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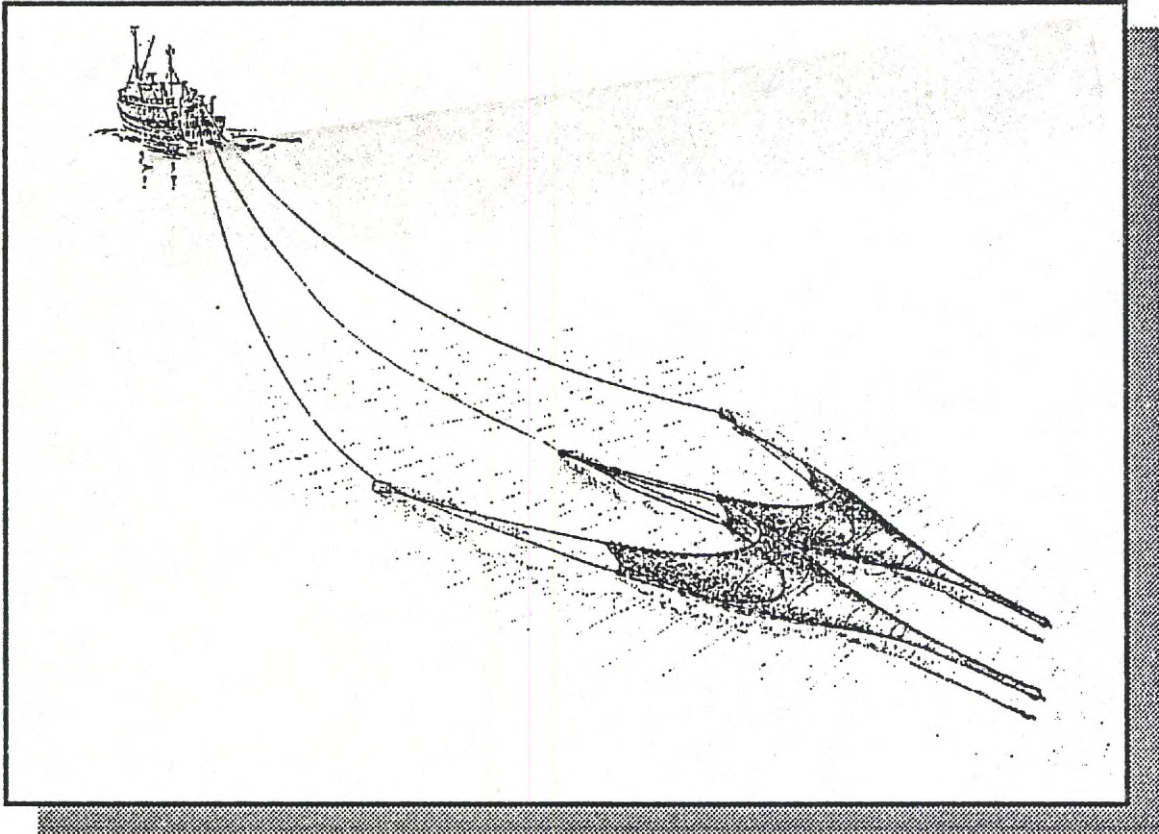
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**SQUARE AND DIAMOND MESH TRAWL CODEND
SELECTION ON *NEPHROPS NORVEGICUS* (L.),
WITH THE CURVE-FIT METHOD
ISOTHONIC REGRESSION**

By

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Lars Ulmestrand

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**SQUARE AND DIAMOND MESH TRAWL CODEND
SELECTION ON *NEPHROPS NORVEGICUS* (L.),
WITH THE CURVE-FIT METHOD
ISOTHONIC REGRESSION**

**(SELEKTION AV HAVSKRÄFTA (*NEPHROPS NORVEGICUS* (L.)), VID
TRÅLNING MED KVADRAT RESP DIAGONALMASKA I STRUTEN,
ANALYSERAT MED
KURVANPASSNINGSMETODEN ISOTON REGRESSION)**

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SAMMANFATTNING

Under 1980-talet har det skett en kraftig ökning av trålfisket efter havskräfta i Skagerrak och Kattegatt. Med den havskräftetrål som används i Sverige (70 mm diagonalformad maska i struten) fångas en stor andel undermåliga kräftor (< 130 mm totallängd). Dessa kräftor slängs tillbaka i havet och man räknar med att 75 % av dem dör. Ett sätt att trygga ett långsiktigt fiske efter havskräfta är att minska fångstandelen undermåliga kräftor, eller med andra ord, minska trålstrutens selektionsbredd. Förutsättningen är att undermåliga kräftor överlever då de passerat genom en trål under fiske. Genom att använda en annan maskform i trålstrutarna skulle man kunna få en trål som släpper igenom en större andel undermåliga kräftor. En tidigare undersökning på havskräfta indikerar att en trålstrut med kvadratmaskor har bättre selektivitet än en trålstrut med diagonalmaskor.

Vi har undersökt selektiviteten av havskräfta hos den havskräftetrål som används i Sverige idag. Selektionskurva och selektionsparametrar redovisas. Mer än hälften av antalet havskräftor som fångades var undermåliga. Dessutom testade vi om det förekom skillnad i selektionsbredd mellan en trål med 60 mm kvadratmaska och en med 70 mm diagonalmaska i struten. Vårt resultat tyder på att det inte är någon signifikant skillnad i selektionsbredd. Därmed skulle inte ett byte till en 60 mm kvadratmaskig trålstrut vara ett sätt att minska fångstandelen undermålig kräfta.

Hittills mest använda metoder att anpassa en selektionskurva till observerade värden har flera brister. I denna undersökning används kurvanpassningsmetoden isoton regression, oss veterligen inte tidigare använd i fiskeribiologiska sammanhang. Metodens för- och eventuella nackdelar diskuteras.

ABSTRACT

With a twin trawl the selectivity of *Nephrops* in the *Nephrops* trawl used in Sweden today (70 mm codend mesh size) was investigated. Selectivity parameters are presented. More than half of the number of *Nephrops* were undersized in this trawl. In addition any difference in selection range between 60 mm square mesh codend trawl and 70 mm diamond mesh codend trawl was tested. Our results indicate that there is no significant difference in selection range. Most used methods of fitting a selection curve to observed values have several disadvantages. In this experiment we use the curve-fit method isotonic regression, to our knowledge previously not used in fisheries biological contexts. Advantages and possible disadvantages of the method are discussed.

INTRODUCTION

Trawl fishing catches of Norway lobster, *Nephrops norvegicus* (L.), in Skagerrak and Kattegat have increased during the 1980's, from 2700 tons in 1980 to 4400 tons in 1990. This is due to: trawl limit being moved inwards, an increase in the number of *Nephrops* trawlers, new electronic equipment making it possible to trawl in partly rocky bottom areas and the trawlers are increasingly equipped with a twin trawl instead of a single trawl (M. Ulmestrand, pers. comm.). It is difficult to estimate the sizes of the populations and TAC's are not practiced.

With the smallest permissible mesh size in the codend (70 mm diamond mesh), a large number of undersized *Nephrops* (<130 mm total length, which corresponds to < about 40 mm carapace length) are caught. From the assessments made in the North Sea, 75% of undersized discarded *Nephrops* are believed to die (Anon. 1990a). One way to ensure long term fishing of *Nephrops* is to reduce the proportion of undersized *Nephrops*, on condition that undersized *Nephrops* passing through a trawl survive.

Experiments with square mesh (for definition see Robertson and Stewart 1988) codends have been conducted for a long time. This has been done to reduce the proportion of undersized catch and to reduce undesired by-catch. In fish experiments 50% selection length (L₅₀) is usually less with square mesh codends compared with diamond mesh codends of the same mesh size (Isaksen and Valdemarsen 1986; Robertson 1983; Robertson and Stewart 1988). Since L₅₀ can be adjusted to the desired length by changing the mesh size, the selection range (SR=L₇₅-L₂₅) is particularly interesting in experiments with the object to reduce the proportion of undersized *Nephrops*. The less SR the lesser proportion of undersized *Nephrops*, at a certain L₅₀. Robertson and Stewart (1988) show that with haddock square mesh codend has less SR than diamond mesh codend; with whiting they found no difference. Robertson *et al.* (1986) indicate that with *Nephrops* square mesh codend have lesser SR than diamond mesh codend.

It is a problem to draw a selection curve from observed proportion retained values. To draw the curve by hand is a simple method but unfortunately also subjective; two persons draw different curves from the same values. Objective methods to draw a selection curve therefore have an advantage. Up to now, objective methods most in use assume a symmetric selection curve. A symmetric curve can be described with a logistic function (logit model) or a cumulative normal distribution function (probit model) (Holden 1971; Pope *et al.* 1975). Two methods of calculating the constants for a logistic function are linear regression of logit transformed proportion retained values (Charuau 1979), and a maximizing procedure (for instance iteratively reweighted least squares) to obtain a maximum likelihood estimation (as in Millar and Walsh 1990). Logit transforming can not be carried out when proportion retained =0 and ≥1; these values must be excluded when calculating the selection curve. Holden (1971) states that there does exist data indicating that a selection curve is not necessarily symmetric. It is a disadvantage that some proportion retained values must be excluded, and also a disadvantage to be restricted to a certain function. Isotonic regression is an objective method, to our knowledge not yet used in fisheries biological contexts, that uses all values when calculating the selection curve and that is not restricted to a certain function. We have used isotonic regression in our experiment.

The objects of this experiment were to compare SR between a trawl with a square mesh codend and the *Nephrops* trawl used in Sweden today (70 mm diamond mesh codend), and to estimate selection parameters for this trawl.

MATERIALS AND METHODS

The data collection was carried out on a commercial stern trawler, GG 55 "Rokard", of length 12.0 m and engine power 2*272 hp.

The twin trawl method was used (Anon. 1990b). We assume that with random variation the same number of *Nephrops* of each length class are entered in each of the two codends, *i.e.* a 50:50 split. Measures and materials of the trawl included in the twin trawl are shown in Fig. 1. The footrope was 27.4 m long and was furnished with plastic bobins and rubber discs.

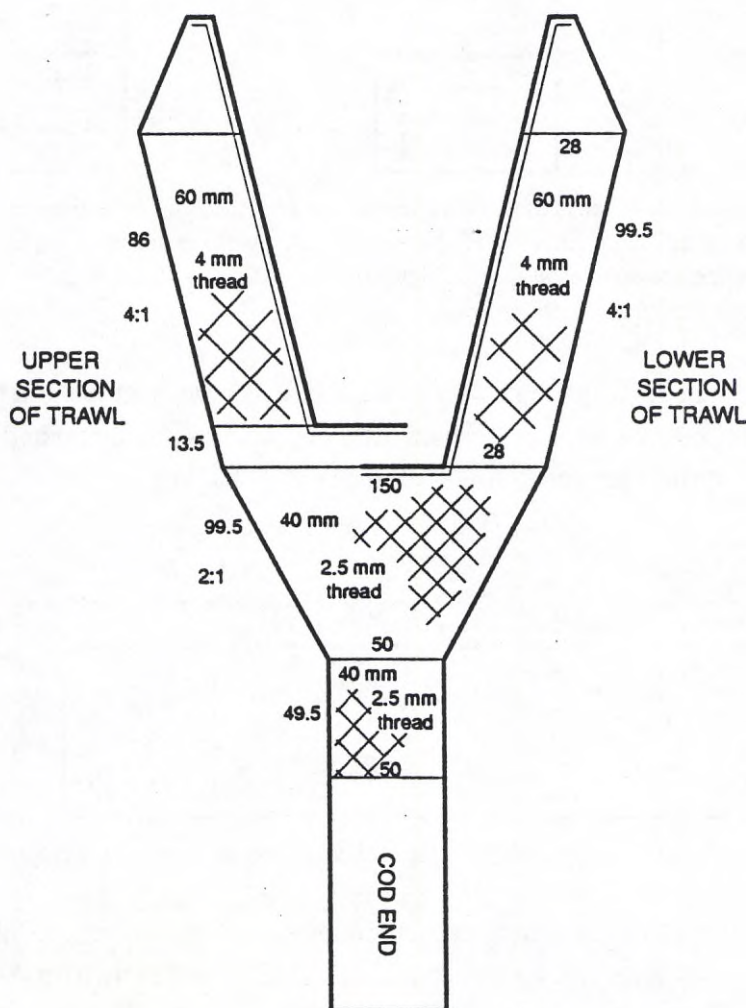


Figure 1. The trawl used in the experiment. The net was knotted and made of single, braided polypropylene (PP) twine. The twine diameter varied according to the figure. The lengths of the different parts of the trawl are given as number of meshes and the degree of tapering with colon in between. The mesh sizes are given as bar length, *i.e.* length between knots.

At half of the hauls a 70 mm diamond mesh codend was used in one trawl and a small mesh diamond mesh codend in the other. With other hauls a 60 mm square mesh codend was used in one trawl and a small mesh diamond mesh codend in the other (Fig. 2). The trawl with small mesh codend is assumed to catch all *Nephrops* in the range L25-L100. The test coden (70 mm diamond and 60 mm square) were shifted during the experiment between starboard and port trawls to eliminate any differences in catching power of the trawls.

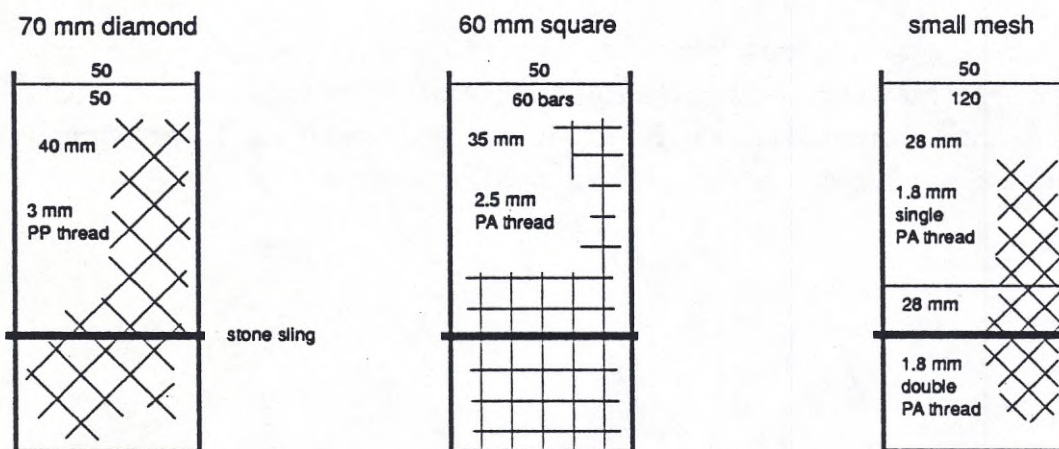


Figure 2. Measures and materials in the codends used. All codends were 8 m long. The mesh sizes are given as bar length. The twine was made of PP in 70 mm diamond and polyamide (PA, nylon) in the other codends. In the end of the small mesh codend the twine was double, otherwise single. The stone sling prevented boulders from entering the codend and thereby destroying trawl and catch.

The mesh sizes in the codends (MS) were measured with an ICES mesh gauge at a pressure of 4 kg. Measurements of wet meshes were performed after hauls at the beginning and end of the experiment. A total of 40 meshes per mesh size were measured (Table 1).

Mesh name	Bar length	Single/double twine	Average MS	SE	Range
70 mm diamond	40	single	68.6	1.5	65 - 70
60 mm square	35	single	61.6	1.5	58 - 64
Small mesh 1	28	single	54.0	1.1	51 - 56
Small mesh 2	28	double	38.3	1.1	36 - 41

Table 1. Codend mesh data. Bar length, average MS, SE (standard error) and range are given in mm.

From April 22 to May 16 1991, 21 hauls were carried out on *Nephrops* grounds within Swedish fishing zone, north of Väderöarna in Skagerrak (position 58°31' - 58°43' N, 10°53' - 11°00' E), and north of Nidingen in Kattegat (position 57°23' - 57°27' N, 11°44' - 11°48' E) (Fig.3). The trawling was performed during the evening, night and morning at depths of 35-75 m and at a speed of 2-3 knots. Each haul lasted for 2.5 - 4.5 h.

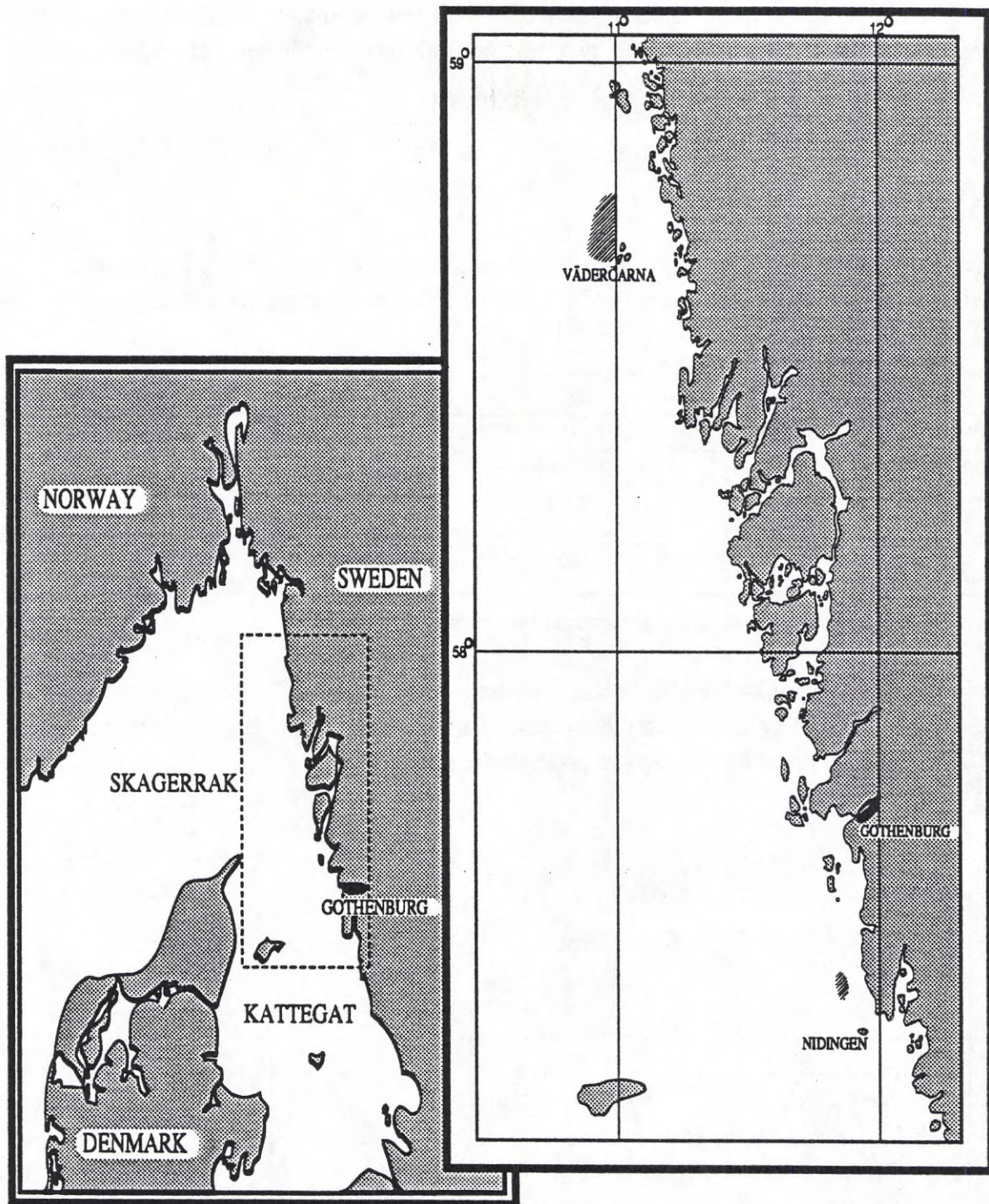


Figure 3. Areas trawled during the experiment (indicated with hatched area).

After each haul the catch was sorted in *Nephrops* above and below minimum landing size and weighed. Normally the whole catch was measured, but at large catches the catch was divided and half or a third of the catch was measured. *Nephrops* carapace length was measured with caliper and grouped in mm length classes.

All of the 70 mm diamond mesh hauls were combined and treated as one haul. The same was done with 60 mm square mesh. Estimations of their selection curves, including L50, selection factor ($SF = L50/MS$) and SR, were calculated using isotonic regression (see appendix, moment I).

We obtained margins of error of the selection ranges estimations by simulations of 100 selection ranges per test codend (see appendix, moment II). With this simulation significant test of difference ($p < 0.05$) in SR between the two test codends was conducted (see appendix, moment III).

RESULTS

The catch in the trawls (*Nephrops*, fish, sea urchins, sediments etc.) was about 50-200 kg per trawl and haul. Number of *Nephrops* measured and estimation of the selection parameters are given in Table 2.

Mesh name	Number of hauls	Number of Nephrops	L50 (mm)	SF	SR (mm)
70 mm diamond small mesh	10	6415	26.4	0.385	11.5
60 mm square small mesh	11	4696	40.1	0.660	13.4
		10651			

Table 2. Number of *Nephrops* measured and estimations of the selection parameters.

In terms of number, the proportion of undersized *Nephrops* was 59% in the 70 mm diamond mesh codend. The corresponding number in the 60 mm square mesh was 45%. Length distribution curves and selection curves for the two test codends are shown in Figs. 4-6.

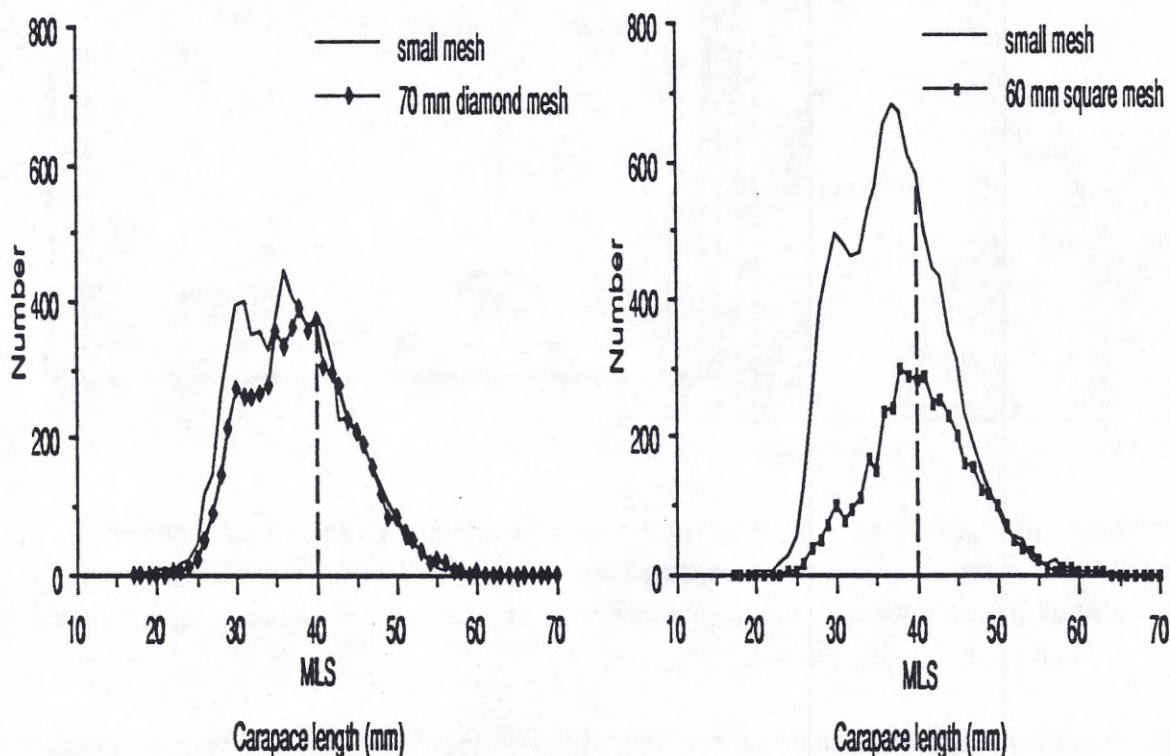


Figure 4. Length distribution curves for 70 mm diamond mesh and 60 mm square mesh. MLS = Minimum legal landing size.

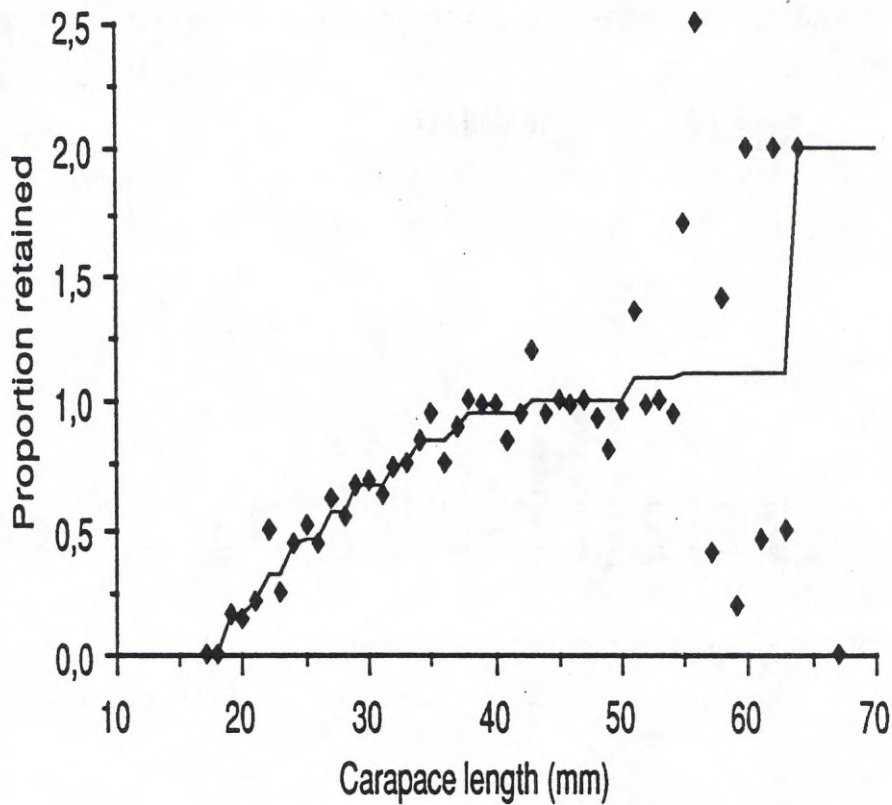


Figure 5. Selection curve for 70 mm diamond mesh, calculated using isotonic regression.

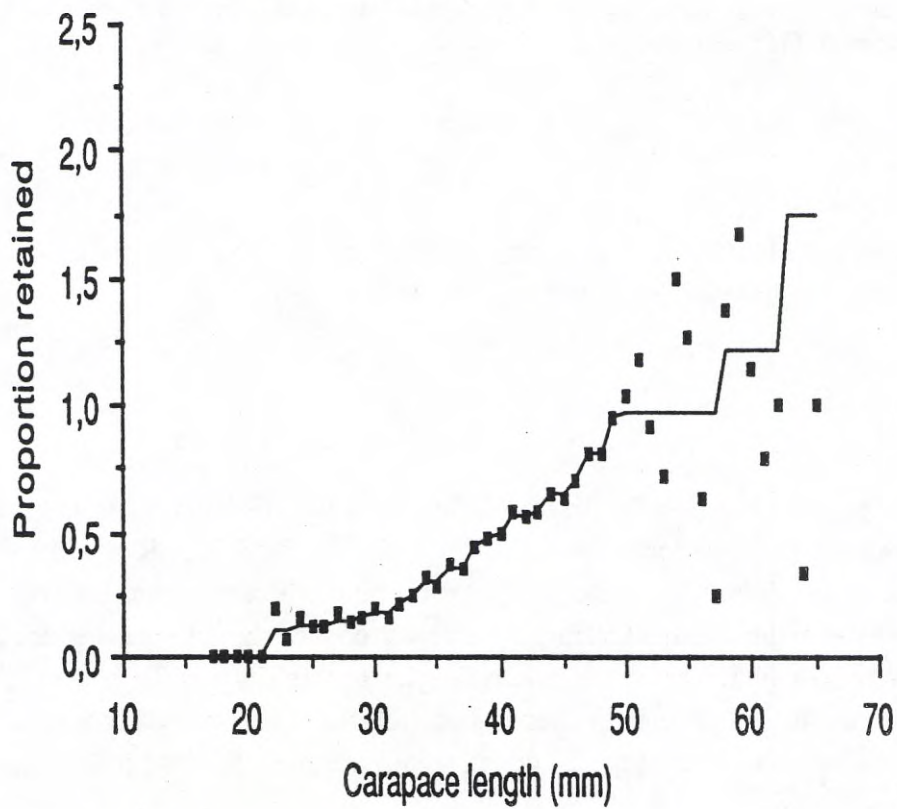


Figure 6. Selection curve for 60 mm square mesh, calculated using isotonic regression.

Results of selection range simulation as a measure of the margin of error in the estimations are shown in Fig. 7 and Table 3.

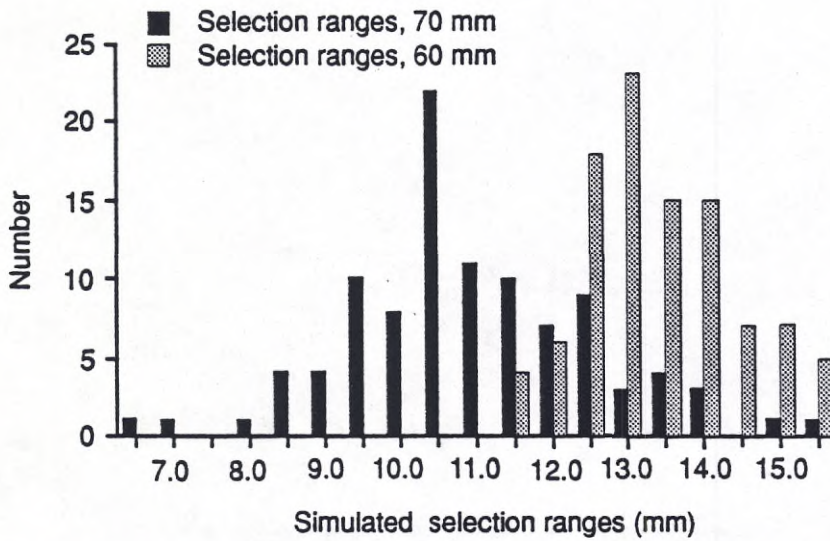


Figure 7. Distributions of simulated selection ranges of the two test codends. The distributions are obtained from simulations of the estimated selection curves in figure 6 and 7 (see appendix, moment II).

Mesh name	Estimated SR	Margin of error of estimation
70 mm diamond	11.5	7.5 - 14.5
60 mm square	13.4	11.6 - 15.5

Table 3. Estimations of SR and 95 % range of simulated selection ranges of the two test codends as a measure of the margin of error in the estimations. The unit is mm.

There was no significant difference in SR ($p < 0.05$) between 70 mm diamond mesh and 60 mm square mesh codend.

The captain of the fishing vessel observed a larger proportion of meshed *Nephrops* in the square mesh codend compared to the diamond mesh codend.

DISCUSSION

The selection parameters found in works by Briggs (1984) and others (Robertson *et al.* 1986; Nicolajsen 1988) show a weak correlation between SR and L50 (Fig. 8). Since SR may depend on L50 we wanted to compare SR between two codends with similar L50. On basis of L50 values in Robertson *et al.* (1986) we estimated that a 60 mm square mesh codend should have similar L50 as a 70 mm diamond mesh codend. However, our results suggest there is a large difference in L50. It is thus necessary to be careful when comparing SR. It is possible that a square mesh codend with L50 corresponding to L50 of the diamond mesh codend would have less SR than the diamond mesh codend.

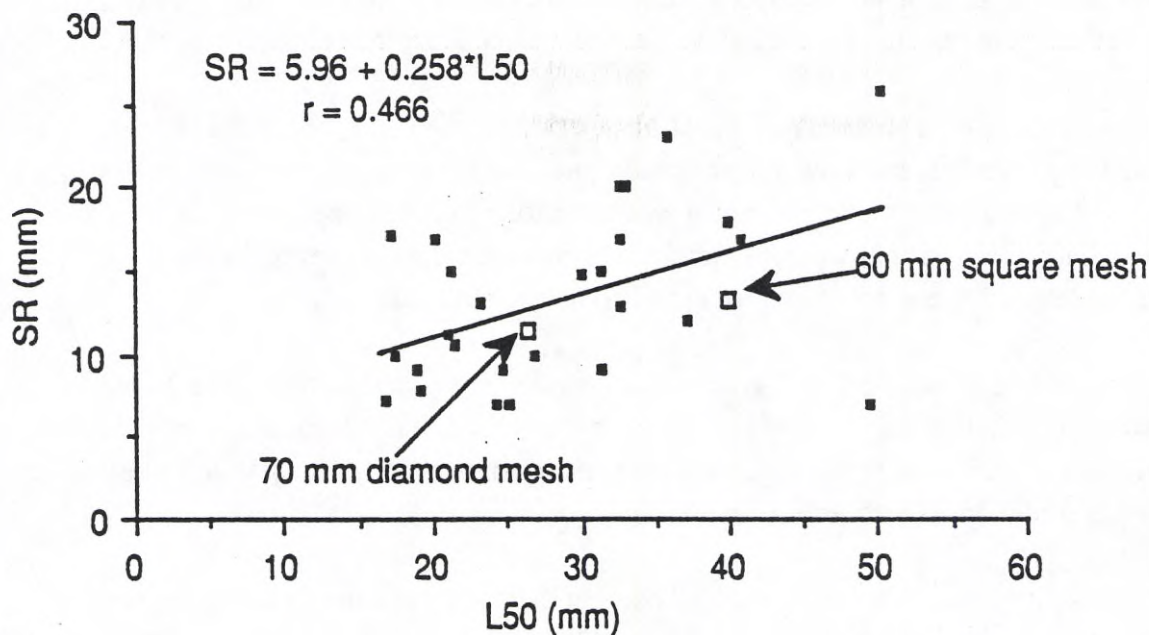


Figure 8. Connection between SR and L50 (based on Briggs 1984, and others). r show coefficient of correlation. Our estimations are shown in the figure.

Pope *et al.* (1975) recommend MS in small mesh codend not to exceed 50% of MS in test codend. Unfortunately we were not able to follow this recommendation. It is therefore possible that the small mesh codend did not catch all *Nephrops* in range L25-L100, contrary to what we assumed. If that is the case, then L50 is actually somewhat higher than obtained L50 values. L50 may have been underestimated in the 70 mm diamond mesh codend, which has the lowest L50.

A condition of isotonic regression is that with random variation an equal amount of *Nephrops* of each length class enter the test codend as the small mesh codend, *i.e.* a 50:50 split. This can be examined by comparing catch of large *Nephrops*, since these *Nephrops* are not able to escape through the test codend or the small mesh codend. The above condition may not be applicable in two codends with different water resistance due to the different water flows (Pope *et al.* 1975). Another method (Millar and Walsh 1990) is not restricted to a 50:50 split, but is instead restricted to a logistic function. The length distribution curves (Fig. 4.) show that the assumption of a 50:50 split was probable in our experiment.

The large variation of the proportion retained values at carapace length > 50 mm, in Fig. 5 and 6, is due to the fact that there are few *Nephrops* caught in these length classes. When few *Nephrops* are caught the importance of chance increases, which in this case leads to large variations of proportion retained.

Our selection curves, obtained through isotonic regression, seem improbable at carapace length > 55 mm. This is due to the influence of chance when the calculation is based on a small number of *Nephrops*. However, the shape of this part of the curve does not affect the result of the three selection parameters. If the curve is based on a considerably smaller number of *Nephrops* than in our experiment L75 may be estimated too highly. At carapace length < 25 mm there are also small numbers of *Nephrops* per length class, but the calculation of this part of the curve is also based on all length classes > 25 mm (see appendix, moment I).

We consider isotonic regression to be an appropriate curve-fit method. The method is objective, not restricted to a certain function and uses all values when calculating the curve.

The simulation moment is not necessary. It is possible to calculate selection parameters for each haul and then do a parametric test. However, the condition is that the selection parameter values from the hauls show normal distribution, which was not fulfilled in our experiment. To avoid using a weaker non-parametric test we made simulations from the values of the combined hauls. We were thus able to calculate the margins of error and do a significance test.

The trawl used in Sweden today has bad selectivity properties for undersized *Nephrops*. In our experiment more than half of the *Nephrops* caught were undersized. It is therefore important to use more selective gears. However, our study does not give any information as to what such a gear should look like, and more experiments are necessary.

If there are to be further experiments comparing SR between diamond and square mesh we suggest that meshes with more similar L50 are used, for instance 70 mm diamond mesh and about 45 mm square mesh.

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Appendix

ISOTONIC REGRESSION (Moment I)

The curve-fit method isotonic regression (Barlow et al. 1972) is based on the only assumption that the expected proportion retained value (q_i , see below) increases or is even as carapace length (i) increases. Thus the method is not restricted to an increase of q_i according to a certain function, such as a logistic function.

The parameters q_i and p_i are the exact values from nature, values we will never be able to know precisely but which we will try to estimate as accurately as possible from observed values.

$$q_i = \frac{\text{expected number of Nephrops with length } i \text{ in test codend}}{\text{expected number of Nephrops with length } i \text{ in small mesh codend}}$$

According to the assumption above, q_i increases with length i , i.e. $q_1 \leq q_2 \leq \dots \leq q_N$.

$$p_i = \frac{q_i}{(1 + q_i)} = \frac{\text{expected number of Nephrops with length } i \text{ in test codend}}{\text{expected number of Nephrops with length } i \text{ in both codends together}}$$

p_i will always get values from 0 up to 1, but it is expected that p_i will increase from 0 to 0.5 as length i increases. Since q_i increases with length i , p_i will also increase, i.e. $p_1 \leq p_2 \leq \dots \leq p_N$.

p_i values are to be estimated in such a way so the estimates are increasing with increasing carapace length. The p_i estimates, here called \hat{p}_i , are plotted to carapace length. From this curve it is possible to calculate estimates of expected proportion retained (q_i) and draw a selection curve. The selection parameters are given from the selection curve. The estimated selection curve is a maximal likelihood estimation.

One condition of using isotonic regression is that with random variation there is an equal amount of Nephrops of each length class entering each of the two codends, i. e. a 50:50 split.

The method to estimate p_i is described below.

Example

Suppose we have the following data :

i	30	31	32	33	34	35	36	37	38	39	40
x_i	1	0	0	1	2	2	2	3	2	2	0
n_i	1	3	5	5	8	6	5	5	4	3	1

x_i = observed number of Nephrops with length i in test codend

n_i = observed number of Nephrops with length i in both codends together

The smallest Nephrops was thus 30 mm and was caught in the test codend while the largest, 40 mm, was caught in the small mesh codend.

$$\text{Make } z_k = \frac{\sum_{i=1}^k x_i}{\sum_{i=1}^k n_i} \text{ where}$$

$\sum_{i=1}^k x_i$ = total number of Nephrops in test codend with length not more than k mm, and

$\sum_{i=1}^k n_i$ = total number of Nephrops in both codends together with length not more than k mm

In our example we get :

$$k = 30 : z_{30} = x_{30}/n_{30} = 1/1 = 1.00$$

(more correct $(x_1+x_2+\dots+x_{30})/(n_1+n_2+\dots+n_{30})$)

$$k = 31 : z_{31} = (x_{30}+x_{31})/(n_{30}+n_{31}) = (1+0)/(1+3) = 1/4 = 0.25$$

$$k = 32 : z_{32} = (x_{30}+x_{31}+x_{32})/(n_{30}+n_{31}+n_{32}) = (1+0+0)/(1+3+5) = 1/9 = 0.11$$

$$k = 33 : z_{33} = (1+0+0+1)/(1+3+5+5) = 2/14 = 0.14$$

etc.

i	30	31	32	33	34	35	36	37	38	39	40
x_i	1	0	0	1	2	2	2	3	2	2	0
n_i	1	3	5	5	8	6	5	5	4	3	1
z_k	1.00	0.25	0.11	0.14	0.18	0.21	0.24	0.29	0.31	0.32	0.32

Then choose the k that gives the smallest z_k . In our example the smallest value is $z_{32} = 0.11$.

The p_i estimate, called \hat{p}_i , is given the value minimum z_k for all $i \leq k$. Thus, \hat{p}_{30} , \hat{p}_{31} and $\hat{p}_{32} = 0.11$.

i	30	31	32	33	34	35	36	37	38	39	40
x_i	1	0	0	1	2	2	2	3	2	2	0
n_i	1	3	5	5	8	6	5	5	4	3	1
z_k	1.00	0.25	0.11	0.14	0.18	0.21	0.24	0.29	0.31	0.32	0.32
\hat{p}_i	0.11	0.11	0.11								

x_i and n_i values for length classes shorter than or equal to length k are discarded and new z_k values are calculated :

i	30	31	32	33	34	35	36	37	38	39	40
x_i				1	2	2	2	3	2	2	0
n_i				5	8	6	5	5	4	3	1
z_k				0.20	0.23	0.26	0.29	0.34	0.36	0.39	0.38
\hat{p}_i	0.11	0.11	0.11								

The smallest z_k is now $z_{33} = 0.20$. \hat{p}_{33} becomes 0.20. x_{33} and n_{33} are discarded and new z_k values are calculated. The procedure is repeated until all p_i have been estimated with \hat{p}_i .

i	30	31	32	33	34	35	36	37	38	39	40
x_i					2	2	2	3	2	2	0
n_i					8	6	5	5	4	3	1
z_k					0.25	0.29	0.32	0.38	0.39	0.42	0.41
\hat{p}_i	0.11	0.11	0.11	0.20							
		$\hat{p}_{34} = 0.25$									

i	30	31	32	33	34	35	36	37	38	39	40
x_i						2	2	3	2	2	0
n_i						6	5	5	4	3	1
z_k						0.33	0.36	0.44	0.45	0.48	0.46
\hat{p}_i	0.11	0.11	0.11	0.20	0.25						
		$\hat{p}_{35} = 0.33$									

i	30	31	32	33	34	35	36	37	38	39	40
x_i							2	3	2	2	0
n_i							5	5	4	3	1
z_k							0.40	0.50	0.50	0.53	0.50
\hat{p}_i	0.11	0.11	0.11	0.20	0.25	0.33					
		$\hat{p}_{36} = 0.40$									

i	30	31	32	33	34	35	36	37	38	39	40
x_i								3	2	2	0
n_i								5	4	3	1
z_k								0.60	0.56	0.58	0.54
\hat{p}_i	0.11	0.11	0.11	0.20	0.25	0.33	0.40				
		$\hat{p}_{37} - \hat{p}_{40} = 0.54$									

As written above p_i is expected to increase from 0 to 0.5. In the end of our example \hat{p}_i was >0.5 , a fact that happened by chance. \hat{p}_i as a function of length i is plotted and the dots are connected with straight lines (figure 1).

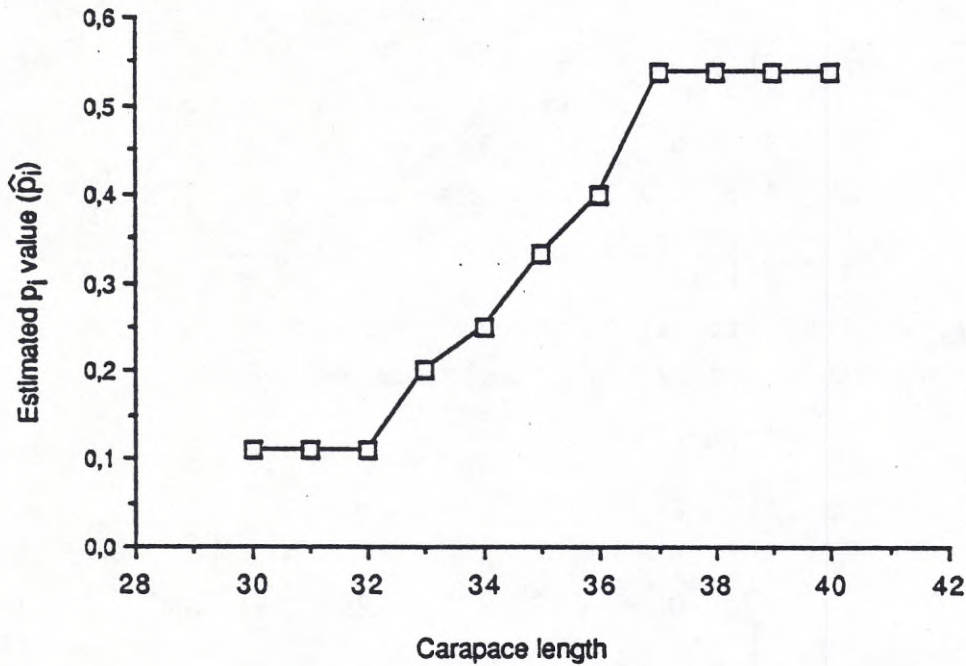


Figure 1. Estimated p_i (\hat{p}_i) value as a function of carapace length.

The selection parameters L25, L50 and L75 can now be read from the graph.

Estimated L25 value is obtained at $q = 0.25$. Then we get

$$\hat{p} = q/(1+q) = (1/4)/(1+(1/4)) = (1/4)/(5/4) = 1/5 = 0.2.$$

The length i at $\hat{p} = 0.20$ is read from the graph.

In a similar way we estimate

$$\text{L50 at } q = 0.5 \text{ and } \hat{p} = 1/3 = 0.33, \text{ and}$$

$$\text{L75 at } q = 0.75 \text{ and } \hat{p} = 3/7 = 0.43.$$

In the example we get the following selection parameters :

$$\text{L25} = 33 \text{ mm}$$

$$\text{L50} = 35 \text{ mm}$$

$$\text{L75} = 36 \text{ mm} \quad \text{SR} = \text{L75} - \text{L25} = 3 \text{ mm}$$

\hat{p}_i can be transformed to expected proportion retained, q_i :

$$q_i = \hat{p}_i / (1 - \hat{p}_i)$$

q_i as a function of length i will give a selection curve. In the same graph observed proportion retained values may be put (figure 2).

observed proportion retained =

$$= \frac{\text{observed number of Nephrops of length } i \text{ in test trawl}}{\text{observed number of Nephrops of length } i \text{ in small mesh trawl}} = \frac{x_i}{(n_i - x_i)}$$

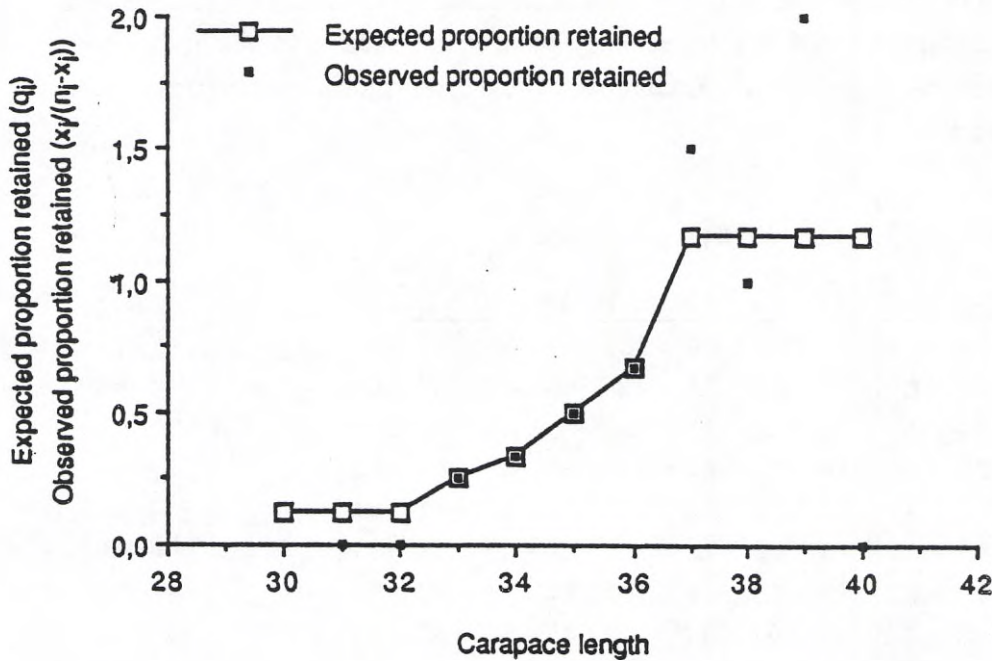


Figure 2. Expected proportion retained (q_i) as a function of carapace length (selection curve) and observed proportion retained ($x_i/(n_i-x_i)$) as a function of carapace length.

SIMULATION (Moment II)

By simulating new selection curves from each of the two estimated selection curves it is possible to get a measure of the margin of error of the estimations of SR. This is used to test significant difference in SR between the two test codends.

We assume that the *Nephrops* individuals enter and pass out through the trawls independent of each other (Poisson distribution). Given n_i and \hat{p}_i , new x_i values are simulated from the binomial distribution. $x_{i,sim}/(n_i-x_{i,sim})$ as a function of i give a simulated selection curve, from which SR are calculated. Hundreds of selection curves should be simulated for each test codend. In this moment a computer is necessary.

SIGNIFICANCE TEST OF DIFFERENCE (Moment III)

Selection ranges from the simulations are used in the significance test. The difference $SR(\text{test codend 1}) - SR(\text{test codend 2})$ is calculated for all combinations of the simulations. The differences are sorted in order of size. With 5% level of significance ($p < 0.05$), the middle 95% range of the differences is indicated. If there are only positive or negative values in the range there is significant difference ($p < 0.05$) in SR. Otherwise there is no significant difference in SR (see example in figure 3).

		SR (test codend 1)									
		8.5	9.4	9.6	9.9	10.2	11.4	12.0	12.1	13.1	
SR (test codend 2)	7.1	1.4	2.3	2.5	2.8	3.1	4.3	4.9	5.0	6.0	← largest 2.5% of the differences
	7.4	1.1	2.0	2.2	2.5	2.8	4.0	4.6	4.7	5.7	
	7.4	1.1	2.0	2.2	2.5	2.8	4.0	4.6	4.7	5.7	
	7.8	0.7	1.6	1.8	2.1	2.4	3.6	4.2	4.3	5.3	
	7.9	0.6	1.5	1.7	2.0	2.3	3.5	4.1	4.2	5.2	● middle 95% range of the differences
	8.0	0.5	1.4	1.6	1.9	2.2	3.4	4.0	4.1	5.1	
	8.3	0.2	1.1	1.3	1.6	1.9	3.1	3.7	3.8	4.8	
	8.9	-0.4	0.5	0.7	1.0	1.3	2.5	3.1	3.2	4.2	→ smallest 2.5% of the differences
	9.0	-0.5	0.4	0.6	0.9	1.2	2.4	3.0	3.1	4.1	

Figure 3. Example in calculating differences between simulated selection ranges from two test codends. 9 simulations per test codend are described, but as a total hundreds of simulations per test codend should be carried out. The middle 95% range of the differences are shown. In this example there is no significant difference in SR.

REFERENCE

Barlow, R.E., Bartholomew, D.J., Bremner, J.M. and Brunch, H.D. 1972. Statistical inference under order restrictions. The theory and application of isotonic regression. John Wiley & Sons Ltd, London, New York, Sydney, Toronto, 390 pp.

