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Investigation of Sampling Bias on Length Distribution of *Pandalus borealis*

When Sampling From the Hatch.

by

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INTRODUCTION.

The fishery for *Pandalus borealis* represents one of the most valuable economical resources for Greenland. The Greenland Fisheries Research Institutes trawl surveys for *Pandalus borealis* are conducted each year. Besides this annual survey, a series of surveys was carried out in 1990, to investigate trawl selectivity and shrimp discards. Due to uncertainties about a possible mechanic sorting of the shrimps in the trawl, sampling has usually been carried out by taking several subsamples from the cod-end on deck immediately after hauling (Carlsson & Kanneworff, 1989, Degel et al., 1991). When sampling has to be done on board commercial trawlers, this procedure is however often cumbersome and sometimes conflicts with security on board. Because of these problems it would be advisable to sample from the hatch. If the catch when emptied to the hatch mix well, then this would moreover be preferable as any possible sorting occurring in the cod-end could be removed. This paper investigates whether the size distribution vary from samples of shrimps (*Pandalus borealis*) taken in the beginning, in the middle and in the end of the process of emptying the hatch.

MATERIALS AND METHODS.

Samples of shrimp were taken on board the shrimp trawler TASERMIUT, between November 14. and November 25. 1990 in NAFO-division 1B. During the trip two types of gear were used, a Skjervoy 3600, with 43 mm mesh size and an Angmassa-liq 3360, also with 43 mm mesh size in the cod-end. For each haul three subsamples each of about 2 kg were taken (1) in the beginning, (2) in the middle and (3) in the end of the process of emptying the hatch. This sampling was repeated in 33 hauls. The oblique carapace length (OCL) was measured with 0.1 mm accuracy using a sliding gauge connected to a computer.

The length-frequency-distributions of the shrimp samples showed non-normal distributions (Fig. 1). For this reason non-parametric statistics were used and the median length, the 25% percentile (Q25) and 75% percentile (Q75) were considered to give adequate descriptions of each subsamples length-frequency-distribution. The median length gives the central value for the distribution (Campbell, 1981), and the two other values together gives a measure of the width of the distribution.

The within-haul test for comparing the length-frequency-distributions for each haul was performed with a non-parametric one-way analysis of variance on ranked data (NPAR1WAY medianscore test from the SAS-system, SAS Institute Inc., 1988). To detect whether there were any overall systematic differences between the length-frequency-distributions from the subsamples taken in (1) the beginning, (2) the middle or (3) the end of the emptying of the hatch, all three measures for each subsample were also plotted (Fig. 2 left). To minimize the "between haul" variance the residual values for the median length, Q25 and Q75 for each subsample of each haul were plotted (Fig. 2 right). The residual values were calculated as:

$$\text{Residual median length} = (\text{median length}_{ij}) - (\text{mean median length}_i)$$

median length_{ij}: the median length of subsample j from haul i.

mean median length_i: the mean median length of all three subsamples from haul i.

Analogous:

$$\text{Residual Q25} = Q25_{ji} - mQ25_i$$

$$\text{Residual Q75} = Q75_{ji} - mQ75_i$$

The residual values were then tested using an one-way varians analysis (NPAR1-

WAY medianscore test) and with linear regression analysis (GLM test from the SAS system).

RESULTS AND DISCUSSION.

Table 1 summarizes the median lengths for all 99 subsamples and the results of the non-parametric one-way analysis of variance on ranked data. In seven of the 33 hauls the test gave p-values less than 0.05. In these seven hauls, three hauls had their maximum median length in subsample (1), two had their maximum median length in subsample (2) and two had theirs in subsample (3). This pattern doesn't indicate that there are any obvious within haul trends in the differences between the median lengths from subsample (1) to (3).

The pooled material (e.g. all 33 hauls) were analyzed both with linear regression analysis (GLM test from the SAS system) and one-way varians analysis. The results of the GLM test are given in table 2. As can be seen the values for the slopes are all close to zero and non significant. This means that there is no trend in the median length vs. time in the process of emptying the hatch.

Table 3 sums up the results from the varians analysis on the residual values. Again all the results are very close to zero, and the p-values are non significant on a 5% level. This means that there are no major overall systematic differences between the length-frequency-distributions from subsample (1) to (3).

It may therefore be concluded, that the catch is mixed effectively during handling. This homogeneous size distribution in the hatch means that the required sampling intensity might be less than when sampling on deck. Even if the total sample size would remain unchanged, the practical importance of a reduction in the number of subsamples to be taken from each haul, is of course interesting considering the intense sampling of *P. borealis* carried out in the recent years.

The results also suggest that the difference in length distributions that is sometimes seen in hauls taken in the same area and period during shrimp surveys are rather due to a size wise patchy distribution of the shrimps and can thus not be explained by sample biases. Finally it is to be stressed that this has only been investigated for *P. borealis*, and does not automatically apply for other species.

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Table 1: The median length (carapace length in millimeter) of *P. borealis* from three subsamples taken from 33 trawl catches in NAFO division 1B, Nov. 1990. N is the total number of *P. borealis* sampled from one haul. NS indicates that the p-value from the one-way varians analysis on ranked data is non significant on a 5% level.

* Indicate that the gear was an Angmassaliq 3360, in all the other hauls the gear used was a Skjervoy 3600 (43 mm mesh size in the cod-end of both gear).

| Haul | N | 1.st sample median length | 2.nd sample median length | 3.rd sample median length | p-value |
|------|-----|---------------------------|---------------------------|---------------------------|---------|
| 1 | 886 | 23.0 | 22.5 | 23.6 | NS |
| * 2 | 841 | 24.0 | 24.4 | 24.6 | NS |
| 3 | 666 | 22.8 | 23.7 | 23.8 | NS |
| 4 | 657 | 25.0 | 25.1 | 25.4 | NS |
| 5 | 846 | 23.1 | 24.0 | 23.9 | NS |
| * 6 | 749 | 24.2 | 23.9 | 24.4 | NS |
| 7 | 756 | 24.8 | 24.4 | 24.5 | NS |
| 8 | 639 | 25.7 | 25.1 | 24.8 | NS |
| 9 | 661 | 25.6 | 25.4 | 25.5 | NS |
| 10 | 734 | 24.1 | 22.4 | 23.1 | NS |
| * 11 | 877 | 23.9 | 22.7 | 22.9 | NS |
| 12 | 784 | 23.3 | 23.0 | 22.5 | NS |
| * 13 | 698 | 24.8 | 24.9 | 24.3 | NS |
| 14 | 716 | 22.9 | 22.6 | 22.3 | NS |
| 15 | 821 | 21.8 | 21.8 | 22.1 | NS |
| 16 | 682 | 22.8 | 22.3 | 23.3 | NS |
| 17 | 866 | 22.3 | 22.4 | 23.5 | P<0.05 |
| 18 | 683 | 23.2 | 23.2 | 22.8 | NS |
| 19 | 788 | 22.6 | 21.7 | 22.3 | P<0.05 |
| 20 | 728 | 23.0 | 22.4 | 22.6 | NS |
| 21 | 694 | 24.0 | 24.1 | 23.4 | NS |
| 22 | 796 | 21.4 | 21.4 | 21.6 | NS |
| 23 | 943 | 21.8 | 21.6 | 21.9 | NS |
| 24 | 872 | 22.3 | 21.6 | 21.7 | NS |
| 25 | 781 | 21.8 | 21.7 | 21.6 | NS |
| 26 | 703 | 21.8 | 22.1 | 21.8 | NS |
| 27 | 710 | 23.2 | 22.9 | 22.1 | P<0.05 |
| 28 | 749 | 23.1 | 22.5 | 21.7 | P<0.01 |
| * 29 | 771 | 23.4 | 23.3 | 24.6 | NS |
| 30 | 729 | 22.6 | 23.5 | 23.9 | P<0.05 |
| 31 | 568 | 22.1 | 23.7 | 22.4 | P<0.05 |
| * 32 | 689 | 22.9 | 24.6 | 23.8 | P<0.01 |
| 33 | 738 | 23.4 | 23.2 | 24.0 | NS |

Table 2: Intercepts, slopes, standard errors (Std. err.) and p-values from the linear regression analysis (GLM, from the SAS system) performed on the pooled residuals of the median lengths, the Q25's and the Q75's, from the subsamples of *P. borealis* taken from catches in NAFO-division 1B, November 1990.

| | residual median length | residual Q25 | residual Q75 |
|-----------|------------------------------|-----------------|-----------------|
| Intercept | 0.003 +-0.105 | 0.002 +-0.059 | 0.059 +-0.070 |
| Slope | -0.015 +-0.049 | -0.001 +-0.027 | -0.030 +-0.032 |
| P-value | 0.975 - | 0.978 - | 0.364 - |

Table 3: The median of the residual of the median length, the median of the residual of the 25% percentile (Q25), the median of the residual of the 75% percentile (Q75) and the p-values from the non parametric one-way varians analysis (NPAR1WAY median score test from the SAS system, SAS Institute Inc., 1988.) performed on the pooled material of subsamples of *P. borealis* from trawl catches from NAFO division 1B, November 1990.

| median of the residual | subsample | | | P-value |
|------------------------------|-----------|-------|-------|---------|
| | (1) | (2) | (3) | |
| length | 0.03 | -0.07 | 0.00 | 0.43 NS |
| Q25 | 0.05 | -0.07 | -0.03 | 0.76 NS |
| Q75 | 0.10 | -0.07 | 0.02 | 0.08 NS |

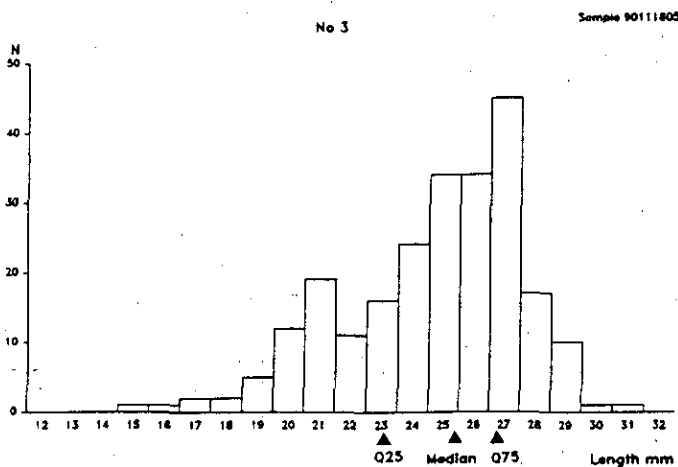
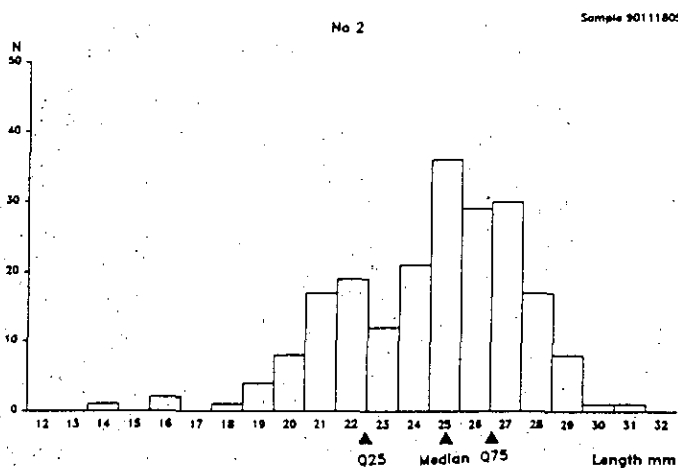
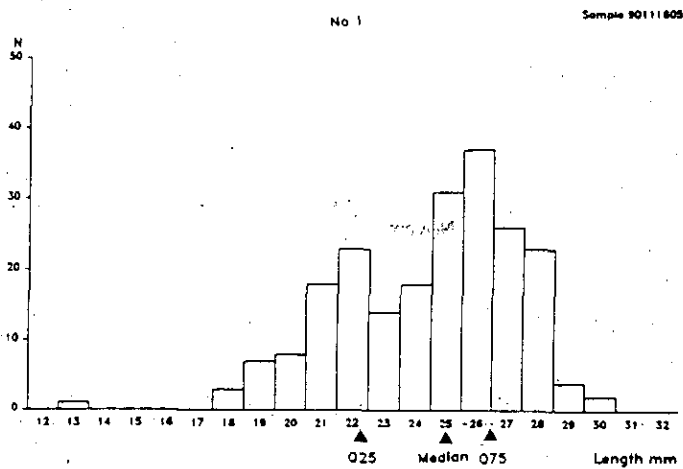


Figure 1: The median length, the 25% percentile (Q25) and the 75% percentile (Q75) for three subsample from a random catch of *P. borealis* taken from the hatch during a survey in NAFO division 1B, November 1990. (Sample 90111805).
Median mm: (1) 25.0 (2) 25.1 (3) 25.4. Q25 mm: (1) 22.3 (2) 22.5 (3) 23.2.
Q75 mm: (1) 26.6 (2) 26.7 (3) 26.9.

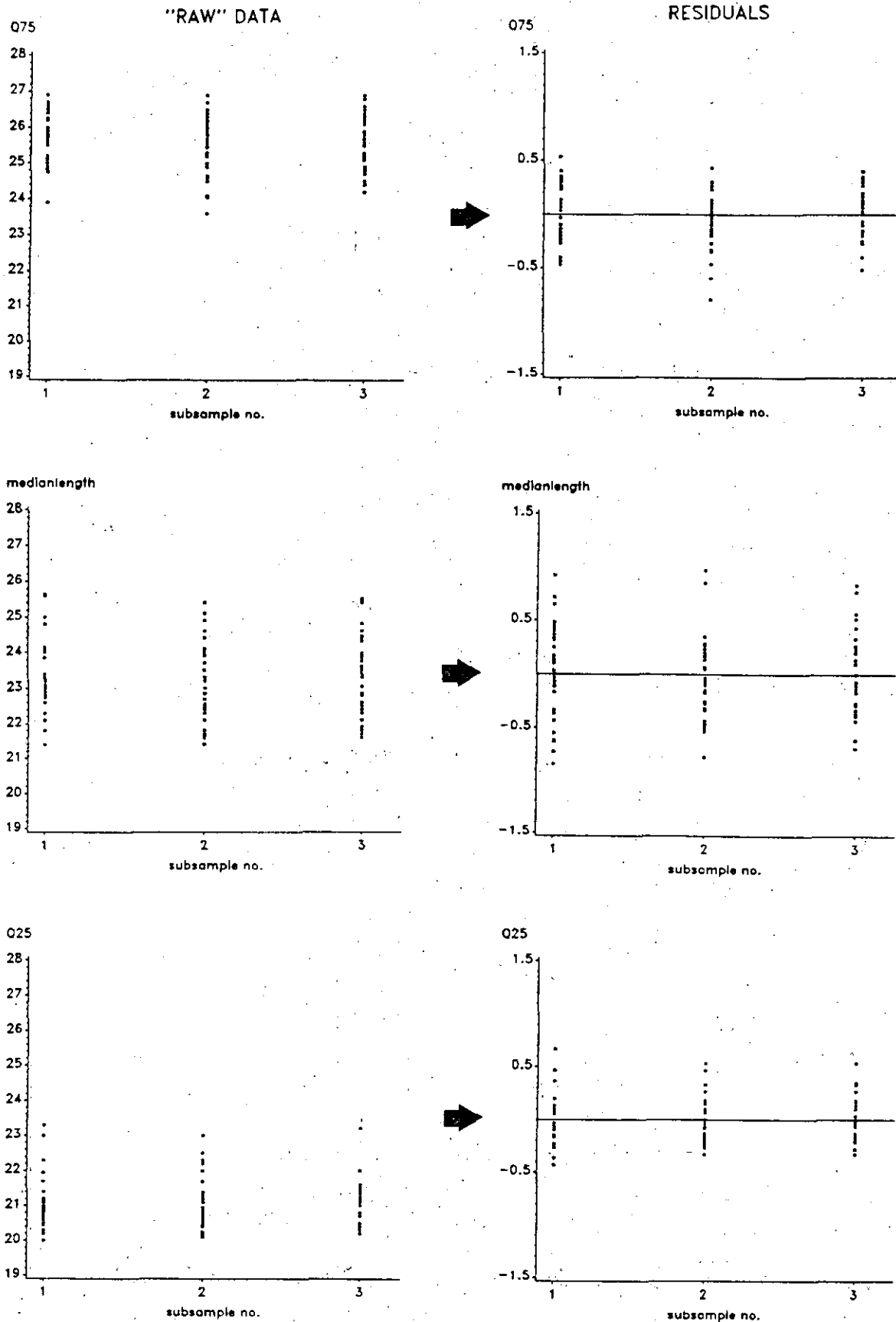


Figure 2: (Left) The median length (carapace length in millimeter), Q25 and Q75 for each haul plotted against the subsample number. (Right) The residual values for the median length, Q25 and Q75 for each haul plotted against the subsample number.