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AN ANALYSIS OF FISH ABUNDANCE AND DISTRIBUTION DATA, MAYOR IS. (TUHUA) MARINE RESERVE BASELINE SURVEY, 1993

(Short Answers in Conservation Science)

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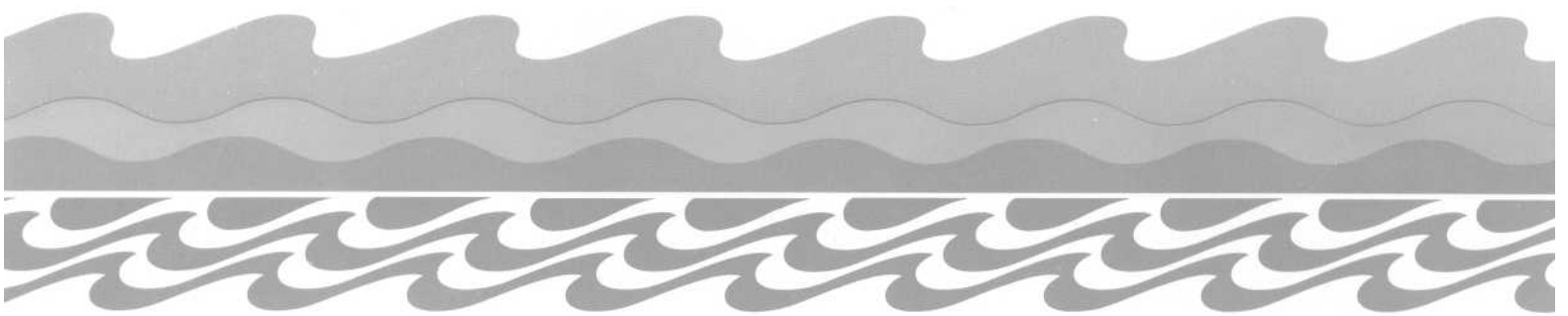

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An Analysis of Fish Abundance and Distribution Data, Mayor Is (Tuhua) Marine Reserve Baseline Survey, 1993

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1. INTRODUCTION

The Mayor Island (Tuhua) marine reserve was created in January 1993. A pre-reserve survey had already compiled algae, invertebrate, and fish species lists, with distributional data and habitat descriptions (Jones & Garrick 1991). They recorded a total of 54 fish species and presented the relative abundances of each. These data were essential for site selection and replication in the present survey, which was undertaken in March/April 1993, only 3 months after the reserve was established. Fieldwork for the present survey was undertaken by Department of Conservation (Bay of Plenty Conservancy) and NIWA-Oceanographic staff, as well as 2nd-year marine biology students from the Bay of Plenty Polytechnic. It was designed to provide background data on numbers of fish species present, numbers of individuals, their distribution within sites and depth, and to ascertain whether there were differences between "reserve" and "control" sites. These data would then be available for comparisons with those obtained after the reserve had been in place for some time, and would provide assistance for reserve management as well as the wider scientific questions recently outlined by Rowley (1992) on whether marine reserves act as spillover areas to enhance fisheries adjacent to their boundaries.

2. METHODS

Based on the previous survey (Jones & Garrick 1991), sites around Tuhua were chosen to cover most of the expected habitats both within and outside the reserve. Sites within the reserve were paired with controls outside, based on similar habitat descriptions, slope, exposure, algal cover, and substrate. These sites are shown in figure 1.

At each site, 2 sets of transects were sampled, stratified by depth. Within each depth zone (which depended primarily on available habitat), 3 (occasionally 4) randomly placed replicate 50m x 10m transects were swum by two divers. A very small number of transects were sampled as 25m x 10m; counts for these were scaled before analysis. All fish seen were identified, counted, and their lengths estimated. Pairs of divers were continually rotated throughout the survey to reduce observer bias, and all personnel involved in fish counts practiced estimating sizes of plastic fishes underwater before commencing the quantitative counts.

Transformations of the raw data were performed on some site plots to reduce the dominance of abundant species obscuring smaller values. Accordingly, counts of individuals >100 were transformed using natural logs simply to reduce the size of those bars on the plots. All such counts are easily identifiable in the site plots. Untransformed raw data were, however, used for all summary statistics and analyses of variance.

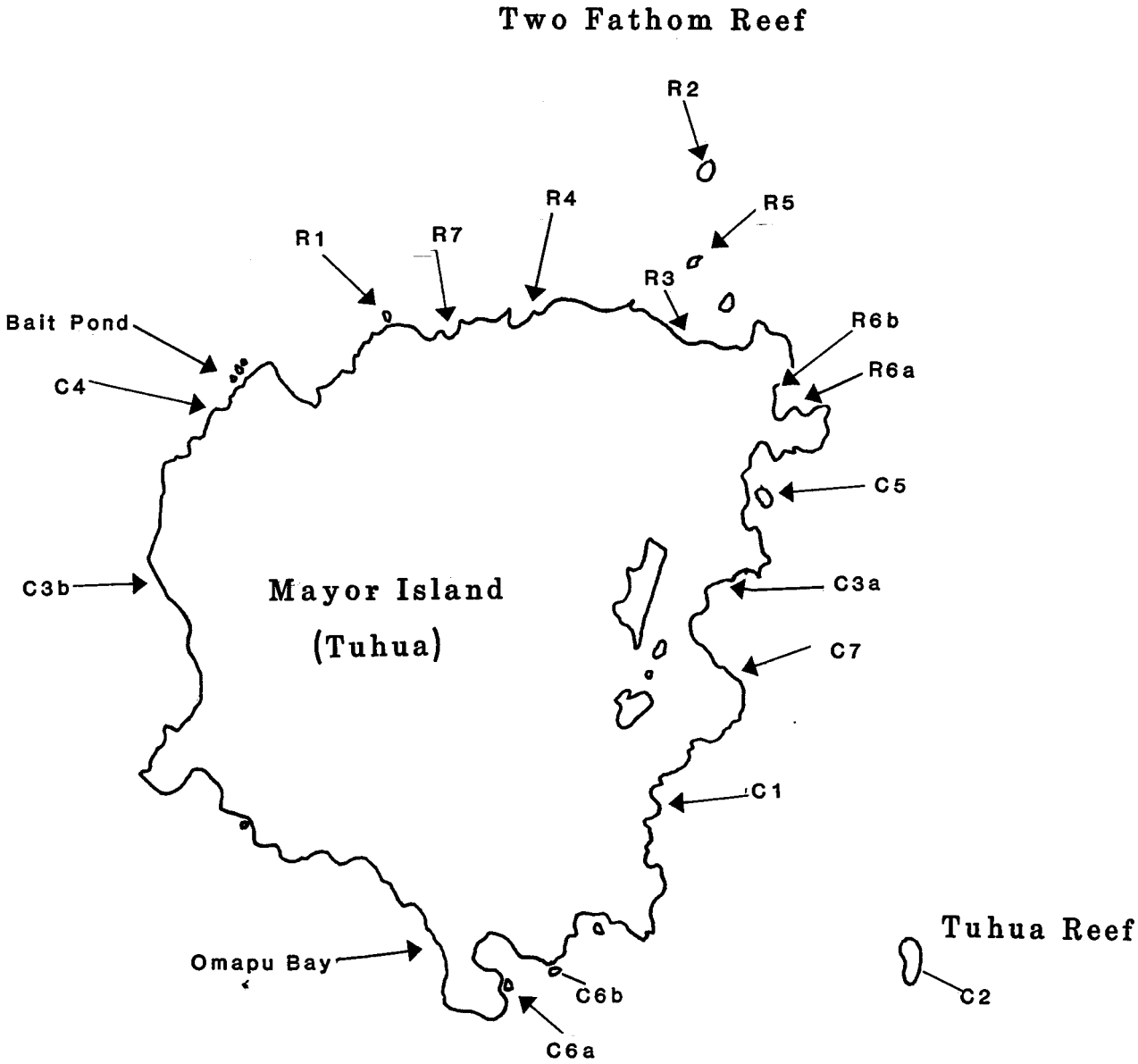


Figure 1. Sites of quantitative fish transect counts, 1993

3. RESULTS

The baseline survey recorded a total of 51 species of fish. The most widespread of these were black angelfish, 2-spot demoiselle, and spotty, all of which occurred at all sites. A ranking of all fish species among reserve and control sites is given in Table 1.

Table 1. Ranking of all fish species recorded among sites.

Species	Reserve sites	Control sites	Total (%)
Black angelfish	8	11	19(100)
2-spot demoiselle	8	11	19(100)
Spotty	8	11	19(100)
Leatherjacket	8	10	18 (94.7)
Banded wrasse	8	9	17(89-5)
Goatfish	7	10	17 (89.5)
Red moki	7	9	16 (84.2)
Big eye	6	8	14 (73.7)
Sweep	6	8	14 (73.7)
Marblefish	5	7	12 (63.2)
Sandagers wrasse	7	5	12 (63.2)
Blue maomao	6	5	11 (57.9)
Hiwihiwi	5	6	11 (57.9)
Yellow moray	5	3	8(42.1)
Scarlet wrasse	4	4	8(42.1)
Slender roughy	4	4	8(42.1)
Crimson cleaner	4	3	7(36.8)
Pink maomao	5	2	7(36-8)
Butterfly perch	3	3	6(31-6)
Jack mackerel	2	4	6(31.6)
Koheru	4	2	6(31-6)
Tarakihi	2	4	6(31-6)
Porae	3	2	5(26.3)
Butterfish	1	3	4(21.1)
Green wrasse	3	1	4(21-1)
Silver drummer	3	1	4(21.1)
Snapper	2	2	4(21-1)
Trevally	1	3	4(21.1)
John dory	1	2	3(15.8)
Grey moray	2	1	3(15.8)
Half-banded perch	2	1	3(15.8)
Scorpionfish	1	2	3(15.8)
Long-tail stingray	0	3	3(15.8)
Oblique-swimming triplefin	1	2	3(15.8)
Blue moki	2	0	2(10.5)
Red pigfish	2	0	2(10.5)
Splendid perch	1	1	2(10.5)
Short-tail stingray	1	1	2(10.5)

Table 1 Contd.

Banded triplefin	1	1	2(10.5)
Blue knifefish	1	0	1(5.3)
Bluefish	1	0	1(5.3)
Clown toado	1	0	1(5.3)
1-spot demoiselle	1	0	1(5.3)
Eagle ray	1	0	1(5.3)
Kahawhai	0	1	1(5-3)
Kingfish	1	0	1(5.3)
Mosaic moray	0	1	1(5-3)
Orange wrasse	1	0	1(5.3)
Common triplefin	1	0	1(5-3)
Mottled triplefin	1	0	1(5.3)
Spectacled triplefin	1	0	1(5-3)

A total of 48 species or over 94% of all fish species were recorded within the reserve, while 39 or just over 76% were recorded at the control sites.

The numbers of fish of each species recorded at each site are presented in Appendix l. Each plot shows a comparison of which species were recorded along the shallow and deep transects as means ± 1 standard error. In general, there is a close similarity between the species at shallow and deep transects for any one site.

Figure 2 shows the mean numbers of individual fishes counted at each site. There are no clear trends. Some sites had more fish in shallow water while other sites had more in deep. The large standard deviations are caused mainly by a small number of species occasionally occurring in large numbers, eg, Jack mackerel, 2-spot demoiselles, and pink maomao. Differences between sites were examined by performing a Kruskal Wallis analysis of variance on these data. The raw data did not have a normal distribution, due to the occasional large numbers in individuals belonging to a small number of species, so a non-parametric test had to be used (Table 2). The ANOVA shows no differences in the numbers of individuals at any site ($p>0.05$).

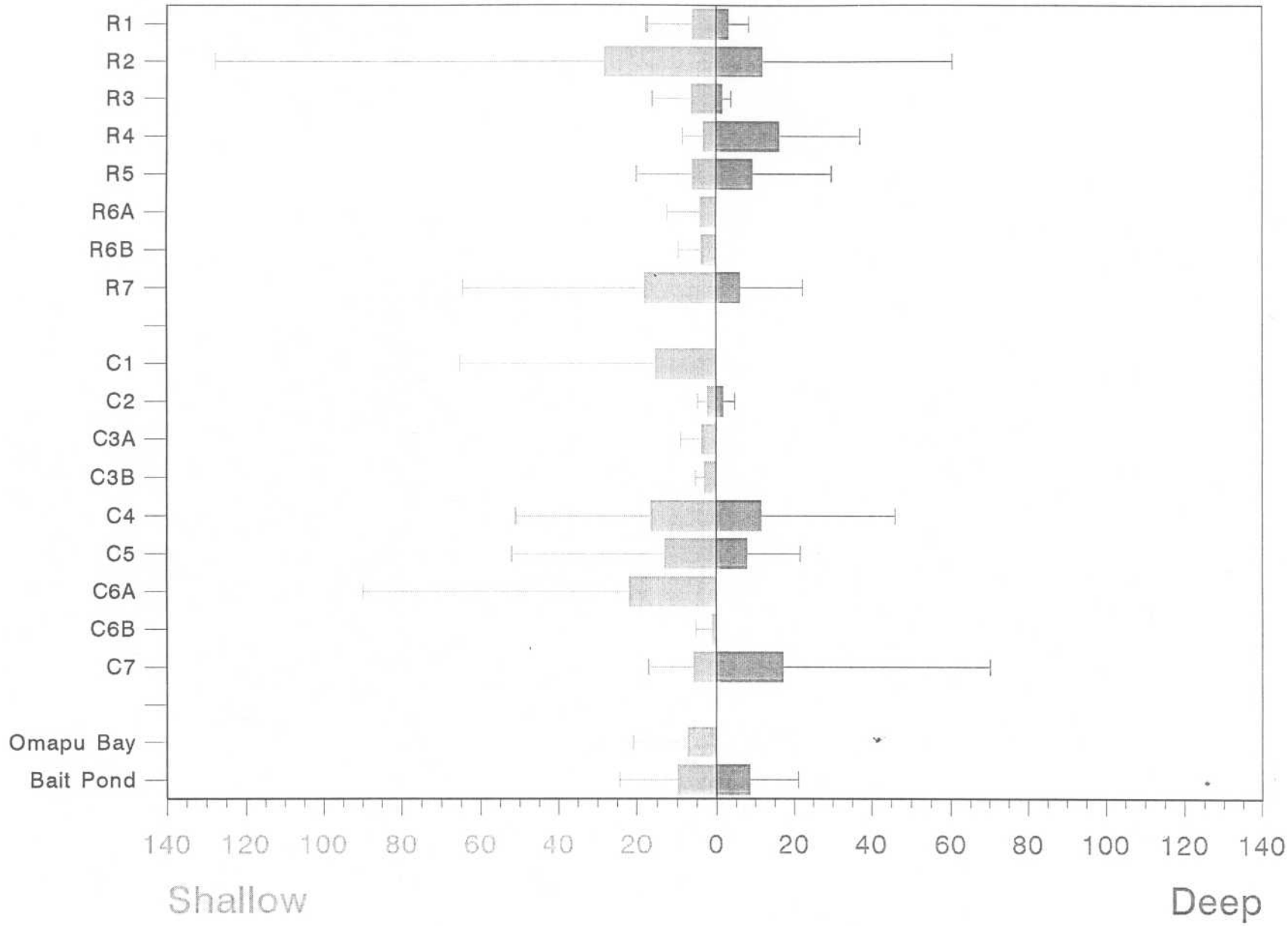


Figure 2. Mayor Is Baseline Survey 1993. Mean numbers (± s.d.) of individual fishes at each site.

Table 2. One way analysis of variance. Mean numbers of fish at all sites.

Normality Test: Failed (P < 0.001)
Use nonparametric test because assumptions for parametric test were violated.
KRUSKAL-WALLIS ONE WAY ANOVA ON RANKS:

Group	Median	25 - 75	Percentiles
R1 shallow	1.300	0.300	2.700
R1 deep	1.000	0.375	3.175
R2 shallow	1.500	1.000	2.875
R2 deep	0.900	0.300	1.500
R3 shallow	1.850	1.000	7.500
R3 deep	1.000	0.600	1.850
R4 shallow	1.300	0.600	3.600
R4 deep	1.000	0.300	1.750
R5 shallow	2.300	1.400	3.575
R5 deep	1.700	0.600	3.775
R6a shallow	1.000	0.300	2.750
R6b shallow	2.000	0.300	4.675
R7 shallow	1.000	0.300	2.825
R7 deep	0.700	0.300	1.225
C 1 shallow	1.800	0.400	3.400
C2 shallow	2.000	1.150	3.400
C2 deep	0.850	0.300	3.500
C3a shallow	2.000	0.400	5.900
C3b shallow	2.300	1.600	4.800
C4 shallow	2.300	0.700	4.350
C4 deep	1.300	0.300	4.600
C5 shallow	1.330	0.330	3.830
C5 deep	1.500	0.330	15.670
C6a shallow	2.165	0.835	8.000
C6b shallow	0.330	0.330	1.670
C7 shallow	1.670	0.585	6.250
C7 deep	1.000	0.585	3.333
Omapu shallow	3.500	1.000	6.000
Bait shallow	4.670	0.670	12.580
Bait deep	1.665	0.500	15.000

H = 33.699 with 29 degrees of freedom. P = 0.250
The differences in the median values among the treatment groups are not great enough to exclude the possiblility that the difference is just due to random sampling variability; there is not a statistically significant difference (P = 0.250).

The total numbers of fish species at each site are shown in figure 3. At most sites there are more species in deep transects than shallow, but no clear trends in distribution among sites are apparent. The highest

number of species at any one site was 26 (site R2; deep) (Two Fathom Reef), and between 10 and 15 species were recorded at most sites. When the shallow and deep transects are combined for each site, the maximum number of fish species recorded was 30 (site R2), with 15-20 at most sites.

To examine whether there were any significant differences in numbers of species or individuals between reserve and control sites, analyses of variances were performed by pooling results from all shallow and deep transects within the reserve and comparing with those transects outside. Since it had already been established that no significant differences occurred at any one site, it was valid to pool the data for these tests. The results are shown graphically in figure 4. The statistical results of the ANOVAs are presented in tables 3 and 4. There were no differences between reserve and control sites for any parameter (number of species, number of individuals, shallow transects, deep transects).

Table 3. One way analysis of variance. Mean numbers of fish species, reserve vs control sites.

Normality Test:	Passed (P > 0.200)
Equal Variance Test:	Passed (P = 0.436)

Group	Mean	Std Dev	SEM
Reserve/shallow	13.500	2.3905	0.8452
Reserve/deep	15.833	6.2102	2.5353
Control/shallow	11.545	3.2974	0.9942
Control/deep	14.000	4.0620	1.8166

Source of Variation	DF	SS	MS	F	P
Between Treatments	3	75.1061	25.0354	1.597	0.214
Residual	26	407.5606	15.6754		
Total	29	482.6667			

The differences in the mean values among the treatment groups are not great enough to exclude the possibility that the difference is just due to random sampling variability; there is not a statistically significant difference (P = 0.214).

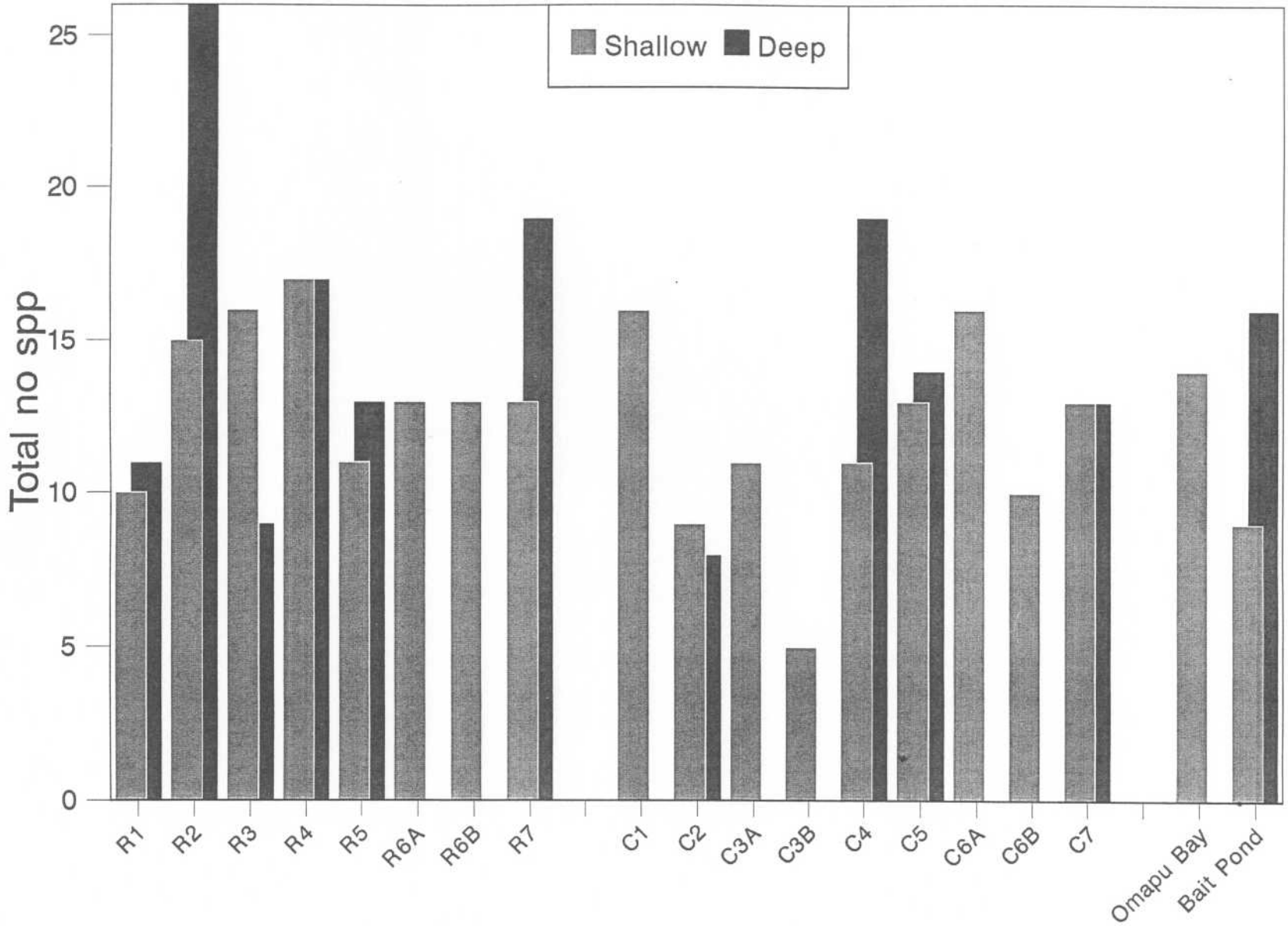
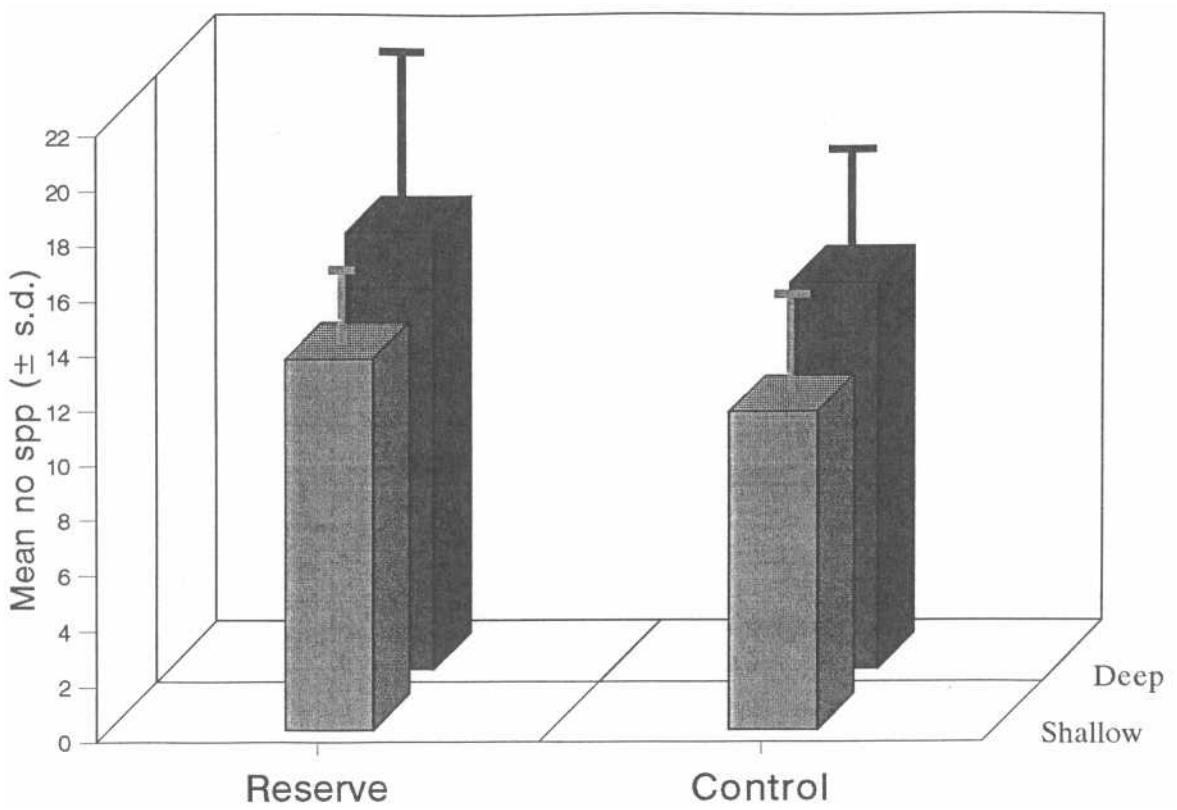


Figure 3. Mayor Is Baseline Survey 1993. Fish counts at each site.



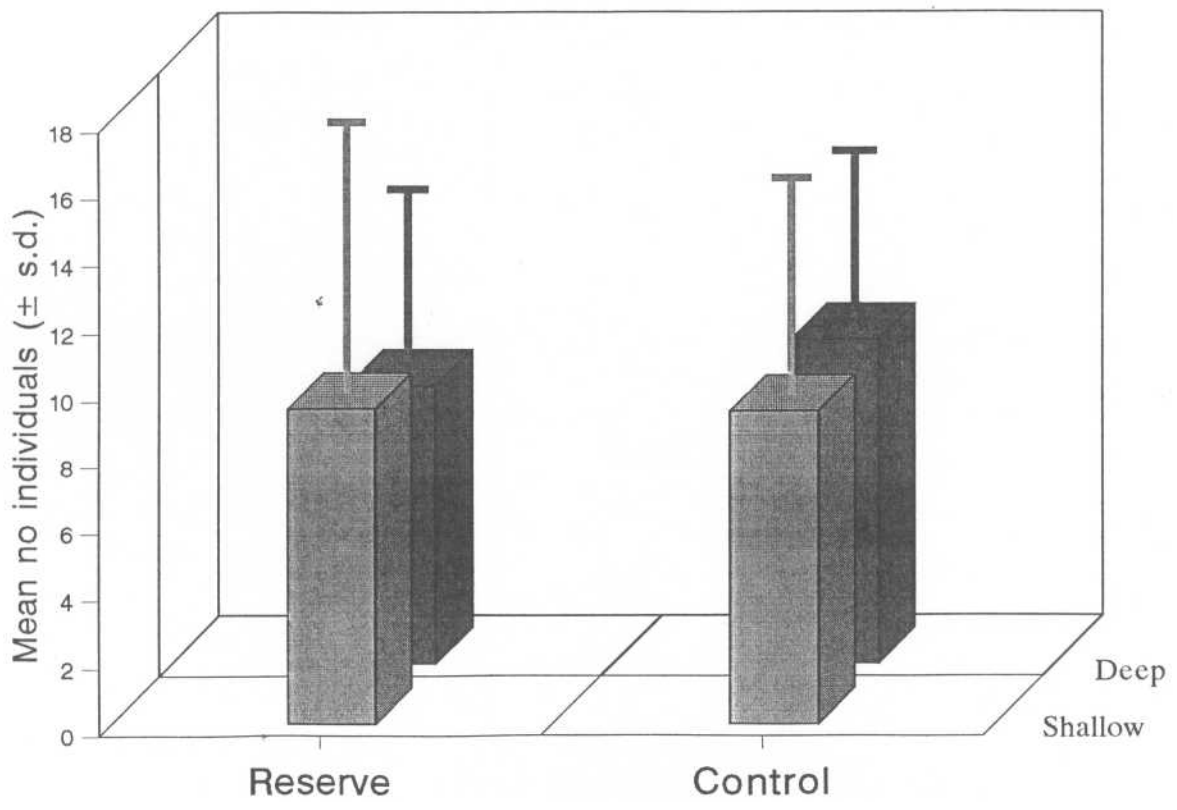


Figure 4. Mayor Is baseline survey. Reserve vs Control Sites; Fish Species.

Table 4. One way analysis of variance. Mean numbers of fish individuals, reserve vs control sites.

Normality Test:	Passed (P = 0.085)
Equal Variance Test:	Passed (P = 0.939)

Group	Mean	Std Dev	SEM
Reserve/shallow	9.408	9.0249	3.1908
Reserve/deep	8.300	5.5636	2.2713
Control/shallow	9.338	6.8264	2.0582
Control/deep	9.660	5.6087	2.5083

Source of Variation	DF	SS	MS	F	P
Between Treatments	3	6.4723	2.1574	0.043	0.988
Residual	26	1316.7389	50.6438		
Total	29	1323.2112			

The differences in the mean values among the treatment groups are not great enough to exclude the possiblility that the difference is just due to random sampling variability; there is not a statistically significant difference (P = 0.988).

4. DISCUSSION

A previous survey (Jones & Garrick 1991; Appendix 4) reported a total of 54 fish species at Tuhua, including pelagics such as flying fish, mako shark, and yellowfin tuna. This survey recorded 51 species, so the methods appear to have sampled most of the fish population.

The species recorded by Jones & Garrick (1991) as "very common" were blue cod, crested blenny, hiwihiwi, leatherjacket, spotty, sweep, and 2-spot demoiselle. These species (other than crested blenny) were also the most widespread in this survey. Crested blenny are cryptic, and would not have been adequately sampled by the methods used for this survey.

This survey has produced results very similar to an equivalent survey undertaken at White Island, where a total of 57 fish species were recorded in transects (Grange et al 1992). The numbers per site at White Is (34 maximum, 20-30 generally) are higher than those from Tuhua (30 maximum, 15-20 generally). This may reflect the increased fishing and extraction pressure on fish stocks at the more accessible Tuhua in the past, and it will be fascinating to follow these populations over time to record changes following reservation.

The 1993 baseline survey will provide useful information against which to measure any subsequent changes in fish populations associated with establishment of the marine reserve. At the time of this survey there were no significant differences in the numbers of species or individuals at any site, and no differences could be found between reserve and control sites. These lack of differences between sites may be due, in part, to the variability within sites. This is difficult to overcome, as overall counts are low, making small differences in numbers appear large when compared to the means. If numbers increase following reservation the same differences in raw data counts will produce less variability. For subsequent surveys, however, it may be advantageous to increase the number of replicate transects at each depth and site to 5, if sufficient resources are available. This would help reduce the standard deviations and increase the power of the ANOVA to detect site differences.

5. REFERENCES

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