

Abstract—Although subsampling is a common method for describing the composition of large and diverse trawl catches, the accuracy of these techniques is often unknown. We determined the sampling errors generated from estimating the percentage of the total number of species recorded in catches, as well as the abundance of each species, at each increase in the proportion of the sorted catch. We completely partitioned twenty prawn trawl catches from tropical northern Australia into subsamples of about 10 kg each. All subsamples were then sorted, and species numbers recorded. Catch weights ranged from 71 to 445 kg, and the number of fish species in trawls ranged from 60 to 138, and invertebrate species from 18 to 63. Almost 70% of the species recorded in catches were “rare” in subsamples (less than one individual per 10 kg subsample or less than one in every 389 individuals).

A matrix was used to show the increase in the total number of species that were recorded in each catch as the percentage of the sorted catch increased. Simulation modelling showed that sorting small subsamples (about 10% of catch weights) identified about 50% of the total number of species caught in a trawl. Larger subsamples (50% of catch weight on average) identified about 80% of the total species caught in a trawl.

The accuracy of estimating the abundance of each species also increased with increasing subsample size. For the “rare” species, sampling error was around 80% after sorting 10% of catch weight and was just less than 50% after 40% of catch weight had been sorted. For the “abundant” species (five or more individuals per 10 kg subsample or five or more in every 389 individuals), sampling error was around 25% after sorting 10% of catch weight, but was reduced to around 10% after 40% of catch weight had been sorted.

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Does the size of subsamples taken from multispecies trawl catches affect estimates of catch composition and abundance?

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Concerns are held worldwide regarding the sustainability of bycatch species taken in trawls, particularly prawn trawls. Under the voluntary FAO Code for Responsible Fisheries, managers are required to “take measures to conserve target species, associated or dependent species and nontarget species and their environment” (FAO, 1995). An essential part of this process is the accurate monitoring of population sizes and structures.

With large trawl catches, subsampling is often the only cost-effective or feasible way to describe the bycatch composition. How well these subsamples represent the total catch depends on how diverse the catch is, how well the catch is mixed before the subsamples are taken, and what proportion of the catch is taken as a subsample.

There is a large literature on subsampling theory for terrestrial insect studies (Van Ark and Meiswinkel, 1992), aquatic macroinvertebrate studies (Vinson, 1996; Walsh, 1997), and marine ecological studies (Andrew and Mapstone, 1987). However, in most of these studies, samples of very small animals collected in the field can be resuspended in fluid and mixed evenly in the laboratory before the subsam-

ples are taken. In fisheries, in direct contrast, large catches are extremely difficult to manipulate and redistribute evenly before subsampling. A few fisheries studies have examined the impact of subsampling on estimates of the abundance and different size ranges of one or a few dominant species. For example, in the *Crangon* trawl fisheries in Belgian waters, sampling strategy had only a minor effect on the reliability of estimates of size selectivity for the targeted shrimp (Polet and Redant, 1999). In UK waters, subsampling trawled fish (both target species and discards) from either the sorting conveyor or the pound made no difference to catch composition estimates (Tamsett et al., 1999).

However, in tropical trawl fisheries, over one hundred species can be recorded in a single catch. Under ESD (ecological sustainable development) guidelines, all these species (both target and bycatch) are equally important but there has been very little research on subsampling techniques applicable to such diverse catches. A recent study in Australia’s Northern Prawn Fishery (NPF) examined the accuracy of subsampling from large, diverse catches of fish and invertebrates (Heales et al., 2000). For most of the “abundant”

species, their position on trawler sorting trays from which the bycatch subsamples were collected, had little effect on the accuracy in representing the catches.

Although the accuracy of subsampling is a general problem for all multispecies fisheries, few other studies have been published on the topic. Reliable techniques for subsampling are needed, however, especially with the demands that bycatch species, as well as the target species, should be ecologically sustainable. We describe here research done in Australia's NPF but the results and methods are applicable to many sampling problems in fisheries.

The NPF is a large tropical trawl fishery that extends from Cape York in Queensland to Cape Londonderry in Western Australia. In addition to catching penaeid prawns (e.g. 8531 metric tons (t) in 1997–98, Taylor and Die, 1999), its bycatch component is estimated at over 38,000 t a year (Pender et al., 1992) or more than 80% of the total catch in the tiger prawn fishery (Brewer et al., 1998). The neighboring Torres Straits Prawn Fishery (TSPF) also has an estimated annual bycatch of 4800 t (Williams, 1985).

The NPF has a management requirement to assess the impact of trawling on nontarget species. The bycatch of both these prawn trawl fisheries (NPF and TSPF) is very diverse. Ramm et al. (1990) recorded 115 fish taxa in their study of NPF waters, and Brewer et al. (1998) recorded over 250 species from one area of the NPF. At least 390 fish species, 234 invertebrate taxa, and 43 elasmobranch species have been recorded in a current bycatch project in the NPF (Stobutzki et al., 2000).

Despite the lack of knowledge on the ability of subsamples to accurately represent such diverse catches, many studies of trawl communities in Northern Australia have used subsampling techniques to estimate catch rates. In two bycatch studies of the NPF, the smaller catches were entirely sorted and the larger catches subsampled (Poiner and Harris, 1986; Harris and Poiner, 1991). Trawl catches in another bycatch study were spread evenly over the sorting tray and a visually estimated fraction of the catch was subsampled (Ramm et al., 1990). Other workers simply subsampled without confirming the accuracy of their subsampling techniques (Blaber et al., 1990 and 1994; Martin et al., 1995; Brewer et al., 1998; Wassenberg et al., 1998).

A lack of knowledge of trawl impacts on nontarget species has led to the present CSIRO study that describes the bycatch from the NPF and provides a framework for any future bycatch monitoring program. As part of that study, we made the first assessment of the accuracy of subsampling over a range of subsample sizes as a tool for estimating the total catch composition of a large multispecies fishery.

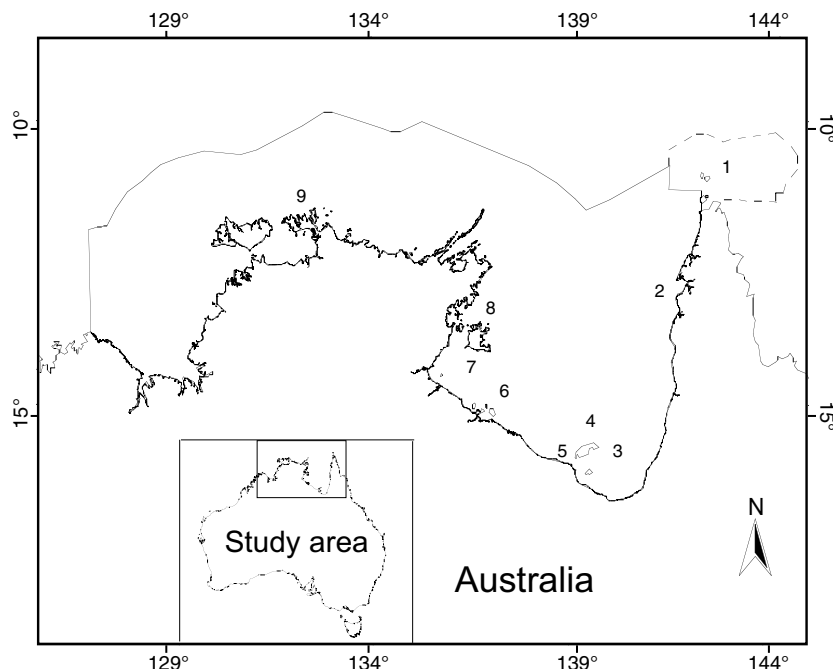


Figure 1

Map of the Torres Straits Fishery (area 1—broken line) and Northern Prawn Fishery (unbroken line), Australia, showing the managed area of the fisheries and the regions where samples were collected. Regional codes are 1 = Torres Straits, 2 = Weipa, 3 = east of Mornington Island, 4 = north of Mornington Island, 5 = west of Mornington Island, 6 = east of Vanderlin Islands, 7 = south of Groote Eylandt, 8 = north of Groote Eylandt, 9 = Melville Island.

Materials and methods

Data were collected from a series of 14 trawl samples taken during two research cruises of the RV *Southern Surveyor*. These samples were collected from one region of the Torres Straits Prawn Fishery (TSPF), and from eight of the major tiger prawn (*Penaeus esculentus* and *P. semisulcatus*) fishing regions of the Northern Prawn Fishery (NPF), (namely Weipa, east of Mornington Island, north of Mornington Island, west of Mornington Island, north of Vanderlin Islands, south of Groote Eylandt, north of Groote Eylandt, and Melville Island) (Fig. 1). All trawls were undertaken in either late summer 1997 (February–March, the end of the wet season) or in mid-spring 1997 (September–October, the dry season). We used a single 14-fathom Florida-Flyer prawn trawl net so that the data would be comparable with data from either of the two nets used by the twin-rigged commercial NPF vessels in the tiger prawn fishery. All trawls were done at night, again to be comparable with the fishery. Duration of trawls ranged from 1 to 3 hours (Table 1), and depths ranged from 23 to 42.3 m.

A further six trawl catches were sampled by a scientific observer on board commercial NPF vessels fishing for tiger prawns north of Mornington Island in late May 1997, and north of Groote Eylandt in late September 1997. Each trawl sample consisted of the entire catch from one of the two 14-fathom Florida-Flyer prawn trawl nets used by these vessels. All trawls were done at night. Their duration

Table 1

Summary of catch data for 20 entirely sorted trawls from the Northern Prawn Fishery and Torres Straits Prawn Fishery. "Bycatch individuals" refers to the total number of bycatch animals (fish and invertebrates) in each trawl. "Fish species" refers to the total number of fish species recorded in the bycatch of each trawl. (*n*) is the total number.

Region	Duration of trawl (h)	Start time of trawls	Catch weight (kg)	Subsamples (<i>n</i>)	Bycatch individuals (<i>n</i>)	Fish species (<i>n</i>)	Invertebrate species (<i>n</i>)	All species (<i>n</i>)
Torres Straits	1.2	0400	94	9	4151	74	21	95
Weipa	2.7	0220	166	16	4911	92	36	128
East of Mornington Island	1.0	0415	274	24	7313	90	18	108
East of Mornington Island	2.9	0250	87	8	2019	77	45	122
North of Mornington Island	3.3	1845	182	16	9762	101	36	137
North of Mornington Island	3.0	2215	194	17	11015	94	42	136
North of Mornington Island	3.2	1840	445	36	13,826	114	52	166
North of Mornington Island	2.0	0350	71	7	1771	60	30	90
North of Mornington Island	2.2	0330	100	10	5067	77	34	111
West of Mornington Island	1.6	0415	174	16	5976	100	21	121
West of Mornington Island	1.7	0400	269	26	6967	87	24	111
North of Vanderlin Islands	2.7	0310	156	15	7182	71	19	90
South of Groote Eylandt	2.0	0345	315	27	23,751	105	25	130
South of Groote Eylandt	2.7	0250	165	17	3856	64	25	89
North of Groote Eylandt	2.5	2230	147	12	5558	68	28	96
North of Groote Eylandt	3.0	0215	85	9	2792	60	34	94
North of Groote Eylandt	3.5	1830	158	13	5664	89	43	132
North of Groote Eylandt	3.5	2215	169	15	8289	96	63	159
North of Groote Eylandt	3.5	2215	189	16	5748	96	43	139
Melville Island	3.0	0130	170	14	4635	60	30	90
Total			3610	323	140,253			

ranged from 3 to 3.5 hours (Table 1), and depths ranged from 29 to 41 m.

Sample collection

On the research vessel, catches were spilled from the codend onto the flat deck (equivalent to the sorting tray on commercial vessels). The entire catch of each trawl was progressively partitioned by shovelling the catch into consecutively numbered boxes (subsample replicates), each of about 10 kg (according to the methods described by Heales et al., 2000). Partitioning of the catch began at the outer edges and continued in a clockwise direction, and subsamples were taken from each of four major compass directions: north, east, south, and west until the entire catch had been collected in successively numbered boxes. The direction of the ship's bow was always designated as north.

Samples on the research vessel were sorted immediately. Fish and invertebrates were identified to the lowest taxonomic level possible (mostly species). Where this was not possible, the data were grouped to genus and in a few cases to family. Total numbers and weights were recorded for each species in each subsample and entered directly into a relational database.

On the commercial vessels, the catches were spilled onto the sorting tray and the commercial-size prawns were removed. The bycatch would then normally move down

a trash chute and spill overboard. However, to sample a catch, the trash chute was diverted so that all the bycatch was collected in consecutively numbered boxes (subsample replicates) each of approximately 10 kg.

All samples collected from commercial vessels were frozen on board and transported to the laboratory for subsequent sorting, identification, and data entry according to the methods described above.

Although most bycatch species were identified to species level, some could only be identified to genus and in a few cases to family. In order to be consistent in terms used throughout this study, we use the term species (plural form) even when referring to multispecies groups.

The methods used to collect subsamples on both the research and commercial vessels differed only in the position from which subsamples were taken (see earlier "Material and methods" section). However, a previously published study (Heales et al., 2000) showed that the majority of the "abundant" bycatch species were evenly distributed throughout the catch. Consequently, for all analyses we combined the 14 catches collected from the research vessel with the six catches from commercial vessels.

Data analysis

Abundance groupings Within each catch, there was a large range of species (both fish and invertebrates) and they

occurred at many different levels of relative abundance. To obtain an overview of how rarely, or how frequently, different species occurred in catches, we reduced each occurrence of a species in a catch to an index of relative abundance. We concentrated solely on determining the accuracy of taking different size subsamples in representing the range of relative abundances (from very low to very high) of the species in these catches.

The relative abundance indices were based on the average number of individuals of a given species that were recorded in a standardized 10-kg subsample taken from that catch. To generate this index, we used the following equation:

$$n = 10 \times (TotNum / Weight), \quad (1)$$

where n = the mean number of individuals of a given species per 10-kg subsample;

$TotNum$ = the total number of individuals of that species in the whole catch; and

$Weight$ = the total weight of the catch in kg.

We derived a separate index of abundance for each species in every catch where it was recorded. Thus, a species that occurred in all 20 catches would have 20 different abundance indices in the analysis.

To highlight the differences in distribution between the two extremes of the “rare” species and the “abundant” species when estimating catch composition, we grouped the indices of abundance into 11 categories, ranging from less than one individual per 10-kg subsample, up to 10 or more individuals per subsample. Species with abundance indices of less than one individual per 10-kg subsample were classed as “rare”; those with one to less than five individuals were classed as “common”; and those with five or more individuals per 10-kg subsample were classed as “abundant.”

For example, the common ponyfish (*Leiognathus moretoniensi*), was classed as “abundant” in 11 of the 20 catches, as “common” in eight catches, and “rare” in one catch. Because a species could have different abundance indices in each catch, individual species are not referred to by name in the results. Instead, we refer to the occurrence of each species in a catch, as one *case* of some relative abundance index that was recorded in that catch (i.e. one “case” of species by trawl abundance). The relative frequency of all the cases (i.e. abundance indices) in each of the three abundance categories (throughout the combined 20 catches) was then calculated.

To calculate the average number of bycatch individuals per 10-kg subsample (over all the catches), the following equation was used:

$$X = 10 \times (Total\ number / Total\ weight) \quad (2)$$

where X = the mean number of bycatch individuals (per 10-kg subsample);

$Total\ number$ = the total number of all bycatch individuals (summed over all 20 catches); and

$Total\ weight$ = the total weight (kg) of all bycatch individuals (summed over all 20 catches).

We then examined the average occurrence ratios within 10-kg subsamples for the “rare,” “common,” and “abundant” species.

Catch composition To examine the relationship between the number of recorded species and the weight of sorted catch, the subsamples were first analyzed in the order that they were collected. The cumulative number of species (both fish and invertebrates) was plotted against the cumulative weight of sorted catch, for each of the 20 catches. Each catch was also summarized in terms of the percentage of species recorded for each 10% increment of weight of sorted catch.

The order (position on the sorting tray) where the subsamples were collected on both the research and commercial vessels was just one of the many possible ways that a catch can be divided into 10-kg subsamples. To determine the level of accuracy in recording the number of species in a catch, we examined 200 combinations of subsample selection (with no replacement), by randomly reordering the subsamples using Monte Carlo simulations for each catch. We also calculated the cumulative number and percentage of species recorded, as well as the cumulative weight and percentage of the sorted catch, for each catch. The proportion of species recorded was fitted as a power function of the proportion of the weight of sorted catch, as described by the following asymptotic equation (Snedecor and Cochran, 1980):

$$y = p^k + \varepsilon, \quad (3)$$

where y = the proportion of species recorded;

p = the proportion of the weight of catch sorted;

k = the mean exponential parameter; and

ε = the random normal error term, with unequal variance.

The variance of ε is assumed to be $p(1-p)\sigma^2$ to ensure that the variance of y is fixed at zero when $p = 0$ and 1. This formulation has the property that, when none of the catch has been sorted, no species will have been recorded. It also ensures that $y = 1$ when $p = 1$, i.e. when all the catch has been sorted, all of the species have been recorded. The estimate of σ^2 was obtained by fitting the following model according to the SAS procedure NLIN (version 7, SAS Inst., Cary NC):

$$y^* = p^k / \sqrt{p(1-p) + \varepsilon^*}, \quad (4)$$

where $y^* = y / \sqrt{p(1-p)}$ and $\varepsilon^* = \varepsilon / \sqrt{p(1-p)}$; and

ε^* now has homogeneous variance structure.

Different k values were estimated for each catch to reflect the variation in the relationship. The mean k_i value for a given catch ($i=1-20$) was obtained from 200 analyses for that catch. The predicted y values i.e. \bar{y}_p (at $p=0.1, 0.2$ etc. to 1.0) were obtained by averaging p^k values across the 20 catches (note that this is different from $p^{\bar{k}}$ where \bar{k} is the mean k value for the 20 catches). We defined the \bar{y}_p values as the predicted expected proportion of species recorded after p proportion of catches had been sorted.

The corresponding 95% confidence interval for the predicted mean values (\bar{y}_p) was evaluated by using the width $1.96 \sigma_m$ where σ_m^2 is the variance of \bar{y}_p given by

$$\begin{aligned} \sigma_m^2 &= V(p^k) + V(\varepsilon) \\ &= (\log(p)\bar{y}_p\sigma_k)^2 + p(1-p)\sigma^2, \end{aligned} \quad (5)$$

where \bar{y}_p = the predicted mean proportion;
 σ^2 = obtained from the mean squared residuals across 20 catches by 200 analyses; and
 σ_k^2 = the estimated variance of k across 20 catches by 200 analyses.

All p and y values are presented as percentages in results.

Abundance estimates The effect of taking different size subsamples, on estimating the total number of a given species in a catch, was determined by using a running mean (of the estimate of abundance) calculated from the equation

$$s = |(n/p - TotNum) / TotNum|, \quad (6)$$

where s = the absolute proportion of sampling error;
 n = the observed number of that species after p proportion (by weight) of the catch has been sorted; and
 $TotNum$ = the total number of individuals of that species in the whole catch.

The values for s are truncated at 1 for ease of presenting results.

We used the following statistical model in which s is subtracted from 1 in order to correspond to the equation used for species composition:

$$1 - s = p^k + \varepsilon, \quad (7)$$

where $1 - s$ is fixed at 1 when $p = 1$, and the $\text{var}(\varepsilon) = (1-p)\sigma^2$ to ensure that there is no sampling error when the entire catch has been sorted.

To obtain estimates of σ^2 , we fitted the following model:

$$(1-s) / \sqrt{(1-p)} = p^k / \sqrt{(1-p)} + \varepsilon / \sqrt{(1-p)}, \quad (8)$$

where the errors for this model have homogeneous variance structure. The variance of a predicted $(1-s)$ is given by an equation similar to Equation 5 (for species composition):

$$\sigma_m^2 = (\log(p)(1-s)\sigma_k)^2 + (1-p)\sigma^2. \quad (9)$$

To examine the accuracy in recording the abundance of all the species in a catch, we modeled the order (200 times) in which subsamples were taken (as described above for catch composition estimates). For each (species by trawl) case, i.e. where a species was recorded at any level of abundance, we calculated the sampling error s for ranges of p from 0.1 to 0.9. We grouped all the (species by trawl) cases

of different levels of abundance into eight categories for these analyses. They were <1; 1 to <2; 2 to <3; 3 to <4; 4 to <5; 5 to <10; 10 to <50 and 50 or more per 10-kg subsample respectively.

The SAS procedure NLIN was used to fit the power curve for catch composition, as well as the separate power curves for sampling error for the different abundance classes.

Results

General results

Catches ranged in size from 71 to 445 kg, with an average of 117 species per trawl (84 fish and 33 invertebrate species). A total of 140,253 fish and invertebrates were recorded from 323 subsamples taken from the 20 prawn trawl catches that were sorted entirely (Table 1). Subsamples weighed, on average, 11.2 kg and contained 434 individuals (or 389 individuals per standardized (std) 10-kg subsample). We identified a total of 276 fish and 141 invertebrate species.

A total of 69.3% (1617 out of 2333) of the (species \times trawl) cases of relative abundance were recorded at ratios of less than one individual per std 10-kg subsample (or less than one in every 389 individuals), when averaged over all 20 catches; they were classed as "rare" (Fig 2). A further 19% (442 out of 2333) of the (species \times trawl) cases of relative abundance were recorded at ratios that fell between one individual per std 10-kg subsample and less than five individuals per 10-kg subsample (or between one in 389 and less than five in 389 individuals), when averaged over all 20 catches; they were classed as "common." The remaining 11.7% (274 out of 2333) of the (species \times trawl) cases of relative abundance were recorded at ratios of five or more individuals per std 10-kg subsample (or five or more in every 389 individuals), when averaged over all 20 catches; they were classed as "abundant" (Fig 2).

Catch composition

The number of species recorded increased as the weight of sorted catch increased in 19 of the 20 catches. This relationship appeared to reach an asymptote in the remaining large catch of 445 kg (Fig 3, A and B).

After 10% of all 20 catches were sorted, the cumulative percentage of species recorded ranged from 31% (in the 315 kg catch) to 78% (in the 182 kg catch) (Table 2). To detect 80% of the species present in a single catch, from 20% to 70% of the catch had to be sorted.

Simulation modelling showed that sorting 10% of catch weight detects (on average) 50% of the species present, with the confidence interval ranging from 44% to 57% (Fig 4). Sorting 50% of the catch was necessary to detect 80% of the species present.

Abundance estimates The simulation model showed that the mean sampling error curves (for the eight abundance categories) decreased as increasing percentages of the catch had been sorted (Fig 5). After 10% of the weight of

Table 2

The percentage of species recorded as more of the catch is sorted (10% increments). Percentages were calculated separately for 20 trawl catches that were completely sorted. The demarcation line denotes where 80% or more of the species in each catch were recorded.

Region	Catch weight (kg)	Number of species	Cumulative % of species recorded (in 10% Wt increments)								
			10%	20%	30%	40%	50%	60%	70%	80%	90%
North of Mornington Island	71	90	51	62	70	76	81	86	90	94	97
North of Groote Eylandt	85	94	49	60	69	75	81	85	89	93	97
East of Mornington Island	87	122	56	66	74	79	84	88	91	95	97
Torres Straits	94	95	60	70	76	81	86	89	92	95	98
North of Mornington Island	100	111	56	66	74	79	84	88	91	95	97
North of Groote Eylandt	147	96	50	61	69	76	81	86	90	93	97
East of Vanderlin Islands	156	90	39	52	61	69	75	81	86	91	96
North of Groote Eylandt	158	132	65	74	80	84	88	91	94	96	98
South of Groote Eylandt	165	89	51	63	71	77	82	86	90	94	97
Weipa	166	128	54	65	73	78	83	87	91	94	97
North of Groote Eylandt	169	159	57	68	75	80	85	88	92	95	98
Melville	170	90	46	58	67	73	79	84	89	93	97
West of Mornington Island	174	121	52	63	71	77	82	86	90	94	97
North of Mornington Island	182	137	78	84	88	91	93	95	96	98	99
North of Groote Eylandt	189	139	61	71	77	82	86	90	93	95	98
North of Mornington Island	194	136	67	76	81	85	89	92	94	96	98
West of Mornington Island	269	111	52	63	70	77	82	86	90	94	97
East of Mornington Island	274	108	40	53	62	69	76	82	87	92	96
South of Groote Eylandt	315	130	31	44	54	63	70	77	84	89	95
North of Mornington Island	445	166	61	71	77	82	86	90	93	95	98

catches had been sorted, only two abundance categories (from ≥ 10 to <50 , and ≥ 50 per subsample) had mean sampling error rates below 25%.

For the “rare” species (<1 per subsample), the gradient of the mean sampling error curve was close to constant (Fig 6). The 95% upper confidence interval was over 100% until more than 40% of the catches had been sorted. Even when 90% of the catches had been sorted, the mean sampling error was just below 10%, and the 95% upper confidence interval remained above 25%.

For the “abundant” species (five or more per subsample), the mean sampling error curve started just below 25% after 10% of catches had been sorted, and fell below 10% when more than 40% of the catches had been sorted (Fig 6). The 95% confidence interval did not fall below 25% until 50% of catches had been sorted.

Discussion

This study shows that a large subsample is required to accurately represent the species composition of a large multispecies catch from

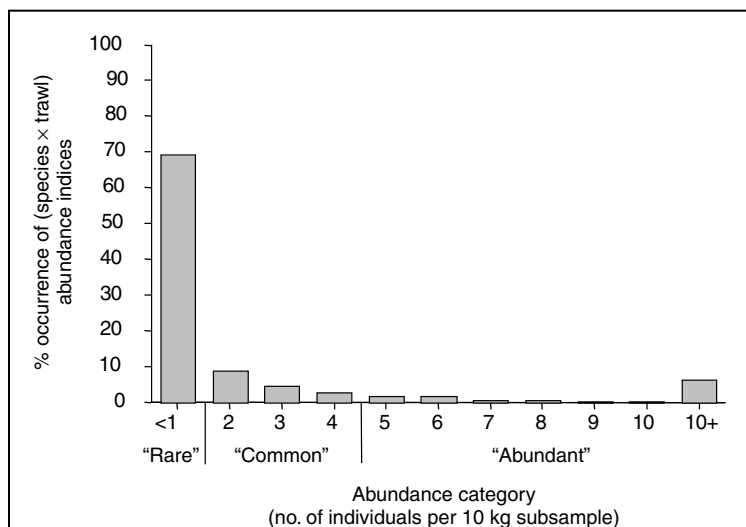
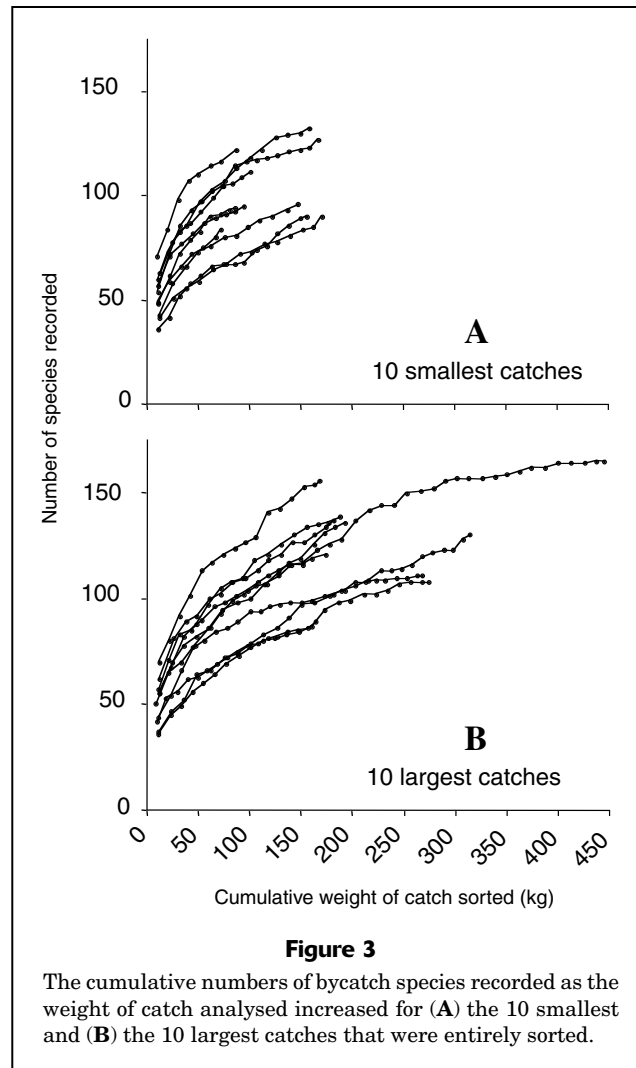


Figure 2

The percentage frequency of occurrence of 2333 cases of (species × trawl) relative abundance for bycatch species recorded from 20 trawl catches. The cases are grouped into 11 categories of abundance indices based on the average number of a species recorded per 10-kg subsample of catch.

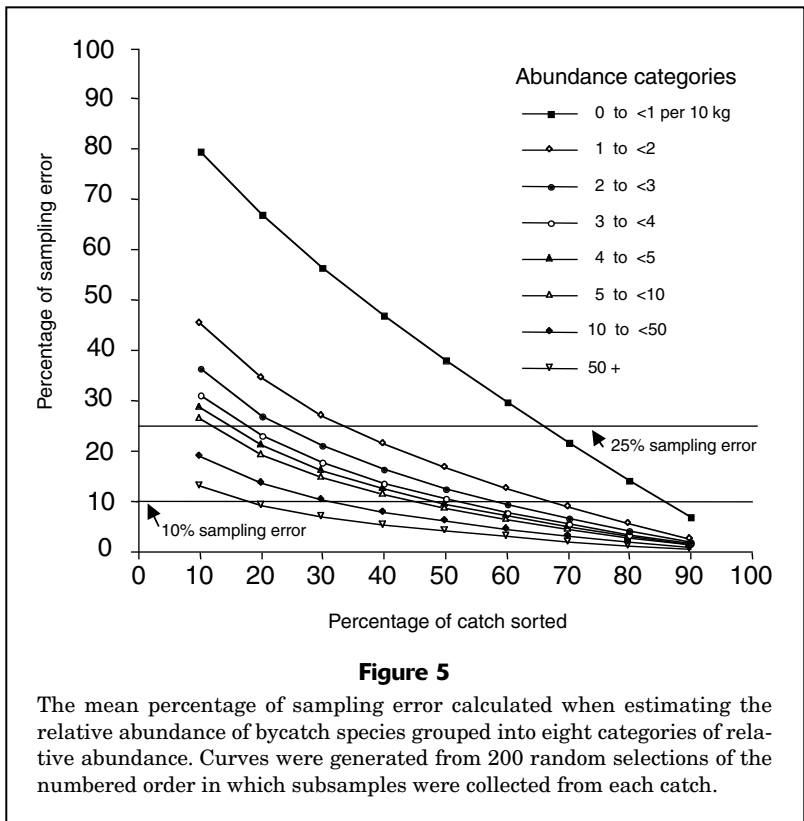
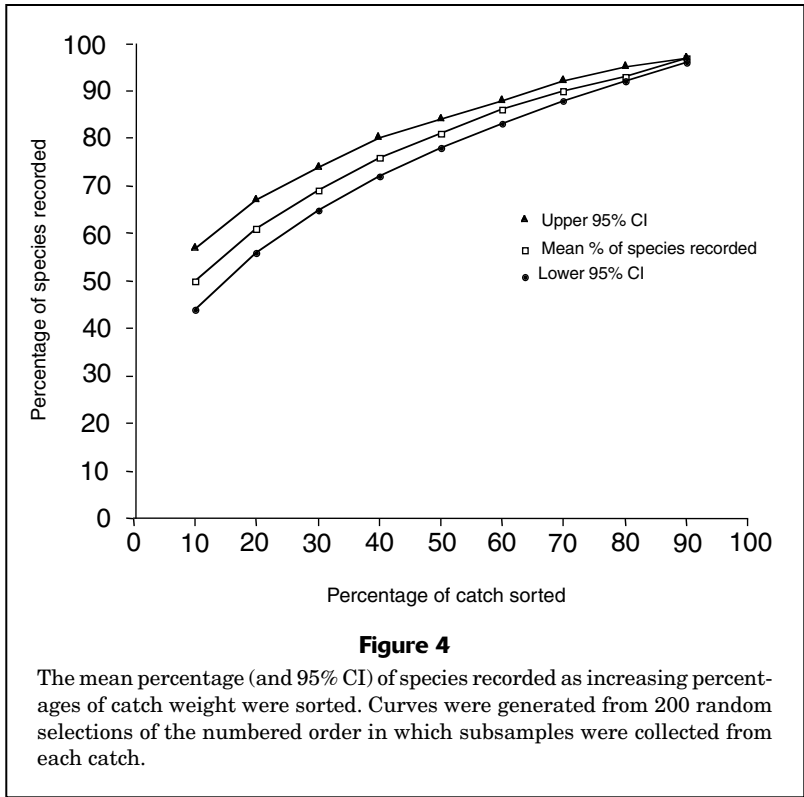


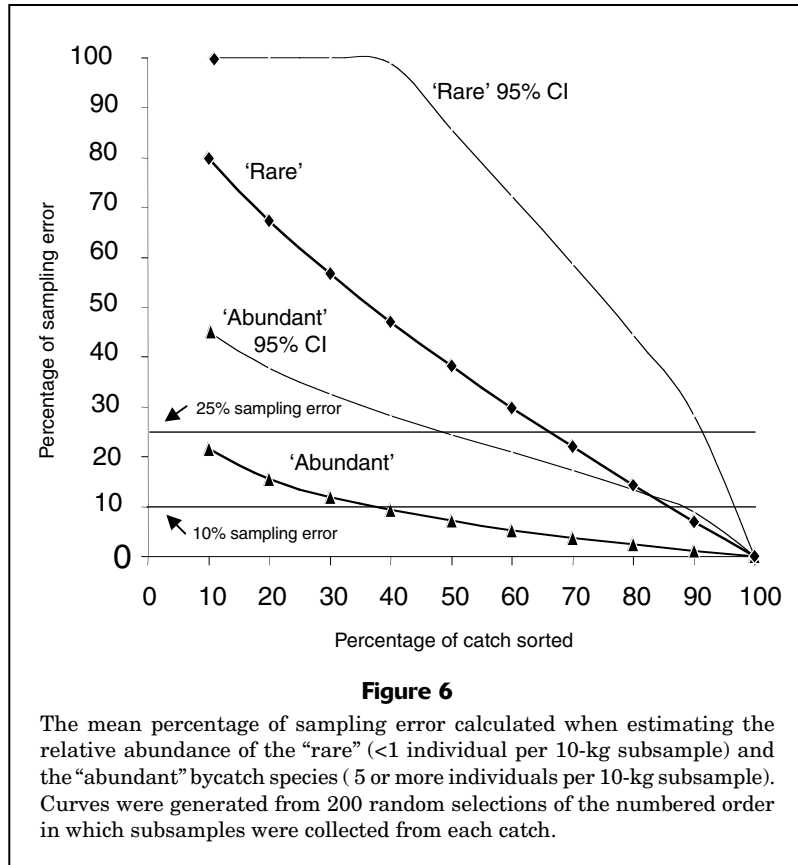
the Northern Prawn Fishery (NPF). As more of the catch is sorted, more new species are encountered. On average, 50% of the catch weight needs to be sorted to record 80% of the species in a single catch. Our data suggest that taking subsamples of between 10% and 30% of catch weight can result in highly variable percentages (from 31% to 88%) of the total species in the catch. When estimating the relative abundance of individual species within a catch, subsampling small percentages of catch weight (around 10%) results in a sampling error around 80% for “rare” species, and around 25% for “abundant” species.

The sampling error (when estimating the relative abundance of a species in a trawl) is a function of the total number of bycatch individuals caught in that trawl. For example, 10 individuals of species “X” may occur in one trawl, at a ratio of one in every 100 bycatch individuals. In the very next trawl, 10 individuals of species “X” may occur at a ratio of only one in every 1000 bycatch individuals because other “abundant” species have swamped its occurrence ratio. As a consequence, the sampling error for the same number of individuals of species “X” varies greatly between trawls.

There are two sources of within-trawl variation to take into account when calculating catch rates for individual species. The first is due to changes in catchability at the trawl-species interface (either on the sea floor or in the water column). The second is due to on-deck subsampling techniques. This study has been able to allocate percentages of sampling error based on the occurrence rate of a species of interest within individual catches. To do this, we calculated the average occurrence ratios for the different categories of relative abundance used in this study. For example, “rare” species occurred at a rate of less than one individual in every 389 bycatch individuals; “abundant” species occurred at a rate of five or more individuals in every 389 bycatch individuals. These ratios can now be applied to species of interest recorded in other trawl catches and the average sampling errors can be calculated.

Monitoring catch rates of a suite of “indicator” bycatch species is a possible future option for measuring the health of nontarget species in trawl fisheries such as the NPF. Stobutzki et al. (2001) identified a suite of small NPF fish species that are more likely to be impacted by trawling.





The catch rates of many of these most-at-risk species are extremely low. Our data suggest that extremely high sampling errors will be incurred if monitoring catch rates of species on this list is undertaken. These errors must be incorporated into any models that assess the impact of trawling on populations of these species.

The range of data in the present study includes many of the sources of variation likely to be encountered in setting up a wide-ranging bycatch monitoring program. The results we present are a valuable guide to the accuracy of subsampling. In particular, this study emphasizes the value of collecting large subsamples, especially when one is restricted to representing the bycatch of an area by only one or a few trawls. This problem is common for research cruises when many regions need to be sampled in a short time (e.g. Blaber et al., 1994), and is also a common problem for observers on commercial fishing vessels where catch sampling is often restricted by the nature of commercial practices. Because there is a high level of sampling error when estimating the abundances for “rare” species, reliable estimates will require either taking large subsamples or sorting entire catches.

The size of some catches in our study may be larger than those of many other tropical prawn trawl fisheries in Australia and overseas. However, the data in the matrix on the range of cumulative species (per proportion of catch sorted, Table 2) will allow managers of other trawl fisheries to better understand the implications and likely accuracy of bycatch sampling programs.

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