Exploring the fishery and ecological effects of Lamlash Bay No-Take Zone

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- Science report for COAST April 2012 -

**Picture taken by Leigh Michael Howarth within Lamlash Bay No-Take Zone of a spider crab (Macropodia spp) inside a plumose anemone.*

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Isle of Arran COAST Community Of Arran Seabed Trust

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Investigating the fishery and ecological effects of Lamlash Bay No-Take Zone

Introduction

In September 2008, Scotland's first fully protected marine reserve was established within the Firth of Clyde in Lamlash Bay, Isle of Arran, under the rationale that it would "help regenerate the local marine environment and enhance commercial shellfish and fish populations" (for further background see Thurstan 2007; Howarth 2010; Thurstan & Roberts 2010; Howarth et al. 2011). Shortly after its designation, Marine Scotland Science and Scottish Natural Heritage (SNH) conducted baseline surveys of the area (e.g. Axelsson et al. 2009) followed by some additional surveys carried out by contractors on behalf of SNH in 2010. However, no monitoring schemes were in place that directly investigated the effects of the marine reserve. Therefore, in the summer of 2010, the University of York in conjunction with the Community of Arran Seabed Trust (COAST), conducted a series of underwater surveys to investigate how the 2.67km^2 "No-take zone" (NTZ) was responding to protection.

What initially began as a series of basic SCUBA surveys has grown to become an extensive marine monitoring program utilising a number of different survey techniques. With each survey technique designed to gather data on the different ecological components that make up Lamlash Bay. Once complete, these datasets will be brought together, allowing the effects of protection upon the larger ecosystem to be investigated. This report attempts to do this for the first time by combining data collected from dive surveys and baited remote underwater video cameras.

Materials and methods

- Dive surveys

Dive surveys, scallop collection and subsequent dissections followed the methods outlined in Howarth et al. (2011). A total of 28 dive surveys were conducted between June and August 2011 (Appendix 1). Of these, 14 were inside Lamlash Bay NTZ and 14 were outside. A wide distribution of surveys was intended to provide a good representation of Lamlash Bay whilst being limited to areas of the seabed that were shallow enough to remain within no-decompression limits. Surveys were also conducted parallel to relief contours to ensure the depth of a single survey did not change by more than 3 m.

- Baited remote underwater video camera (BRUV)

A Cannon Powershot S95 camera was fitted with an internal colour correction filter suitable for green water. The camera was then placed inside a Cannon WP-DC38 underwater housing along with silica gel sachets to help absorb condensation. The camera was mounted on an Ikelite tray with two Ikelite pro-v8 LED video lights. Based on designs by Bullimore (2011), this camera system was then

fitted to one end of a 22 inch commercial lobster pot frame. A bait box with several drilled holes was fitted to the other end in view of the camera. The frame of the lobster pot was marked with evenly spaced 10mm white bands, allowing the length of individuals recorded on video to be estimated. Rope was spliced to all four ends of the frame and joined at the centre by snap-shackles along with three cork floats to prevent the ropes from sinking in view of the camera.

Prior to deployment, 200g of coarsely cut mackerel was placed inside the bait box. The camera was turned on and switched to video mode using the underwater white balance setting with "vivid red" colour adjustments in an attempt to offset the greenness of the water. Once recording began, a 40m long rope with surface marker buoy was attached to the central snap-shackle and the BRUV was carefully lowered to the seafloor. The system's negative buoyancy ensured the BRUV landed upright and remained in a stable position. After 1 hour, the BRUV was hauled back to the boat, the bait replaced, and the BRUV was ready for redeployment at a new site. Overall, this set-up provided a highly cost-effective, low maintenance and robust baited remote underwater video camera (BRUV) system that could be hauled and deployed without the need of a hydraulic winch (Fig. 1; Bullimore 2011).

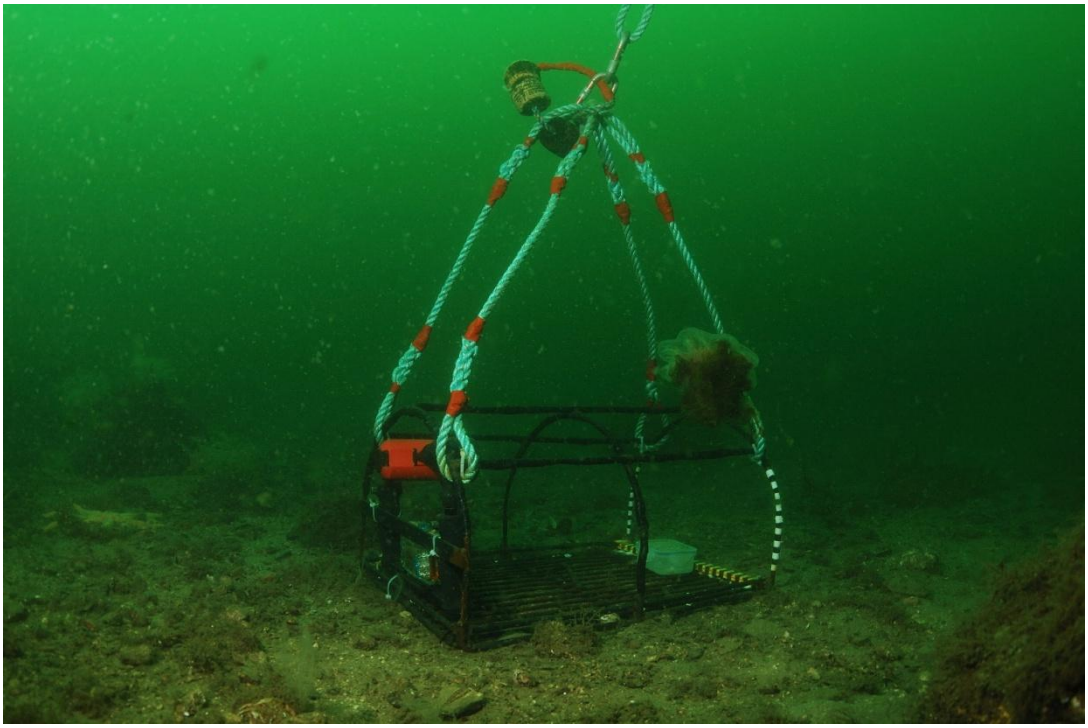


Figure 1 | The baited remote underwater video camera system deployed on the seabed. The camera and lights on the left faced the bait box on the right. In the picture, the 10mm white markings can be seen, as can the three cork floats lifting the ropes and snap-shackles out of view from the camera.

All deployments were conducted between 18th July and 25th August 2011 between 0800 and 1600 hours (Appendix 3). The date, time and weather conditions were recorded for every deployment. All sites had been previously surveyed, meaning data was already available on their depth, substrate type and benthic community composition. It was originally intended that every site dive surveyed in 2011 would also be subject to at least one BRUV deployment. However, due to early technical issues and time constraints, only 20 sites were BRUV surveyed.

- Video analysis

After reviewing the footage, only 17 videos were deemed appropriate for analysis, eight from inside the NTZ and nine from outside. The hue, saturation, sharpness and contrast of all videos were adjusted for the clearest picture possible using VLC player (http://www.videolan.org/vlc). To standardise video lengths, analysis began from two minutes after the BRUV hit the seabed and terminated 50 minutes after. For each video the following variables were recorded: (*i*) the total number of species; (*ii*) the total number of families; (*iii*) the time of first appearance for each species; (*iv*) the maximum number of individuals of a species observed within the same frame (MaxN); and (*v*) the time MaxN occurred. As the camera was always the same distance from the measurement markers, the length of fish and carapace width of crustaceans could be estimated when individuals aligned between both posts of the frame and faced parallel to the camera.

- Data analysis: Biometrics

Data obtained from scallop dissections were used to explore relationships between shell length and age, exploitable biomass and reproductive biomass. Exploitable and reproductive biomass were plotted against shell length in simple scatter charts and fitted with power trendlines in Microsoft Excel 2007. Equations derived from the trendlines were then extrapolated for the entire sampled population, allowing for the exploitable biomass and reproductive biomass to be estimated for all scallops measured during the diver surveys. The relationship between length and age differed in that it was explored using the software package SIMPLY GROWTH (http://www.pisces-conservation.com/softgrowth.html) and by fitting the data with a non-linear Von-Bertalanffy growth curve. This provided the values for the following equation:

$$t = t_0 + \ln (1 - L_t/L_\infty)/(-k)$$

The Von-Bertalanffy equation (Brody 1945; Ricker 1958) | where t = age; L_t = length at age t; L_∞ = the asymptotic length; k = the rate at which length reaches L; t_o = the hypothetical age at which fish would have zero length.

Any differences observed in biometrics between sites in and outside the NTZ were tested for significance through a one-way Analysis of Variance (ANOVA) once variables were tested for normality using histograms, boxplots, normal QQ plots and the Shapiro-Wilk test. The Shapiro-Wilk test was chosen as it is widely accepted to be the most suitable for small and medium size samples (*n* up to 2000, Royston 1982; Conover 1999). These exploratory measures were conducted on all variables within this study using the statistical package R (www.r-project.org).

- Population structure of king and queen scallops

After every survey, the mean density of scallops was plotted on a line graph incorporating ±1 Standard Error (SE) bars. It was expected that, for the first several dives, the mean density of scallops encountered would fluctuate and the error bars would be large. Then, once a sufficient number of dive surveys had been conducted, the mean density of scallops would level out and the error bars

would narrow. This provided a rough indicator that enough dive surveys had been conducted to generate an accurate estimate of the density of scallops in and around the Lamlash Bay NTZ.

Densities of king and queen scallops were compared between the two treatments (i.e. 'NTZ' and 'outside') using the Mann-Whitney U test in SPSS v 17.0. This test was chosen as the two groups were independent and both variables were found to have a non-normal distribution. The Mann-Whitney U test was also performed on the estimated abundance of juvenile scallops between both treatments. These data were then plotted in bar graphs. The mean size and age of scallops in and outside the NTZ were also plotted in bar graphs and tested for significance using a one-way ANOVA. Finally, the size and age (age estimated from biometrics) distribution of scallop populations in and outside the NTZ were compared using bar charts and tested for significance using a Kolmogorov-Smirnov (K-S) analysis.

To compare scallop data between the years 2010 and 2011, the size and age composition of both king and queen scallops were plotted in a bar graph, split by year and grouped based on whether they were in or outside the NTZ. Any observable differences were tested with a one-way ANOVA. Any change in scallop density over the two years was measured by plotting the mean density of scallops from sites in and outside the NTZ using simple line graphs.

- Investigating the composition of other species encountered during dive surveys

A species sample matrix suitable for analysis in the software package PRIMER v. 6.1.5 (Clarke & Gorley 2001) was generated. This matrix contained both count data and SACFOR estimates of colonial benthic organisms (e.g. maerl, macroalgae and bryozoans) obtained from the dive surveys. Sites were labelled as being either "NTZ" or "OUT" and were assigned a habitat type based on their depth and substrate (Table 1).

The DIVERSE function in PRIMER was used to generate univariate measures of biodiversity including total number of species, total number of individuals, Pielou's evenness and Shannon's biodiversity index (the latter 3 required count data and therefore colonial organisms were excluded). These were tested for differences using bar charts and a two-way ANOVA using protection (i.e. NTZ or outside) and habitat as fixed factors. Unfortunately, the model violated the assumption of equal variances and could not be transformed. As there was no significant interaction between the two factors, it was decided that a series of separate one-way ANOVAs would be more suitable despite the increased risks of running a Type I error.

A resemblance matrix using the Bray-Curtis similarity measure (Bray & Curtis 1957) was then created based on the count data. A non-parametric multi-dimensional scaling (MDS) ordination was then performed on the resemblance matrix to identify how similar the samples were based on their ecological assemblages. To test for differences between NTZ and outside, as well as differences between habitats, a two-way crossed Analysis of Similarity (ANOSIM, Clarke 1993) was executed. A Similarity Profile (SIMPROF) routine was then used to highlight if any alternative *a posteri* groups existed in the data. Lastly, a two-way Similarity of Percentages (SIMPER) program was run to determine the contribution of individual species to the average dissimilarity between samples.

Table 1 | How sites were assigned a habitat type. Based on their depth and substrate type, similar sites were grouped together. For meaningful analysis, every habitat type needed at least one representative in and outside the NTZ. This proved difficult in some cases. MPA 6, for example, was identified to be a "mud" habitat, but no mud habitats have been detected inside the NTZ. Based on its substrate and supporting ecological community (determined from dive survey and BRUV data) NTZ 11 was deemed the closest site to "mud" and was therefore paired with MPA 6. Sites inside the NTZ have been highlighted green.

Habitat	Site	Depth (m)	Substrate type
Kelp forest	NTZ 7	6.8	Kelp, sand, some dead maerl & shell
	OUT 11	8	Kelp & dead maerl
Sandy mud	NTZ 16	11.25	Sandy mud, cobbles & shell
	OUT 3	11.6	Sandy mud, shell & pebbles
Maerl bed	NTZ 13	11.2	Dead maerl, sandy mud & shells
	OUT 7	10.7	Dead maerl & some shell
	NTZ 3	8.45	Dead maerl & sandy mud
Shallow muddy sand	NTZ 14	15.1	Muddy sand & shell
	MPA 4	15.2	Muddy sand, shells & pebbles
	OUT 6	15	Muddy sand, shells & pebbles
Shallow boulders	NTZ 5	13.8	Boulders, sandy mud, shell & pebbles
	MPA 2	14.35	Boulders, sandy mud, shell & cobbles
	NTZ 17	15.2	Boulders, dead maerl & shells
	OUT 4	15.4	Boulders, dead maerl, muddy sand & shells
	NTZ 12	10.8	Boulders, sand, dead maerl, shells, & cobbles
Shallow sand	NTZ 4	15.2	Sand & very small quanities of dead maerl & shell
	MPA 1	16.48	Sand
	OUT 10	17	Sand, shell & small quanities of dead maerl
	NTZ 21	17.4	Sandy mud & small amounts of shell
Deep boulders	NTZ 8	17	Boulders, muddy sand, shell & cobbles
	OUT 1	18.5	Boulders, sandy mud, shell & pebbles
Deep muddy sand	MPA 3	19.3	Muddy sand & small quanities of shell
	NTZ 10	19	Muddy sand & small quanities of shell
Deep sand	NTZ 15	20.8	Sand with shell & cobbles
	OUT 8	22.8	Sand, shell & few cobbles
	MPA 5	21.5	Sand, shell & pebbles
Mud	MPA 6	24	Mud
	NTZ 11	15.6	Very fine sandy mud

Deciding whether the outputs from PRIMER displayed a difference between samples and how much confidence could be expressed in the statistical tests performed depended on the following factors: (1) The stress value of the MDS ordination. A stress value gives an indication of how well the two-dimensional plot represents the multi-dimensional sample relationship. Values between 0.05 and 0.2 generally correspond to a good representation of sample similarities (Clarke & Warwick 1994; Boyd *et al.* 2004). (2) The Global R value from the ANOSIM and its significance level. An R value ranges from -1 to 1. A value of 1 would indicate treatments are completely dissimilar, whilst a value of -1 would indicate that variation within treatments is greater than the variation between

treatments. Low significance values would indicate high reliability of the Global R values produced. (3) The average similarity within treatment replicates. Here, large values would signify that samples taken from within the same treatment share a large proportion of their ecological community characteristics. (4) The species identified to be important in characterising treatments.

- Analysis of BRUV data

To investigate if a recording time of 50 minutes was sufficient to capture most of the species likely to appear at a site, the cumulative number of species observed was plotted against time in simple line graphs for each BRUV recording. If the number of species observed plateaued towards the end of a video, then it is likely that most species found at that site had been recorded. If the number of species observed continued to increase, then the recording time may not have been long enough and should be increased for next year's surveys.

To look for overall differences between sites in and outside the NTZ, the size and abundance of all individuals were compared in simple bar charts. Species were then grouped into broad groups (e.g. gadoids, flatfish, and wrasse) and their abundance and size were compared again in bar charts and tested by one-way ANOVA.

- Exploring the larger ecosystem

As both methodologies used in this study gathered abundance data on very different groups of organisms, the combining of both datasets was trialled in this study. Only sites where both BRUV and dive surveys had been conducted were included in this dataset.

For statistical analysis, the SACFOR scale used to estimate the abundance of benthic taxa was converted into numerical categories ranging from 0-6, where a value of 0 would indicate the absence of a taxon and 6 would represent the superabundance of a taxon, as denoted by the SACFOR scale (Connor *et al*. 2004). It was our intention to create a generalised linear model (GLM) using Shannon's biodiversity index as a response variable to explore how benthic organisms and their conferring structural complexity interacted with the biodiversity of Lamlash Bay. However, scatterplots and intercorrelation matrices revealed that the abundance of different benthic taxa were highly intercorrelated (Table 2) meaning they would not be allowed together in a GLM (Crawley 2005). This result was not surprising. In theory, a site containing a large abundance of coral and hydroids would likely encompass a large abundance of other benthic taxa as these organisms are extremely fragile, requiring low disturbance and a stable substrate to attach to. Similarly, the presence of photosynthetic maerl and kelp will decline with increasing depth. Therefore, instead of a GLM, the estimated abundances of benthic taxa were combined to assign each site a numerical value indicating its level of bottom complexity. This was done using the equation below:

$$BC = \frac{\sum SACFOR}{MaxS}$$

Equation used to assign a numeric value of bottom complexity | where *BC* = Bottom complexity; *ΣSACFOR* = The sum of SACFOR estimates for every benthic taxon measured; *MaxS* = The maximum possible score for each taxon. The SACFOR scale had 7 possible values (i.e. absent - 1, rare - 2, occasional - 3, frequent - 4, common - 5, abundant - 6 and superabundant - 7) meaning each taxon could achieve a maximum score of 7.

To determine how the structural complexity of the seafloor was influencing biodiversity, the bottom complexity of sites was plotted against Shannon's biodiversity index, number of species and number of individuals in simple scatter charts incorporating linear trendlines. The resulting R^2 values were used to assess the strength of the correlation and tested for significance using Pearson's Product Moment Correlational Analysis.

For meaningful analysis in PRIMER, the dataset combining dive survey and BRUV data was reduced to include only those samples which had comparable habitats both in and outside the NTZ. This step was to allow, for example, the ecological assemblages of kelp forests inside the NTZ to be compared with the assemblages of kelp forests outside the NTZ. Unfortunately, this made sample sizes even smaller, meaning extra caution must be taken in interpreting the results.

Table 2 | Intercorrelation matrix of several explanatory variables. Many variables were strongly intercorrelated (i.e. $-0.7 \leq r \geq 0.7$) and therefore could not be used in a GLM together. These variables have been highlighted in red. Values represent Pearson's correlation.

-	Depth	Maerl	Macroalgae	Kelp	Sponge	Anemones	Coral	Tunicates	Hydroids
Depth									
Maerl	-0.51								
Macroalgae	-0.70	0.26							
Kelp	-0.71	0.69	0.51						
Sponge	-0.30	0.03	0.34	0.34					
Anemones	-0.18	0.37	0.17	-0.08	-0.06				
Coral	-0.36	0.14	0.37	0.48	0.70	-0.09			
Tunicates	-0.13	0.22	0.22	0.30	0.34	0.04	0.29		
Hydroids	0.06	0.06	0.17	-0.03	-0.01	0.17	0.09	0.48	
Bryozoans	-0.44	0.35	0.57	0.71	0.56	0.04	0.79	0.68	0.33

As the combined dataset now met the assumption of equal variances, a two-way ANOVA was conducted using protection and habitat as fixed factors against several univariate measures of biodiversity. The resulting estimated marginal means were then plotted against protection in simple line graphs. Estimated marginal means have the advantage that they are suitable for unbalanced designs such as the one used in this study (Dytham 1999).

Results

- Were enough dive surveys conducted?

Sites varied greatly in their scallop density, as reflected by the large error bars and shifting mean in Figure 2. Nonetheless, the mean does level out with number of surveys conducted and the error bars do narrow, suggesting the number of dive surveys conducted was adequate. Interestingly, almost no queen scallops were observed for the first six dive surveys inside the NTZ.

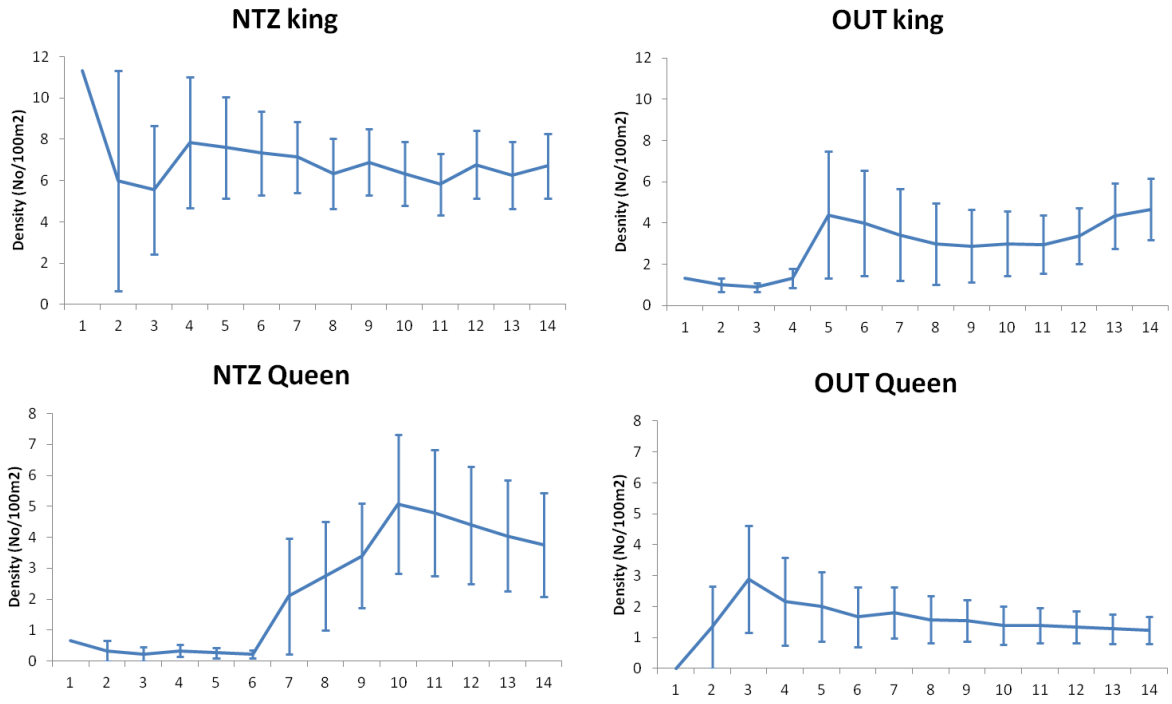


Figure 2 | The number of dive surveys appeared to be adequate. Graph shows the cumulative mean density of scallops plotted against number of dive surveys conducted (*x* axis). Error bars represent ±1 SE.

- Comparisons of scallop density and abundance

The mean density of adult king scallops per 100 m^2 in and outside the marine reserve was 6.71 (±SE = 1.5) and 4.67 (±SE = 1.56) respectively (Fig. 3). Despite king scallop density being 1.5 times higher inside the NTZ, the difference was found to be non-significant (Mann–Whitney U test, U = 88. 5, N = 28, P > 0.05). The mean density of adult queen scallops per 100 m^2 in and outside the marine reserve was 4.05 (±SE = 1.68) and 1.23 (±SE = 0.44) respectively (Fig. 4), over three times higher inside the NTZ. Once again though, this difference was found to be non-significant (Mann–Whitney U test, U = 97.5, N = 28, P > 0.05). The large variation between sites likely made any significant differences difficult to detect, and may explain these results. Surprisingly, no juvenile scallops were found outside the NTZ in 2011 and very few were recorded inside (Fig. 5).

Comparing between years, the density of queen and juvenile scallops in and outside the NTZ declined considerably between 2010 and 2011. Juvenile scallops saw the strongest decline, going from “rare” to completely “absent” outside the NTZ, and “occasional” to “rare” inside the NTZ. King scallop density outside the NTZ was 1.62 times lower in 2011 than in 2010. Whilst queen scallop

density was 4.9 times lower. The declines were less pronounced inside the NTZ, with king scallop density increasing slightly inside the NTZ, and queen density becoming 1.5 times lower (Fig. 5 & 6). A two-way ANOVA showed all these trends as being non-significant (Table 3). Again, this may be a result of great variation in scallop abundance between sites. The estimated abundance of juvenile scallops was not subjected to a two-way ANOVA because SACFOR data is unsuitable for such analysis.

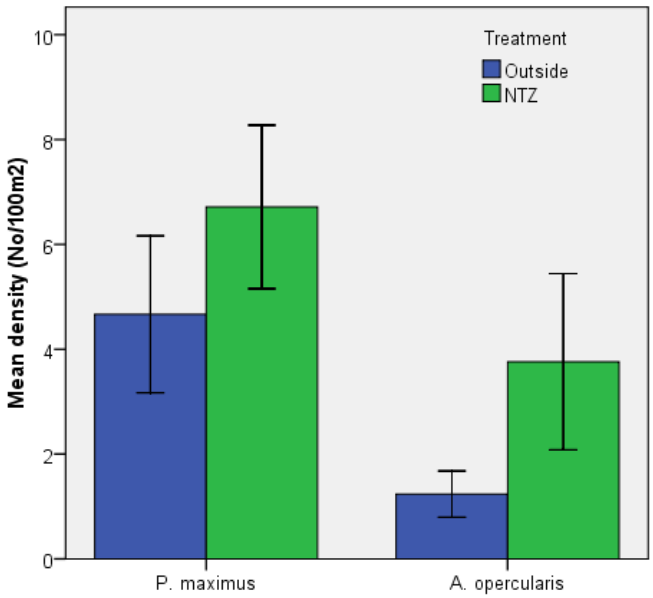


Figure 3 | The density of both king and queen scallops appeared higher inside the NTZ in 2011. Error bars represent ±1 SE.

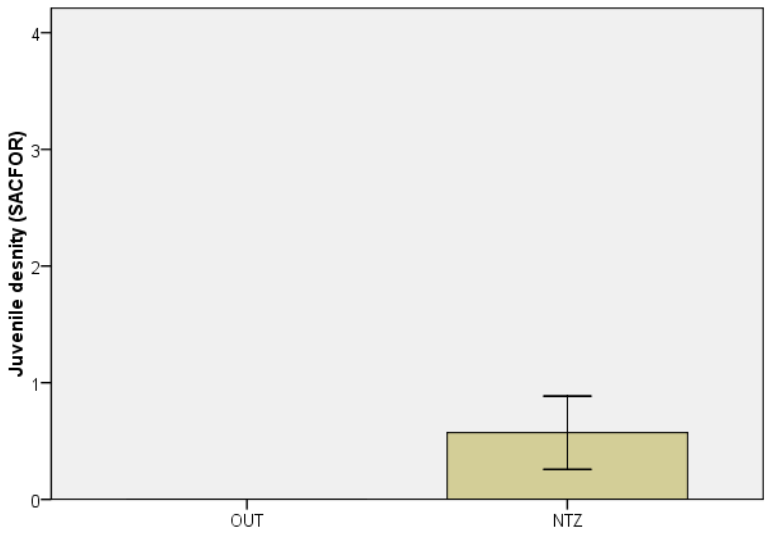


Figure 4 | The estimated abundance of juvenile scallops was slightly higher inside the NTZ in 2011. Error bars represent ±1 SE.

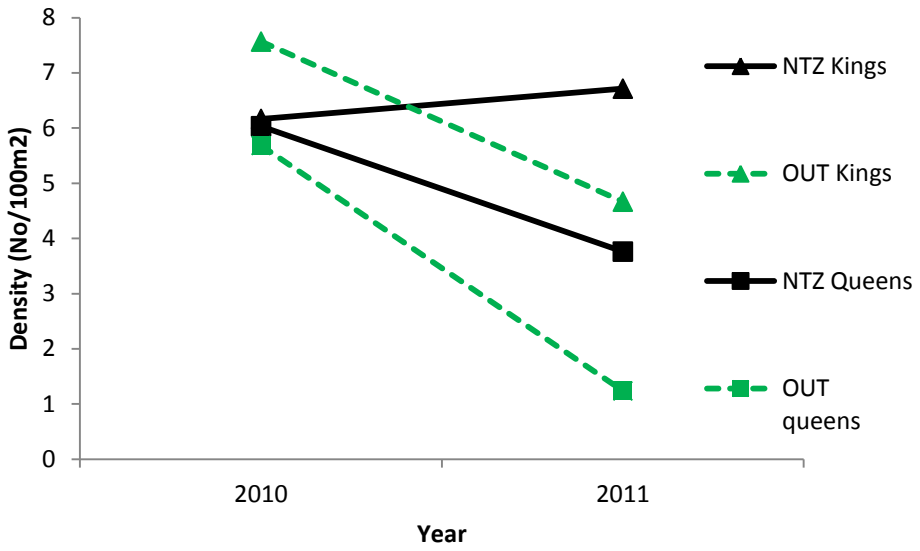


Figure 5 | The density of scallops declined dramatically in 2011 except for king scallops, which increased slightly inside the NTZ. No error bars were incorporated in this graph due to great variation about the mean.

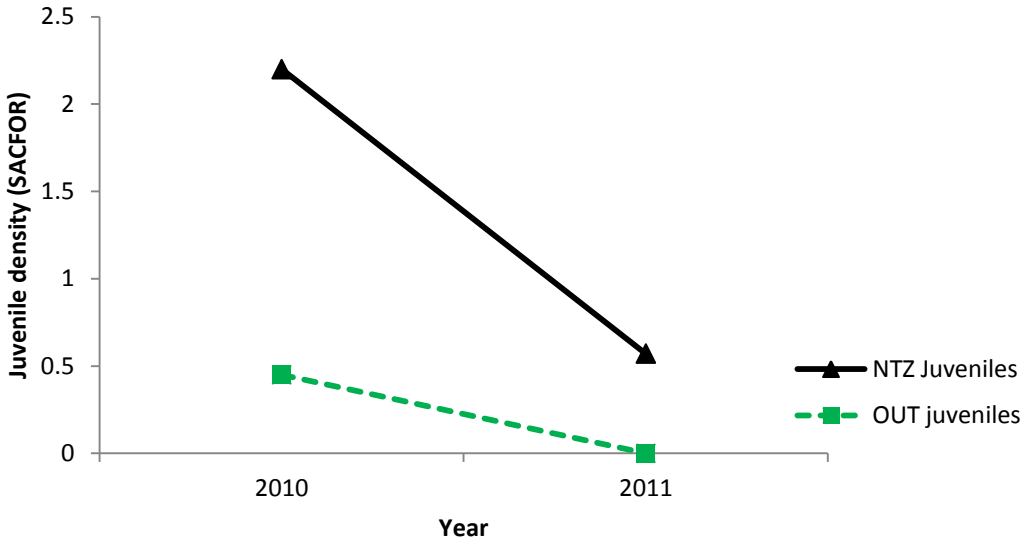


Figure 6 | The estimated abundance of juvenile scallops declined both in and outside the NTZ between years. No error bars were incorporated in this graph due to great variation about the mean.

Table 3 | The decline in king and queen scallop density were flagged as non-significant in a two-way ANOVA. Where SS = Type III sum of squares; df = degrees of freedom; MS = Mean square.

Source	SS	df	MS	F	p
a) King scallops					
Year	22.786	1	22.786	.318	.575
Protection	1.727	1	1.727	.024	.877
Protection x Year	48.943	1	48.943	.683	.412
b) Queen scallops					
Protection	41.042	1	41.042	.784	.379
Year	170.421	1	170.421	3.257	.076
Protection * Year	14.716	1	14.716	.281	.598

- Biometrics

All biometric graphs along with their trendline equations, associated R^2 values and Von-Bertalanffy values are available in Appendices 3-6. Relative confidence could be expressed in all the biometric trends produced (i.e. $R^2 \geq 0.7$). Through extrapolating the biometrics to the entire sampled population (Fig. 7), the mean exploitable biomass per $100m^2$ of king scallops in and outside the NTZ was 295.61g (±SE = 66.32) and 147.69g (±SE = 38.95) respectively. Exploitable biomass of king scallops was therefore 2 times higher inside the NTZ, a difference found to be significant (ANOVA, $F_{(1,27)} = 36.52$, $P < 0.05$). Similarly, the mean reproductive biomass per $100m^2$ of king scallops inside the NTZ was 64.17g (±SE = 10.37) and 27.1 outside (±SE = 10.1). The reproductive biomass of king scallops was therefore 2.3 times higher inside the NTZ, again, a significant difference (ANOVA, $F_{(1,27)} = 8.51$, $P < 0.05$).

In contrast, the mean exploitable biomass per $100m^2$ of queen scallops was 16.16g (±SE = 7.03) and 4.67g (±SE = 1.41) respectively. Despite being over three times higher inside the NTZ, this difference was non-significant (ANOVA, $F_{(1,27)} = 2.56$, $P < 0.05$). Likewise, the mean reproductive biomass per $100m^2$ was 3.68g (±SE = 1.58) and 1.79g (±SE = 0.74) respectively, over two times higher but was not significant (ANOVA, $F_{(1,27)} = 1.27$, $P < 0.05$). As before, the variation between sites was very large and likely made the detection of statistical differences very difficult.

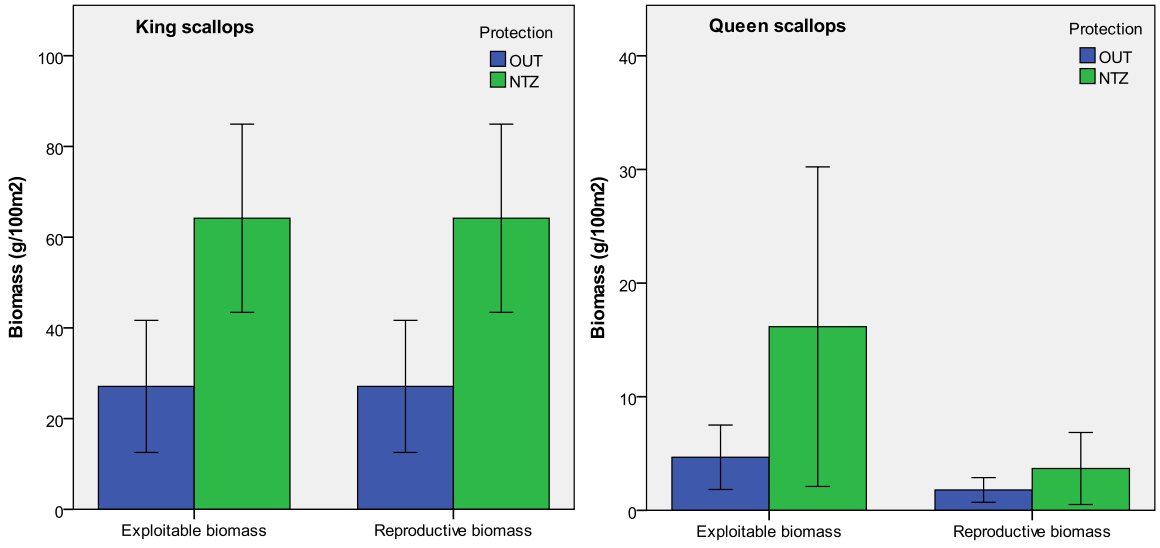
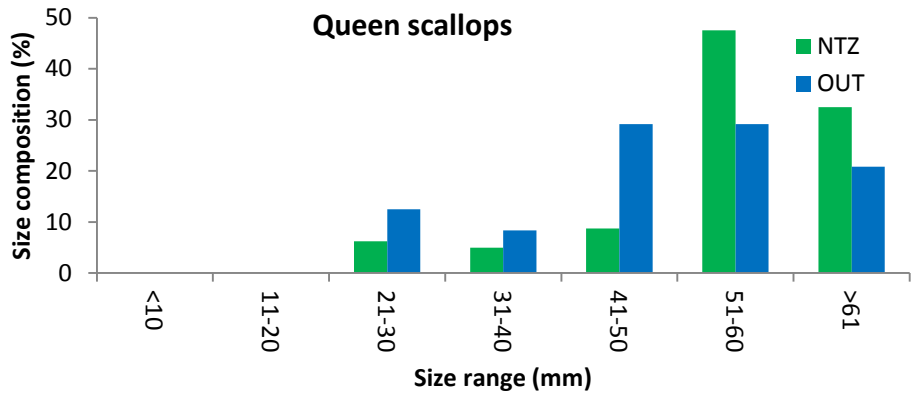


Figure 7 | The exploitable and reproductive biomass of king and queen scallops were higher inside the NTZ. Error bars represent 95% confidence intervals to illustrate the great variation observed about the mean. Variation was particularly high in queen scallops, making it difficult for statistical tests to find a significant difference between the 2 samples.

- Comparisons of scallop population structure

Comparisons of age structure between treatments suggested that scallop populations within the NTZ were composed of larger and older individuals (Fig. 8). These differences in age and size structure between sites within and outside the NTZ were found to be significant for both species (Table 4). In fact, the mean age of king scallops was 1.3 times higher inside the reserve and 1.2 times greater in size. Similarly, the mean age of queen scallops was 1.6 times higher inside the reserve and 1.1 times greater in size. Again, there is evidence that very little recruitment occurred in 2011.

A



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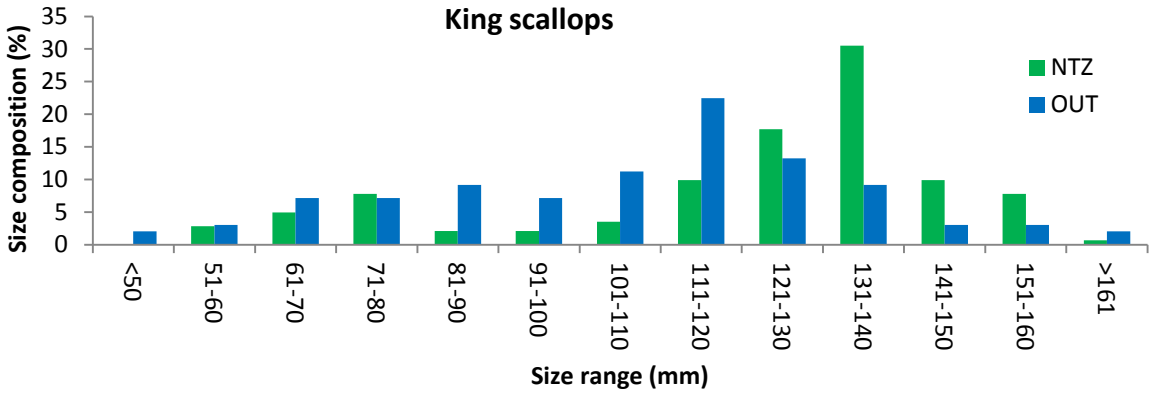

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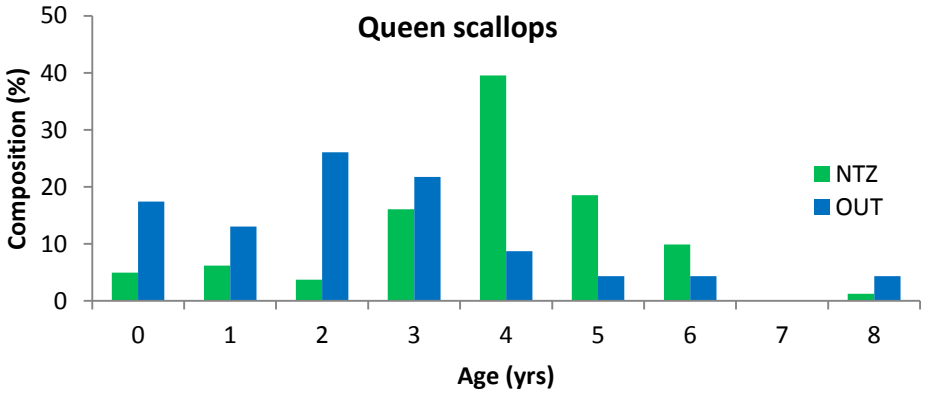

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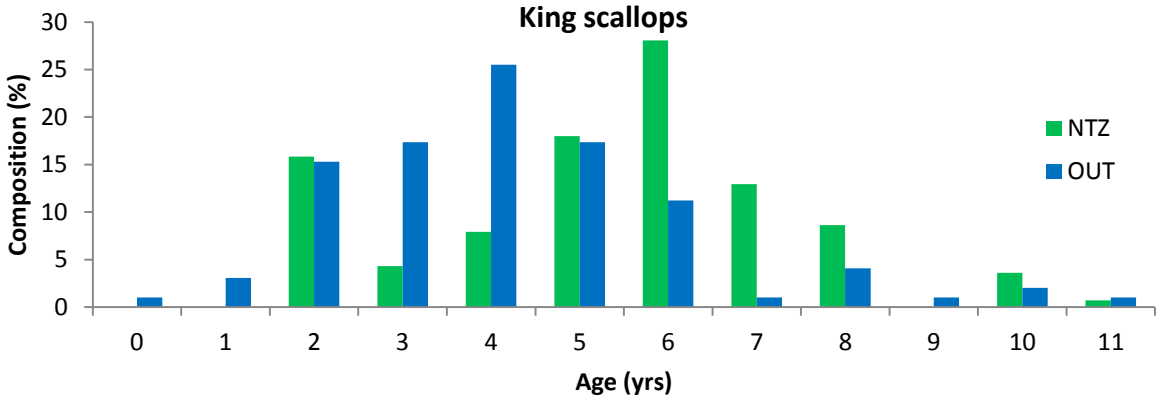

Figure 8 | Scallops were both older and larger inside the NTZ. Graphs show the size structure of queen (A) and king scallop (B) populations in and outside the NTZ. Also plotted is the age structure (estimated from biometrics) of queen (C) and king (D) scallops in and outside the NTZ.

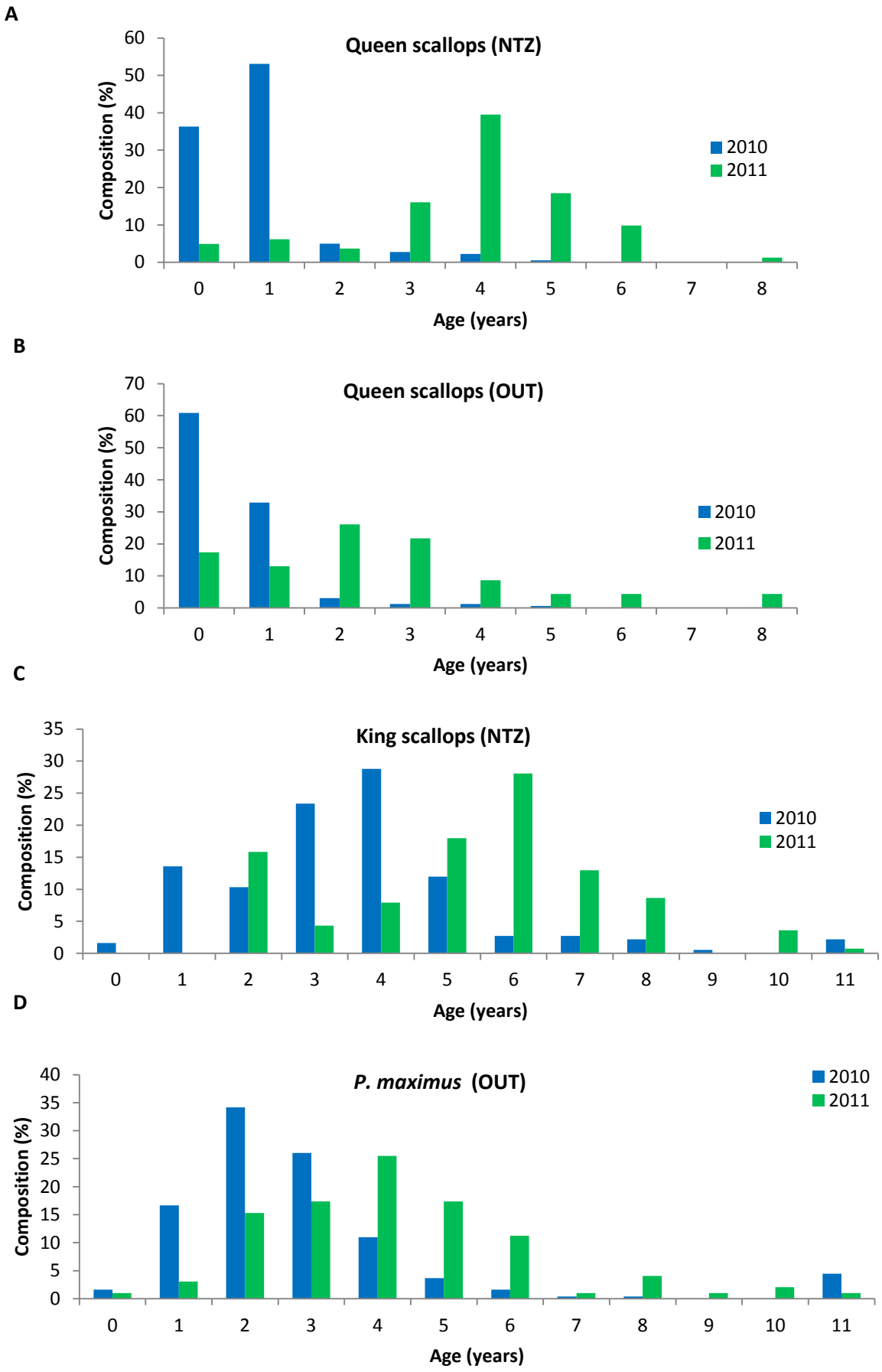

Figure 9 | Scallops were older and in 2011 than in 2010. Graphs show the age structure of queen scallops in (A) and outside (B) the NTZ, and king scallops in (C) and outside (D) the NTZ.

Table 4 |Differences observed in age and size structure were significant. Outputs from the Kolmogorov-Smirnov (K-S) 2 sample tests used to compare the size and age structure (age structure estimated from biometrics) of populations in and outside the NTZ for both scallop species. All comparisons were significant at $p < 0.05$ and denoted by (*).

Test variable	NTZ (n)	Outside (n)	K-S *Z*	*p*
Size - *P. Maximus*	139	98	2.696	0.001*
Age - *P. Maximus*	139	98	2.592	0.001*
Size - *A. Opercularis*	81	24	1.394	0.41*
Age - *A. Opercularis*	81	24	2.078	0.001*

Comparisons of age structure between 2010 and 2011 indicated that scallop populations were made up of older individuals in 2011 compared to 2010. In all cases, the peak age class of each population had shifted to the right, suggesting many scallops had survived 2010 to enter 2011 as a higher age class. Populations showed substantial recruitment of 2nd year age classes but again it appears very little recruitment occurred in 2011, with very few 0-1 age classes in 2011 compared to the previous year.

- Comparisons of ecological assemblages recorded from dive surveys

A resemblance matrix based on Bray-Curtis similarity measures revealed a wide range of similarity between samples, with values ranging between 10% (low similarity) and >70% (high similarity). The MDS ordinations (Fig. 10) based on these values indicated that the samples collected from the sites within and outside the NTZ were not clearly separated. There was therefore a need to further distinguish between these sites on a level other than just “in” or “out”. Labelling sites based on their habitat revealed clear clustering between sites of similar habitat, suggesting there is higher similarity within habitats than between them. It appears then, that designating samples to these different habitat types was justified.

The ANOSIM between the two levels of protection produced a Global R value of 0.35 and a significance value of 7%. This indicated that there was little overall difference between sites sampled in and outside the NTZ. However, when conducted between the different habitats a Global R value of 0.64 was produced with a significance value of 0.1%. This provided strong evidence that the ecological assemblages differ between different habitats.

The results of the SIMPROF test are graphically represented by a dendogram in Figure 11 and suggest that, out of the 10 different habitats sampled, there are only 3 statistically distinguishable groups. The first group encompasses “mud” and “deep muddy sand” habitats. The second group is the most diverse, containing “deep sand”, “deep boulder”, “sand”, and “muddy sand” habitats. The last encompasses “sandy mud” and “kelp forest” habitats. “Shallow boulders” and “maerl” were the only habitats to be split between two groups, meaning there were statistical differences between sites of the same habitat. This may indicate that protection from fishing is causing the ecological assemblages of some sites to diverge, or that shallow boulders and maerl habitats are highly variable in the assemblages they support, or may be an artefact of these habitats being inappropriately labelled.

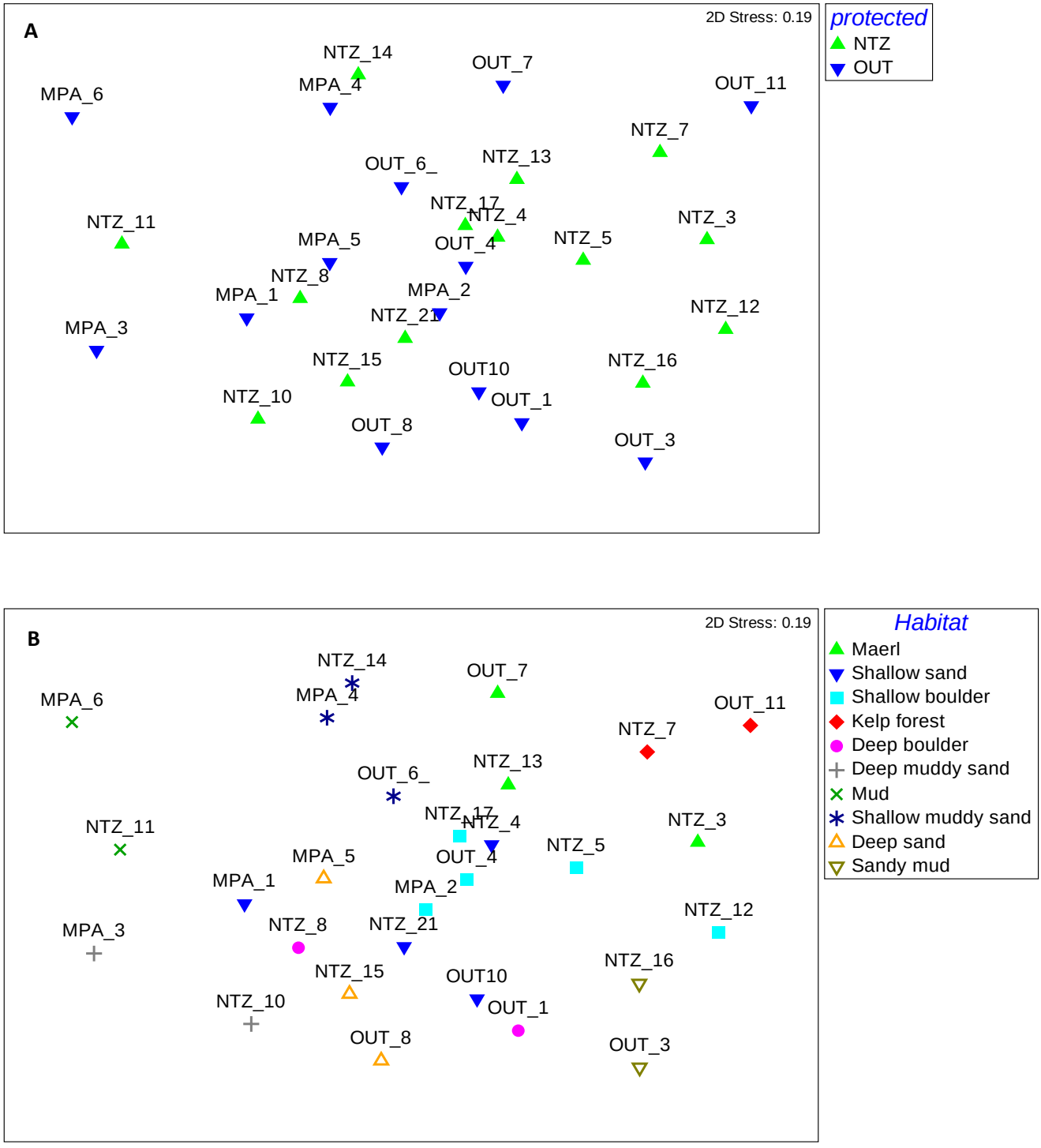

Figure 10 | There is no overall difference between samples taken in and outside the NTZ (A). However, when samples were labelled by their habitat type, clear clustering of similar habitats was observed (B). Charts show MDS of Bray–Curtis similarity values derived from untransformed species abundance (colonial organisms excluded) data recorded during dive surveys.

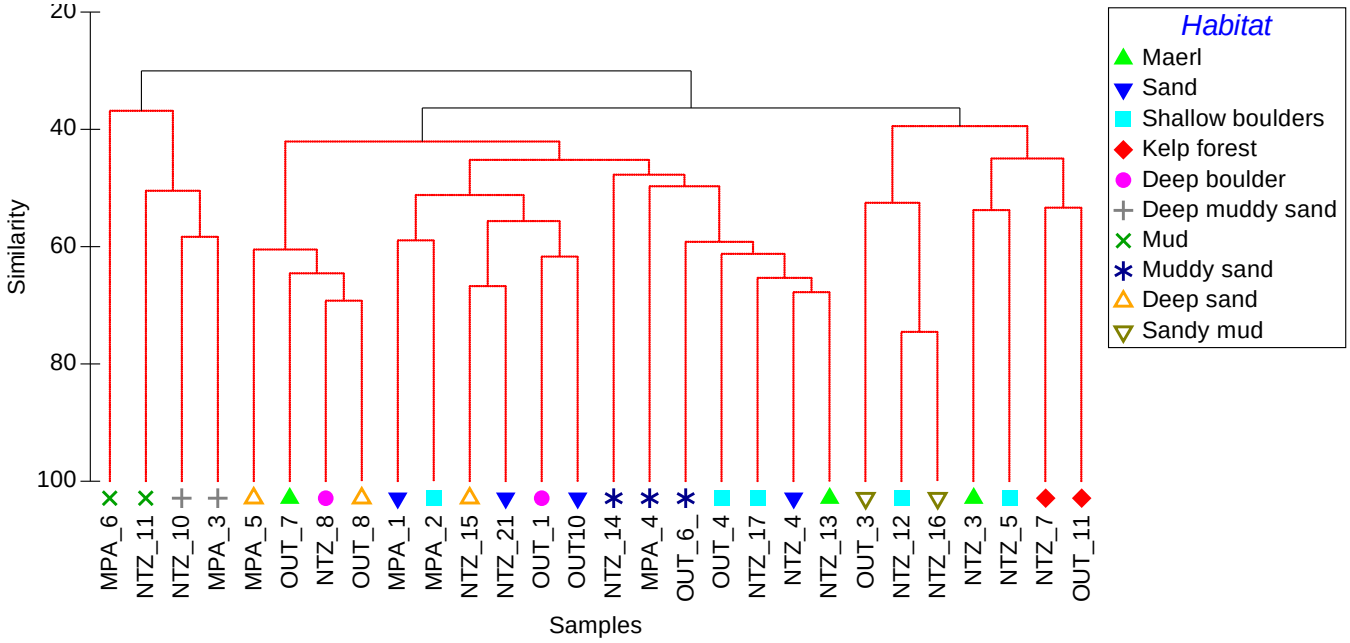

Figure 11 | Only 3 statistically distinguishable groups existed in the dataset. This group average dendogram created from the SIMPROF test based on Bray-Curtis similarities was derived from untransformed species abundance (colonial organisms excluded) data. All sites are connected by a red dotted line representing they are statistically indistinguishable at $p>0.05$. Whereas a black line would indicate significant assemblages at $p<0.05$.

The results from the SIMPER analysis are summarised in Table 5. The analysis found very little difference between all sites inside the NTZ and outside, with both treatments sharing very similar species. However, the NTZ was characterised by 13 species that contributed towards over 90% of the faunal assemblages inside the NTZ. The three most important species inside the NTZ were identified to be gobies (of the group Gobidae), parchment worms (*Chaetopterus spp*) and king scallops (*P. maximus*). In contrast, sites outside the NTZ were characterised by just 10 species that contributed towards 90% of faunal assemblages, suggesting sites outside the NTZ were dominated by a smaller number of species. The three most important species that characterised sites outside the NTZ were the starfish (*Asterias reubens*), the harbour crab (*Liocarcinus depurator*) and hermit crabs (*Pagurus spp*).

Analysis between habitats was not possible for many samples as SIMPER analysis requires at least three samples of each group. However, where SIMPER analysis was possible all habitats were composed of similar ecological assemblages consisting largely of crabs and starfish. Based on these results, Lamlash Bay appears to be an area of low biodiversity, with assemblages heavily dominated by crustaceans and invertebrates.

To further test for differences in biodiversity between sites in and outside the NTZ, the graphs in Figure 12 were created. For the majority of habitats sampled, the number of species, number of individuals (excluding colonials) and Shannon's biodiversity index (excluding colonials) were all substantially higher inside the NTZ, and were found to be significant (ANOVA, $F_{(1,27)} = 7.4$, $P < 0.05$). Evenness, on the other hand, did not differ between samples (ANOVA, $F_{(1,27)} = 2.56$, $P < 0.05$).

Table 5 |Results from SIMPER analysis of untransformed macrofauna data (colonial organisms excluded) listing the main characterising species from samples subject to the two different levels of protection. Average abundance, average similarity and the % contribution to similarity made by each characterising species are shown. Also listed are the cumulative percentage and the overall average similarity between replicate samples from within each group.

Treatment	Species	Average abundance	Average similarity	Similarity /SD	% Contribution	Cumulative %	Overall average similarity
NTZ	GOBIDAE	16.57	10.21	1.88	20.31	20.31	**50. 27**
	Chaetopterus spp	10.79	5.37	2.27	10.67	30.98	
	Pecten maximus	10.07	5.35	2.72	10.64	41.62	
	Asteria reubens	13.43	4.73	1.17	9.42	51.04	
	Marthasterias glacialis	9.36	4.13	1.61	8.22	59.26	
	Liocarcinus depurator	13.43	3.06	0.9	6.08	65.34	
	Porania pulvillus	5	2.91	3.06	5.79	71.13	
	Necora puber	5.71	2.41	2.14	4.8	75.93	
	Pagurus spp	12.21	1.98	3.08	3.93	79.86	
	Aequipecten opercularis	5.64	1.69	0.45	3.37	83.23	
	Macropodia spp	5.36	1.44	0.56	2.87	86.1	
	Cancer pagurus	2.36	1.22	0.84	2.42	88.52	
	Munida rugosa	5.29	0.83	0.45	1.65	90.17	
OUT	*Asterias reubens*	17.86	10.75	0.96	20.62	20.62	**52.15**
	Liocarcinus depurator	13.64	9.76	1.53	18.72	39.34	
	Pagurus spp	14.14	5.92	1.33	11.34	50.68	
	GOBIDAE	9.43	5.25	1.22	10.07	60.75	
	Chaetopterus spp	7.86	2.89	1.62	5.54	66.29	
	Pecten maximus	7	2.8	1.79	5.37	71.67	
	Munida rugosa	7.29	2.74	0.65	5.25	76.91	
	CRINOIDEA	10.86	2.71	0.55	5.2	82.11	
	Necora puber	2.86	2.17	0.71	4.16	86.28	
	Porania pulvillus	6.14	2.11	1.41	4.05	90.33	

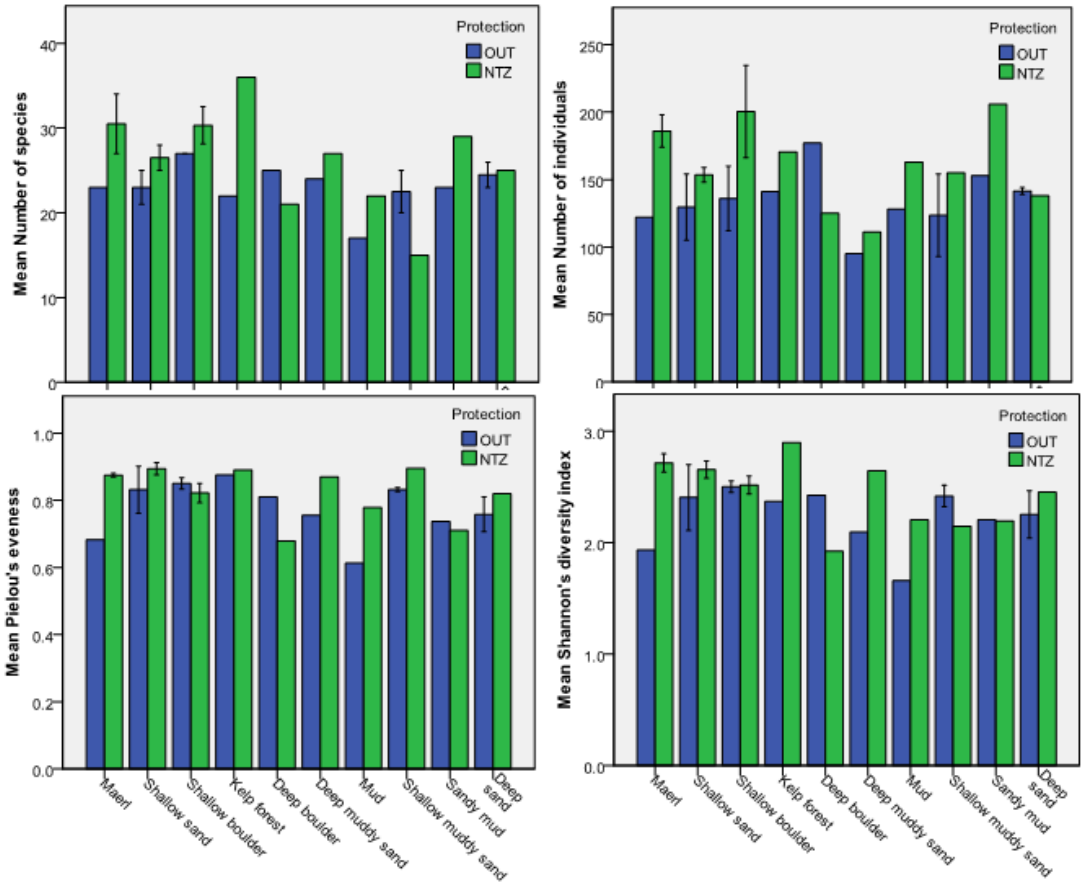

Figure 12 | For the majority of habitats sampled, univariate measures of biodiversity were highest inside the NTZ. For samples with at least 2 replicates, error bars represent ±1 SE.

- Was a 50 minute recording time sufficient?

For the majority of sites, results suggested that most species that were likely to be recorded had been observed (Fig. 13) However, for some sites the cumulative number of species observed continued to rise at the end of the 50 minutes recording time. It may therefore be best to increase recording time for next year's surveys.

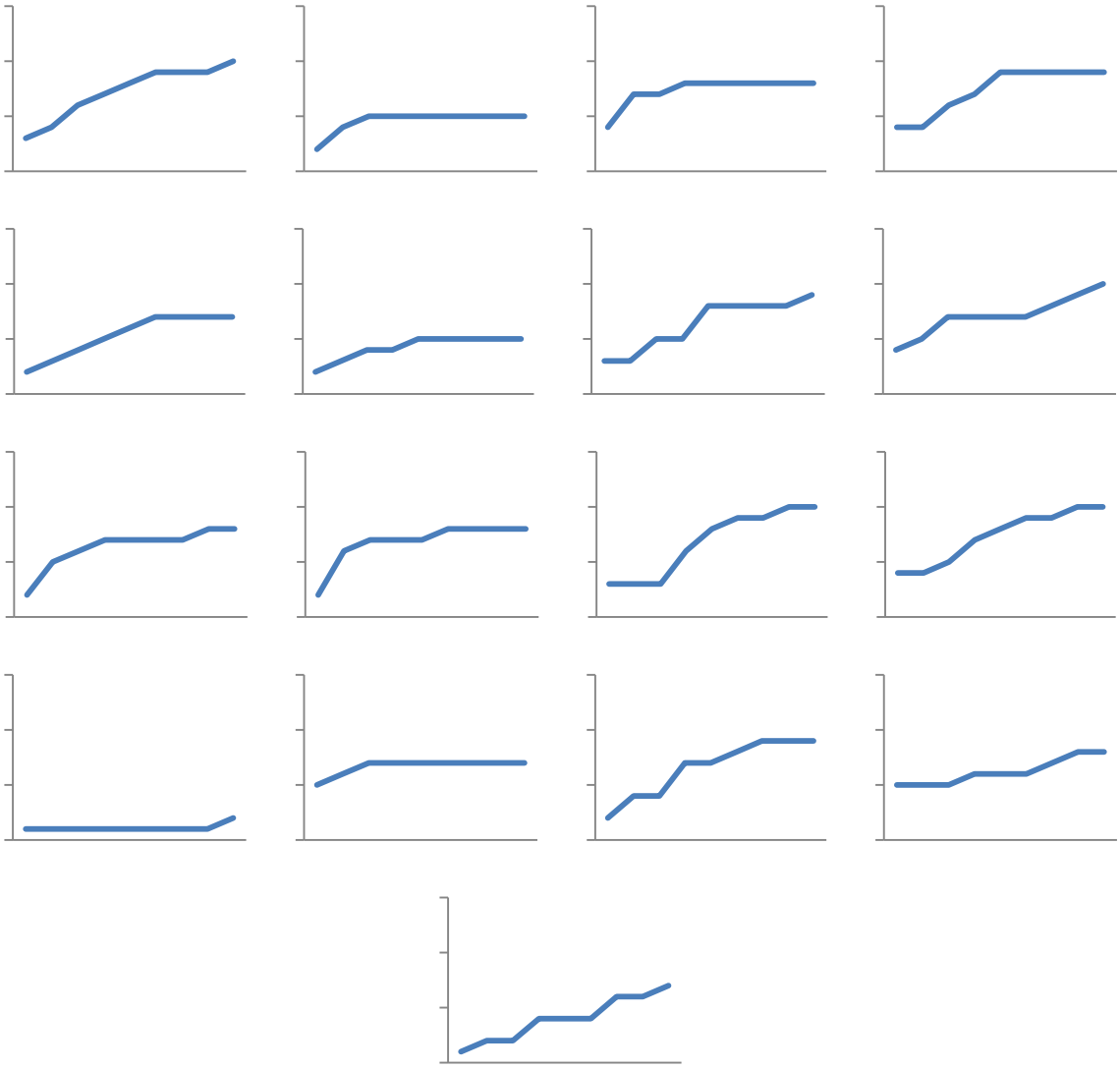

Figure 13 | Most species that were likely to be caught on camera for each site had been observed. Graphs show the cumulative number of species observed (*y* axis) plotted against minutes into each recording (*x axis*).

- Analysis of fish and crustacean populations from BRUV data

A total of 303 individuals were recorded from 27 species of 12 different families. Despite one less BRUV deployment being conducted inside the NTZ, 163 individuals were recorded inside the NTZ compared to 140 outside, a difference found to be significant (Mann–Whitney U test, $U = 2248.5$, N = 17, $P < 0.05$). This difference appears to be down to the NTZ containing large quantities of gadoids (Fig. 14). Conversely, sites outside the NTZ had greater diversity with 24 species from 12 families

being recorded, compared to 20 species from 10 families inside the NTZ. There was no difference in the size of individuals (Mann–Whitney U test, U = 1248.6, N = 303, P > 0.05). Overall, the most common species were whiting (*Merlangius merlangus*, 73 observations), followed by the harbour crab (*Liocarciuns depurator*, 52 observations), cod (*Gadus morhua*, 25 observations) and haddock (*Melanogrammus aeglefinus*, 24 observations). Interestingly, all individuals of cod and haddock were in their juvenile form.

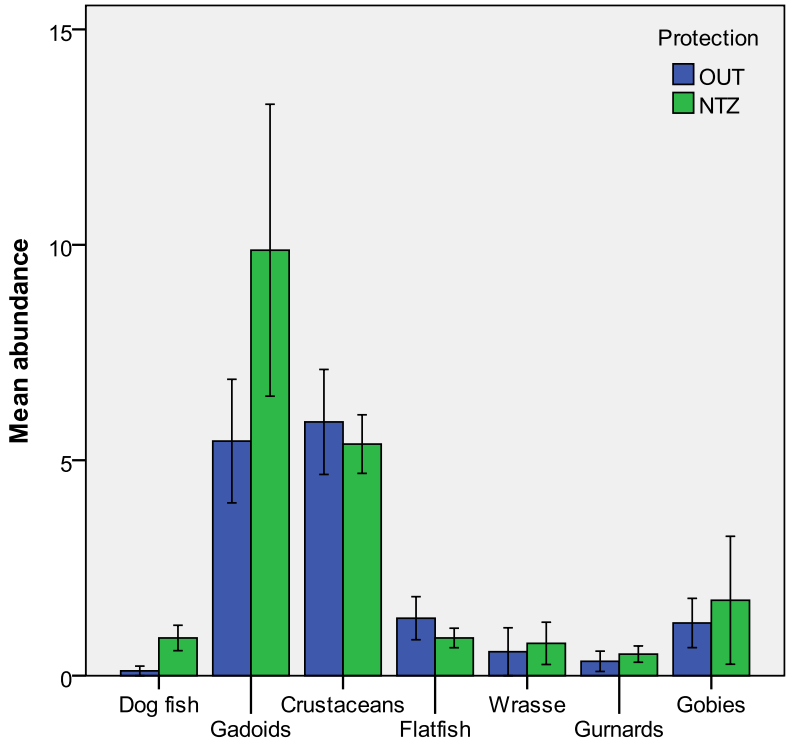

Figure 14 | The abundance of fish was significantly higher inside the NTZ. However, the graph shows that this was not the case for all groups, suggesting the difference was largely due to the high abundance of gadoids inside the NTZ. Error bars represent ± 1SE.

- Investigating the larger ecosystem

After combining the BRUV and dive survey data, it was found that the number of species, number of individuals and Shannon's biodiversity index positively correlated with bottom complexity (Fig. 15). Although these positive relationships are not particularly strong (i.e. R^2 ranges between 2.6 - 4.9) they are very clear and Pearson's correlation found them all to be significant (Pearson's Correlation, r = 0.51 - 0.72, N = 17, P <0.05).

The dataset was then reduced to include only comparable habitats. As before, MDS ordinations (Fig. 16) revealed that sites within and outside the NTZ were not clearly separated. Labelling sites based on their habitat showed clear clustering, suggesting once again that there was higher similarity within habitats than between them. Again, confidence can be expressed in labelling the different habitats.

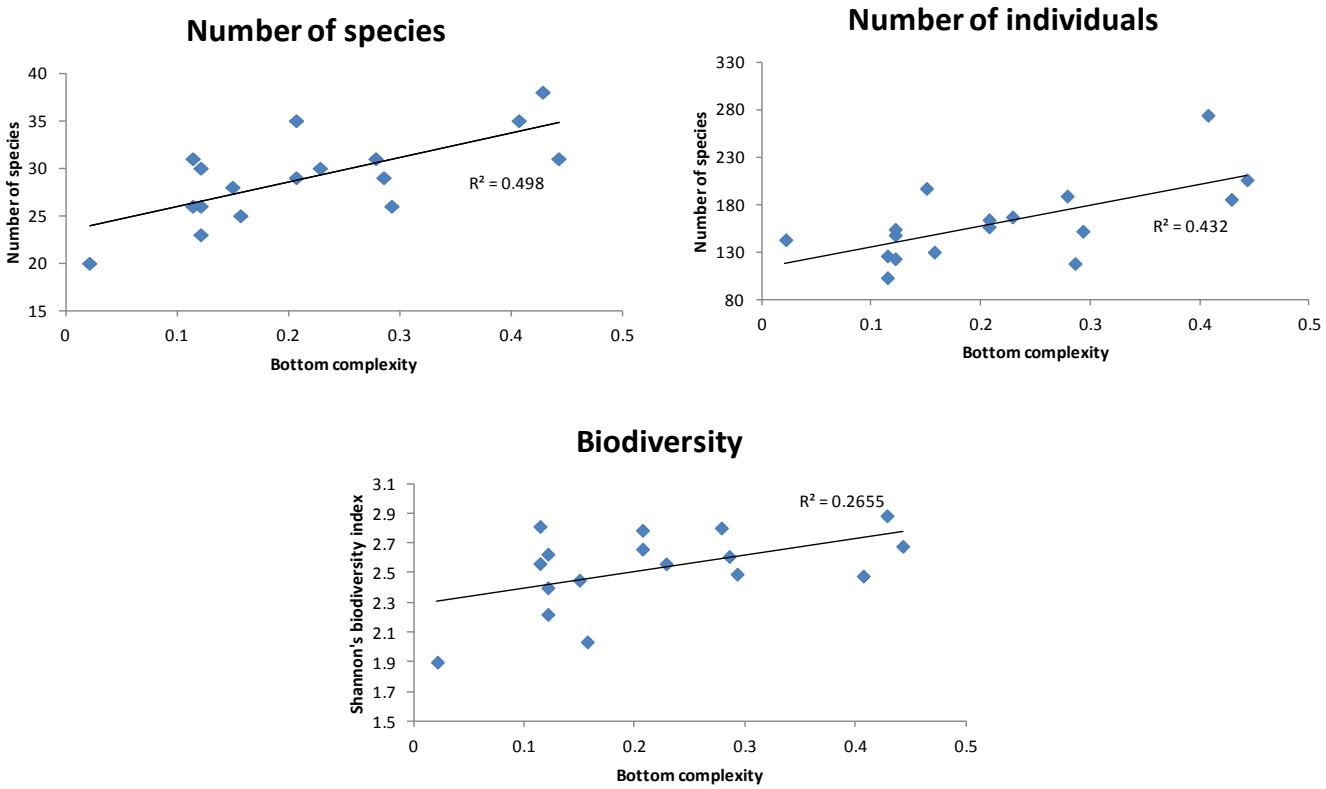

Figure 15 | **Sites with greater bottom complexity (a numerical value based on the abundance of various benthic taxa) conferred greater biodiversity.** Data fitted with a linear trendline, of which the R^2 values are displayed.

The ANOSIM between the two levels of protection produced a Global R value of 0.167 and a significance value of 40%. This indicates that there is great variation between samples and little overall difference between sites sampled in and outside the NTZ. However, when conducted between the different habitats an R value of 0.71 was produced with a significance value of 0.6%. This provides strong evidence that, again, the ecological assemblages do differ between different habitats.

The results of the SIMPROF test are graphically represented by a dendogram in Figure 17 and suggest that, out of the four different habitats sampled, there are only two statistically distinguishable groups. “Mud” supports ecologically unique assemblages compared to other sites. This allows confidence to be expressed in pairing the site MPA 6 with the shallower NTZ 11, as mentioned earlier. In contrast to previous analyses, “Kelp forest”, “maerl” and “shallow boulders” are now statistically indistinguishable after combining BRUV and dive survey data.

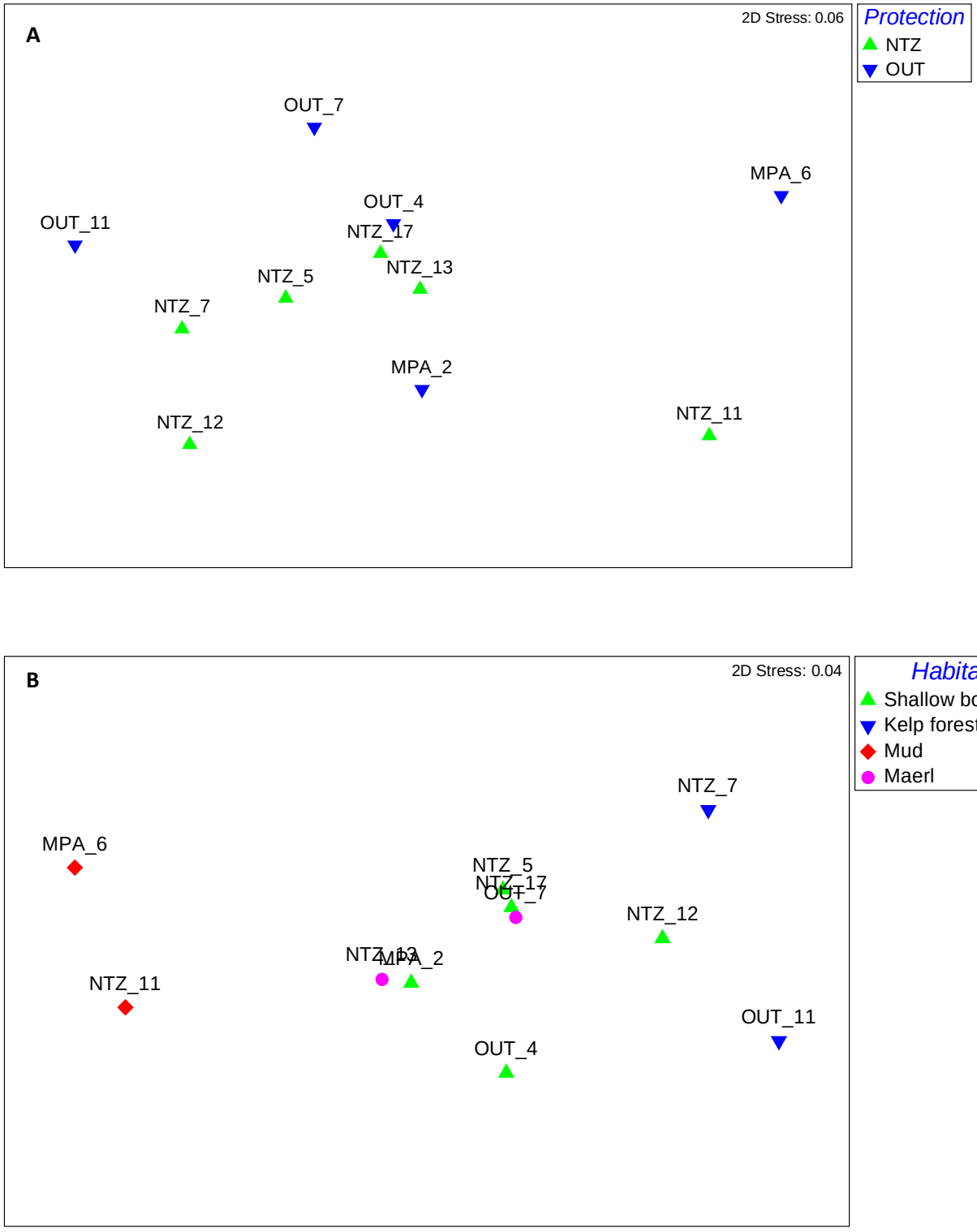

Figure 16 | There was no overall difference between samples taken in and outside the NTZ (A). However, when samples were labelled by their habitat type, clear clustering of similar habitats was observed (B). Charts show MDS of Bray–Curtis similarity values derived from untransformed species abundance (colonial organisms excluded) data recorded during dive and BRUV surveys. Only comparable habitats were included.

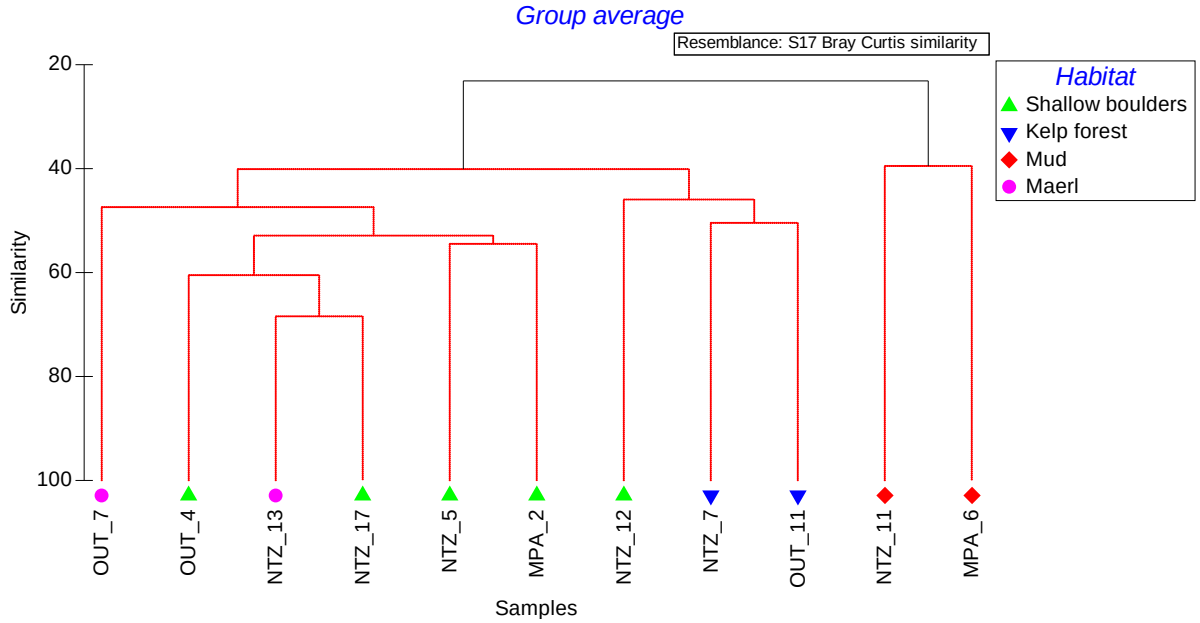

Figure 17 | Only 2 statistically distinguishable groups existed in the combined dataset. This group average dendogram created from the SIMPROF test based on Bray-Curtis similarities was derived from untransformed species abundance (colonial organisms excluded) data. All sites are connected by a red dotted line representing they are statistically indistinguishable at $p>0.05$. Whereas a black line would indicate significant assemblages at $p<0.05$.

The results from the SIMPER analysis are summarised in Table 6. Now the dataset encompasses both BRUV and dive survey data some differences between NTZ and outside are beginning to emerge. The average similarity between sites within the NTZ was 5% lower than outside, indicating that sites inside the NTZ may be slightly more variable and more diverse. This is further supported by the result that 12 species contributed towards over 90% of ecological assemblages inside the NTZ, whereas sites outside the NTZ were characterised by only 8 species, suggesting they are less diverse. Species were similar to previous analyses utilising only dive survey data, except that both cod (*Gadus morhua*) and haddock (*Melanogrammus aeglefinus*) were now considered important species in characterising sites inside the NTZ and not outside.

To further test differences in biodiversity between sites in and outside the NTZ, a two-way ANOVA found that the number of species, number of individuals and Shannon's diversity index all significantly differed between NTZ and outside, but not between different habitats (Table 7). Figure 18 shows that these three measures of biodiversity were higher inside the NTZ for all habitats. There was no significant difference in Pielou's evenness between sites in and outside the NTZ and there was no interaction between protection and habitat. This lack of interaction may be a result of the small sample size used.

Table 6 |Results from SIMPER analysis of untransformed macrofauna data (colonial organisms excluded) from BRUV and dive survey data listing the main characterising species from samples subject to the two different levels of protection. Average abundance, average similarity and the % contribution to similarity made by each characterising species are shown. Also listed are the cumulative percentage and the overall average similarity between replicate samples from within each group.

Treatment	Species	Average abundance	Average similarity	Similarity /SD	% Contribution	Cumulative %	Overall average similarity
NTZ	GOBIDAE	21.5	12.9	6.98	25.86	25.86	**49.87**
	Asterias reubens	13.5	5.37	1.36	10.76	36.63	
	Pecten maximus	11.67	4.89	1.85	9.81	46.44	
	Marthasterias glacialis	9.5	4.57	1.57	9.16	55.6	
	Chaetopterus spp	14.17	3.97	1.73	7.96	63.56	
	Necora puber	7	2.8	5.53	5.63	69.18	
	Porania pulvilus	6.83	2.74	2.21	5.5	74.69	
	Gadus morhua	8	2.7	4.6	5.41	80.1	
	Pagurus spp	9.33	1.99	2.44	3.99	84.09	
	Liocarcinus depurator	13.33	1.43	6.98	2.87	86.96	
	Munida rugosa	4.67	1.29	0.58	2.58	89.54	
	Melanogrammus aeglefinus	5	1.11	3.96	2.23	91.77	
OUT	*Liocarcinus depurator*	14.4	12.63	6.48	23.08	23.08	**54.74**
	GOBIDAE	15.8	9.82	1.31	17.95	41.03	
	Munida rugosa	5.8	8.42	1.81	15.38	56.41	
	Pagurus spp	8.8	4.91	1.57	8.97	65.38	
	Asterias reubens	16.4	4.21	1.74	7.69	73.08	
	Marthasterias glacialis	8.6	4.21	5.55	7.69	80.77	
	Chaetopterus spp	4.8	3.51	2.22	6.41	87.18	
	Pecten maximus	6.4	2.81	5.6	5.13	92.31	

Table 7 | Level of protection was flagged as in a two-way ANOVA. Where SS = Type III sum of squares; df = degrees of freedom; MS = Mean square. Significant terms are highlighted by (*).

Source	SS	df	MS	F	p
a) Number of species					
Protection	133.175	1	133.175	35.778	.009*
Habitat	98.241	3	32.747	8.798	.057
Protection * Habitat	22.833	3	7.611	2.045	.286
b) Number of individuals	6838.248	1	6838.248	2.514	0.11*
Protection	469.083	3	156.361	.057	.979
Habitat	471.935	3	157.312	.058	.979
Protection * Habitat					
c) Evenness	.015	1	.015	9.255	.071
Protection	.024	3	.008	5.155	.106
Habitat	.019	3	.006	4.015	.142
Protection * Habitat					
d) Biodiversity					
Protection	.461	1	.461	27.585	.013
Habitat	.360	3	.120	7.175	.070
Protection * Habitat	.208	3	.069	4.141	.137

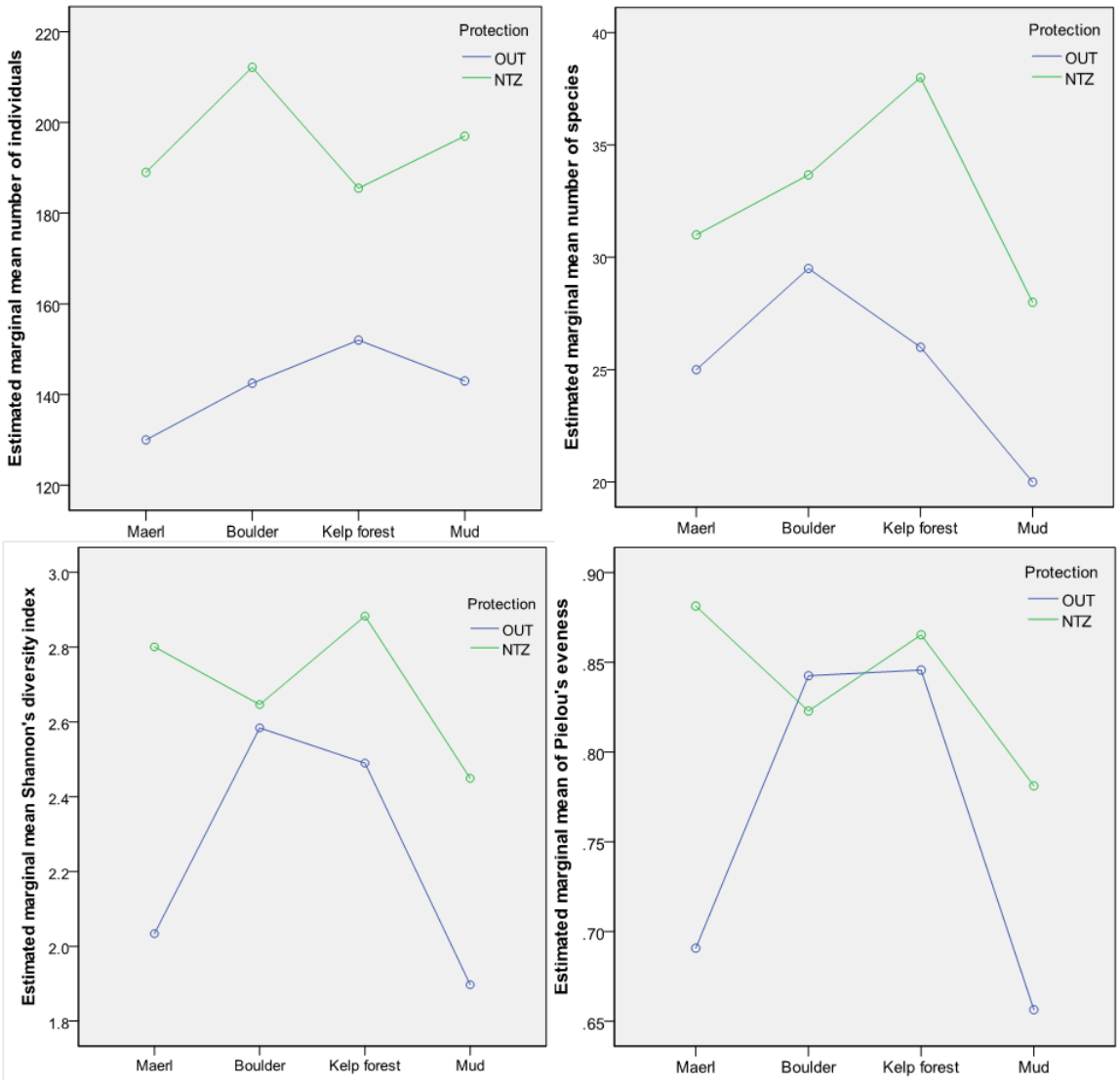

Figure 18 | In all cases but one the estimated marginal mean number of individuals, species, evenness and biodiversity were highest inside the NTZ. Estimated marginal means derived from a two-way ANOVA on data combining BRUV and dive survey data.

Discussion

This study was designed to investigate the effects of closed area protection on the structure of megafaunal communities by sampling areas of different habitat in and outside Lamlash Bay NTZ. Analysing data from the dive surveys indicated that the number of species, number of individuals and overall biodiversity were all greater inside the NTZ. However, there was very little difference in their community composition. All habitats, regardless of their level of protection, appeared to be heavily dominated by low-level, opportunistic invertebrates such as starfish, crabs and other crustaceans. This suggests Lamlash Bay is an area characterised by low biodiversity. However, using the novel approach of combining data from baited camera surveys with dive surveys allowed investigation into the larger ecosystem and revealed several differences between sites in and outside the NTZ. The species that characterised the NTZ now included cod and haddock, whereas the species that characterised sites outside the NTZ remained largely unchanged. Further analysis found

the abundance of gadoids (such as cod and haddock) to be significantly higher inside the NTZ and that, overall, the number of species, number of individuals and biodiversity were all greater inside the NTZ.

In recent years, cod and haddock have been considered to be largely absent from the Firth of Clyde as a result of severe overfishing (Thurstan & Roberts 2010), but this study suggests that populations of gadoids are still present, although they are made up almost entirely of juveniles within Lamlash Bay, and the Firth of Clyde in general (Heath & Speirs 2011). Previous evidence suggested that Lamlash Bay NTZ was enhancing the recruitment of commercially important scallops by protecting vital nursery habitats from fishing, thereby allowing juveniles to experience greater growth and survival (Howarth et al. 2011). A similar effect may be occurring in commercially important fish species as it was found that sites which encompassed the greatest structural complexity (due to the high presence of benthic taxa such as maerl, hydroids and bryzoans) conveyed the greatest levels of biodiversity. Whether sites within the NTZ have greater complexity is currently under investigation.

For the second year running, scallop densities were substantially higher inside the NTZ. The density of king scallops was 1.5 times higher inside the NTZ, and queen scallops were 3.3 times higher. However, the density of scallops within treatments, and within transects, was hugely variable and made any significant differences too difficult to detect. As in 2010, scallop populations were composed of significantly older and larger individuals suggesting a return to natural, more extended age structures as, on average, king scallops were 16mm larger and 1.25 times older. Likewise, queen scallops were 5mm larger and 1.6 times older inside the NTZ.

Despite the positive results above, scallop densities had actually declined considerably between 2010 and 2011, a trend which was most pronounced outside the NTZ. The density of king scallops outside the NTZ had declined by over 37%, whilst the density of queen scallops had declined by over 79%. In contrast, queen scallops had reduced by just 33% and king scallop density had actually risen by 9.5% inside the NTZ. It was also observed that, in contrast to predictions made in 2010 (see Howarth et al. 2011), very little recruitment had occurred in 2011. Only two sites were observed to contain any juvenile scallops inside the NTZ, and none were found outside. A dramatic difference compared to the previous year. Similarly, there had been very little recruitment of 1st and 2nd year age classes of adult king and queen scallops. The factors behind this apparent failure in recruitment are unknown, but may be due to unusually cold waters (around 2°C lower than the previous year) which have been known to negatively influence reproduction and recruitment in UK scallops (Shepherd et al. 2010).

Analysis into the effectiveness of this study suggested that enough dive surveys had been conducted and that the labelling of sites to different habitats was appropriate. However, there were also several limitations to this study which mean caution must be taken in interpreting the results. Firstly, the sample sizes used in several of the analyses were particularly small, especially those involved in analysing the dataset combining the baited camera and dive survey data. Also, the study design was very unbalanced, with uneven numbers of habitat representatives in and outside the NTZ. Furthermore, some habitats had so few representatives in and outside the NTZ that useful comparisons could not be made of the data using two-way ANOVAs and other multivariate tests. Therefore, next year's surveys should attempt to address this by ensuring that each habitat has at least two representatives in and outside the NTZ. However, for this to occur, some sites/habitats

may have to be dropped entirely from the dataset. Lastly, the recording time of the baited underwater video camera was probably not always sufficient to record all the species of a site and should be extended for next year's surveys. Overall though, the University of York developed a highly cost-effective monitoring strategy suitable for monitoring temperate marine reserves, such as that on Arran.

Conclusion

After two years of surveying Lamlash Bay using a wide variety of techniques and statistical analyses, the majority of evidence appears to be pointing in the same direction; that ecological communities within Lamlash Bay are more diverse and more abundant within the NTZ than outside, and that scallop populations within the NTZ are made up of older, larger and a greater number of individuals.

A key objective of the recent Marine Acts in Scotland and the United Kingdom is to establish an ecologically coherent network of Marine Protected Areas (MPAs). As Lamlash Bay No-Take Zone is currently the only fully protected marine reserve in Scotland (and one of only three in the UK) it clearly has a key role to play in informing the development of this network. Results from our monitoring programme will therefore provide vital information on the range of effects that can be expected from MPAs in Scottish waters. As our results provide encouraging signs of recovery both in scallop populations and seafloor habitats, as well as the promise of recovery in fish populations, our research will be of great interest to the community of Arran, to other biologists studying closed area protection, and of particular interest to stakeholders and decision-makers involved in marine resource management both in the UK and further afield.

Acknowledgements

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Appendix

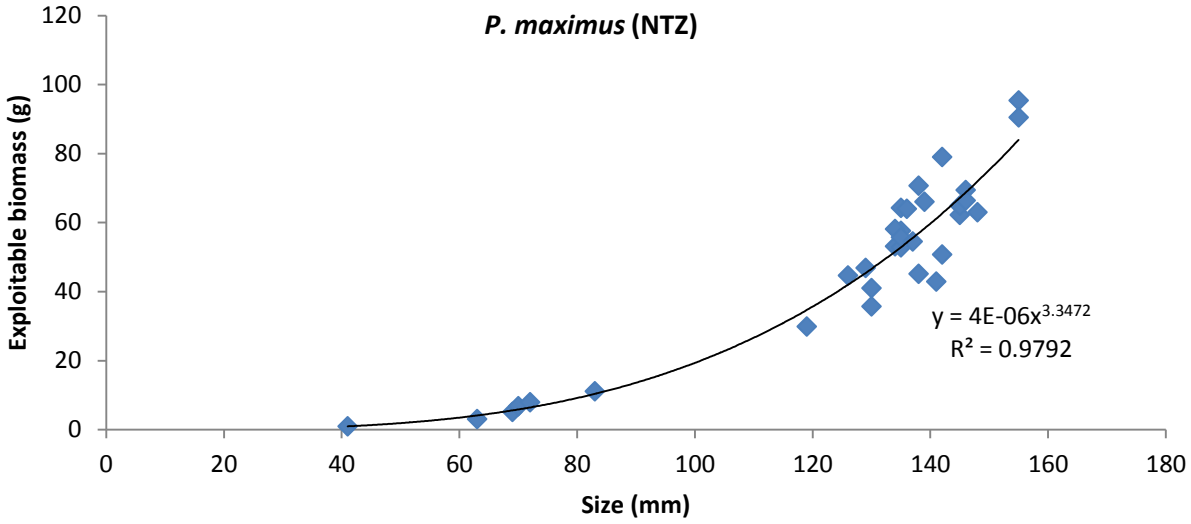
Site	Date	Time	Depth (m)	Substrate type	Start lat	Start long	End lat	End long
NTZ 5	21/06/2011	10:07	13.8	Sandy mud, boulders, shell & pebbles	55 32 511	005 05 213	55 32 536	005 05 176
NTZ 14	22/06/2011	10:01	15.1	Muddy sand & shell	55 32 737	005 05 428	55 32 742	005 05 469
NTZ 17	30/06/2011	11:15	15.2	Dead maerl, shells & boulders	55 32 354	005 05 609	55 32 363	005 05 661
NTZ 16	03/07/2011	10:35	11.25	Sandy mud, cobbles & shell	55 32 106	005 05 501	55 32 132	005 05 482
NTZ 13	06/07/2011	12:20	11.2	Dead maerl, sandy mud & dead shells	55 32 379	005 04 866	55 32 354	005 04 867
NTZ 7	12/07/2011	14:27	6.8	Kelp, sand, some dead maerl & shell	55 32 681	005 04 897	55 32 707	005 04 866
NTZ 21	24/07/2011	16:29	17.4	sandy mud with some pebbles & shell	55 32 352	005 05 869	55 32 375	005 05 842
NTZ 10	25/07/2011	13:59	19	muddy sand with some shell	55 32 422	005 05 782	55 32 437	005 05 809
NTZ 4	01/08/2011	13:57	15.2	sand, shell & some dead maerl	55 32 249	005 05 241	55 32 244	005 05 292
NTZ 15	11/08/2011	14:00	20.8	Sand with shell & some cobbles	55 32 187	005 05 507	55 32 198	005 05 479
NTZ 11	15/08/2011	13:51	15.6	Fine sandy mud	55 31 945	005 05 535	55 31 928	005 05 514
NTZ 12	23/08/2011	13:29	10.8	Sand, dead maerl, shells, cobbles & boulders	55 32 550	005 04 841	55 32 564	005 04 870
NTZ 8	25/08/2011	11:33	17	muddy sand, shell, cobbles & few boulders	55 32 581	005 05 499	55 32 589	005 05 482
NTZ 3	26/08/2011	12:25	8.45	dead maerl, sandy mud	55 32 390	005 04 841	55 32 413	005 04 813
OUT 6	20/06/2011	11:58	15	Sandy mud, shells, pebbles	55 31 209	005 03 560	55 31 184	005 03 560
MPA 4	27/06/2011	12:09	15.2	Muddy sand, with shells & pebbles	55 31 330	005 04 829	55 31 347	005 04 347
MPA 3	30/06/2011	13:53	19.3	Muddy sand & some shell	55 32 059	005 06 233	55 32 057	005 06 166
OUT 4	10/07/2011	13:30	15.4	dead maerl, muddy sand, shells & some boulders	55 32 197	005 04 434	55 32 207	005 04 463
MPA 2	11/07/2011	13:07	14.35	Sandy mud, shell, cobbles & few boulders	55 31 389	005 06 026	55 31 958	005 06 081
OUT 7	18/07/2011	16:48	10.7	dead maerl & some shell	55 30 735	005 03 466	55 30 759	005 03 460
MPA 6	19/07/2011	17:29	24	mud	55 32 214	005 06 108	55 32 227	005 06 138
OUT 11	26/07/2011	15:00	8	kelp, dead maerl, boulders & shell	55 30 600	005 30 964	55 30 583	005 03 930
OUT 3	02/08/2011	12:09	11.6	sand, shell & pebbles	55 31 689	005 04 051	55 31 703	005 04 066
MPA 1	05/08/2011	16:48	14.7	fine sand	55 30 702	005 04 847	55 30 710	005 04 886
MPA 5	13/08/2011	1344	21.5	sand, shell & pebbles	55 31 061	005 04 460	55 31 027	005 04 471
OUT10	17/08/2011	1459	17	sand, shell & dead maerl	55 32 017	005 04 198	55 32 041	005 04 187
OUT 1	22/08/2011	09:00	18.5	sandy mud, shell, pebbles & boulders	55 33 335	005 04 763	55 33 318	005 04 738
OUT 8	30/08/2011	14:12	22.8	sandy mud, shell & few cobbles	55 32 677	005 04 453	55 32 649	005 04 435

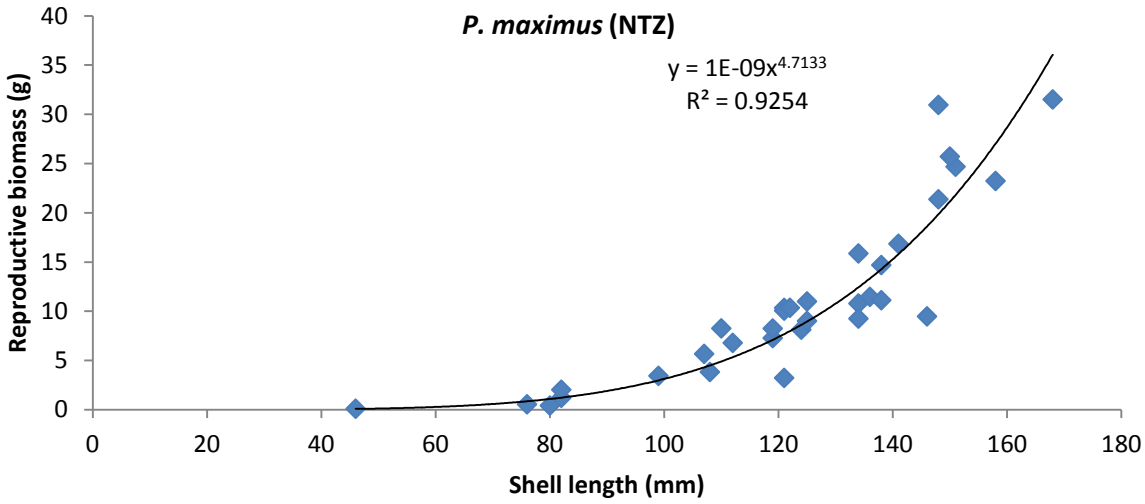
Appendix 1 | The location, depth and predominant substrate types of all dive surveys. Location is represented by the latitude and longitude taken from the starting and finishing ends of the 50m transect.

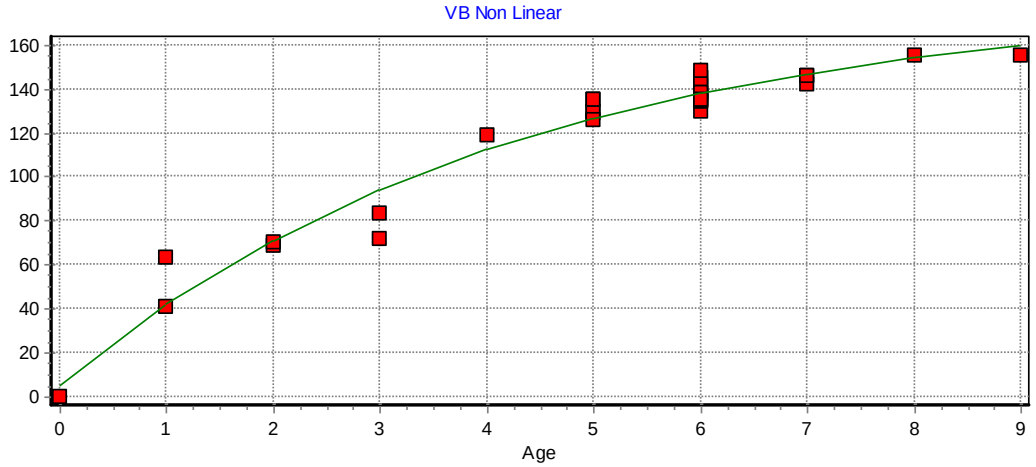
Site	Date	Time
OUT 7	18/07/2011	1453
OUT 6	18/07/2011	16:04
MPA 6	19/07/2011	1510
MPA 2	20/07/2011	1602
NTZ 10	22/07/2011	1600
NTZ 5	25/07/2011	1033
OUT 11	27/07/2011	1250
MPA 4	27/07/2011	1422
OUT 3	02/08/2011	1301
MPA 1	13/08/2011	1133
NTZ 11	13/08/2011	1300
NTZ 15	15/08/2011	12:00
OUT 4	17/08/2011	13:15
NTZ 17	21/08/2011	15:05

NTZ 7	22/08/2011	08:38
NTZ 13	22/08/2011	13:07
NTZ 12	25/08/2011	11:08

Appendix 2 | The date and time of BRUV deployments.

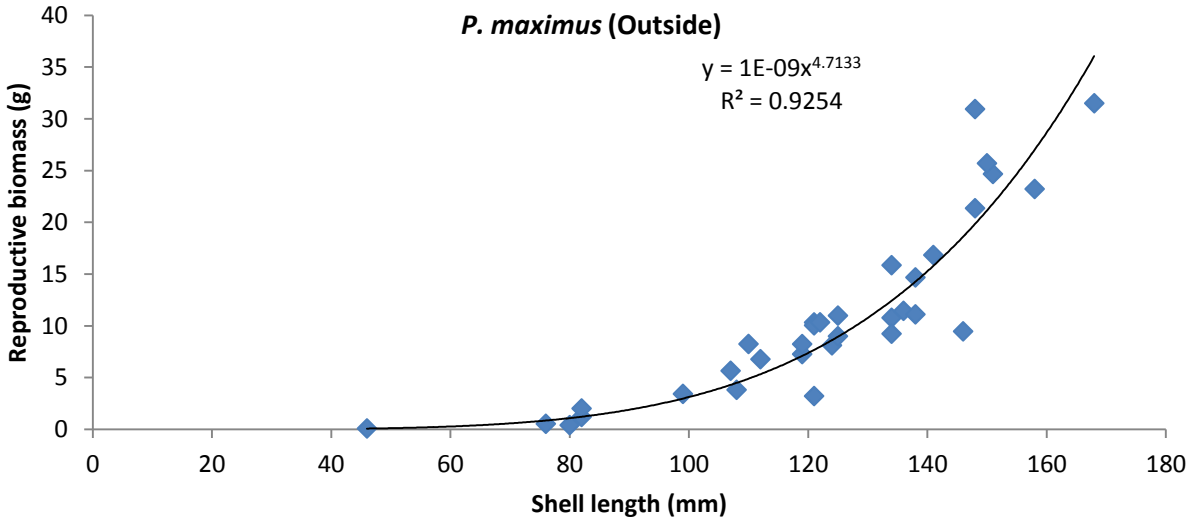


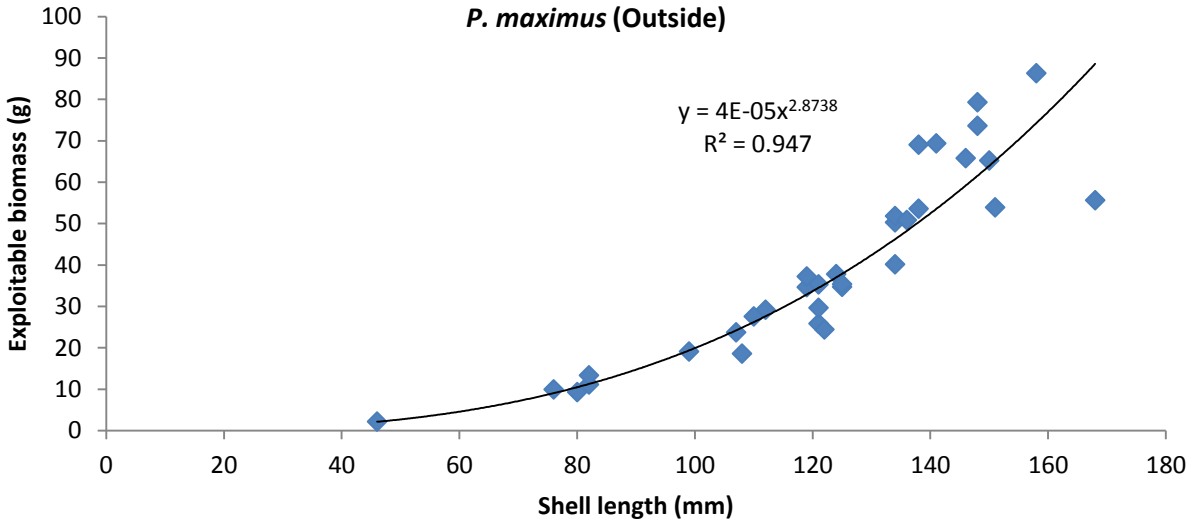


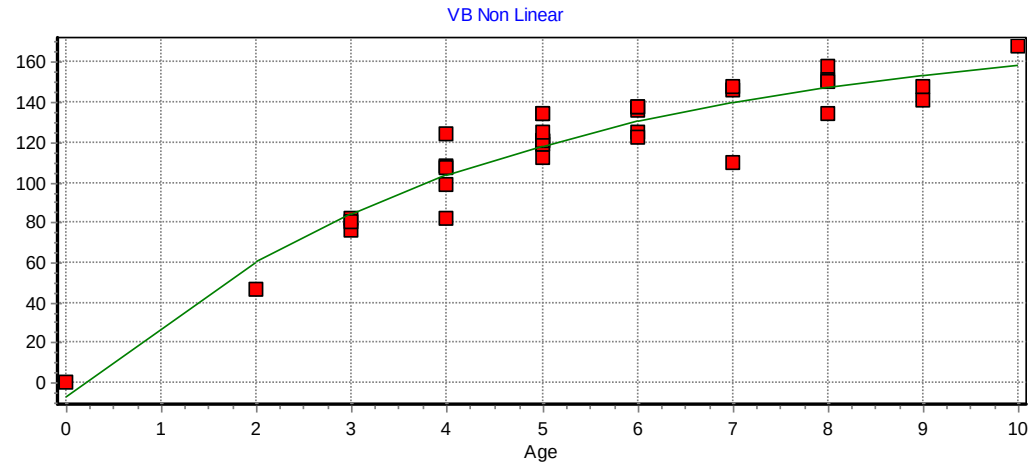


k	0.228614
L_∞	177.297
T_0	0.16497

Appendix 3 | Biometric plots for dissected *P. maximus* (n = 32) individuals collected from inside the NTZ. Trendline for above 2 graphs represents a power relationship and its associated equation and R^2 value are on display. The lower graph represents a Von-Bertalanffy non-linear trendline and the resulting variables are available on the right.

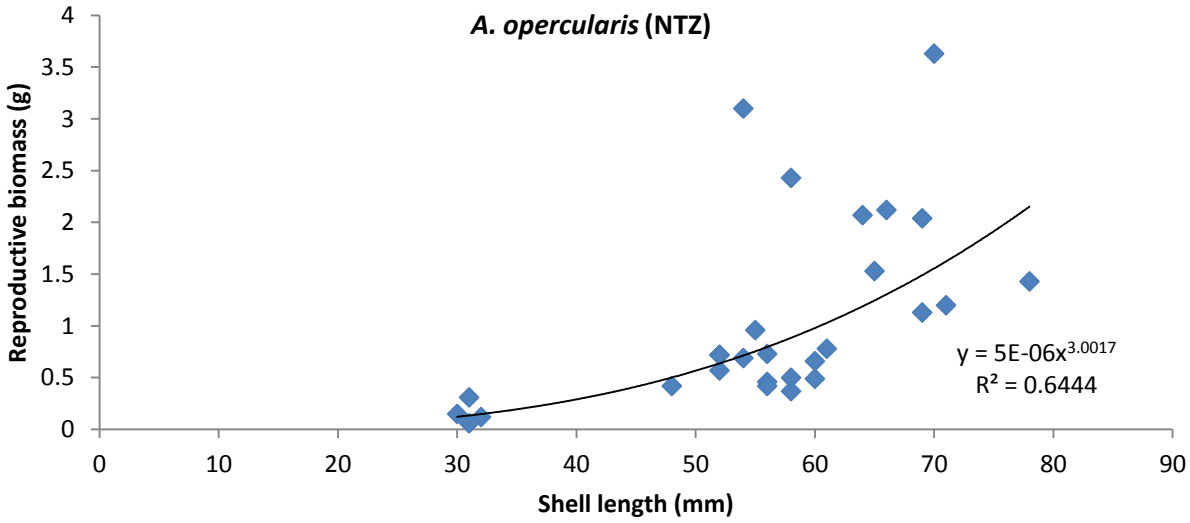


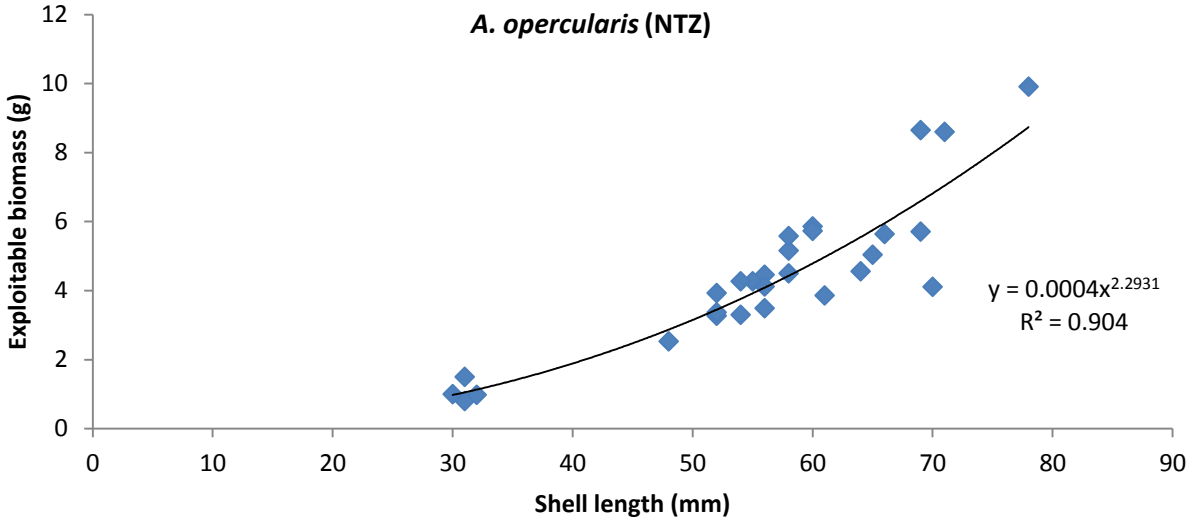


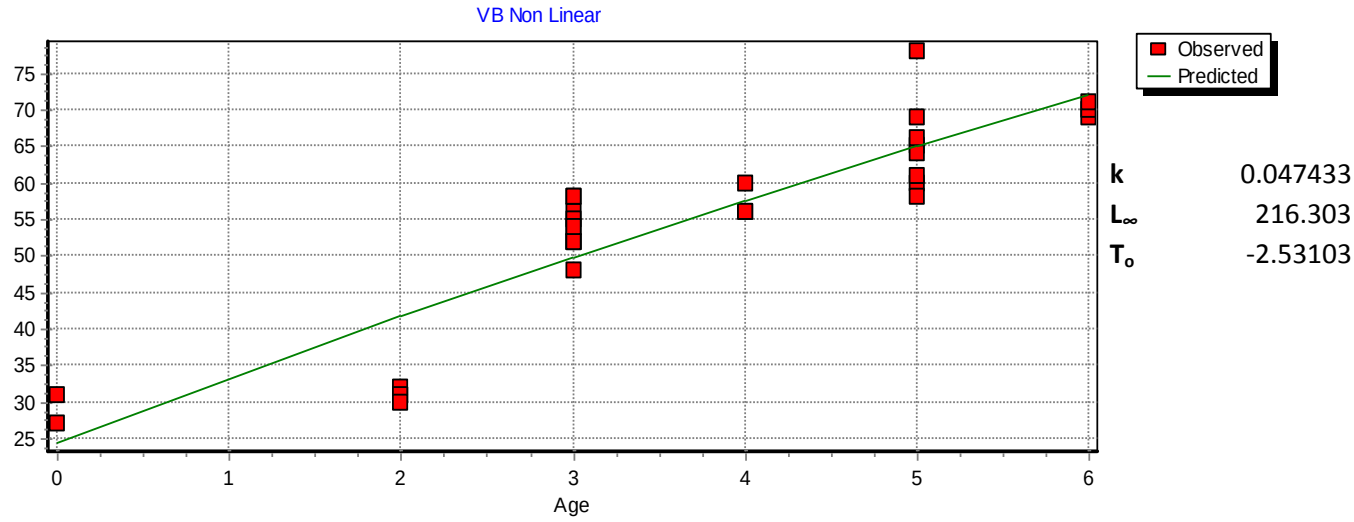


k	0.228614
L_∞	177.297
T_0	0.16497

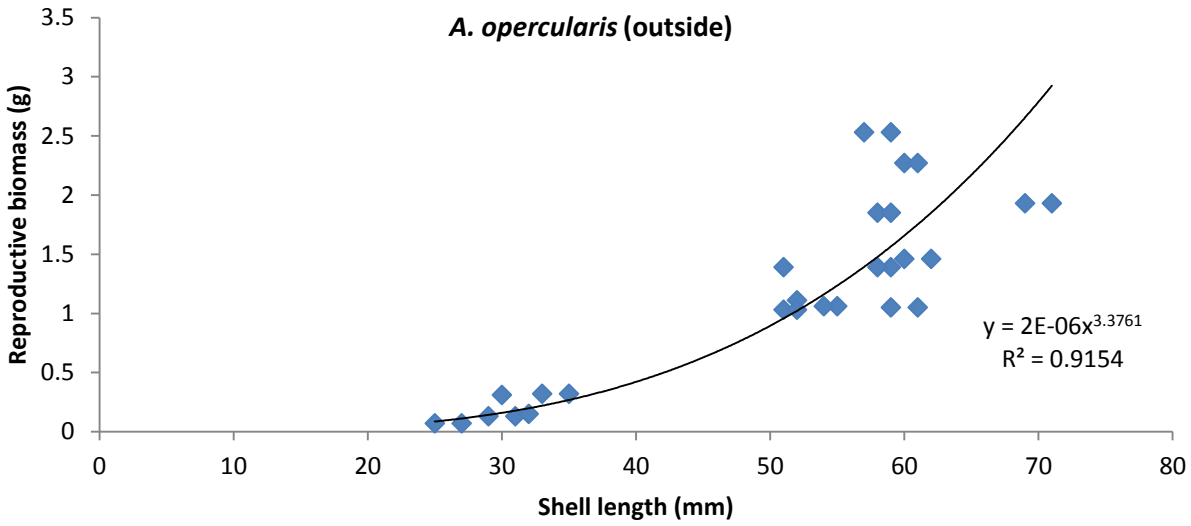
Appendix 4 | Biometric plots for dissected *P. maximus* (n = 33) individuals collected from outside the NTZ. Trendline for above 2 graphs represents a power relationship and its associated equation and R^2 value are on display. The lower graph represents a Von-Bertalanffy non-linear trendline and the resulting variables are available on the right.

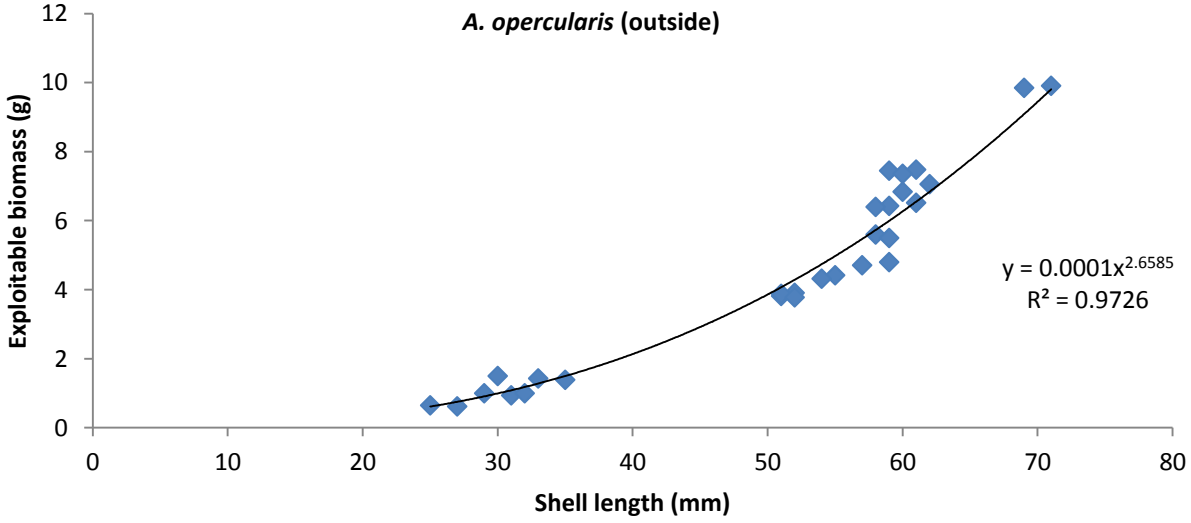


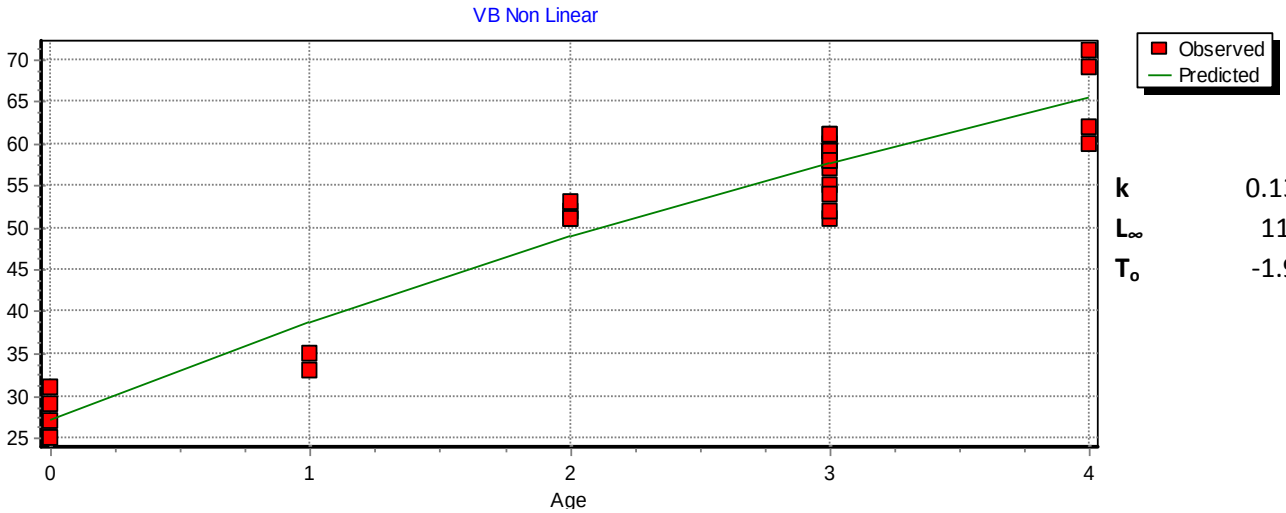




Appendix 5 | Biometric plots for dissected *A. opercularis* (n = 30) individuals collected from inside the NTZ. Trendline for above 2 graphs represents a power relationship and its associated equation and R^2 value are on display. The lower graph represents a Von-Bertalanffy non-linear trendline and the resulting variables are available on the right.







Appendix 6 | Biometric plots for dissected *A. opercularis* (n = 28) individuals collected from outside the NTZ. Trendline for above 2 graphs represents a power relationship and its associated equation and R^2 value are on display. The lower graph represents a Von-Bertalanffy non-linear trendline and the resulting variables are available on the right.