Sample Size Requirements for Detecting Length Differences of White Shrimp

- Jeff F. Doerzbacher,¹ Coastal Fisheries Branch, Texas Parks and Wildlife Department, 4200 Smith School Road, Austin, TX 78744
- Steven R. Marwitz, Coastal Fisheries Branch, Texas Parks and Wildlife Department, 100 Navigation Circle, Rockport, TX 78382

Abstract: Subsampling to obtain length measurements is often necessary when large numbers of organisms are captured with bag seines in a resource monitoring program. Catches of white shrimp were used to examine the representativeness of the subsamples and to construct sample size selection curves for determining the number of length measurements required to detect a given percentage difference between samples. A wide size range of white shrimp (*Penaeus setiferus*) is often captured in the same sample. Subsampling to measure 19 white shrimp from Texas Parks and Wildlife Department (TPWD) bag seine collections to estimate mean lengths was not always completely random but systematic discrepancies were not evident. A subsample of 19 shrimp can be used to detect a 15% difference in mean lengths among collections 80% of the time ($\alpha = 0.01$) with a CV of 13.3%, and in the worst case (CV = 37.9%), can detect a 50% difference in mean length and variance, nor between number caught and variance ($P \ge 0.05$).

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Standardized fisheries monitoring programs should ideally obtain data with known precision within budget constraints. A balance must be achieved between the available resources and the level of precision desired (Thornton et al. 1982). Many times, monetary and man-power considerations are often the dominant influence on the design of the monitoring programs. This can lead to either inadequate or excessive sampling to satisfy objectives (Kirmura 1984).

Precise size information is important for managers to assess the status of a population of organisms. Subsampling procedures are often used to shorten data processing time, but to be effective, subsampling should be unbiased and adequate to obtain a desired level of precision.

¹Present address: Intermedics Orthopedics, Inc., 1300 East Anderson Lane, Austin, TX 78752.

In October 1977, the TPWD initiated a standardized fishery-independent monitoring program using bag seines to assess relative abundance and size of finfish and shellfish in Texas bays. No more than 20, and usually 19, selected finfish and shellfish of each species were measured from each bag seine collection (Hammerschmidt et al. 1985, McEachron and Green 1986). The remaining unmeasured organisms were then counted. However, a subsample of 19 may not be adequate for detecting size differences of white shrimp caught in the fall. McEachron et al. (1977) noted a wide range in white shrimp lengths (post-larvae to individuals > 100 mm TL) and relative abundance among bag seine samples in 3 Texas bays. The objectives of the present study were to: 1) determine if 19 individuals selected during subsampling procedure results in an unbiased mean length estimate of all white shrimp in each bag seine collection, and 2) determine the number of white shrimp caught that should be measured in bag seine collections to detect at least a 50% difference between mean lengths at the 1% and 5% significance levels 80% and 95% of the time.

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Methods

White shrimp were collected at 10 locations in the Lavaca River delta on 26 September 1984. The Lavaca River delta is located near the coastal city of Port Lavaca, Texas. Bag seines (18.3 m long and 1.8 m deep with 1.3-cm stretched nylon multifilament mesh in the 1.8-m wide central bag with remaining webbing 1.9-cm stretched mesh) were pulled parallel to shore for a distance of 15.2 to 30.5 m (McEachron and Green 1986).

All white shrimp caught in each seine were sorted from the remainder of the catch. Nineteen white shrimp were randomly selected, and the total length (tip of rostrum to tip of telson) measured to the nearest 1 mm. The rest of the white shrimp were then measured separately.

The mean (\tilde{L}) , variance $(\sigma_{\tilde{L}}^2)$, and coefficient of variation (CV) were calculated for all lengths (N) of white shrimp in each bag seine collection (sample). Mean length (\bar{x}) , variance (s_x^2) , and CV were also computed for each subsample (n) of randomly selected and measured white shrimp. Because all shrimp in the whole sample were measured, an additional set of statistics $(\bar{y}, s_y^2, \text{ and CV})$ was computed for the complementary subsample comprised of those shrimp (N - n) left over after the subsample was removed.

If the subsample is random and unbiased, then \bar{x} has mean \bar{L} and variance $\sigma_L^2(1/n - 1/N)$ and the linear regression model

260 Doerzbacher and Marwitz

$$\tilde{x} = a + bL + 1/\sqrt{w} \cdot e$$

should hold, where a = 0 and b = 1; $1/\sqrt{w} = \sigma_L \sqrt{1/n - 1/N}$; and *e* is the standard normal error.

If the subsamples are not random, the regression model may still apply although 1 or all of the 3 conditions may be violated. The model was fit using the SAS REG procedure (SAS 1985) with weight

$$(w) = [\sigma_1^2(1/n - 1N)]^1$$

The hypothesis that a = 0 and b = 1 was tested with an *F*-test. The hypothesis that *e* (residual mean square error) was equal to 1 was tested by comparing the residual sum of squares with a χ^2 with 8 degrees of freedom (df) (Weisberg 1980). Rejection of either of these hypotheses indicates that the subsamples were not random, but does not indicate whether the discrepancy was in the means or the variances, or both. An alternate aggregate method of testing a = 0 and b = 1 with the given variances is to compare the sum of squares (Σz^2) of

$$z = (\tilde{x} - \bar{L})/\sigma_L \sqrt{1/n} - 1/N$$

to χ^2 with 10 df. Tests of individual z's help indicate which, if any, of the pairs of subsamples and samples were significantly different.

Separate tests of means and variances made use of each subsample and its complementary subsample. If the subsamples were representative in terms of means but not variability, then a direct 2-sample *t*-test comparison using \bar{x} and \bar{y} and the subsample variances s_x^2 and s_y^2 should reveal no differences. Alternatively, if the subsamples were representative in terms of variation, then both s_x^2 and s_y^2 should be close to σ_t^2 . An approximate test is the F-test s_x^2/s_y^2 with *n* and N - n df.

Correlation coefficients between mean length and variance and between number of shrimp measured (sample size) and variance in each sample were computed and tested for significance. Bartlett's test for homogeneity of variance (Sokal and Rohlf 1981) was performed to test the assumption of equal variance among mean lengths in samples using untransformed data and square root and log transformations of the data. A single classification analysis of variance was performed using each sample as a group to determine an estimate of variance. Significance level was set at P = 0.05. Sample size selection curves determining the number of measurements required to detect a given difference between 2 means within specific confidence limits were calculated using the following equation (Sokal and Rohlf 1981):

$$n \ge 2(CV/d)^2(t_{\alpha[v]} + t_{2(1-P)[v]})^2$$

where n = number of measurements required; CV = coefficient of variation (%); d = smallest difference that is desired to be detected (% of mean); v = degrees of

where n = number of measurements required; CV = coefficient of variation (%); d = smallest difference that is desired to be detected (% of mean); v = degrees of freedom of the sample standard deviation; α = significance level (precision); P = probability a true difference as small as d will be found significant; and $t_{\alpha[\nu]}$ and $t_{2(1-P)[\nu]}$ = values from a 2-tailed *t*-table with v degrees of freedom and corresponding to probabilities of α and 2(1 - P), respectively.

Results

The mean length estimates of white shrimp based on the TPWD subsamples of 19 measurements indicated that some subsamples were not representative of the sample but discrepancies were not systematic in one particular direction. The weighted linear regression estimated a slope (\pm SE) of 0.92 (0.15) and an intercept (\pm SE) of 6.68 (12.28). The hypothesis that the slope b = 1 and intercept a = 0could not be rejected (F = 0.15, P > 0.86); however, the residual error term deviated significantly from 1 as evidenced by the comparison of the residual sum of squares (20.56) with $\chi^2 = 15.15$ (P = 0.05, 8 df). This result was confirmed by computation of $\Sigma z^2 = 21.3$ (P < 0.05; χ^2 , 10 df). Individual standardized mean comparisons revealed significant z scores for the third (z = 2.81, P < 0.01) and sixth (z = -2.27, P < 0.05) samples (Table 1). These tests indicated some problem with the hypothesis of random subsamples but did not indicate if the discrepancies were in the means or variances or both.

The t statistic comparing subsample means and complementary subsample means again showed a significant difference for the third sample (t = 2.44, P < 0.05). The test indicated the third subsample mean was not representative of the whole sample mean. F-tests comparing the variances of subsample and complementary subsample means showed a significant difference for the ninth sample (F = 0.34, P < 0.05).

Correlations between mean length and variance (r = -0.56, P > 0.05) and between sample size and variance (r = -0.58, P > 0.05) were not significant; however, Bartlett's test for homogeneity of variance indicated the assumption of equal variances was suspect. Neither square root nor log transformation gave any improvement and, in fact, resulted in significant correlation between mean length and variance. Therefore, in addition to using a CV (13.3%) based on the within mean square from the analysis of variance on the untransformed data (F = 118.6, P < .01, MSE = 110) and the unweighted mean of all samples (78.9 mm), the highest CV (37.9%) from an individual sample (Table 1) was also used as a worst case example for the computation of sample size.

A 50% difference in mean lengths could be detected with 2–3 shrimp measured per sample if the CV was 13.3% and with 10–21 shrimp measured per sample if the CV was 37.9% (Fig. 1 and 2). Sample size estimates for detecting a 15% difference in mean lengths ranged from 13 to 29 with a CV of 13.3%.

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Table 1.	sample fo

		Samp	ole			Subsa	mple		ŭ	mplementary	subsam	ple	T	est statistics	
Station	N	Mean TL (mm)	ß	CV (%)	r	Mean TL (mm)	SD	CV (%)	n - n	Mean TL (mm)	SD	CV (%)	r Z	qi	F.c
-	57	92	16	16.8	61	68	19	21.6	38	94	13	14.1	- 1.03	- 1.02	2.12
2	65	70	19	27.4	19	69	24	34.1	46	70	17	24.7	-0.27	-0.17	1.88
Э	1425	79	œ	9.6	19	84	6	10.6	1406	79	×	9.9	2.81**	2.44*	1.30
4	804	81	٢	8.9	19	84	×	10.0	785	81	٢	8.8	1.85	1.55	1.37
5	49	84	12	14.7	19	84	11	12.5	30	84	14	16.2	0.0	0.00	0.60
6	167	93	10	11.0	19	88	11	12.7	148	93	10	10.7	-2.27*	-1.86	1.25
7	358	74	12	16.1	19	71	14	19.7	339	75	12	15.8	-1.12	-1.22	1.39
8	69	77	23	29.8	19	75	26	34.8	50	78	22	28.2	- 0.44	- 0.44	1.41
6	49	68	16	24.1	21	2	11	17.3	28	71	19	26.8	- 1.49	-1.62	0.34^{*}
10	117	58	22	37.9	19	59	21	34.9	98	58	22	38.5	0.22	0.19	0.85
** <i>P</i> < ** <i>P</i> < *-St2 ** *-St2 **	 < 0.05. < 0.01. < 0.01. distic comparisatic comparisatic	ares the samplares the subsar ares the subsar	le mean mple and	with the subs 1 the complei riance with th	sample n mentary he comp	ncan. subsample m	eans.					-			Ĩ

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Figure 1. Sample size selection curves for number of white shrimp total length measurements from bag seine collections required to detect a desired percent difference among means at each precision level using a CV = 13.3. A, $\alpha = .05$ (P = 80%); B, $\alpha = .01$ (P = 80%); C, $\alpha = .05$ (P = 95%); D, $\alpha = .01$ (P = 95%).

Discussion

This study indicated that the procedures used in this particular sampling exercise yielded some subsamples that were not completely random but the discrepancies were not systematic in one particular direction. Thus, mean lengths computed should still be useful in assessment of trends in white shrimp populations. However, many different field personnel may be responsible for resource sampling and may be using a variety of subsampling techniques. Because there was some indication of non-random subsampling in this study, it may be advantageous to consider instituing uniform subsampling procedures on a coastwide basis to help insure consistency of the data collected for trend analysis.

Gulland (1966) suggested methods to eliminate or minimize potential bias when subsampling from a large catch. One method is to separate the large sample into groups, a few organisms at a time, until the groups contain about the desired number to be measured. Then one of the groups is randomly selected and the individuals measured. DeVries (1985) described the approach used in North Carolina's statewide trawl survey to minimize bias in selecting subsamples. Samples containing large numbers of individuals (>60) were subsampled by first mixing the separated pile of a particular species, and then randomly selecting (as a group) and measuring 30-60 individuals. By having a range for subsample size and selecting it as a unit, the bias that may be introduced by handling individually a specific-sized subsample was believed to have been eliminated.

White shrimp are only one of many species routinely collected in TPWD bag seine samples (McEachron and Green 1986). Continued evaluation of subsampling procedures for other species would insure that unbiased data are being collected



Figure 2. Sample size selection curves for number of white shrimp total length measurements from bag seine collections required to detect a desired percent difference among means at each precision level using a CV = 37.9. A, $\alpha = .05$ (P = 80%); B, $\alpha = .01$ (P = 80%); C, $\alpha = .05$ (P = 95%); D, $\alpha = .01$ (P = 95%).

with a minimum of effort and cost. The wide size range of white shrimp caught in a single bag seine collection would probably result in greater variance about the mean for white shrimp than for species captured within narrower size ranges. It is reasonable to assume that for these species a subsample size of 19 would also provide means useful for detecting length differences at precision levels at least equal to those achieved for white shrimp.

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