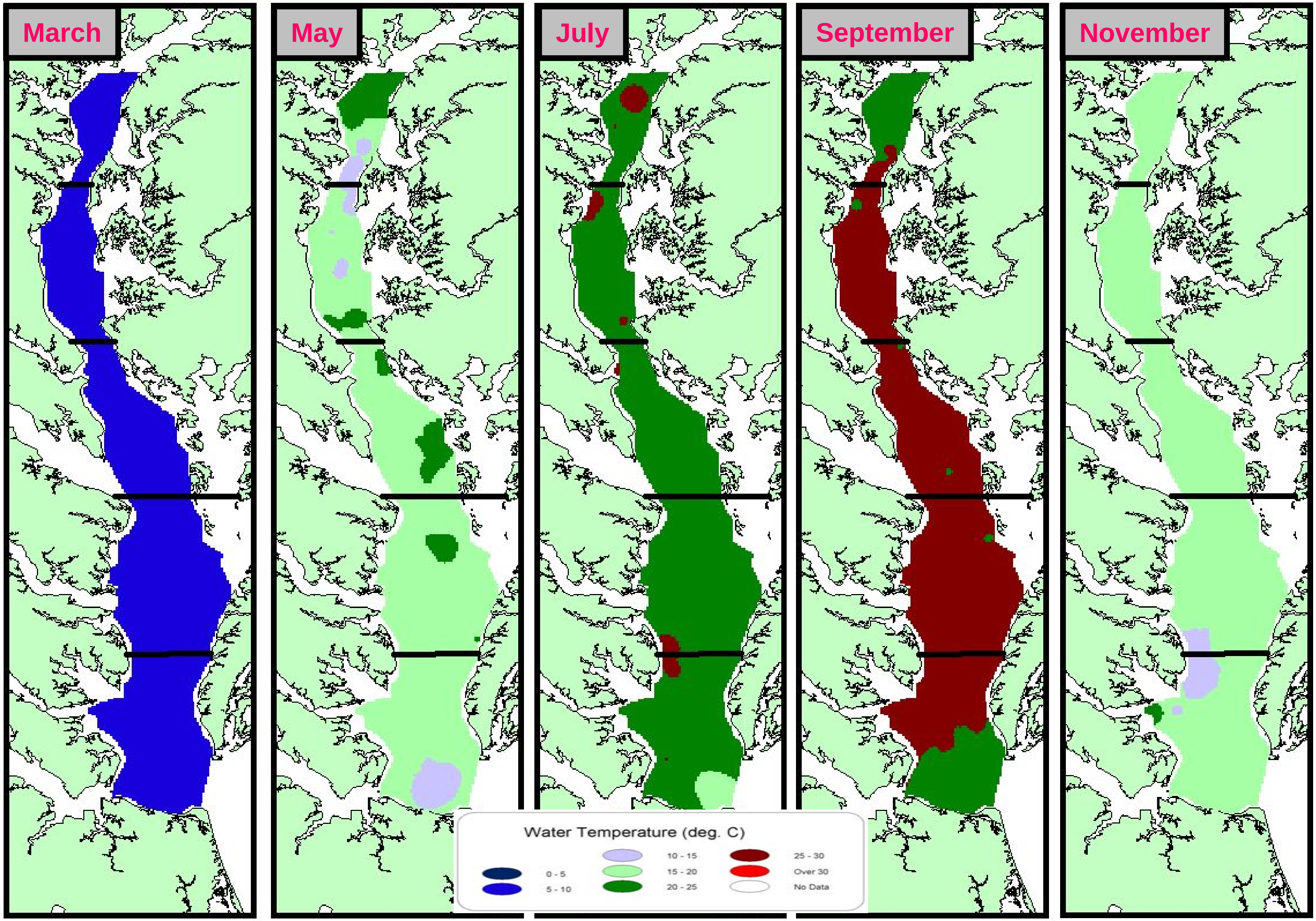


Figure 134. Surface temperature in Chesapeake Bay, 2005.

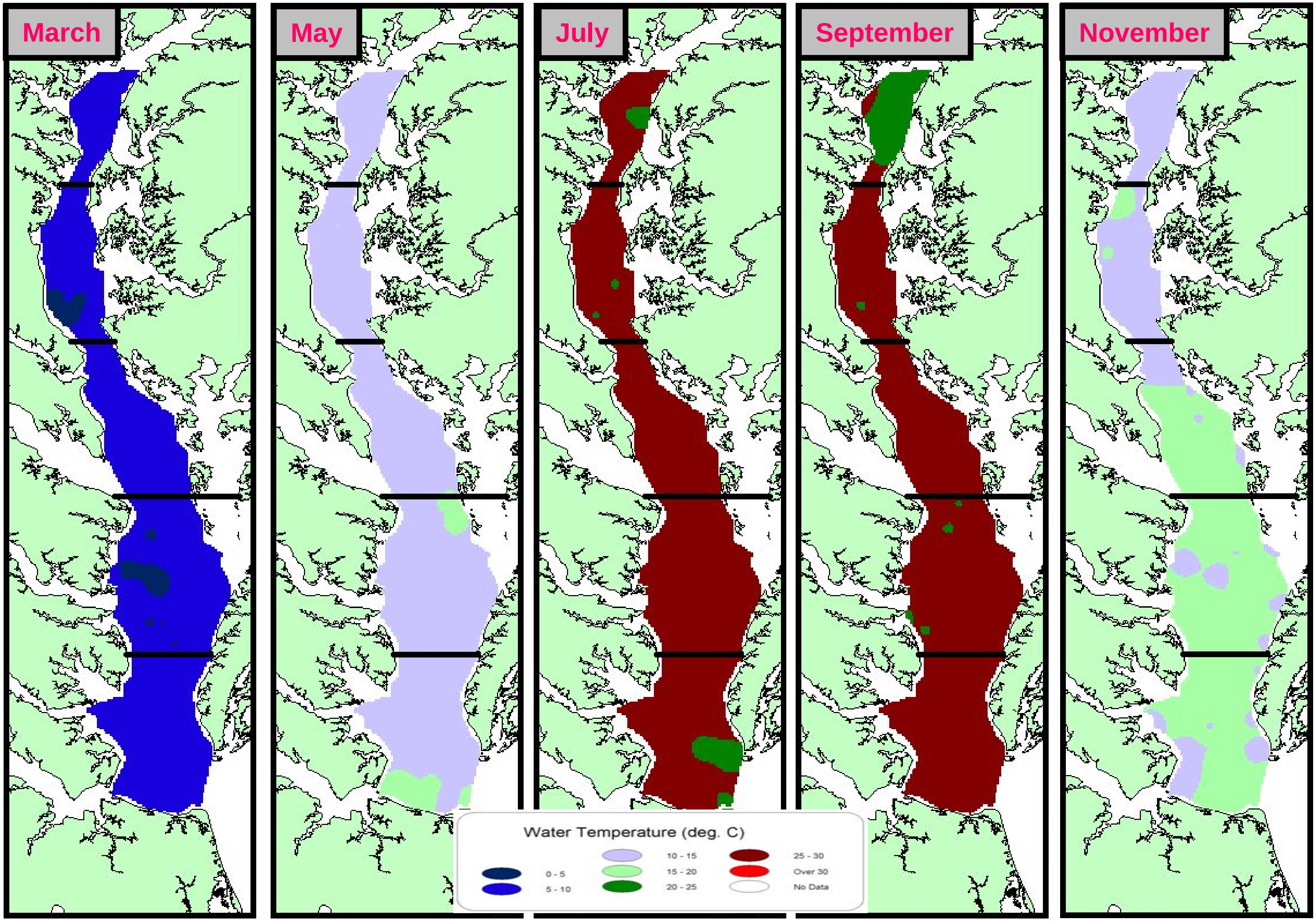


Figure 135. Bottom temperature in Chesapeake Bay, 2005.

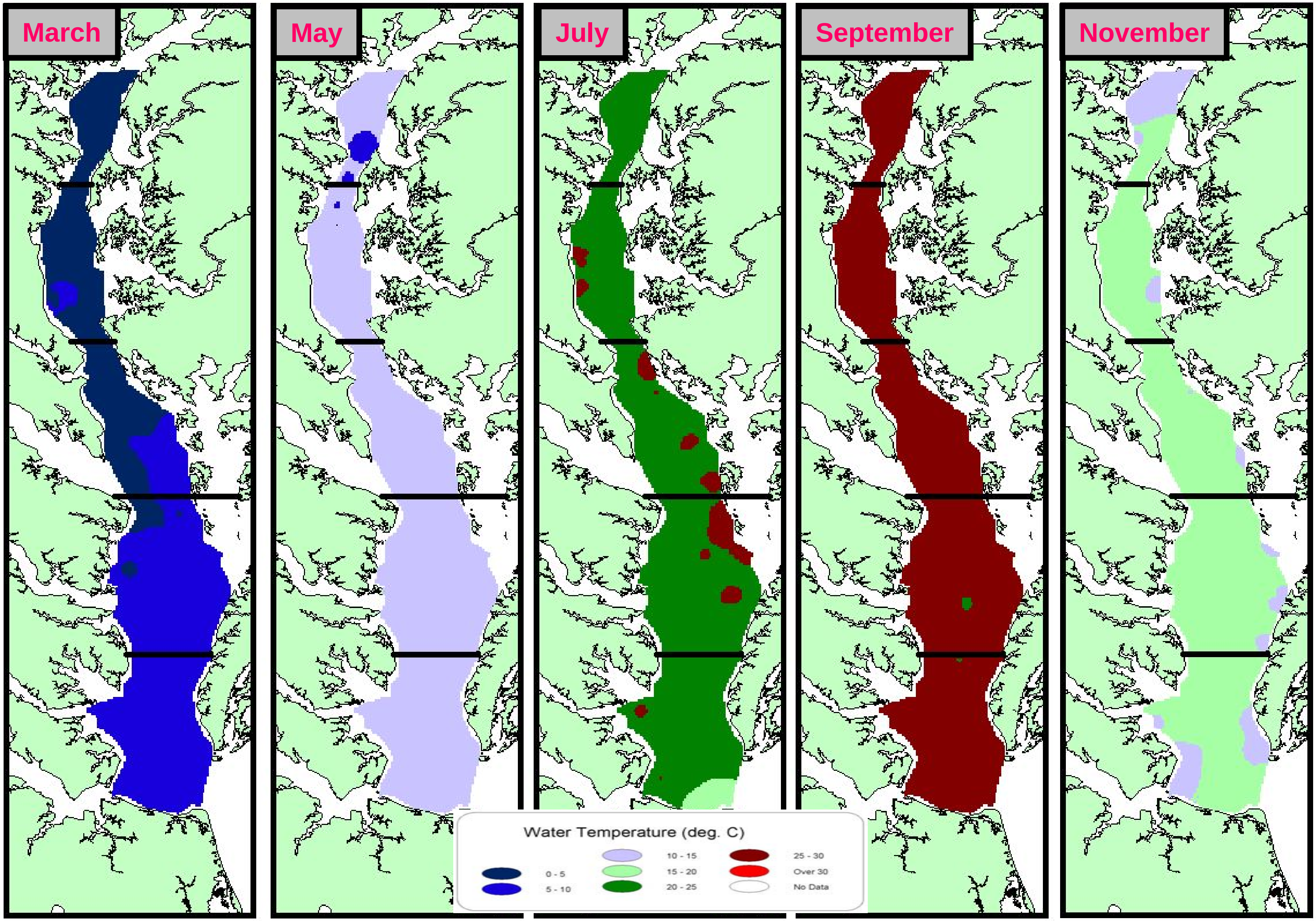


Figure 136. Surface temperature in Chesapeake Bay, 2006.

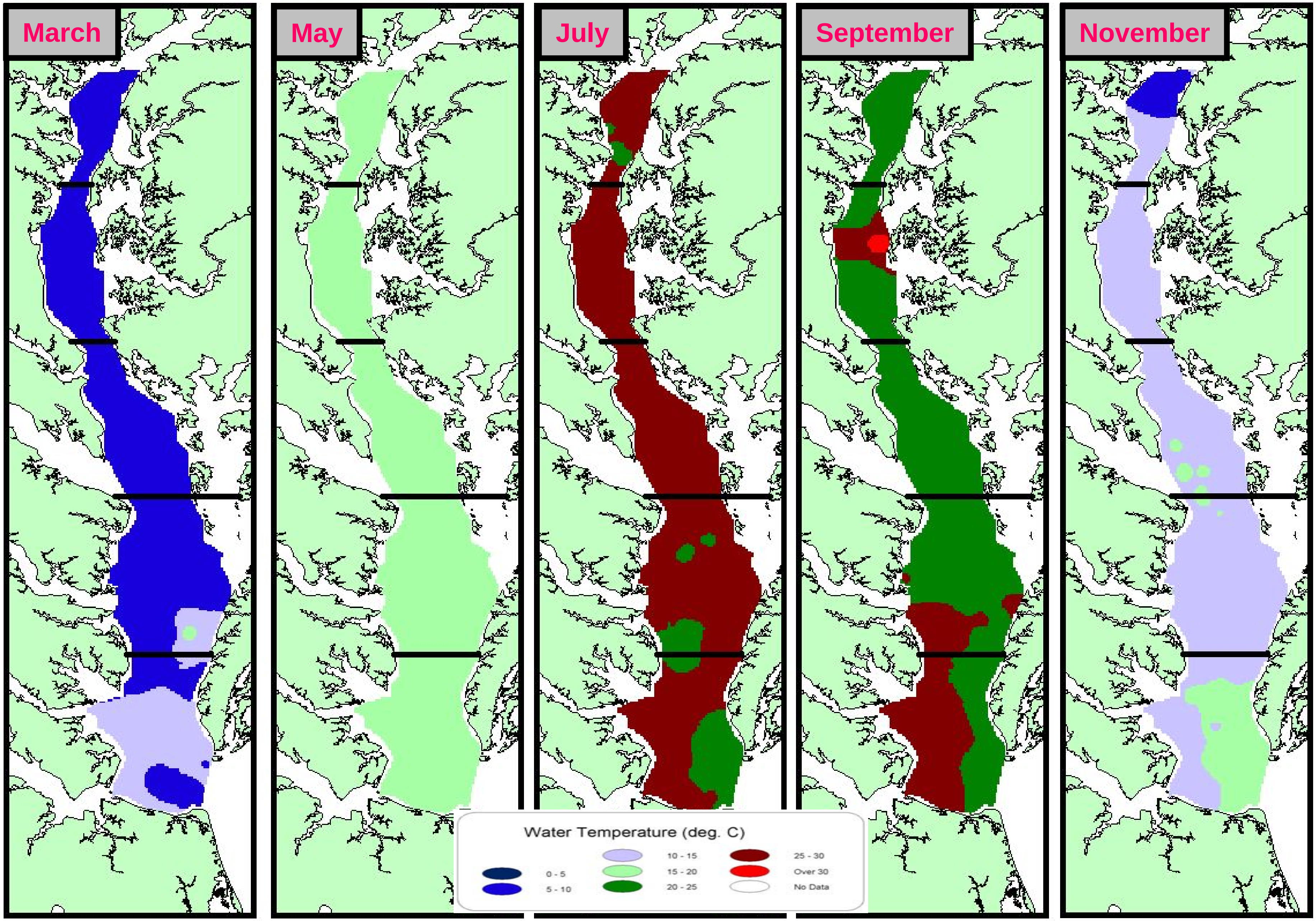


Figure 137. Bottom temperature in Chesapeake Bay, 2006.

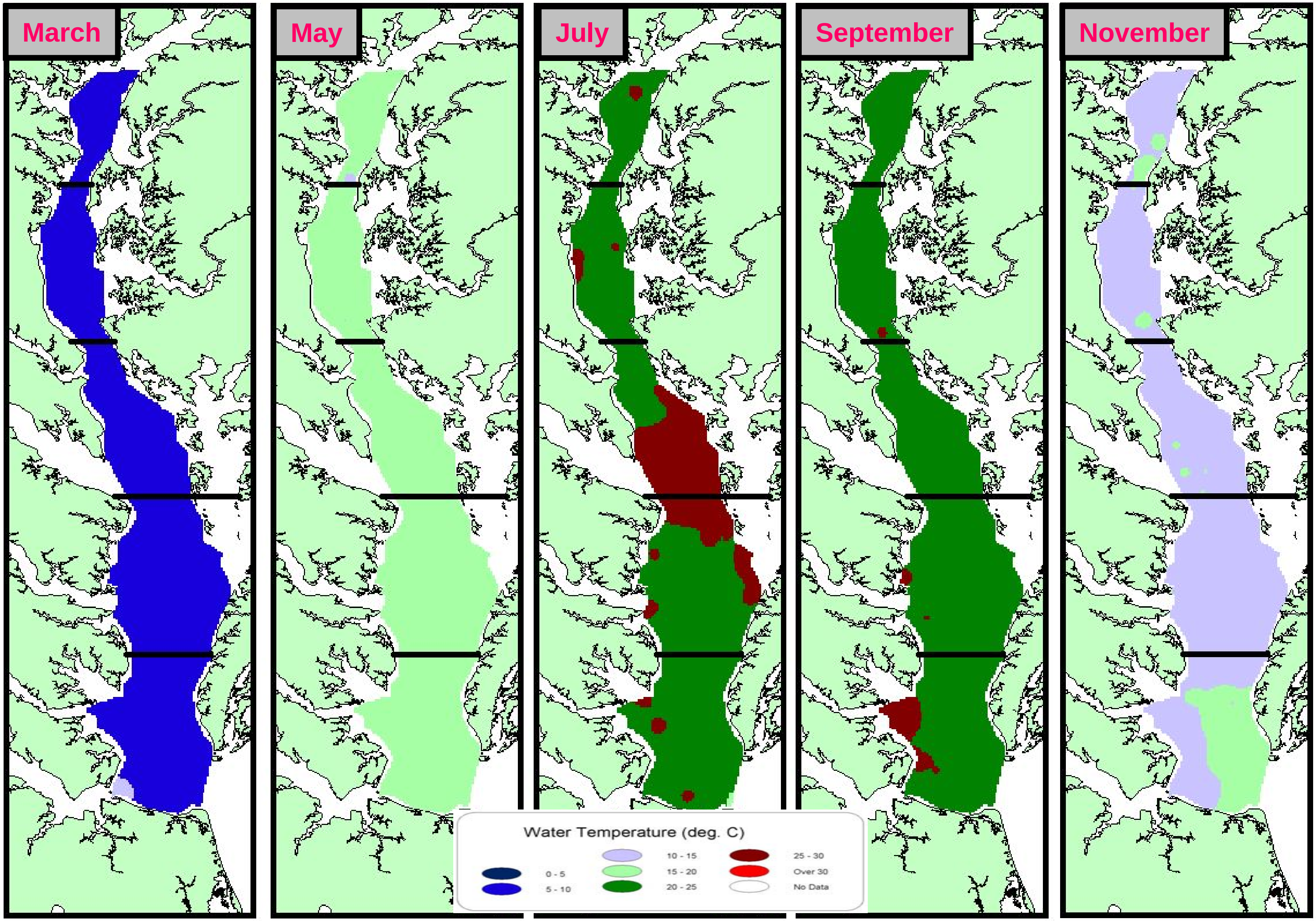


Figure 138. Surface salinity in Chesapeake Bay, 2002.

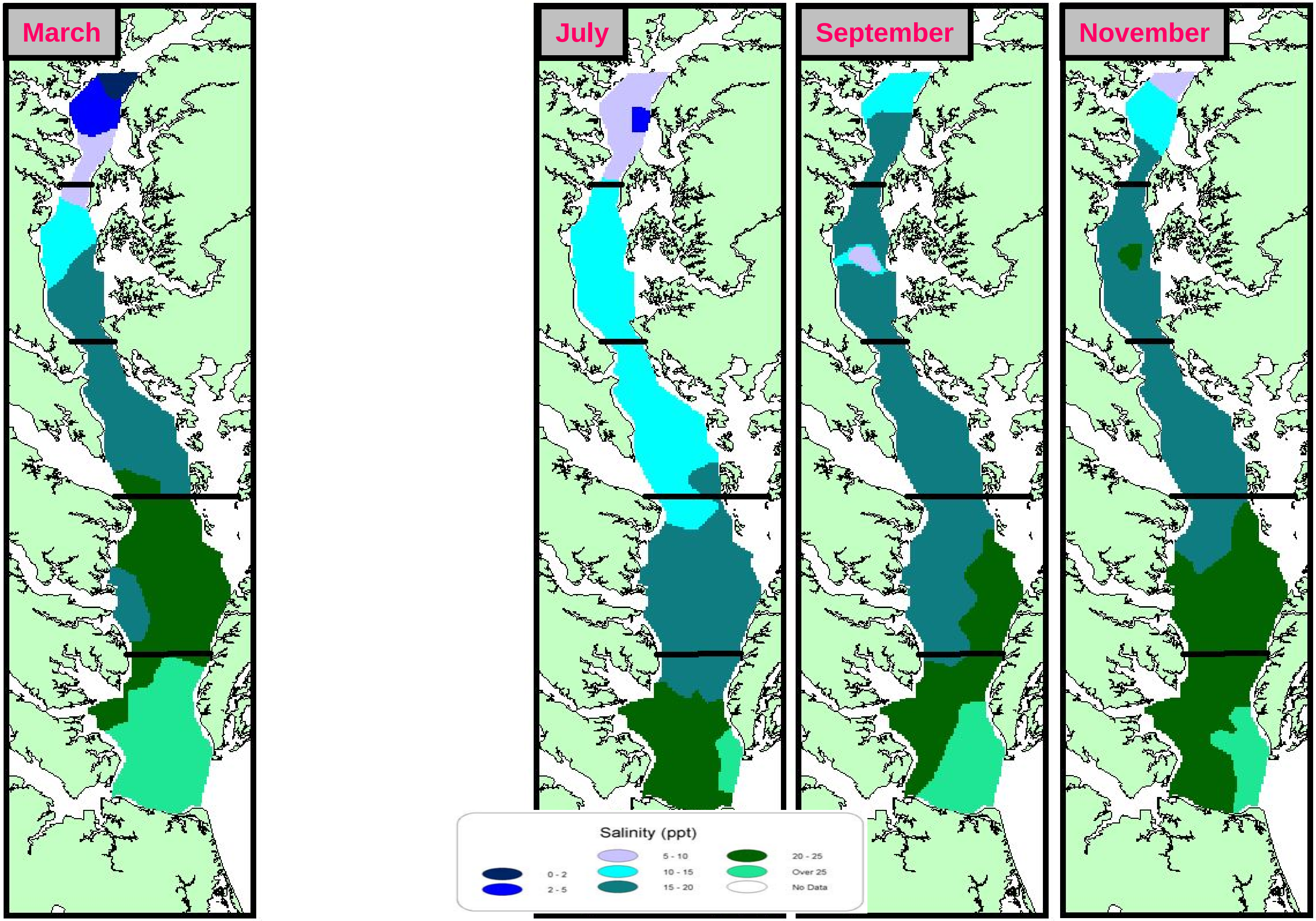


Figure 139. Bottom salinity in Chesapeake Bay, 2002.

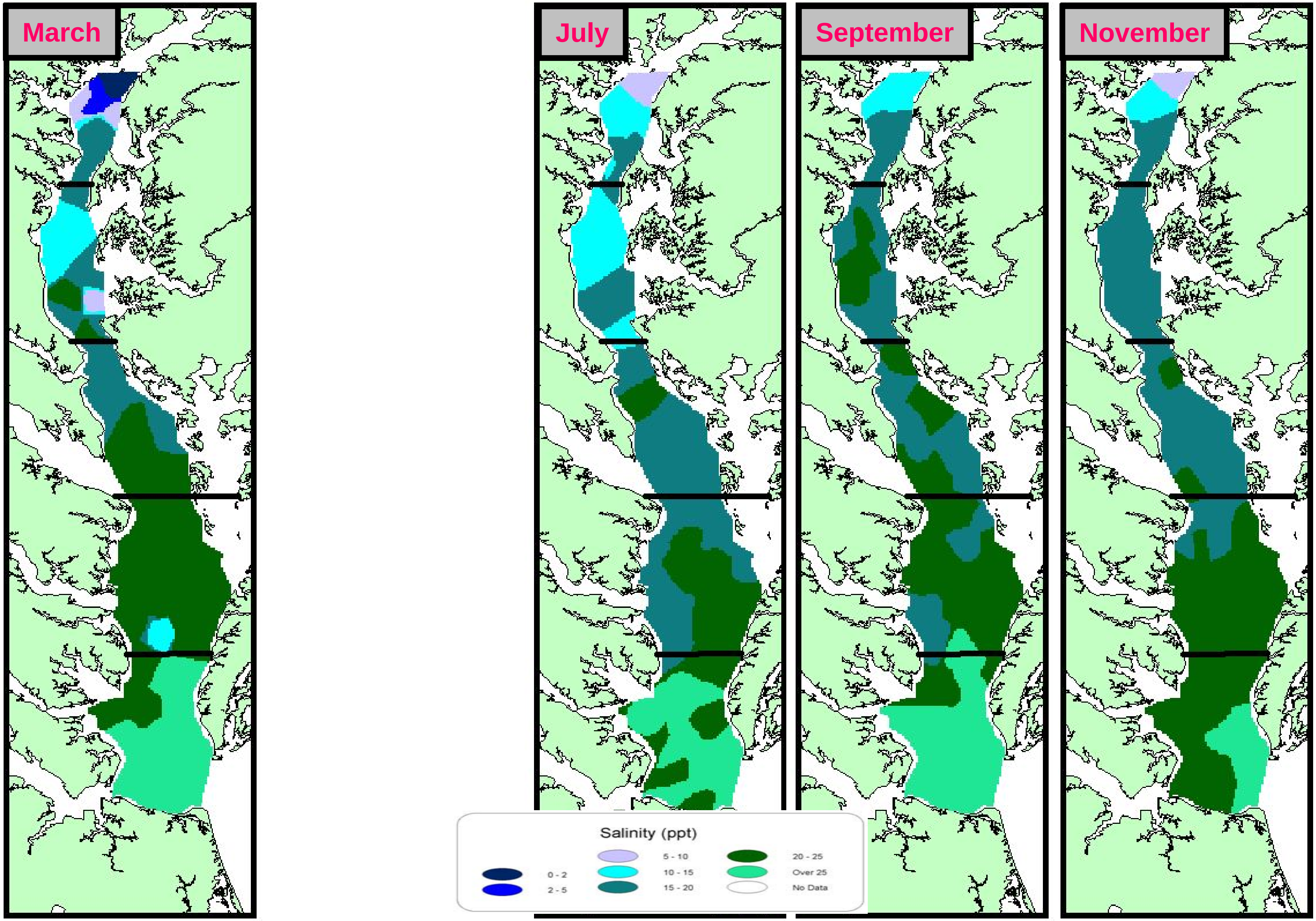
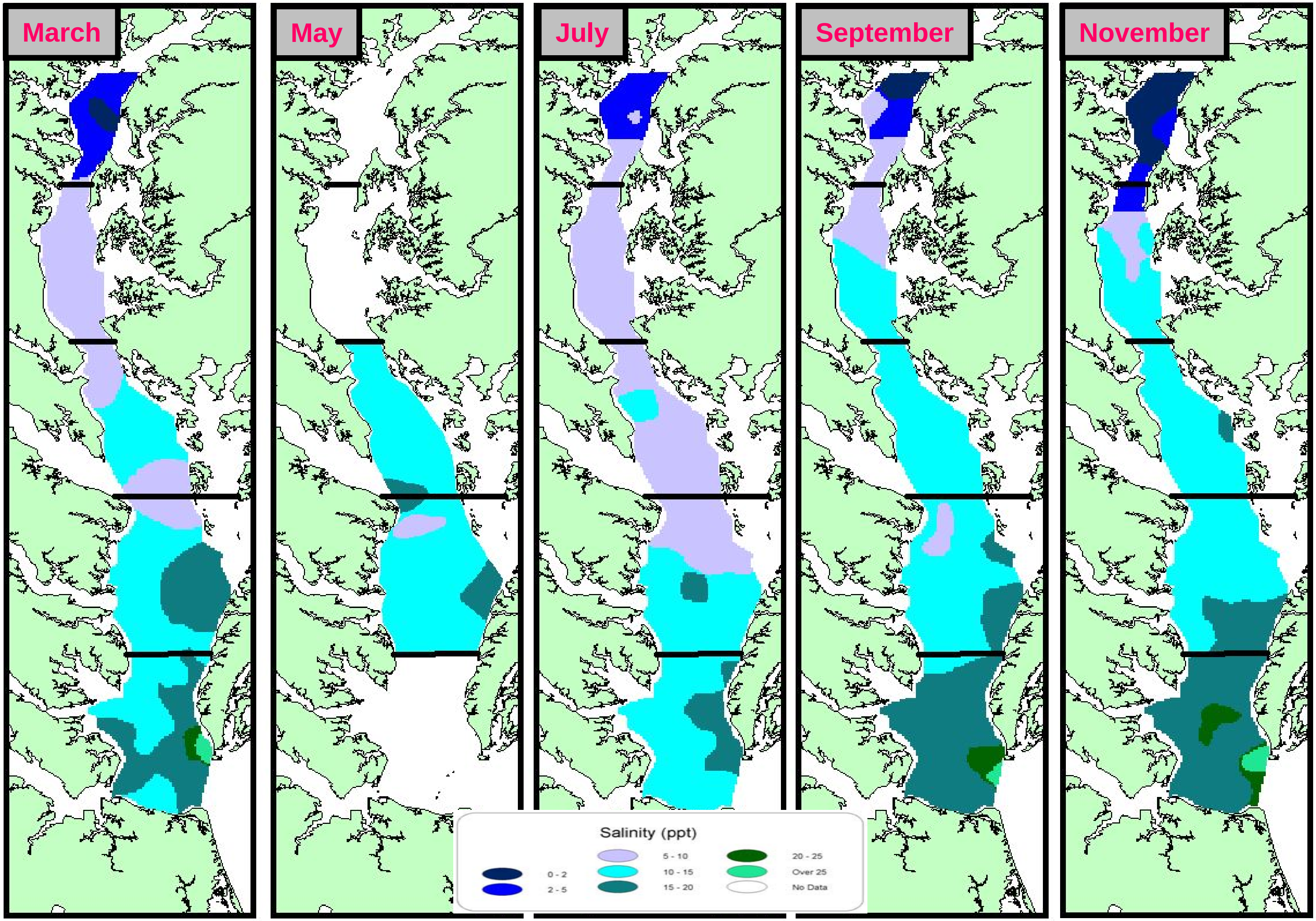


Figure 140. Surface salinity in Chesapeake Bay, 2003.



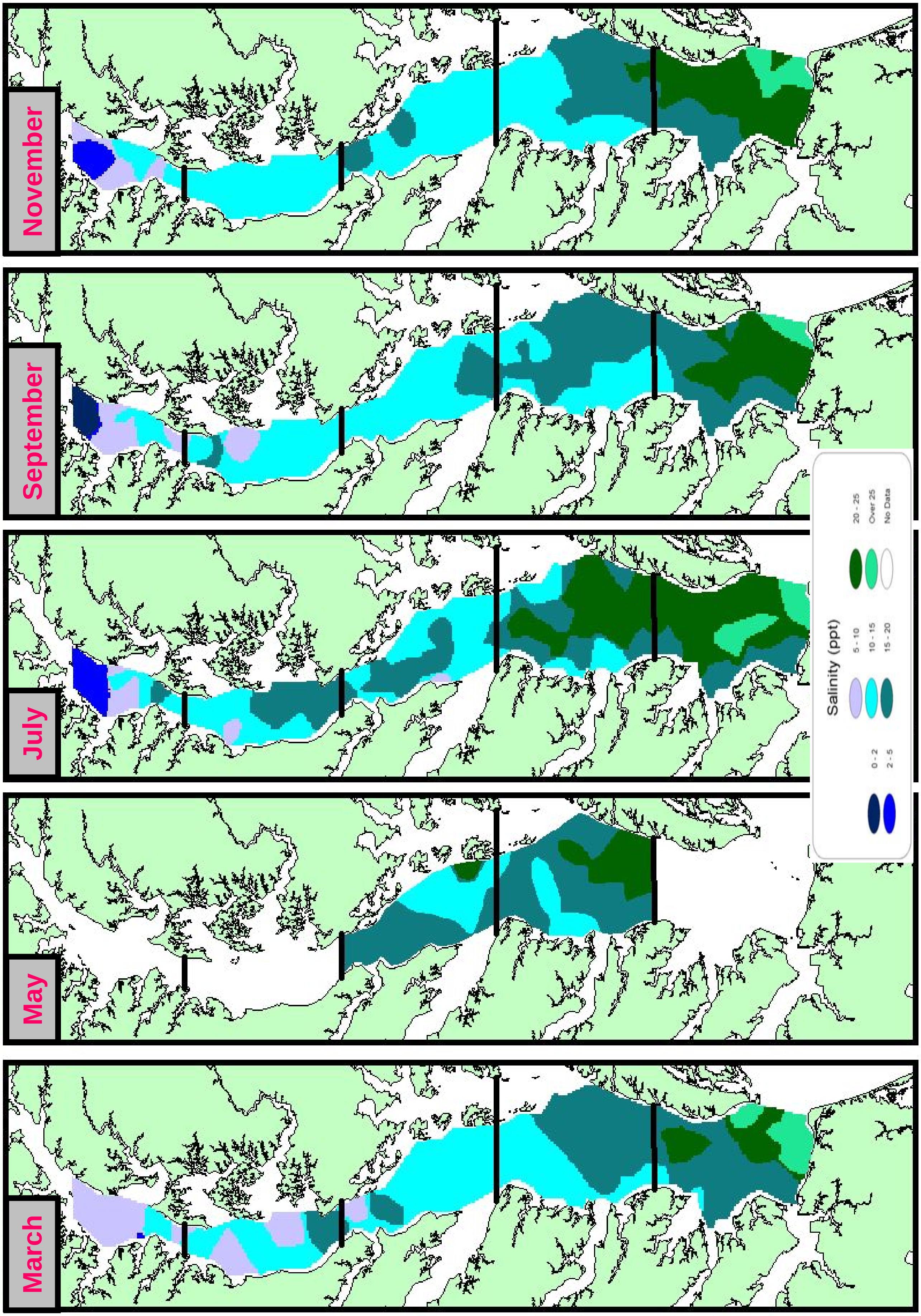


Figure 141. Bottom salinity in Chesapeake Bay, 2003.

Figure 142. Surface salinity in Chesapeake Bay, 2004.

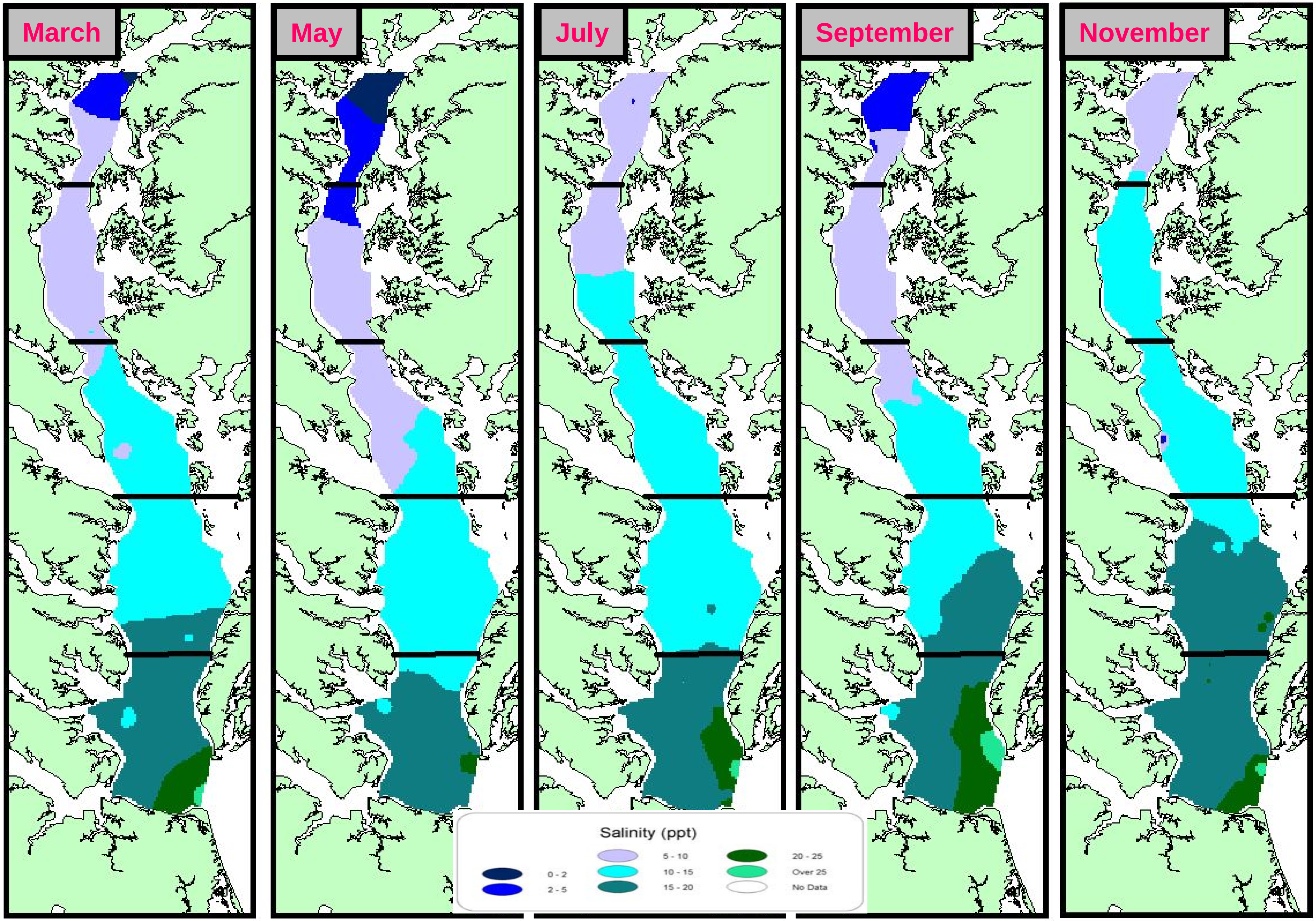
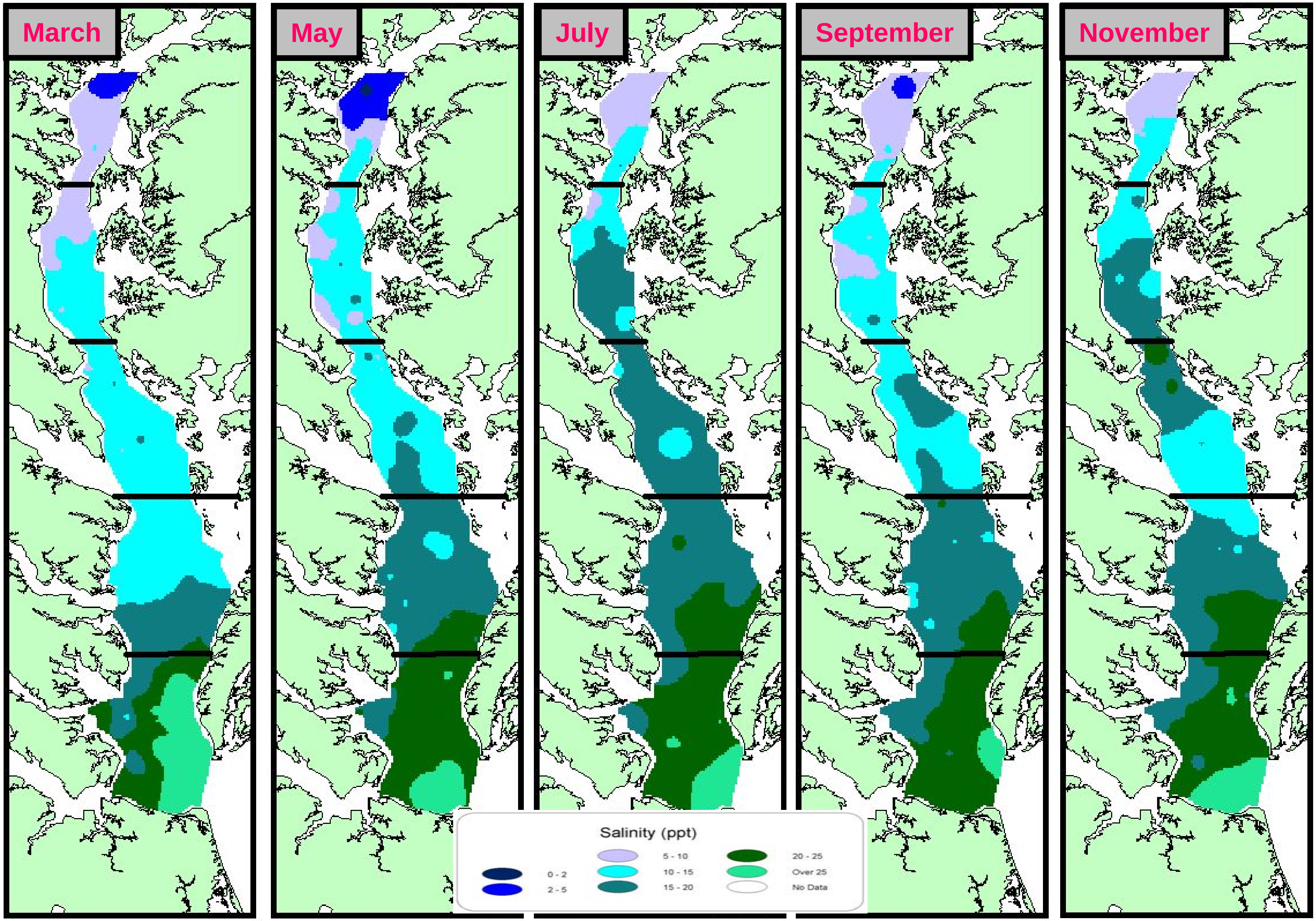


Figure 143. Bottom salinity in Chesapeake Bay, 2004.



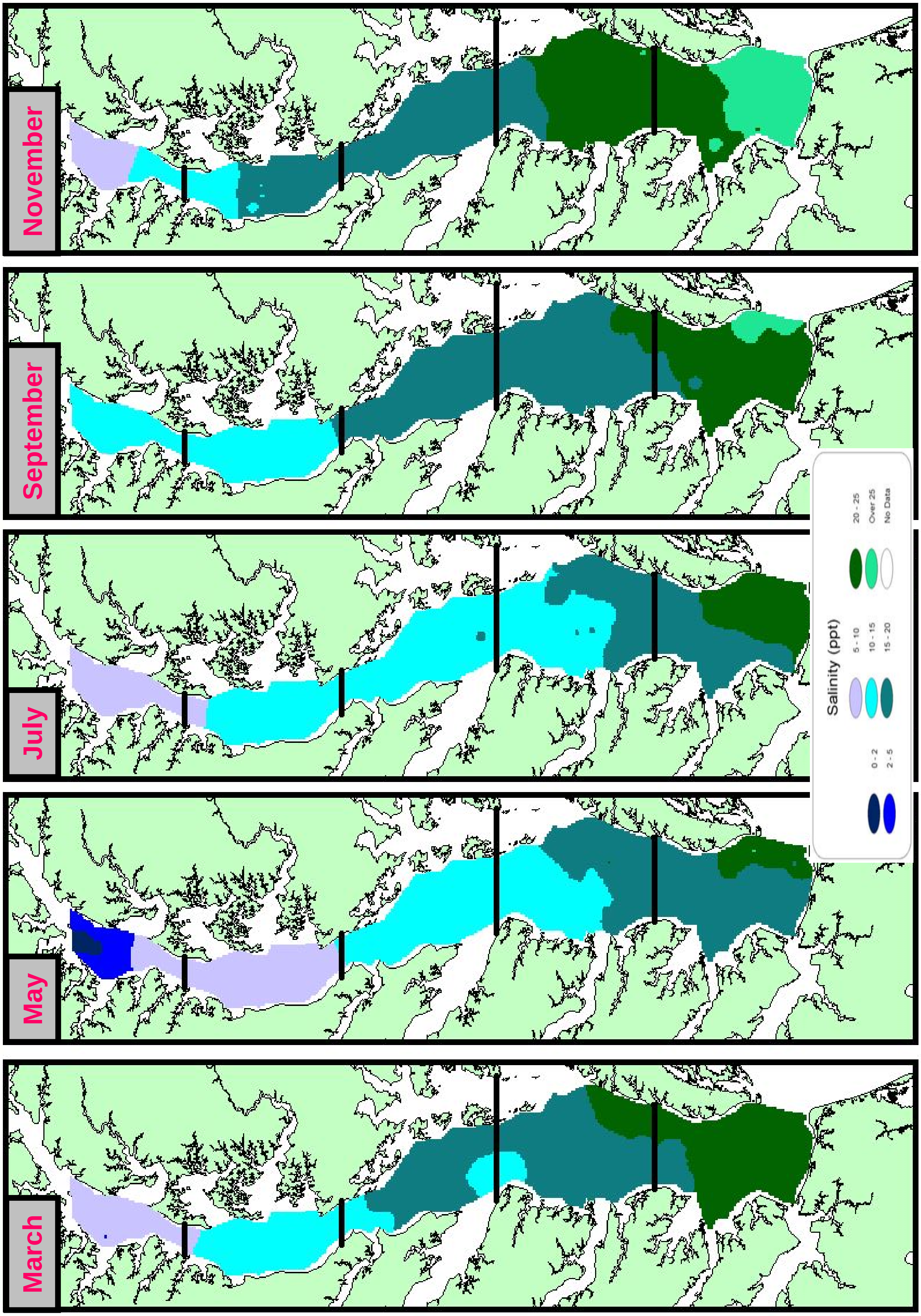


Figure 144. Surface salinity in Chesapeake Bay, 2005.

Figure 145. Bottom salinity in Chesapeake Bay, 2005.

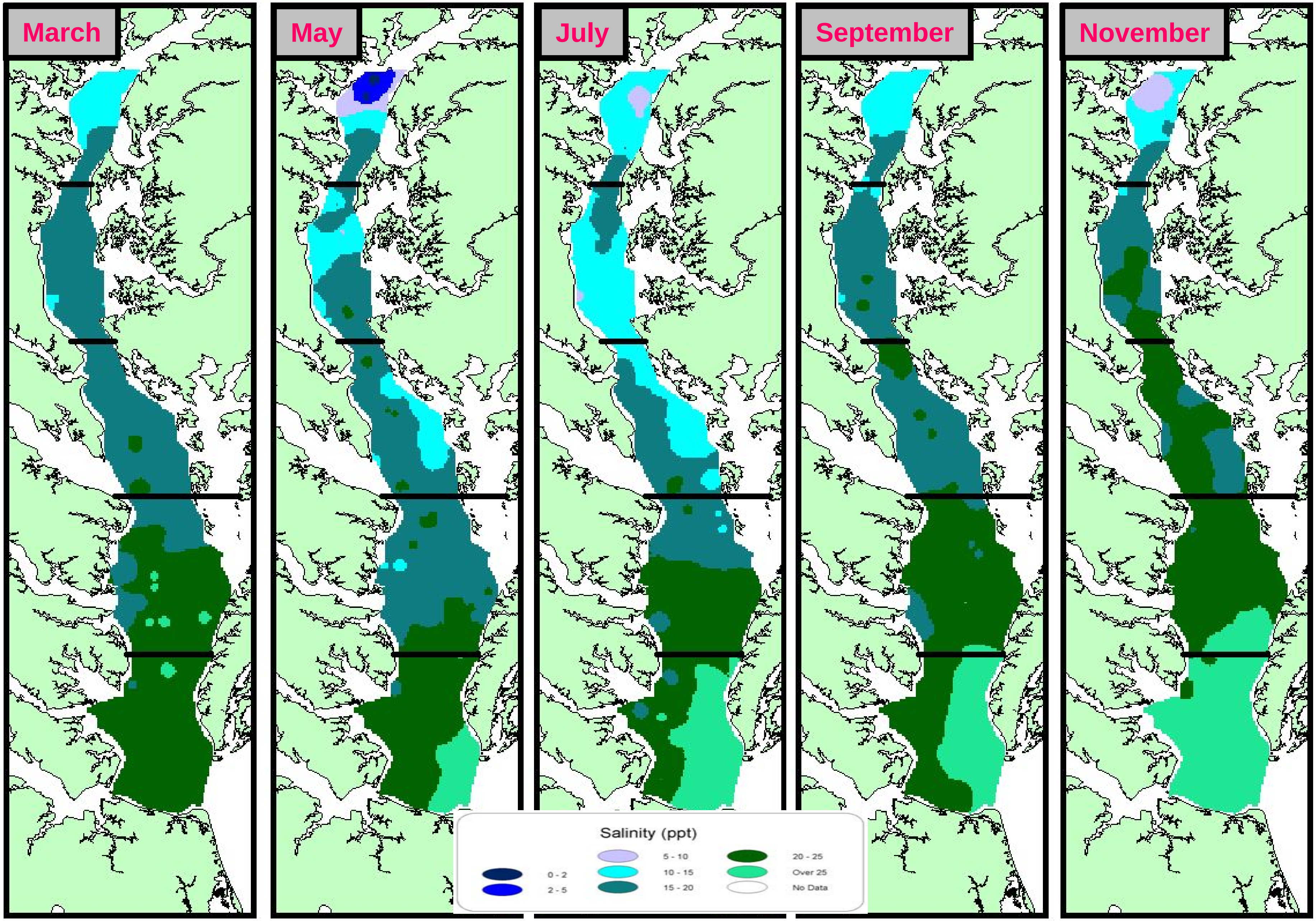


Figure 146. Surface salinity in Chesapeake Bay, 2006.

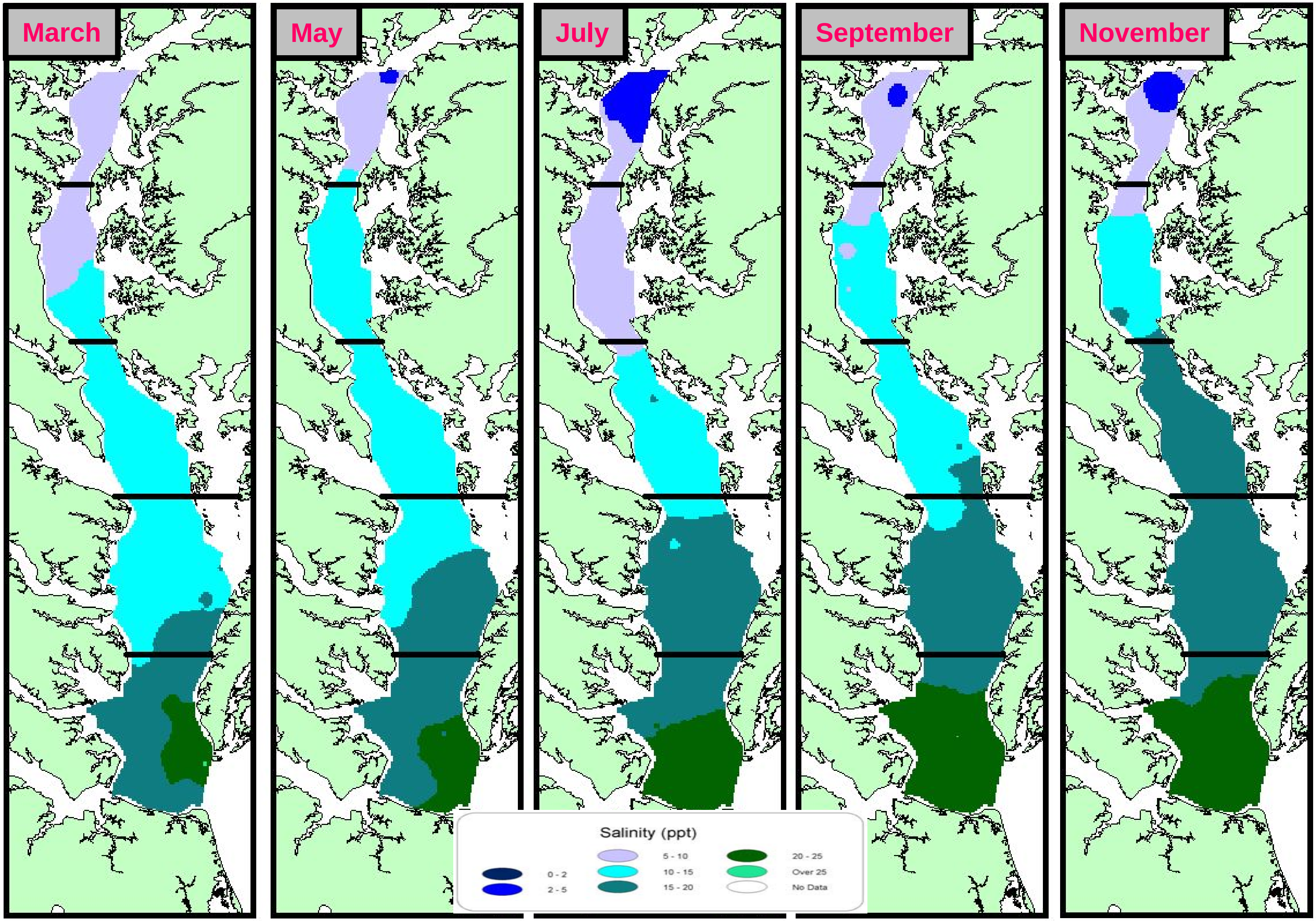


Figure 147. Bottom salinity in Chesapeake Bay, 2006.

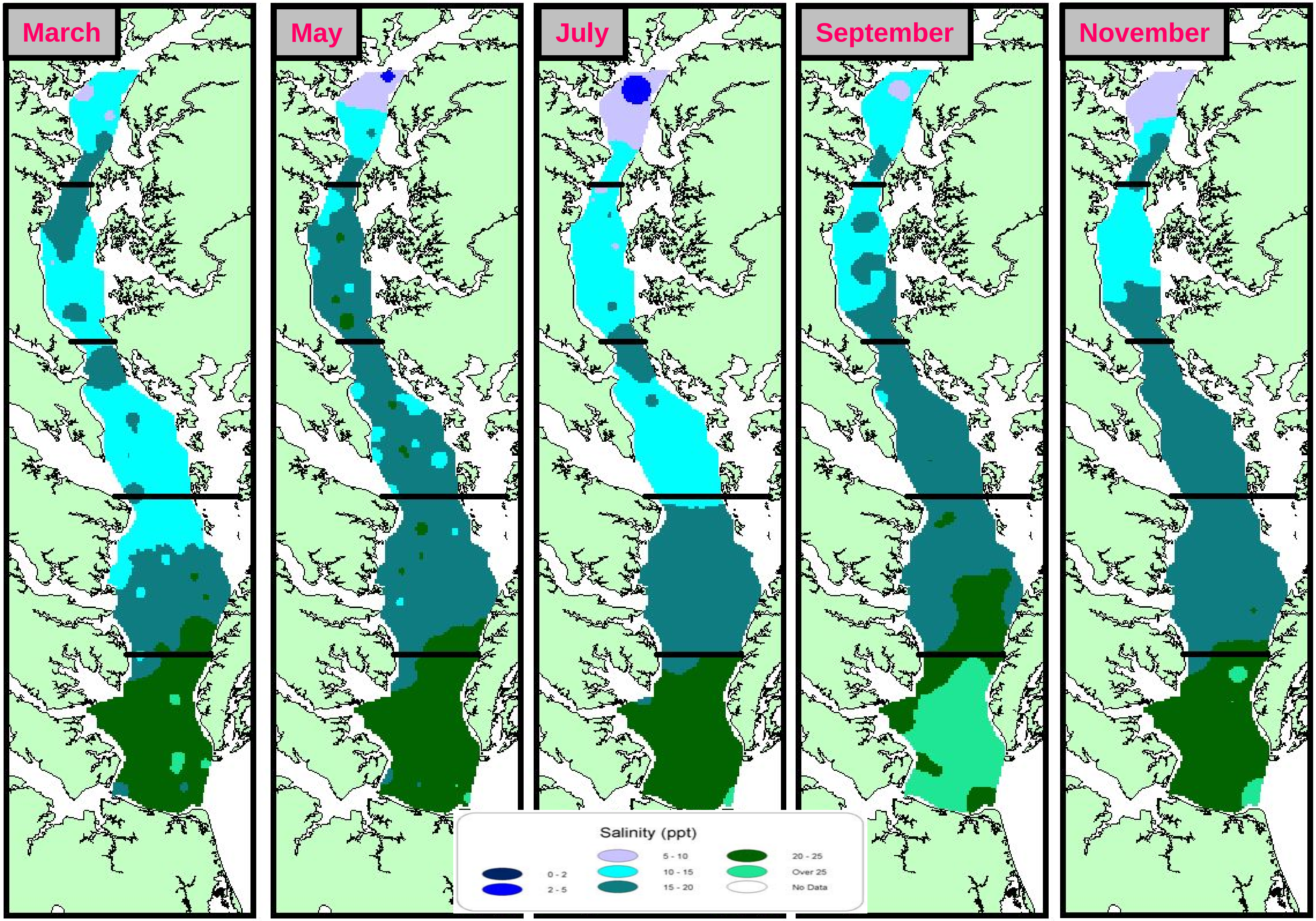


Figure 148. Surface dissolved oxygen in Chesapeake Bay, 2002.

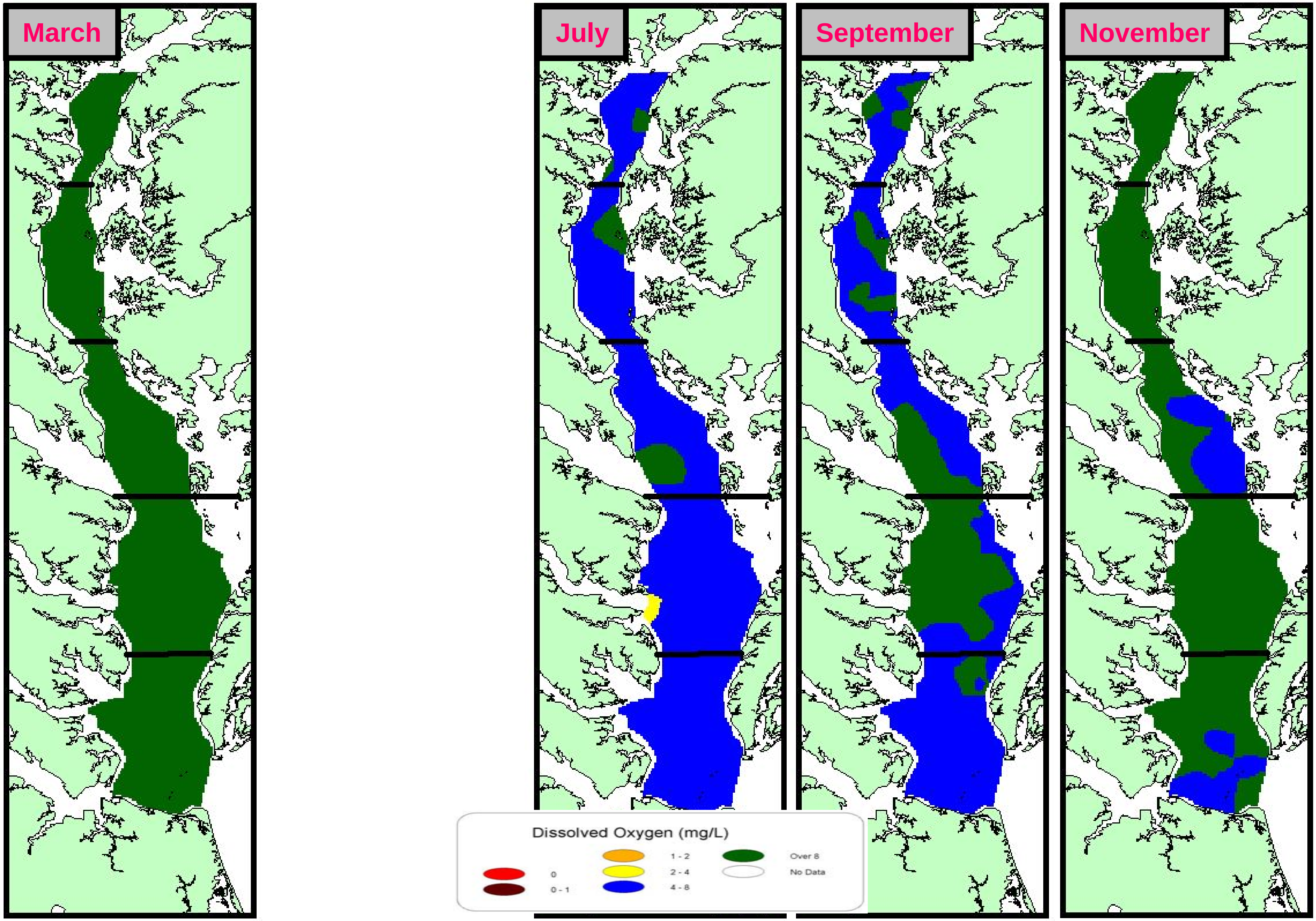


Figure 149. Bottom dissolved oxygen in Chesapeake Bay, 2002.

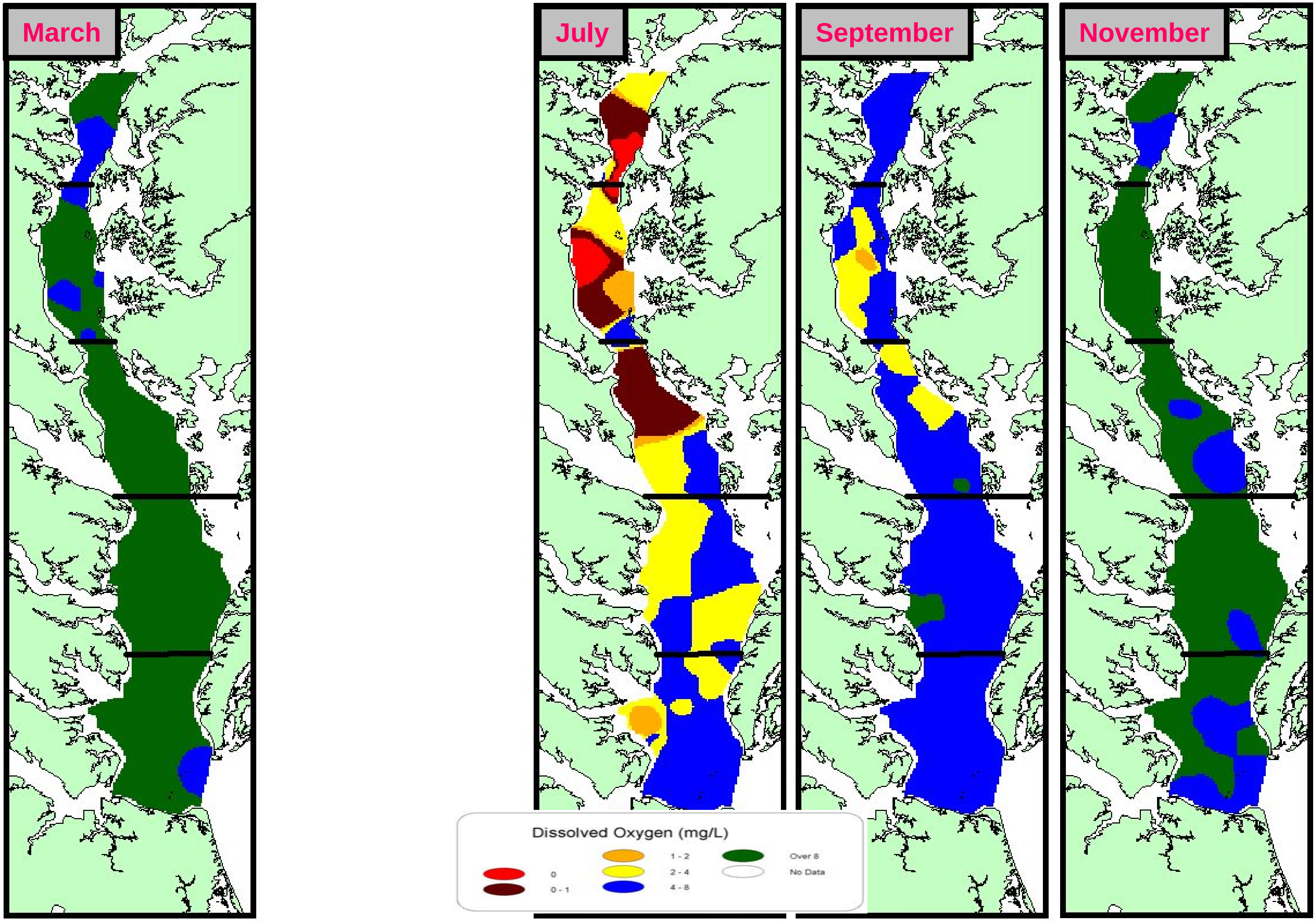


Figure 150. Surface dissolved oxygen in Chesapeake Bay, 2003.

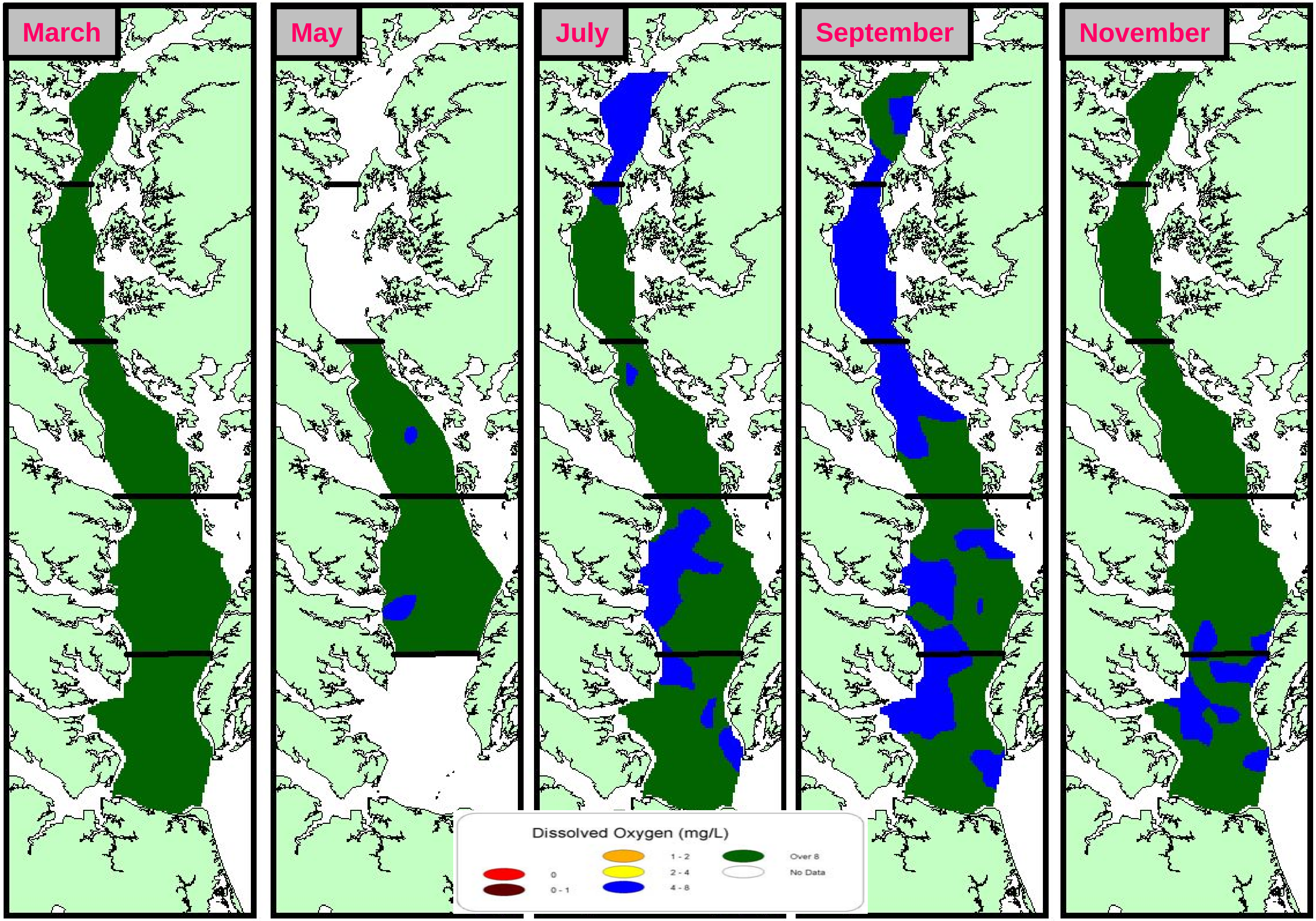


Figure 151. Bottom dissolved oxygen in Chesapeake Bay, 2003.

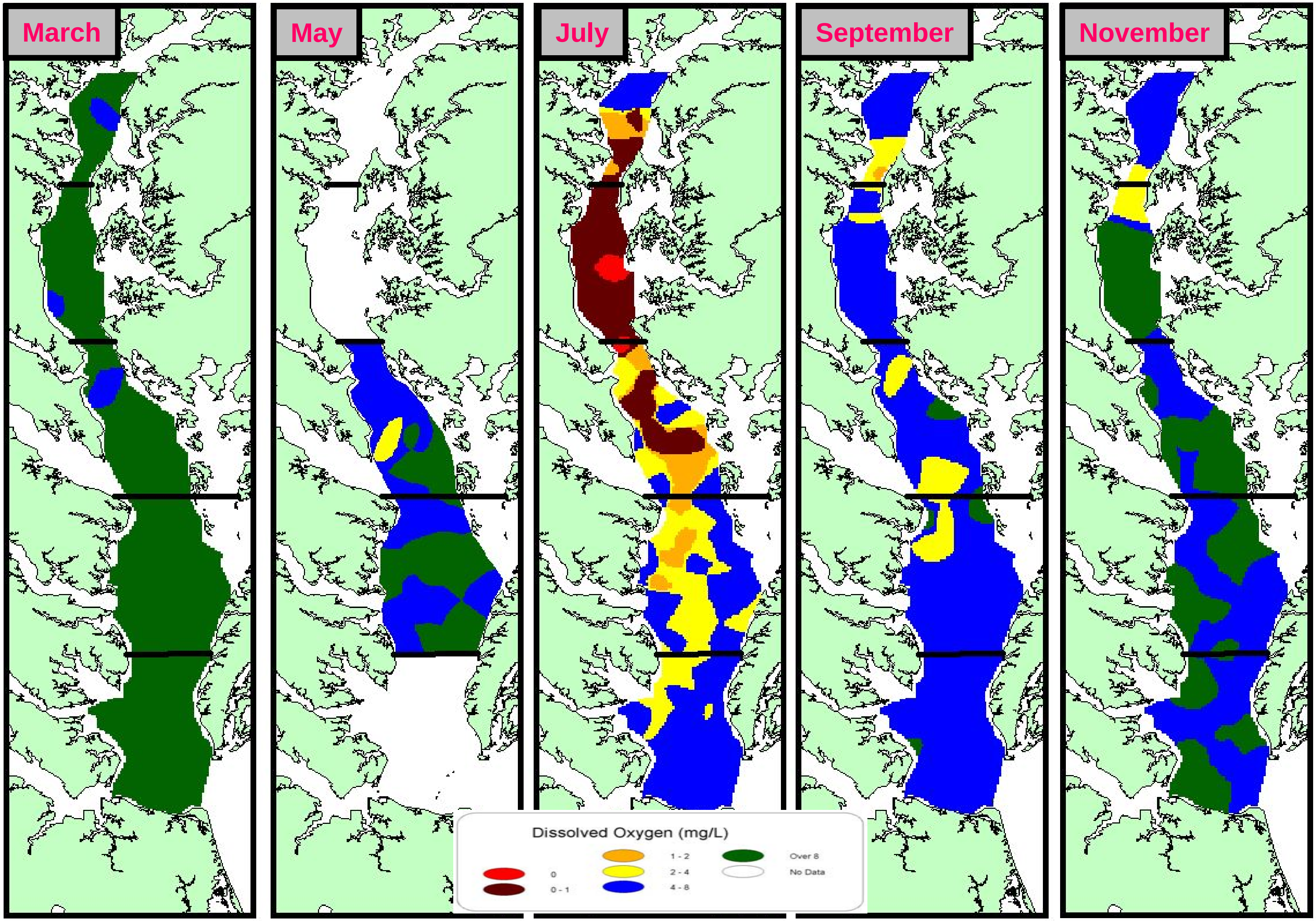


Figure 152. Surface dissolved oxygen in Chesapeake Bay, 2004.

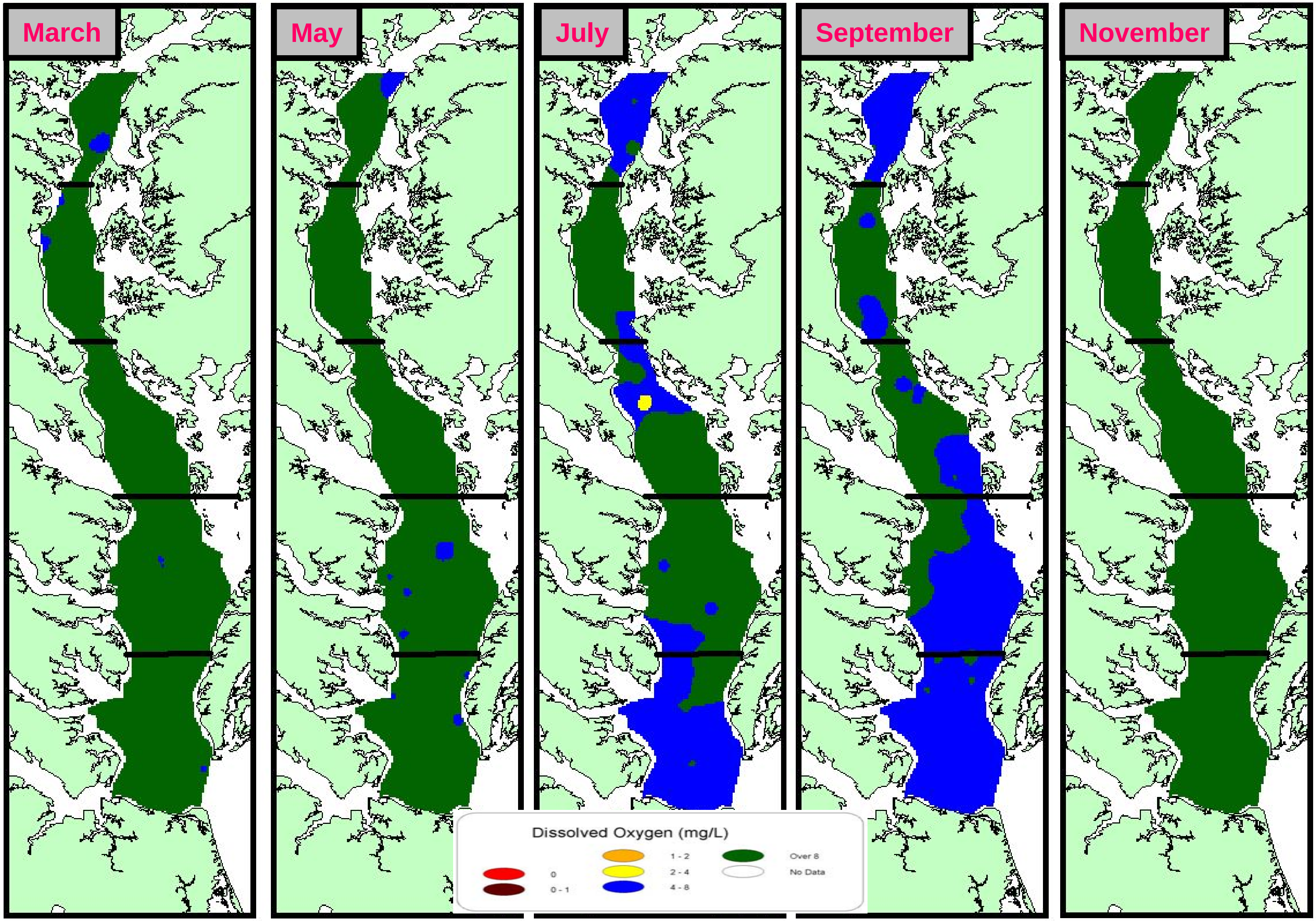


Figure 153. Bottom dissolved oxygen in Chesapeake Bay, 2004.

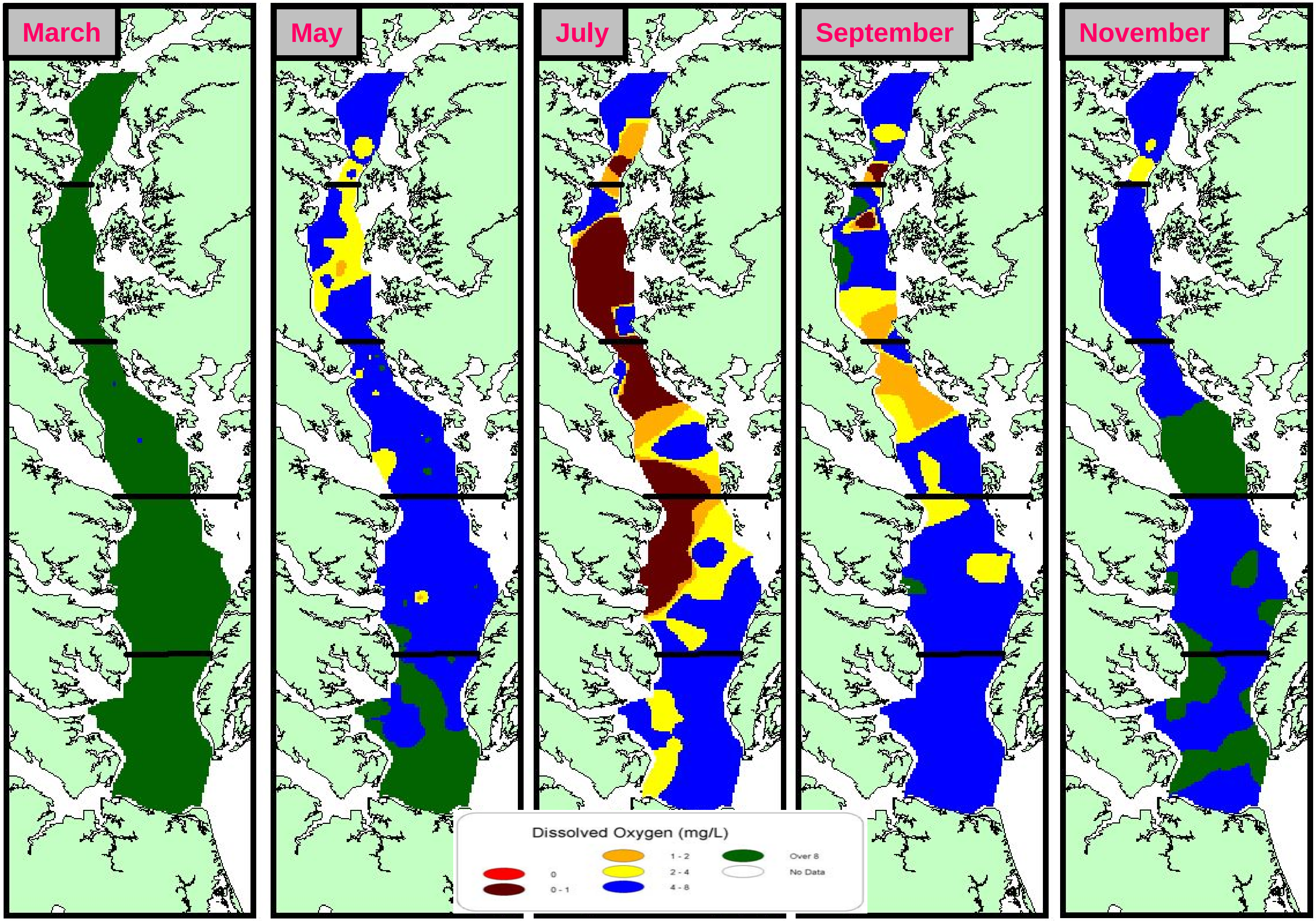


Figure 154. Surface dissolved oxygen in Chesapeake Bay, 2005.

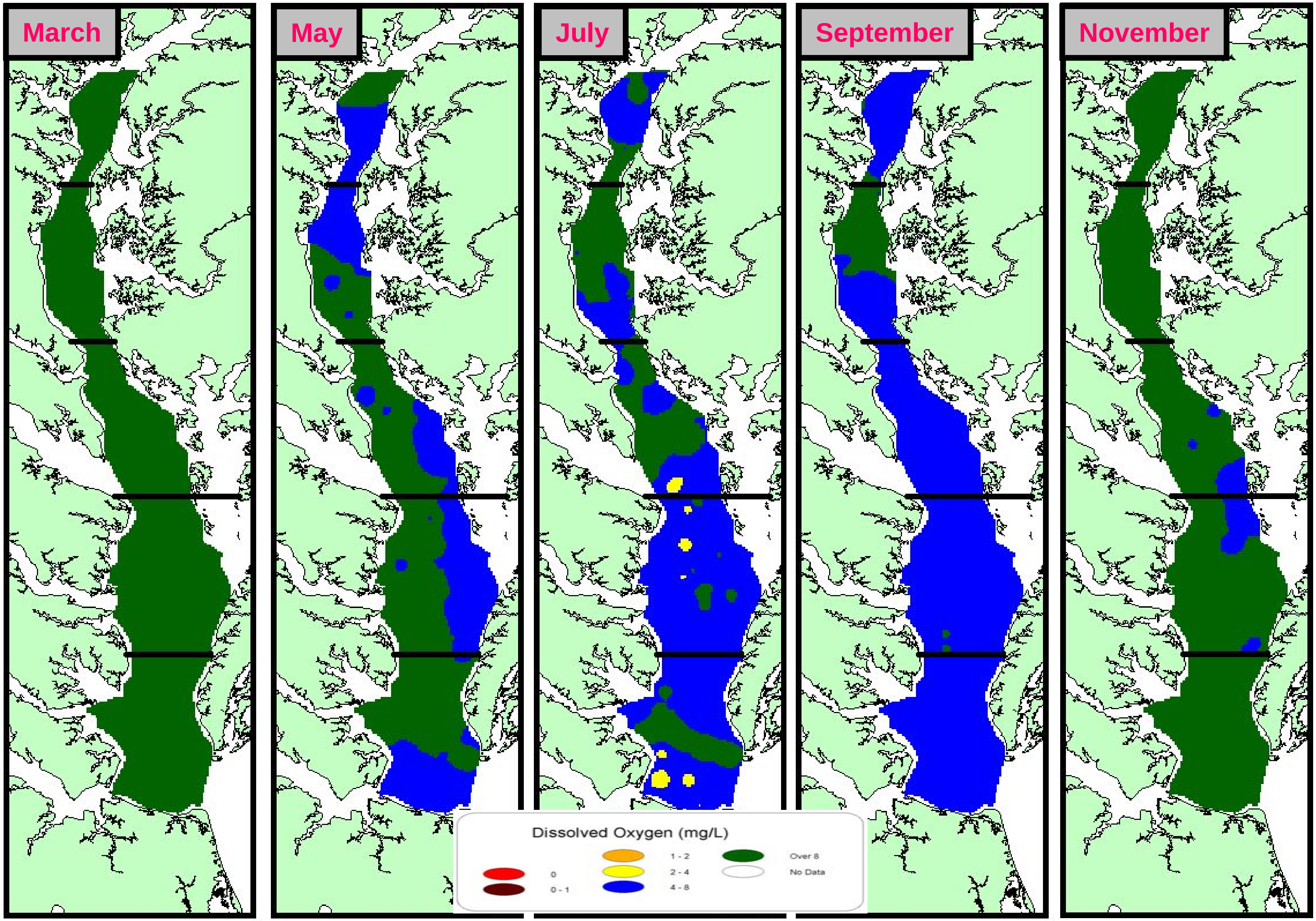


Figure 155. Bottom dissolved oxygen in Chesapeake Bay, 2005.

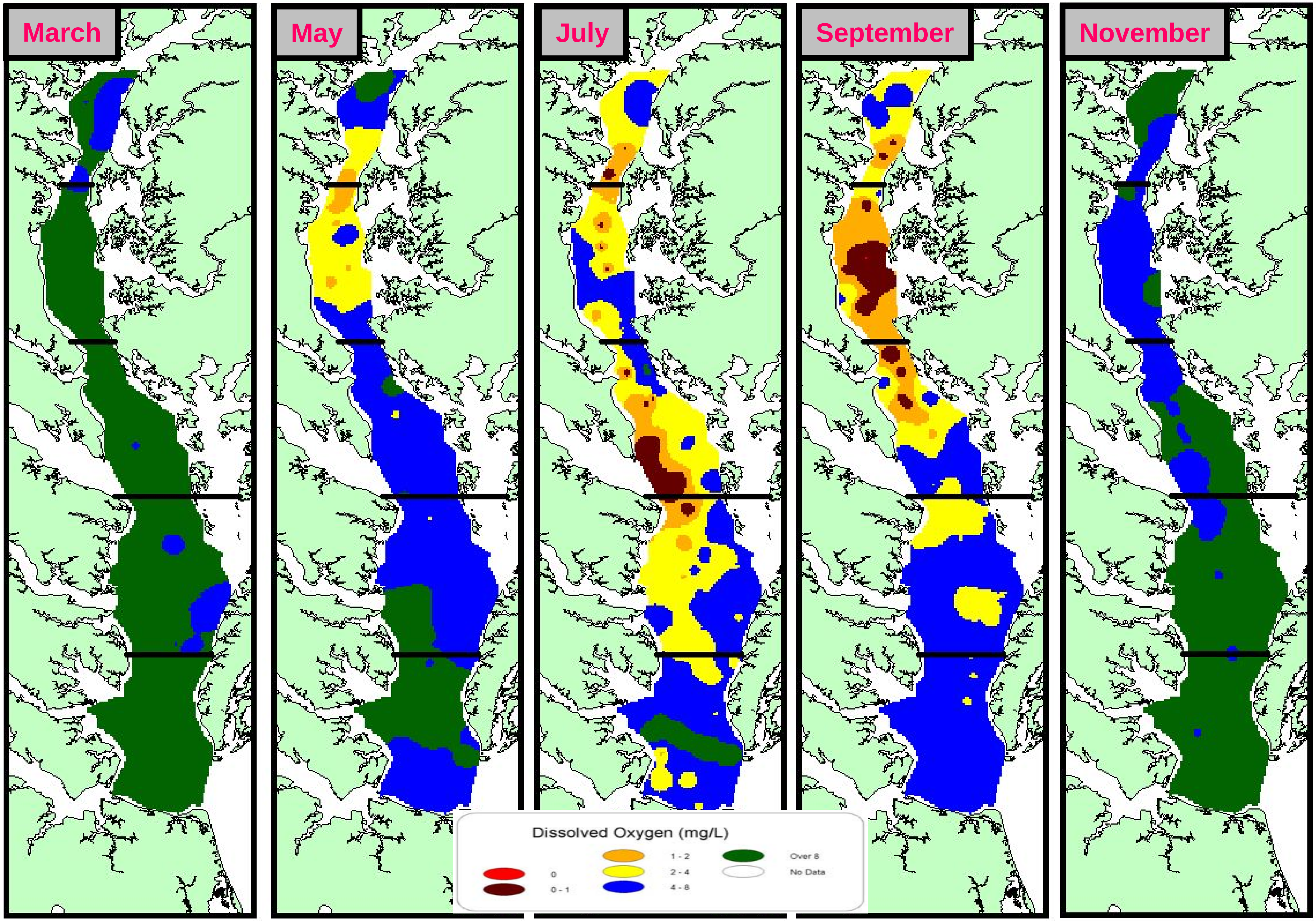


Figure 156. Surface dissolved oxygen in Chesapeake Bay, 2006.

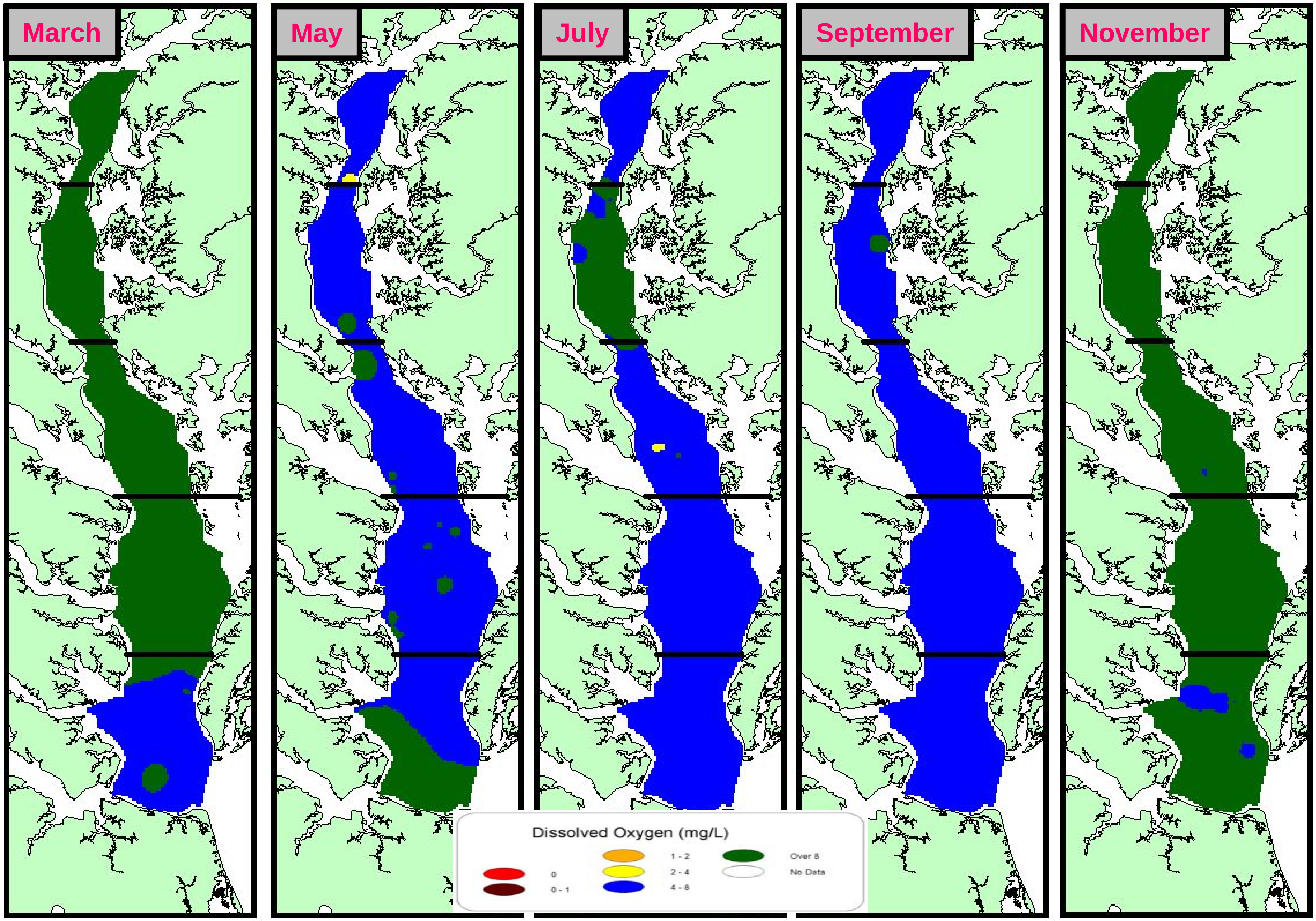


Figure 157. Bottom dissolved oxygen in Chesapeake Bay, 2006.