NATIONAL MARINE BIOLOGICAL ANALYTICAL QUALITY CONTROL SCHEME

ANNUAL REPORT

(Year 7)

2000/2001

October 2001
National Marine Biological AQC Coordinating Committee

NATIONAL MARINE BIOLOGICAL ANALYTICAL QUALITY CONTROL SCHEME

Annual Report 2000/2001

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1. OVERALL SUMMARY

- The National Marine Biological AQC Scheme (NMBAQC Scheme) has completed its seventh year in 2000/2001. The background to the scheme is described in previous annual reports.

- Components of the scheme continue to be based on Ring Tests (RT), whole samples (MB), Laboratory reference (LR) and Own Samples (OS) for biological determinands plus Particle size (PS) tests.

- The aims of the scheme include improving laboratory skills, improving the consistency and quality of marine biological benthic data, screen data for the UK NMMP programme.

- Participation in the scheme remained high with a total of twenty three laboratories participating. Fourteen of these laboratories submitted data for NMMP, six were consultants or private contractors and the remainder non NMMP government labs. Interest had been expressed by some labs in 'selective' participation where particular components of the scheme could be excluded/included for them. Participating laboratories are responsible for communicating their level of participation in the scheme to Unicomarine Ltd. **NMMP labs were required to participate in ALL relevant components**. Overall the scheme was well supported.

- Several laboratories contract out analysis of their own samples and for the NMBAQC Scheme samples. Others supply a central laboratory service with relevant material. This is recognised as a risk in the potential loss of quality control by members of the scheme. Unless directly participating in the scheme, subcontractors are not recognised as being within it. Subcontractors must be made aware of the appropriate scheme deadline.

- There was considerable variation in the way different participating laboratories approached the scheme components. The issuing of reminders has reduced the number of delayed data returns and improved reporting feedback.

- Detailed results of the circulations are presented in the contractors report (Section 7) where individual laboratory performance is described and standards of achievement against the targets tabulated.

- Problems with biomass analysis were again evident with a great deal of variation amongst labs. The scheme needs to address the issue of biomass determination. Trials are required to derive the best method for the "blotted technique". Consideration needs to be given to the preparation of a standardised protocol and reporting format.

- Serious problems still exist in sorting accuracy. Laboratories should target taxa commonly being overlooked and provide additional training. A review of existing extraction techniques and quality control measures may be required.

- Overall participating laboratories performed quite well in the OS exercise. However, this year saw the lowest pass rate (73% excluding deemed fails) since the introduction of the NMBAQC standards. Faunal extraction needs to be improved as major extraction differences were reported between the participating laboratory and the contractor.

- The application of the pass / fail criteria for the Own Sample exercise will be altered in scheme year 8. Data flags will be applied on a sample-by-sample basis using a graded system related to the untransformed Bray-Curtis scores. Those samples which do not reach the required standard will be flagged, along with the other replicates from the same NMMP site. Remedial action will be required to reach a pass standard and will be undertaken to an agreed time scale. The Committee will develop a protocol for tracking and evaluating remedial action.

- All samples submitted for the OS exercise from scheme year 8 will have to be split to species. The NMMP Green Book will be amended accordingly.

- Random selection of the OS samples will be introduced in scheme year 9 (2202/2003).

- Particle size exercises again highlighted the variation in results depending on the technique employed. These differences are further emphasised by certain sediment characteristics. The application of the pass / fail criteria will be suspended for scheme year 8. The standards will be reviewed during this time.

- Data return delays have been reduced with the introduction of deadline reminders. This has resulted in improve data feedback to participants. **Laboratories who miss data or sample return deadlines will be deemed to have failed**. All primary correspondence for scheme year 8 will be conducted via e-mail. Hard copies will be provided where appropriate.

- Laboratories should use feedback to decide if additional training or procedural changes are required to improve their performance.

- NMMP Laboratories achieved a 62% overall pass rate. This is similar to last year but is again partly due to non returns of OS data.

- Failure of some NMMP laboratories to achieve the necessary overall standards may affect the inclusion of their data submissions to the NMMP database.

- A Scheme Statement of Performance will be issued to participants.

- The Co-ordinating Committee commissioned an independent review of standards in 1999. The final report was issued in February 2001. Conclusions and recommendations are detailed in Appendix 5.

- The JNCC organised a ring test for epibiota, using photographic material. This pilot scheme was distributed in March/April 2001 (see Appendix 6).

- Co-ordinating Committee is considering commissioning an independent audit of the scheme.

- Proceedings from the 1997 Humber Benthic Field Methods Workshop are expected to be published in late 2001.

- The contract to operate the scheme was tendered in February 2001. Unicomarine Ltd. were successful and will run the scheme until 2005

- Overall co-ordination of the scheme was undertaken by the National Co-ordinating Committee (Appendix 1) reporting to NMMP Working Group at UK level.

2. SCOPE OF THE SCHEME

The seventh year of the scheme was designed to build on the data from previous years and highlighting the standards achieved, while continuing the emphasis on participant supplied samples. In total nineteen participant supplied samples have now been judged against the standards derived in 1996/97. To this end the format of the scheme in 2000/2001 followed last year's formula.

Scheduled circulations:

a) 3 participant supplied macrobenthic samples (OS) to be (re)analysed by Unicomarine;

b) Ring Tests (RT) as follows;
- one normal ring test of twenty five species to be supplied by the contractor;
- one participant supplied set of twenty five species to be sent to the contractor for validation;
- one ring test targeted at "problem taxa" highlighted throughout the scheme;

c) One contractor supplied macrobenthic sample (MB).

The samples were sent out to participants at staggered intervals during the year with set time scales for sample or data returns to Unicomarine Ltd.

A detailed breakdown of the results from the year, are contained in the contractors report in Section 7.

3. ISSUES ARISING

3.1 The composition and aims of the scheme

The statements made in last year's report hold true for 2000/2001

- **Ring tests** are generally accepted as a method of improving learning skills relating to taxonomy. Laboratories generally achieved good results. Areas of difficulty emerged with particular faunal groups which were tackled by the targeted RT and individual feedback. The standard ring test formed part of the core programme. It is recognised that the contractor supplied ring tests do not necessarily reflect the skills of individual laboratories and for this reason RT's have not been used to set a pass / fail standard for NMMP labs. They can however be used to reflect overall lab performance and improve skills.

- The **Laboratory Reference** was perceived as a parallel to OS returns *i.*e. this component test would apply quality control to 'own specimens'. Initially some laboratories were only beginning to set up marine voucher collections, while others used the LR exercise to acquire a second opinion on their 'difficult specimens' from a consultant. Participating laboratories are now requested to consider fauna recorded in their NMMP samples (where applicable). They are also encouraged to assemble and use reference specimens from NMMP stations, especially for certain molluscs. The use of growth series is also important for molluscs. The LR exercise is not assign a pass / fail standard.

- The **MB sample**, though sourced from a geographical location unfamiliar to many participants, was designed to examine sample processing skills in addition to taxonomic skills. It became apparent that a few labs had some serious problems overlooking a number of taxa in addition to many others overlooking some specimens. While overlooking a few individuals might be deemed to be insignificant, should these individuals comprise several taxa in a sparse community, interpretation

could be compromised. The MB component is considered by many labs to be irrelevant or too time consuming. Some labs opt not to participate in this exercise.

- Determining **biomass** is a new skill for many laboratories that do not complete this analysis routinely. Biomass determination is a requirement of NMMP labs but no standard has been assigned by the AQC Committee. The derivation of a standardised effective protocol and reporting format requires addressing by the committee. Trials are required to derive the best method for the "blotted technique". Biomass procedures should not render the specimens indistinguishable.

- **Own samples**. Pass / Fail Standards for the NMMP data base have been applied only to OS samples for the extraction and enumeration of taxa. The exercise is seen as representing the true reflection of local laboratory skills. There is no doubt that participants give a lot of weight to these samples and to this end may be selecting samples with specimens of which they are confident in order to gain a pass. A technique to avoid this selectivity has been developed and will be introduced in Scheme Year 8 (2001/2002).

- **Particle size** determinations are accepted as a routine biological descriptor and can be carried out by a variety of techniques each of which appears to be fairly consistent in its reproducibility. As a routine and NMMP determinand, this analysis has been assigned a pass / fail standard and must be completed by NMMP labs. Most laboratories in this scheme carried out the analysis by one of the two preferred techniques in common use.

3.2 Participation

The twenty three participants in 2000/2001 comprised private contractors, university labs and Government labs in Scotland, Northern Ireland, England and Wales. Fourteen laboratories provide data or analytical services for NMMP components and submit data to the NMMP data base. A number of the participants subcontract to a second or third party. While it is in the interest of all laboratories to participate in all components of the scheme, in order to gauge their performance, some laboratories may favour completing certain components over others which will be compatible with their commercial interests, budgets or time constraints. This is their choice provided no contractual agreement is broken. **However, all laboratories submitting data to the NMMP should complete the whole programme whether pass / fail standards have been devised or not for individual components.**

3.3 Submission of data

There has been a reduction in the number of laboratories either not submitting data or missing deadlines compared to previous years. This can be partly attributed to the exercise reminders which have been dispatched throughout the scheme year. However, laboratories must give adequate priority to the NMBAQC Scheme components and endeavour to report within the requested time limits. **Laboratories which subcontract work to a second or third party should make the contractor fully aware of the Scheme deadlines.**

Fourteen NMMP laboratories are members of the Scheme. Of these six supplied all the data from all the relevant components. The remaining eight laboratories failed to supply at least one component. Six of these had indicated at the beginning of the scheme year that they would not participate in the MB exercise. Many labs find this exercise irrelevant or too time consuming. Four of these six labs completed all the other components of the Scheme.

Participating laboratories are responsible for informing Unicomarine Ltd. of their level of participation in the Scheme. 'Fail flags' which are applied when no data is submitted are perceived as far worse than a participatory 'fail flag'.

Laboratories recognise the value of flags and tended to favour the supply of OS and PS data at the expense of the rest of the scheme.

3.4 Data feedback

As in previous years considerable problems were encountered feeding back data due to late or non returns and incorrect data formats. **Laboratories who miss data or sample return deadlines will be deemed to have failed**.

Laboratories have been issued with their individual results for circulations to allow review of their own performance. The introduction of ring test bulletins (RTB) has improved feedback and emphasised the learning aspect of this component.

3.5 Targets and Standards

As in 1999/2000, it was agreed that the separate components of the Own Samples and PS only would be scored against the targets. Thus for those labs returning data, 9 separate components can be assigned as pass or fail. These components are a pass or fail for estimation of taxa, estimation of abundance and the similarity index for each of the three OS samples. The committee agreed it would be reasonable that in order to achieve an overall pass, the standards should be achieved or exceeded on >=6/9 components.

Eighteen labs participated in the OS exercise, seven of these failed overall. Three of these seven failures were due to insufficient or no OS data (these are deemed to have failed). A further two labs failed for the first time since joining the Scheme.

One of the main reasons for labs failing was poor extraction efficiency. Participating laboratories are encouraged to study their detailed OS reports and target those taxon or groups of taxa which are commonly overlooked. Additional training or changes to the extraction methods should be considered to improve extraction efficiency.

(**Overall flags** can only be applied to laboratories participating in biological components. They are not applicable to laboratories only participating in PS samples).

Achievement of the biological standards appears to be posing a challenge for a number of laboratories. An independent review of standards was undertaken during 1999/2000. The final report was completed in February 2001 and the conclusions and recommendations can be found in Appendix 5. The Committee propose to change the pass / fail criteria in scheme year 8 to a graded system which will be applied on a sample-by-sample basis. In addition, the Committee will introduce the random selection of Own Samples and prepare a protocol for the evaluation of remedial action applied to failing samples.

Two PS exercises were distributed in 2000/2001. Seventeen laboratories participated in the first circulation, two of which failed. These laboratories failed due to non-return of data. In the second distribution nine out of eighteen labs received 'fail flags'. One of these failures was due to the non-return of data. The remaining labs failed due to the application of the standards and the bias towards labs using laser techniques. The Committee intend to review the PS standards and will suspend the pass / fail criteria in scheme year 8.

4. SCHEME PROPOSAL FOR 2001/2002 (SCHEME YEAR 8)

The core programme for the scheme in the coming year 2001/2002 will contain the following components.

1. Own samples;
2. Ring Tests including a targeted ring test
3. Macrobenthic 'Bucket' sample
4. PSA samples

The Co-ordinating Committee have decided to alter the application of the pass / fail criteria for the Own Sample exercise. Data flags will be applied on a sample-by-sample basis using a graded system related to the untransformed Bray-Curtis scores. The five tier system will be applied as follows:

100% BCSI	Excellent
95-<100% BCSI	Good
90-95% BCSI	Acceptable
85-90% BCSI	Poor - Remedial Action Suggested
<85% BCSI	Fail - Remedial Action Required

Those samples which do not reach the required standard will be flagged, along with the other replicates from the same NMMP site. Remedial action will be required to reach a pass standard and will be undertaken to an agreed time scale.
The Committee will develop a protocol for tracking and evaluating remedial action.

The Committee intend to randomise the selection of samples for the OS exercise. From scheme year 9 (2002/2003) all participating laboratories must submit their previous years completed NMMP data set. Own Samples from non-NMMP labs will be selected on a similar basis. Labs can choose which data set to submit. The Committee believe that contractual confidentiality can be maintained by using codes to disguise the survey location.

All samples submitted for the OS exercise from scheme year 8 will have to be split to species. The NMMP Green Book will be amended accordingly.

During scheme year 8 the Committee will develop protocols to standardise the faunal groups to be extracted from NMMP samples, and to determine what is a reasonable level of identification for all taxa likely to be encountered.

The Committee have agreed to suspend the application of the pass / fail criteria for the PS exercise for 2001/2002. They intend to review the standards during this time.

A complaints form has been developed and is available on the website (www.nmbaqcs.org) or from the contract manager.

All primary correspondence for scheme year 8 will be conducted via e-mail. Hard copies will be provided where appropriate.

A workshop on certain problematic taxonomic groups was held in October 2001 at Portaferry, Northern Ireland.

5. CO-ORDINATING COMMITTEE ACTIVITIES AND PROJECTS

During 2000-01 the scheme has continued to function well despite continuing difficulties in funding. The year saw the start of Unicomarines third period as contractor after successfully tendering for the project. The co-ordinating committee has seen a number of changes throughout the year (Appendix 1) the most notable being the resignation of Anne Henderson as scheme manager.

After a number of false starts the scheme has established its own website with aim of allowing the more efficient dissemination of information. These tools are only of value if updated and participants are encouraged both to use the site and links from there own organisations and also submit items and appropriate links to the site. Www.nmbaqcs.org

The co-ordinating committee has recognised for some time that the scope of the scheme may need to be widened to cover areas other than soft bottom macrofauna. This has become more evident with developments within the NMMP to possibly cover elements of monitoring under the Water Framework Directive and also representation on the scheme by the "country agencies" involved in monitoring for the Habitats Directive. At the start of 2001 JNCC organised a pilot epibiota ring test using photographic images which attracted 36 participants. Initial findings are presented in Appendix 6. Once the outcome of this pilot has been fully assessed it is in intended that a follow up exercise will be undertaken.

At a number of points over preceding years there have been questions raised over the independence of the contractors, who audits the auditors? As part of the new contract issued to Unicomarine they have obliged to submit a proportion of the AQC scheme material for third party assessment to an independent recognised laboratory. The committee have reserved the right to approve or reject the suitability of the third party. On a similar vein the committee recognise that the "paper trail" used by the contractor and the manager should be transparent, traceable and secure. To this end the appointment of an independent auditor is under consideration.

Committee members have participated in two ISO Working Groups on the Sampling Soft Bottom Macrofauna and Sampling Sediments this should ensure that International Standards arising these groups do not deviate widely from NMMP protocols.

In May 2001 committee members participated in a workshop organised under the auspices of the NMMP. The objectives of the workshop were to:

- Outline the requirement for identifying robust indicators of marine environmental quality.
- Enable internal discussions with UK marine scientists to ensure that the UK can play an active role in international fora on indicators.
- The co-ordinating committee was tasked with reviewing biological performance indicators and ranking them into;

a) indicators that can be used now
b) indicators that could be used with a little refinement from the National Marine AQC groups
c) indicators that will require further R&D work before they could be adopted.

The proceedings of the workshop can be viewed on the NMMP website : **www.nmbaqcs.org**

6. FINANCIAL SUMMARY 2000/2001

The seventh year of the scheme has been completed..

Fees in 2000/2001 remained the same as 1999/2000. Non NMMP laboratories were eligible to take advantage of the 'split fee' according to the components required although many elected to participate fully.

The contract continued to be administered by Unicomarine on the basis of their experience, good management and reasonable cost having won the contract in a competitive tendering exercise at the end of 1997/98.

The contract continued to be managed by the Scottish Environment Protection Agency (SEPA) West Region under direction from the AQC committee.

Financial Summary 2000/2001

	INCOME	***EXPENDITURE***
Participant Fees	*£ 54 150.00*	
Interest	*£ 1 257.23*	
Expenditure *Core project/Additional projects* *Travel/Admin etc.*		 *£ 62 497.78* *£ 2 366.30*
Management fee		*£ 3 000.00*
Bank Balance carried forward from 1999/2000	*£ 22 587.35*	
Balance at year end	***£ 10 130.50***	

Report from the contractor

7. REPORT FROM THE CONTRACTOR

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Summary of performance

This report presents the findings of the seventh year of operation of the National Marine Biological Analytical Quality Control Scheme.

The Scheme consisted of five components:

- Analysis of a single estuarine macrobenthic sample.
- Analysis of two sediment samples for physical description.
- Identification of two sets of twenty-five animal specimens.
- Re-analysis by Unicomarine Ltd. of three own samples supplied by each of the participating laboratories.
- Re-identification of a set of twenty-five specimens supplied by each of the participating laboratories.

The analytical procedures of the various components of the Scheme were the same as for the sixth year of the Scheme. The results for each of the Scheme components are presented and discussed. Comments are provided on the performance for each of the participating laboratories in each of the components.

Analysis of the **Macrobenthic sample (MB)** by the participating laboratories and subsequent re-analysis by Unicomarine Ltd. provided information on the efficiency of extraction of the fauna; accuracy of enumeration and identification and the reproducibility of biomass estimations. Overall agreement between the laboratories and Unicomarine Ltd. was generally very good. Extraction efficiency, irrespective of sorting, was better than 90% in 82% of comparisons and better than 95% in 73% of all comparisons.

Comparison of the results from the laboratories with those from analysis by Unicomarine Ltd. was made using the Bray-Curtis similarity index. The value of the index varied between approximately 83.1% and 99.9% and was better than 90% in 82% of comparisons and better than 95% in 73% of comparisons.

The results for the **Own samples (OS)** were slightly reduced compared to those from the Macrobenthic sample. Agreement between the laboratories and Unicomarine Ltd. was generally good. Extraction efficiency, irrespective of sorting, was better than 90% in 76% of comparisons and better than 95% in 64% of all comparisons. The Bray-Curtis similarity index was greater than 95% in 47% of comparisons and in most cases (67%) the value of the index was greater than 90%.

The influence of analytical technique on the results returned for the **Particle Size exercises (PS)** was marked, especially for the muddy fine sand sediment circulated as PS17. As has been previously reported, in most cases there was good agreement between laboratories using the same technique. The second particle size exercise of the scheme year (PS17) resulted in eight 'fail flags'. The current pass/fail criterion based upon the average percentage silt/clay figure recorded by all participating laboratories is unreliable and is under review. The majority of these 'fail flags' were due to one spurious data set and at least one participating laboratory calculating their percentage silt/clay figure incorrectly.

Two **Ring Tests (RT)** of twenty-five animal specimens were distributed. One set contained general fauna and the other set consisted of twenty-five specimens of estuarine origin. For the general set of fauna (RT16) there was fairly good agreement between the identifications made by the participating laboratories and those made by Unicomarine Ltd. On average each participating laboratory recorded 1.9 generic errors and 3.6 specific errors. The 'targeted' set (RT17) posed far more problems. On average each participating laboratory recorded 3.6 generic errors and 4.5 specific errors. Nine taxa were responsible for the bulk of these errors. These comprised two oligochaetes, three cirratulids, one sabellid, two bivalves and one gastropod. All species distributed are common in estuarine regions.

The identification of a set of twenty-five species selected by the participating laboratories from a list distributed by Unicomarine Ltd. were generally accurate. No clear problem areas were identified. However there were differences in the approach to this **Laboratory Reference (LR)** exercise by the individual laboratories. For example, some laboratories used this as a test for confirming voucher specimens whilst others sought a means of having 'unknowns' identified.

Comments are provided on the individual performance of the participating laboratories in each of the above components. A summary of their performance with respect to standards determined for the National Marine Monitoring Plan is presented.

1. Introduction

The Scheme addresses three main areas relating to benthic biological data collection:

- The processing of macrobenthic samples.
- The identification of macrofauna.
- The determination of physical parameters of sediments.

The seventh year of the Scheme (2000/01) followed the format of the sixth year. A series of exercises involved the distribution of test materials to participating laboratories and the centralised examination of returned data and samples. Twenty-three laboratories participated in the Scheme.

As in previous years, some laboratories elected to be involved in limited aspects of the Scheme. Others chose not to submit samples for the Own Sample component. NMMP laboratories were required to participate in all components and standards were applied to agreed components.

In this report performance targets have been applied for the OS and PS components only (See Appendix 2: Description of the Scheme standards for each component). These targets have been applied to the results from laboratories (See Section 5: Application of NMBAQC Scheme standards) and "Pass" or "Fail" flags assigned accordingly. As these data have been deemed the basis for quality target assessment, where laboratories failed to fulfil these components through not returning the data, a "Fail" flag has been assigned. The two flags are indicated in the Tables presenting the comparison of laboratory results with the standards (Tables 15 and 16).

2. Description of the Scheme Components

There are five components; Macrobenthic sample analysis (MB), Ring Test identification (RT), Particle Size analysis (PS), Laboratory Reference (LR) and Own Sample (OS) reanalysis.

Each of the scheme components is described in more detail below. A brief outline of the information which was to be obtained from each component is given, together with a description of the preparation of the necessary materials and brief details of the processing instructions given to each of the participating laboratories.

2.1 General

2.1.1 Logistics

The labelling and distribution procedures employed previously have been maintained and details may be found in the reports for 1994/95 and 1995/96 (Unicomarine, 1995 & 1996). For the majority of laboratories email has become the preferred mechanism of communication. It is considered to be a very useful mechanism but must remain an option until email facilities are available to all participating laboratories.

2.1.2 Data returns

Return of data to Unicomarine Ltd. followed the same process as in previous years. Pre-formatted discs with spreadsheet based forms (tailored to the receiving laboratory) were distributed with each circulation in addition to hard copies. In addition some laboratories were provided with forms via e-mail. A range of file formats were required to cover all applications in use by participating laboratories. All returned data have been converted to Excel 97 format for storage and analysis. Slow or missing returns for exercises lead to delays in processing the data and resulted in difficulties with reporting and rapid feedback of results to laboratories. This year reminders were distributed shortly before and shortly after each exercise deadline. This has markedly improved the number and punctuality of data returns.

2.1.3 Confidentiality

To preserve the confidentiality of participating laboratories the practice of identifying laboratories with a new four-digit Laboratory Code was introduced in April 2000. These new codes are prefixed with the

scheme year to reduce the possibility of obsolete codes being used inadvertently by laboratories, as has occurred in the past. For example, Laboratory 4 in scheme year seven will be recorded as LB0704.
In the present report all references to Laboratory Codes are the post-April 2000 (Scheme Year seven) codes.

2.2 Macrobenthic Samples (MB)

A single unsorted grab sample from estuarine waters was distributed to each participating laboratory. This part of the scheme examined differences in sample processing efficiency and identification plus their combined influence on the results of multivariate analysis. In addition, an examination of the estimates of biomass made by each of the participating laboratories was undertaken.

2.2.1 Preparation of the Samples

Sample MB08 was collected from Pegwell Bay, Ramsgate; in an area of mud with dead shell sediment. A set of forty samples was collected using a 0.1m² Day Grab. Sampling was carried out while at anchor and samples for distribution were collected within a five hour period. All grabs taken were equal in size. Sieving was carried out on-board using a mesh of 0.5mm, followed by fixing in buffered formaldehyde solution. Samples were mixed after a week in the fixative. Prior to distribution to the participating laboratories the samples were washed over a 0.5mm sieve and transferred to 70% IMS.

2.2.2 Analysis required

Each participating laboratory was required to carry out sorting, identification and enumeration of the macrobenthic fauna contained in the sample. Precise protocols were not provided, other than the use of a 0.5mm sieve mesh; participating laboratories were instructed to employ their normal methods. The extracted fauna was to be separated and stored in individually labelled vials. Labels were provided and cross-referenced to the recording sheets.

In addition, measurements of the biomass of the recorded taxa were requested. Detailed instructions were provided for this component; measurements were to be blotted wet weights to 0.0001g and to be made for each of the taxa recorded during the enumeration.

Twenty weeks were allowed for completion of the sample analysis. All sorted and unsorted sediments and extracted fauna were to be returned to Unicomarine Ltd., together with the data on counts and biomass determinations.

2.2.3 Post-return analysis

Upon return to Unicomarine Ltd. the various components of the MB samples were re-examined. All extracted fauna was re-identified and re-counted for comparison with the participating laboratory's own counts. The sample and residue were re-sorted and any missed fauna removed, identified and counted. All fauna weighed by the participating laboratories was re-weighed to 0.0001g by the same member of Unicomarine Ltd. staff using the same technique.

2.3 Own Sample (OS)

This exercise examined laboratory analytical performance on material from their 'home' area. Each laboratory was requested to send a list of samples from which three samples were identified. The selection was in turn notified to the laboratories. NMMP laboratories were advised to use NMMP samples if possible, otherwise there was free choice.

2.3.1 Analysis required

Participating laboratories were instructed to carry out macrobenthic analysis of the samples using their normal procedures. Samples requiring sub-sampling were to be avoided where possible. All procedures were to be documented and details returned with the sample components. All material from the sample was to be sent to Unicomarine Ltd. broken down as follows:

- Sorted residue - material from which all animals had been removed and counted.
- Separated taxa - individually labelled vials containing the identified fauna.
- Other fractions - *e.g.* material containing fauna which had been counted in situ.

Identification was to be to the normal taxonomic level employed by the laboratory (usually species). The names and counts of specimens were to be recorded on a matrix and linked to the vials through a specimen code number. Biomass analysis was to be carried out in the same manner as for the MB exercise.

Upon receipt at Unicomarine Ltd. all OS samples were re-analysed by the same operator. The sorted residue was re-examined and any countable material extracted. Identified fauna was checked for the accuracy of enumeration and identification and all specimens were re-weighed using the same procedure as for the MB exercise. **Twenty-nine weeks** were allowed for preparation of the Own Samples selected for reanalysis (following a deadline extension).

2.4 Particle Size Analysis (PS)

This component was intended to provide information on the degree of variation between participating laboratories in the production of basic statistics on the sediment characteristics. Two samples of sediment, one coarse the other much finer, were distributed in 2000/01. Both samples were derived from natural sediments and prepared as described below. In each case replicates of the distributed samples were analysed using both laser diffraction and sieve analysis techniques.

2.4.1 Preparation of the Samples

2.4.1.1 Natural samples

Sediment for each of the circulations was collected from locations covering a range of sediment types. This was returned to the laboratory and coarse sieved (2.0mm) to remove stones. The sediment for an individual PS circulation was well mixed in a large tray following sieving and allowed to settle for a week. Each sediment was sub-sampled by coring in pairs. One core of a pair was stored as the 'A' component, the other as the 'B'. To ensure sufficient weight for analysis, and to further reduce variation between distributed PS samples, this process was repeated three times for each sample sent, *i.e.* each distributed sample was a composite of three cores.

The numbering of the resulting samples was random. All of the odd-numbered 'B' components (a total of 14) were sent for particle size analysis to assess the degree of inter-sample variation. Half the replicates were analysed using laser and half by sieve and pipette. The 'A' components were assigned randomly and distributed to the participating laboratories.

2.4.2 Analysis required

The participating laboratories were required to carry out particle size analysis on the samples using their normal technique or sub-contractor and to return basic statistics on the sample including mean, median, sorting and skewness. Also requested was a breakdown of the particle size distribution of the sediment, to be expressed as a weight of sediment in half-phi (ϕ) intervals.

2.5 Ring Test Specimens (RT)

This component of the Scheme examined inter-laboratory variation in the ability to identify fauna and attempted to determine whether any errors were the result of inadequate keys, lack of reference material (*e.g.* growth series), or the incorrect use of satisfactory keys.

Two sets of twenty-five specimens were distributed in 2000/01. The first of the year's RT circulations (RT16) was of the same form as for the earlier years - the specimens included representatives of the major phyla and approximately 36% of the taxa were polychaete worms, 28% were crustaceans, and 24% were molluscs. The second circulation (RT 17) 'targeted' specimens of estuarine origin. This would enable participating laboratories to use habitat descriptions to aid their identifications.

2.5.1 Preparation of the Samples

The specimens distributed were obtained from a range of surveys from around the UK. Every attempt was made to provide animals in good condition and of similar size for each laboratory. Each specimen sent was uniquely identifiable by means of a coded label and all material has been retained for

subsequent checking. In a number of instances, particularly with small species, two specimens were distributed. Where relevant, every effort was made to ensure all specimens of a given species were of the same sex.

For the standard RT (RT16) and the 'targeted' RT (RT17), all specimens were taken from replicate grabs within a single survey and in most cases they were replicates from a single sampling station.

2.5.2 *Analysis required*

The participating laboratories were required to identify each of the RT specimens to species and provide the Species Directory code (Howson & Picton, 1997) for the specimen (where available) and brief information on the keys or other literature used to determine the identification. All specimens were to be returned to Unicomarine Ltd. for verification and resolution of any disputed identifications. This was the same procedure as for earlier circulations.

2.6 Laboratory Reference (LR)

This component aims to address the criticism that some of the taxa circulated in the Ring Tests were unlikely ever to be encountered by some of the laboratories, and thus were not a valid test of laboratory skills. The participants were required to submit a reference collection of twenty-five specimens for re-examination by Unicomarine Ltd.

2.6.1 *Selection of fauna*

The different geographical distributions of species meant that a contractor request for a uniform set of species from all laboratories was unlikely to be successful. Accordingly a list of instructions was distributed to participating laboratories (Appendix 1). The specimens were to broadly represent the faunal groups circulated in the general Ring Tests, *i.e.* mixed phyla. Each laboratory was invited to include, if they wished, two problematic specimens, these were to be excluded from the summary statistics. Specimens wherever possible were to be representatives from NMMP reference collections.

2.6.2 *Analysis*

A prepared results sheet was distributed with the list with attached labels for the laboratories to identify each of the specimens. All specimens were re-identified and the identification made by Unicomarine Ltd. compared with that made by the participating laboratories. All specimens were returned to the laboratories after analysis. Results for the exercise were recorded separately at the generic and specific level, in the same manner as for the Ring Test.

3. Results

The exercises in 2000/01 were undertaken, in varying numbers, by twenty-three separate laboratories. Differences in the number of exercises in which laboratories participated meant that some exercises had more data returned than others. There were, as in previous years, large differences between laboratories in their ability to meet the target deadlines, even though these had been extended for some exercises this year due to variations in seasonal workload between laboratories. Sub-contracting by participating laboratories of certain sample analyses may also have contributed to delays.

Some laboratories did not submit returns for a number of the exercises, or the returns were not in the format requested; this is indicated in the tables by a dash (-). The reasons for the dashes are various. In some case samples were not returned by laboratories, in others the data, although returned, were not suitable for the analysis. In some instances, laboratories had elected not to participate in a particular component of the Scheme.

To avoid unnecessary detail in the Tables described below the reason for the dashes is explained in each case under the appropriate heading in Section 6: Comments on individual laboratories.

3.1 Macrobenthic Samples (MB)

3.1.1 General comments

The distributed sediment (MB08) was from an estuarine mud with shell substratum taken from a depth of approximately 4m. The samples contained an average of fifteen species and one thousand three hundred and thirty-six individuals, covering a variety of phyla. The composite list from all samples was approximately thirty-eight species. Seven out of the eleven samples returned had been stained with Rose Bengal during sample processing. All of the eleven laboratories participating in this exercise returned samples and data.

3.1.2 Efficiency of sample sorting

Table 1 presents for sample MB08, a summary of the estimate of numbers of taxa and individuals made by each of the participating laboratories together with the corresponding count made by Unicomarine Ltd. following re-analysis of the same samples. Comparison of the number of taxa and number of individuals between the participating laboratory and Unicomarine Ltd. is given as a percentage in Table 1. Table 2 shows the composition of missed fauna by each participating laboratory.

3.1.2.1 Number of Taxa

It may be seen from Table 1 (column 5) that there was considerable variation between laboratories in the percentage of taxa identified in the samples. Up to four taxa (and 31% of the total taxa in the sample) were either not extracted or not recognised within the picked material. On average Unicomarine Ltd. recorded two more taxa than the participating laboratories.

The values presented for the number of taxa not extracted (column 10) represent taxa not recorded or extracted (even if misidentified) elsewhere in the results, *i.e.* these were taxa completely missed by the laboratory. Only two laboratories extracted representatives of all the species present in their samples and in the worst instances three completely new taxa were missed during the picking stage of this exercise.

3.1.2.2 Number of Individuals

Re-sorting of the sample residue following analysis by the participating laboratories retrieved varied numbers of individuals all eleven samples. These data are presented in columns 11 and 12 of Table 1. The number of individuals not extracted from the sample (column 11) is given as a percentage of the total number in the sample (including those missed) in column 12 (*i.e.* column 12 = column 11 / column 7 %). The proportion of missed individuals in 73% of the samples was less than 5% of the true total number in the sample. In the worst instance 28% of the total number of individuals were not extracted during the initial sample processing. The average number of missed individuals found upon re-sorting the residue was twenty-five. A breakdown of the missed individuals by taxonomic group is presented in Table 2. Excluding nematodes and mites, molluscs were the most frequently missed faunal group, on average 39% of the total numbers of molluscs present are not extracted from the residue during the initial processing.

3.1.2.3 Uniformity of identification

Most of the species in the distributed sample were identified correctly by the participating laboratories. 64% of participating laboratories had no taxonomic differences (Table 1, column 15). In the worst instance four taxonomic differences were recorded. On average less than one taxonomic difference was encountered per sample.

3.1.3 Comparison of Similarity Indices (Bray-Curtis)

The fauna list for each sample obtained by the participating laboratory was compared with the list obtained for the same sample following its re-examination by Unicomarine Ltd. The comparison was made by calculating the Bray-Curtis similarity index for the pair of samples using non-transformed data. The results of this calculation are presented in Table 1 (column 14). There was little variation among laboratories in the values calculated for the index, from 83.1% to 99.9%, with an average value of 95.1%. The index for the majority of laboratories (8 of 11) was in excess of 95%. Only two of the

participating laboratories achieved a Bray-Curtis similarity index below 90%, these were 83.1% and 87.2%. These high Bray-Curtis similarity indices can be attributed to several factors, but in the main the presence of a dominant taxon or group of taxa that are relatively easy to correctly identify will offset any errors that occur in the minor taxa present. Further details of each participating laboratory's performance is given in Section 6: Comments on individual laboratories.

3.1.4 *Biomass determinations*

A comparison of the estimates of the biomass made by the participating laboratories and Unicomarine Ltd. broken down by major taxonomic group for the MB08 circulation is presented in Table 3. Three laboratories did not supply biomass data. The average difference between the two weight values was –9.98%, with the measurement made by Unicomarine Ltd. typically being greater (*i.e.* heavier) than that made by the participating laboratory. There was great variation in biomass estimations between participating laboratories and between taxonomic groups. The range of overall biomass percentage difference results, between participating laboratories and Unicomarine Ltd., was from –44.9% (measurements by laboratory were lighter than those made by Unicomarine Ltd.) to +56.3% (measurements by laboratory were greater than those made by Unicomarine Ltd.).

3.1.5 *Uniformity of samples*

The faunal content of the samples distributed as MB08 is shown in Table 4. Data received from six participating laboratories (LB0703, LB0705, LB0710, LB0717, LB0719 and LB0723) show distinctly higher abundance figures than those of the other participating laboratories. However, the faunal composition of all samples returned was very similar. The samples analysed show that the area sampled has a fairly uniformed taxonomic composition, however two groups of samples can be determined when observing the abundance data. The first group of samples are characterised by comparatively high total abundance figures composed in the main part by their dominant taxon, *Streblospio shrubsolii.* The second group of samples have far lower total abundance figures and *Corophium volutator* as their dominant taxon. Two participating laboratories felt it necessary to sub-sample a proportion of their samples.

3.2 Own Sample (OS)

3.2.1 *General comments*

Following the request to participating laboratories to submit a list of samples for re-analysis, forty-five samples were received from fifteen laboratories, together with descriptions of their origin and the collection and analysis procedures employed. Samples were identified as OS14, OS15 and OS16 on receipt. Four participating laboratories did not supply samples for this component although notification of non-participation was only received from one. The nature of the samples varied markedly. Samples were received from estuarine and marine locations, both intertidal and subtidal. The sediment varied from mud to gravel and from 10ml to 5l of residue. The associated fauna of the samples was also very varied; the number of taxa recorded ranged from 1 to 87, and the number of individuals from 4 to 4109. All NMMP labs were required to participate in this exercise. Overall, of the nineteen laboratories participating in this exercise, fifteen laboratories returned all three Own Samples. One laboratory failed to supply Unicomarine Ltd. with a list of samples from which to select their samples, one laboratory did not submit the requested samples, one laboratory submitted their samples well after the deadline (inadmissible), and one laboratory decided not to take part in this component for this scheme year.

3.2.2 *Efficiency of sample sorting*

Table 5 displays a summary of the data obtained from the analysis of the Own Sample exercise. All taxa identified and enumerated by the participating laboratory were included in the analysis. In fourteen cases (31% of the comparisons) the number of taxa recorded by the participating laboratories was identical to that obtained by Unicomarine Ltd. (column 4). In the thirty-one exceptions, the difference was at most fourteen taxa and the average difference was two taxa.

The data for the numbers of individuals recorded (columns 6 & 7) shows a range of differences from the value obtained from re-analysis of between 0% and 42%. The average difference is 8% (only thirteen samples exceeded this average). Eleven of the samples received showed 100% extraction of fauna from the residue (column 12), and in ten samples various numbers of individuals (but no new taxa) were missed during sorting (column 11). The remaining twenty-four samples contained taxa in the residue

which were not previously extracted, the worst example being thirteen new taxa found in the residue (column 10). In the worst instance residue was found to contain one thousand one hundred and four individuals. A breakdown of the missed individuals by taxonomic group is presented in Table 6. The average number of missed individuals found upon re-sorting the residue was sixty-four, and the average number of missed taxa was two.

3.2.3 *Uniformity of identification*

Taxonomic differences between participating laboratory and Unicomarine Ltd. results were found in thirty of the forty-five samples received. An average of over two and a half taxonomic differences per laboratory were recorded; in the worst instance eleven differences in identification occurred. A great variety of samples (and hence fauna) was received and no particular faunal group was found to cause problems.

3.2.4 *Comparison of Similarity Indices (Bray-Curtis)*

The procedure for the calculation of the similarity index was as used for the MB exercise. The Bray-Curtis similarity index figures (Table 5, column 14) ranged from 71% to 100%, with an average just over the pass/fail margin of 91%. Eleven samples from seven different laboratories achieved a similarity figure of less than 85%. Only one sample gave a similarity figure of 100%. The best overall results were achieved by laboratories LB0702 and LB0721, whose results consisted of 97.14%, 99.55% and 98.30%, and 96.95%, 99.09% and 98.95% similarity scores respectively. It is worth noting that a small number of differences between samples can result in a large difference in the Bray-Curtis index. This difference does not necessarily reflect the laboratory's interpretative ability.

3.2.5 *Biomass determinations*

It was not possible to make a comparison of the biomass determination in all cases; three laboratories did not supply biomass data, in others it was in a different format from that requested (one laboratory reported biomass to three decimal places and two laboratories reported at five decimal places). Audit biomass estimations were not calculated for two samples due to the condition of the fauna received (these were severely dried specimens due to initial biomass procedures). Table 7 shows the comparison of the participating laboratory and Unicomarine Ltd. biomass figures by major taxonomic groups. Thirty-four of the forty-five samples received could be used in this comparative exercise. The total biomass values obtained by the participating laboratories varied greatly with those obtained by Unicomarine Ltd. The average was a +14% difference between the two sets of results, the range was from –93% to +79%. The reason for these large differences is unknown but is presumably a combination of variations in apparatus (*e.g.* calibration) and operator technique (*e.g.* period of, and effort applied to, drying). Further analysis of biomass results by major taxonomic groups indicated an average difference of +16% for polychaetes, +25% for crustaceans and +8% for molluscs. These figures are markedly different to those produced by this same exercise in the last four years , this emphasises the variability caused by not only duration and method of drying but also the consistency of results within each major taxonomic group. The Unicomarine Ltd. biomass data was achieved using a non-pressure drying procedure as specified in the Green Book.

3.3 Particle Size Analysis (PS)

3.3.1 *General comments*

Most participating laboratories now provide data in the requested format, though some variations remain. As previously reported, it should be remembered that the results presented are for a more limited number of analytical laboratories than is immediately apparent since this component of the Scheme is often sub-contracted by participants to one of a limited number of specialist laboratories. For PS16, fifteen out of the eighteen participating laboratories returned data (including labs with grouped results); one laboratory specified not participation for this exercise; two did not. For PS17, seventeen out of the eighteen participating laboratories returned data; one did not.

3.3.2 *Analysis of sample replicates*

Replicate samples of the sediment used for the two PS distributions were analysed using both sieve and laser techniques. This was adopted after the earlier results indicated a clear difference according to the

analytical technique used to obtain them. Half of the replicates were analysed using the Malvern laser and half by the sieve and pipette technique.

There was very good agreement between the *replicate* samples from PS16; the shape of the distribution curves was similar for the two analytical techniques and they were closely grouped. This sample had a very low percentage of sediment in the fine fraction (average of 0.44% <63μm). Results for the individual replicates are provided in Table 8 and are displayed in Figure 1.

Sample PS17 was of a muddy fine sand sediment (average of 41.38% <63μm) although there was a marked difference in the curves between the two techniques. The estimations of <63μm% were clearly different between the two techniques. The average estimation of <63μm% from laser analyses was 53.85%, compared with 28.92% from sieve and pipette analyses. Results for the individual replicates are provided in Table 9 and are displayed in Figure 2.

3.3.3 *Results from participating laboratories*

Summary statistics for the two PS circulations are presented in Tables 10 and 11. After resolution of the differences in data format, the size distribution curves for each of the sediment samples were plotted and are presented in Figures 3 and 4. Included on each of these Figures for comparison is the mean distribution curve for the replicate samples as obtained by Unicomarine Ltd.

It should be noted that four laboratories which normally sub-contract particle size analysis to the same independent laboratory (also participating), elected to utilise the results from this laboratory. These laboratories are indicated in Tables 10 and 11 by an asterisk against their LabCode. Accordingly the results from this laboratory have been used in the Figures and Tables as appropriate though a few points should be noted. In Figures 3 and 4, which present the size distribution curves for PS16 and PS17 respectively, only a single line is shown though it applies to five laboratories (the sub-contractor and the four laboratories utilising their results). In Tables 10 and 11, which present the summary statistics for PS16 and PS17 respectively, although the results are displayed for all five laboratories, the value supplied (by the sub-contractor) has been included only once in the calculation of mean values for the exercise. Performance flags (as discussed in Section 5: Application of NMBAQC Scheme standards) have been assigned in the same manner as for other laboratories.

3.3.3.1 *Sixteenth distribution - PS16*

There was good agreement for PS16 between the results from the analysis of replicates and those from the majority of participating laboratories. The results for a single laboratory (LB0711) were slightly adrift; this is the only laboratory that uses a Coulter Multisizer for its sediment analysis. The difference between the analytical techniques was less marked than has been seen for other PS circulations (see Figure 3).

3.3.3.2 *Seventeenth distribution - PS17*

There was more spread in the results for this sample (which had a much higher proportion of sediment in the silt-clay fraction) and the difference between the techniques was less clearly marked, however this was not true of the replicate samples analysed by Unicomarine Ltd. (see Figures 2 and 4).

3.4 Ring Test Circulations (RT)

3.4.1 *General comments*

The implementation of this part of the Scheme was the same as previous years. A number of labs use this part of the scheme as a training exercise and have selected it preferentially over other components. NMMP labs are required to participate in this component though it is not used when assigning pass or fail flags. Two circulations of twenty-five specimens were made. For RT16 the species were from a variety of Phyla (as for previous years) while for RT17 twenty-five estuarine specimens were 'targeted' for circulation. Other aspects of the two circulations, in particular the method of scoring results, were the same as for previous circulations. Overall nineteen laboratories were distributed with RT16 and RT17 specimens. For RT16, fourteen laboratories returned data; two did not; three specified non-participation for this exercise. For RT17, eighteen laboratories returned samples and data; one specified non-participation for this exercise (using it as a training exercise without submitting data).

3.4.2 *Returns from participating laboratories*

Each laboratory returned a list of their identifications of the taxa together with the specimens. The identifications made by the participating laboratories were then compared with the AQC identification to determine the number of differences. A simple character-for-character comparison of the text of the two names (the AQC identification and the laboratory identification) was the starting point for this determination and provided a pointer to all those instances where (for whatever reason) the names differed. Each of these instances was examined to determine the reason for the difference.

As previously found, the main cause of an identification being different from the AQC identification was through differences in spelling of what was clearly intended to be the same species. There were several reasons for these differences, for example:

- Use of a different synonym for a species, e.g. *Tubifex costatus* for *Heterochaeta costata.*
- Simple mis-spelling of a name, e.g. *Aphelochaete* for *Aphelochaeta.*

NB. For the purposes of calculating the total number of differences in identification made by each laboratory a difference was ignored if it was clearly a result of one of the above.

Tables 12 and 13, respectively, present the identifications made by each of the participating laboratories for each of the twenty-five specimens in RT circulations RT16 and RT17. For clarity the name is given only in those instances where the generic or specific name given by the laboratory differed from the AQC identification. Where it was considered that the name referred to the same species as the AQC identification but differed for one of the reasons indicated above, then the name is presented in brackets "[name]". Errors of spelling or the use of a different synonym are not bracketed in this way if the species to which the laboratory was referring was not the same as the AQC identification. A dash "-" in the Tables indicates that the name of the genus (and / or species) given by the laboratory was considered to be the same as the AQC identification.

3.4.2.1 *Scoring of RT results*

The method of scoring was to increase a laboratory's score by one for each difference between their identification and the AQC identification, *i.e.* for each instance where text other than a dash or a bracketed name appears in the appropriate column in Tables 12 and 13. Two separate scores were maintained: for differences at the level of genus and species. These are not independent values, if the generic level identification was incorrect then the specific identification would normally also be incorrect, though the reverse is not necessarily the case.

3.4.3 *Ring Test distribution results*

The RT component of the Scheme mirrored that of 1998/99 as there was only a single 'standard' exercise (RT16). RT17 was targeted on estuarine taxa. The circulation was designed as more of a learning exercise to discover where particular difficulties lie within these individuals. Results were forwarded to the participating laboratories as soon as practicable. Each participant also received a ring test bulletin (RTB16 and RTB17), which outlined the reasons for individual laboratories identification discrepancies. This year participating laboratories were instructed to retain their ring test specimens, for approximately two week after the arrival of their results, to facilitate an improved learning dimension via the essential 'second look'.

3.4.3.1 *Sixteenth distribution – RT16*

Table 12 presents the results for the RT16. For the majority of the distributed taxa there was good agreement between participating laboratories and the identification made by Unicomarine Ltd. A small number of taxa were again responsible for the majority of differences and these are described briefly below.

Two specimens (*Turtonia minuta* and *Potamopyrgus antipodarum* (specimen 13)) accounted for 38% of the differences at the level of genus. Four specimens (*Ophelia borealis*, *Turtonia minuta, Ampharete lindstroemi* and *Potamopyrgus antipodarum* (specimen 13)) accounted for 36% of the differences at the level of species. Eight of the twenty-five circulated specimens were correctly identified by all

participating laboratories. Further details and analysis of results can be found in the relevant Ring Test Bulletin (RTB16) which was circulated to each laboratory from which results were received.

3.4.3.2 *Seventeenth distribution – RT17*

RT17 contained twenty-five estuarine dwelling specimens. The results from the circulation are presented in Table 13 in the same manner as for the other circulations. For the majority of the distributed taxa there was an reasonable agreement between participating laboratories and the identification made by Unicomarine Ltd. A small number of taxa were again responsible for the majority of differences and these are described briefly below.

The agreement at the generic level was relatively poor, sixty-four errors were recorded. Three specimens (*Mytilus edulis, Cerastoderma* edule and Potamopyrgus *antipodarum*) accounted for 45% of the differences recorded at the generic level. At the species level nine specimens accounted for 76% of the differences recorded (*Paranais litoralis, Tharyx 'A', Mytilus edulis, Aphelochaeta vivipara, Cerastoderma edule, Heterochaeta costata, Potamopyrgus antipodarum, Sabella pavonina* and *Aphelochaeta marioni*). Five of the twenty-five circulated specimens were correctly identified by all participating laboratories. Further details and analysis of results can be found in the relevant Ring Test Bulletin (RTB17) which was circulated to each laboratory from which results were received.

3.4.4 *Differences between participating laboratories*

Figures 5 and 6 present the number of differences recorded at the level of genus and species for each of the participating laboratories, for RT circulations RT16 and RT17 respectively. The laboratories are ordered by increasing number of differences at the level of species. The division of laboratories into three bands (Low, Medium and High) on the basis of the number of differences at the level of species is also shown. These bands are discussed further in Section 6: Comments on individual laboratories.

3.4.5 *Differences by taxonomic group*

Most of the differences of identification in RT16 were of molluscs, despite only six specimens being circulated. Approximately 58% of the total number of generic differences and 38% of specific differences were attributable to Mollusca. Polychaete specimens were responsible for 23% of the total number of generic differences and 32% of specific differences.

Most of the differences of identification in RT17 were also of molluscs, despite only nine specimens being circulated. Approximately 56% of the total number of generic differences and 49% of specific differences were attributable to Mollusca. Polychaete specimens were responsible for 27% of the total number of generic differences and 36% of specific differences.

3.5 Laboratory Reference (LR)

3.5.1 *General comments*

The value of reference material in assisting the process of identification cannot be over-emphasised. Accordingly the Laboratory Reference (LR) component of the Scheme was introduced to assess the ability of participating laboratories to identify material from their own area, or with which they were familiar. Of the eighteen laboratories participating in this exercise, fourteen laboratories returned samples and data; one laboratory indicated their non-participation in this exercise; three did not.

3.5.2 *Returns from participating laboratories*

The identification of the specimens received from the participating laboratories was checked and the number of differences at the level of genus and species calculated, in the same manner as for the RT exercises. The results for this component are presented in Table 14. There was generally very good agreement between the identifications made by the participating laboratories and those made by Unicomarine Ltd.

4. Discussion of Results

The results presented in the Tables and the discussions below should be read in conjunction with Section 6: Comments on individual laboratories.

4.1 Macrobenthic Analyses

The sample distributed as MB08 posed different problems for participating laboratories compared to some of the samples of previous circulations. The extraction of fauna from the sediment was time consuming due to the high numbers of individuals retained after sieving. All participating laboratories failed to extracted all the countable material from the residue. Identification caused very few problems, due to the common estuarine taxa present. However some mistakes were noted involving oligochaetes and confusion between *Macoma balthica* and *Abra tenuis*. Only two of the eleven returning laboratories attained a Bray-Curtis similarity index less than 90%. The average Bray-Curtis figure of 95% is the highest recorded for this exercise to date. However, it is still comparable with those recorded for MB07 (88%), MB06 (91%), MB05 (85%) and MB04 (82%). This years Macrobenthic exercise (MB08) illustrates the benefit of relatively large numbers of one or two taxa within a sample, assuming that these taxa are correctly identified, errors encountered in extraction, enumeration and identification of the minor taxa present will not result in a Bray-Curtis similarity index below 90%. For example, one participating laboratory missed eighty-five individuals in their residue, including two new taxa; enumeration of individuals extracted by the participating laboratory was two hundred and nineteen individuals more than the Unicomarine count of these individuals; however their Bray-Curtis similarity score was over 98%.

Table 4 shows the variation, by major Phyla, between those samples circulated for the macrobenthic exercise (MB08). The area sampled was patchy in its faunal composition. All samples were of relatively equal volume, sediment characteristics and species content, however the faunal composition varied with two discernible groups of samples present.

The 'blot-drying' procedure employed by Unicomarine Ltd. for the determination of biomass was as specified in the Green Book, *i.e.* avoiding excessive pressure when blotting specimens dry. However, there remains a considerable variation between the estimates of total biomass made by the participating laboratories and Unicomarine Ltd. Eight laboratories provided biomass data; four provided data that was heavier than Unicomarine Ltd.; and four supplied data that was lighter than Unicomarine Ltd. estimations. The extremes recorded were 45% lighter (LB0719) and 56% heavier (LB0720) than the Unicomarine Ltd. estimations. Overall the average difference between the values determined by the participating laboratories Unicomarine Ltd. was 4.9% (i.e. laboratory measurements were slightly heavier than those made by Unicomarine Ltd.).

It seems likely that the main reasons for the observed differences between the measurements are more thorough, or less consistent, drying by participating laboratories prior to weighing. A similar observation was made in previous years of the Scheme. The average percentage difference between Unicomarine Ltd. and participating laboratories biomass figures for MB08 was +4.9%, while for MB07 it was –1.67%, MB06 it was +26%, MB05 it was +32% and for MB04 it was +20%. There are likely to be several reasons for the differences between years, though the nature of the fauna in the distributed samples is likely to of particular importance.

Clearly, determination of biomass remains a problem area warranting further examination. Although each laboratory is following the same protocol it is apparent that different interpretations are being made of the degree of drying required. When single specimens of small species are being weighed (*e.g.* amphipods) very small differences in the effectiveness of drying will make large percentage differences in the overall weight recorded. It must be noted that the techniques specified are derived from the conversion factors used, *i.e.* which technique best reflects the methods specified by the conversion factors to be subsequently used. A series of trials should be commissioned to ascertain the best methods for accurate and consistent 'blotted' dry weight figures which can in turn be reliably applied to existing or new conversion factors.

4.2 Own Sample analyses

Considering just the Bray-Curtis index as a measure of similarity between the results obtained by the participating laboratories and those obtained from the same sample by Unicomarine Ltd. Participating laboratories performed similarly in the OS exercises and the MB08 exercise. The average value of the

index was 91% for the OS, compared with 95% for MB08. The average values of the other individual measures of processing performance (% of taxa extracted and identified, % individuals extracted) were similar for the MB08 exercise. The most apparent difference between these exercises was the far better identification of the fauna in the MB08 sample, the average number of taxonomic differences for the OS samples was more than two and a half compared with the figure of less than one for the MB returns. This is the reverse of last years exercises (OS11, 12, & 13, and MB07). The Bray-Curtis index is influenced more by differences in the identification of a number of taxa than by relatively small differences in the estimated abundance of any given taxon. Also in this instance MB08 contained high numbers of relatively easy dominant taxa which resulted in the diminishing significance, in Bray-Curtis similarity, of any errors involving the less abundant taxa. In summary although the average Bray-Curtis figures between these two exercises are similar, the OS returns had more taxonomic differences and contained more missed individuals in their residues compared with the MB08 returns, and MB08 contained fewer taxa and higher numbers of individuals per taxon than the Own Samples (85 and 20 individuals per taxon respectively) .

There were forty-five samples submitted for this component. This was facilitated by an extended deadline for returns and the distribution of timely reminders. The average Bray-Curtis similarity index achieved was 90.8%. Approximately 67% of samples exceeded the 90% Bray-Curtis pass mark. Approximately 44% of the samples exceeded 95% Bray-Curtis similarity. In the 1999/2000 year (OS 11, 12 and 13) the average Bray-Curtis figure was 91.4%, and 73% (of the fifty-one samples received) achieved more than 90% Bray-Curtis results. In the 1998/99 Scheme year (OS 08, 09 and 10) the average Bray-Curtis figure was 89.3%, and 71% (of the forty-two samples received) achieved more than 90%. In the 1997/98 year (OS 05, 06 and 07) the average Bray-Curtis figure was 93.6%, and 83% (of the forty samples received) achieved more than 90%.

Since the beginning of the OS component two hundred and twenty-nine samples have been received (OS01 – 16). The average Bray-Curtis similarity figure is 92%. Fifty-nine samples have fallen below the 90% pass mark (26%). Twenty-seven samples have achieved a similarity figure of 100% (12% of all returns). Whether laboratories are giving special attention to the samples that they submit for the OS component remains to be seen. However it must be noted that the extraction of fauna is an area in which several participating laboratories could review their efficiency. All countable fauna must be extracted to record a truly representative sample, although this is rarely the case due to time restraints or inefficient methods used. A sample that has been poorly picked stands high possibility of being unrepresentative regardless of the quality of subsequent faunal identifications, and should the sorted residue be disposed of this cannot be rectified. Laboratories should study their detailed OS and MB reports and target the particular taxon or groups of taxa that are being commonly overlooked during the picking stages of sample analysis. It must be resolved whether the individuals are either not recognised as countable or not scanned using the extraction methods employed. If it is the former, then training is appropriate. If the latter is the case then a review of current extraction methods should be conducted. An assortment of approaches would be appropriate in accordance to sediment type and faunal composition.

4.3 Particle Size Analyses

The difference between the two main techniques employed for analysis of the samples (laser and sieve) was again apparent in the results from the analysis of the replicates samples and from those from the participating laboratories. The sample distributed as PS16 appeared from an analysis of replicates (Figure 1) to be very uniform and, with few exceptions, the results from participating laboratories (Figure 3) were closely grouped.

There was more scatter in the results for PS17 from participating laboratories and a much less clear division between the two analytical methods. This may reflect variations in the use of sieves to pre-process samples analysed by laser (and therefore flagged as being analysed by laser). The participating laboratories were required to complete an additional data field for the analysis of this sediment sample. The laboratories were asked to provide a description of the sediment, *e.g.* the sediment circulated as PS17 could best be described as 'muddy fine sand'. Eight of the fourteen participating laboratories provided definitions of the sediment. One laboratory described the sediment as 'fine sand'; two laboratories recorded 'very fine sand'; one recorded 'muddy sand'; one recorded 'silt'; two recorded 'mud'; and one laboratory described the sediment as 'muddy'. Clearly a more scientific approach to describing sediment characteristic needs to be developed. The sediment circulated as PS17 yielded summary statistics from the majority of participating laboratories that placed the median particle as very

fine sand and less than 50% silt/clay content. Hence, the descriptions provided by the laboratories should not contain exclusively the words; 'fine sand' or 'mud'.

It is essential that the analytical method is stated when attempting to compare results. The situation is complicated further by the fact that the difference between the techniques also varies with the nature of the sediment sample. In Figures 3 and 4 the technique employed is indicated (as far as could be determined from the returns made by the laboratory). In most cases either sieve or laser analysis was used though in a few cases a mixed technique was employed.

4.4 Ring Test distributions

The results were in general comparable with those from the first six years of the Scheme, with a high level of agreement between participating laboratories for the majority of distributed species. The RT component is considered to provide a valuable training mechanism and be an indicator of problem groups and possible areas for further 'targeted' exercises. The ring test bulletins (RTB) have further emphasised the learning aspect of this component. RT16 identified discrepancies with literature used by some participating laboratories for their identification of the *Ophelia borealis* specimen. All participating laboratories have been made aware of this via the ring test bulletin (RTB16). However, the recommended literature had been stated on the NMBAQCS literature list circulated to all participating laboratories several years earlier.

4.5 Laboratory Reference

In view of the different species sent by laboratories for identification it is inappropriate to make detailed inter-lab comparisons. Some overall assessment of the performance is considered of value. For the laboratories returning a collection, the average number of differences at the level of genus was 1.4, and in most cases (9 of 14) laboratories had no differences or only a single difference. The situation was similar for identification at the level of species where the majority of laboratories achieved at most two differences in identification (8 of 14 laboratories). The average number of specific differences was 2.9. In the majority of instances identifications made by the participating laboratories were in agreement with those made by Unicomarine Ltd. In view of the range of species submitted it was not possible to identify a single taxon causing the majority of problems.

The results for this exercise should be viewed bearing in mind the different approach of different laboratories. Some clearly are sending well known species while others elect to obtain a 'second opinion' on more difficult species. Thus the scores are not comparable. The results presented in Table 14 are arranged by LabCode; it is not considered appropriate to assign any rank to the laboratories. Each participant should deliberate therefore on the aim of this component in terms of data quality assessment.

5. Application of NMBAQC Scheme standards

The primary purpose of the NMBAQC Scheme is to assess the reliability of data collected as part of the National Marine Monitoring Plan. With this aim a target standard has been defined for certain of the Scheme components. These standards are unchanged and have been applied to the results for the present year; each is described in detail in Appendix 2. Laboratories meeting or exceeding the required standard for a given component would be considered to have performed satisfactorily for that particular component. A flag indicating a 'Pass' or 'Fail' would be assigned to each laboratory for each of the components concerned. It should be noted that, as in previous years, only the OS and PS exercise have been used in 'flagging' for the purposes of assessing data for the National Marine Monitoring Plan.

As the Scheme progresses, additional components may be included. In the mean time, the other components of the Scheme as presented above are considered of value as more general indicators of laboratory performance, or as training. This follows the same approach as used when reporting the results for the year 1996/97 (Unicomarine, 1997).

As mentioned in the Introduction, non-return of samples or results for the PS and OS components resulted in the assignment of a "Fail" flag to the laboratory (see also Sections 3: Results). The only exception to this approach has been in those instances where laboratories had elected not to participate in a particular component of the Scheme.

5.1 Laboratory Performance

The target values for each component and the corresponding laboratory results are presented in Table 15 (OS) and Table 16 (PS). The assigned flags for each laboratory for each component are also given. An assessment is performed separately for each of the three OS samples. Pooling the results for the samples and applying a single flag was inappropriate because of the wide variation in the nature of the samples received from an individual laboratory. The tables should be should be read in conjunction with the comments on individual laboratories' results made in Section 6: Comments on individual laboratories.

Where no returns were made for the exercise this is indicated in Tables 15 and 16 with a "-". The reason for not participating, if given, will be stated in Section 6: Comments on individual laboratories.

It can be seen from Table 15 that for the OS exercise the majority of laboratories are considered to have met or exceeded the required standard for three of the OS targets - the enumeration of taxa and individuals and the Bray-Curtis comparison. Overall 80% of the comparisons were considered to have passed the enumeration of taxa standard; 80% exceeded the enumeration of individuals standard and 67% passed the Bray-Curtis comparison standard. Of the nineteen laboratories participating in this component fifteen supplied samples for reanalysis; one decided not to submit samples this scheme year; eleven achieved an overall pass flag; four failed; three laboratories which failed to supply samples or indicate their intentions have been flagged as 'Fail'.

Performance with respect to the biomass standard was much poorer with only 41% of the submitted samples meeting the required standard. It should be noted that there were laboratories for which the results from the biomass exercise should be considered unsuitable for comparison with the standard (expressed as three or five decimal places instead of four, and fauna rendered dry by initial biomass procedures).

Application of the standards to the results for the PS component is shown in Table 16. Three laboratories failed to meet the standard in PS16 due to non-return of data. All other participating laboratories passed this exercise. It must be noted that the current NMBAQCS standard applied to PS results allows a ten percentage point margin of error both above and below the mean of participating laboratory's results for % silt/clay in the circulated sample. As PS16 was a sandy sample containing only a nominal silt/clay volume achieving a 'Pass' was virtually predetermined by the sediment circulated. Sediment that contains either very small volumes or very high volumes of silt/clay particle fractions are far easier to achieve a 'pass' grade than mixed sediments. PS17 illustrates the different scenario when a mixed sediment is circulated. One laboratory failed to meet the standard in PS17 due to non-return of data. Eight laboratories, which submitted data, failed to meet the standard; nine laboratories passed. One laboratory provided spurious data (100% silt/clay) that dramatically altered the standard that the remaining laboratories must achieve. At least one laboratory submitted incorrect data for the % silt/clay content, which in turn was used to create the average % silt/clay figure and target range for a 'Pass' flag. Alternative 'Pass/Fail' criteria for this component are being reviewed.

5.2 Statement of Performance

Each participating laboratory have received a 'Statement of Performance', which includes a summary of results for each of the schemes components and details the resulting flags where appropriate. These statements were first circulated in with the 1998/1999 annual report, for the purpose of providing proof of scheme participation and for ease of analysing year on year progress.

5.3 Comparison with results from previous years

A comparison of the overall results for recent years is presented in Table 17. The Table shows the number of laboratories assigned 'Deemed Fail' (non-return), 'Fail' and 'Pass' flags for the OS and PS exercises over the last five years. For the OS component, this year resulted in the lowest pass rate (73% excluding deemed failures) since the introduction of the NMBAQCS standards. A similarly poor pass rate was achieved for the PS component (75% excluding deemed failures). However, for both components the numbers of 'Deemed Fails' have been either reduced or maintained at a low level. This can be attributed to the 'deadline reminders' dispatched throughout the Scheme year. Table 18 shows the trend of OS flags for participating laboratories over the past five years. There appears to be a fairly high level of consistency within each laboratory. Monitoring the situation over a longer period is required before a firm statement about changes in laboratory standards could be made.

6. Comments on individual laboratories

Brief comments on the results for individual laboratories are provided below. These are not intended to be detailed discussions of all aspects of the results but provide an indication of the main issues arising for each of the exercises. Clearly different laboratories have encountered different analytical problems. Broadly, these fell into the following areas:

- Incomplete sorting and extraction of individuals from whole samples.
- Particular taxonomic problems in RT's and whole samples
- Accuracy in biomass measurement
- Particle size % silt/clay calculations

Where possible these are noted for each laboratory listed below.

Also in the comments below, the results for RT16 and RT17 are expressed in terms of their position relative to the results from all laboratories. The overall range of differences at the level of genus and species was used to define three categories according to the number of differences: **Low**, **Mid** and **High** (based on the number of differences with the Unicomarine identifications). Each laboratory has been placed into a group for information only, on this basis.

This year five laboratories which normally use a centralised sediment analysis centre for the PS exercises, have decided to pool their data from just one laboratories analysis of PS samples. Their data is indicated accordingly in all figures and tables. In the comments below they are termed 'Data from centralised analysis'.

Laboratory – LB0701

Macrobenthos

MB08 - Not participating in this component.

Own Sample

OS14 – Five taxonomic differences. Seven vials contained mixtures of species. Two hundred and eighty-six individuals not picked from residue, including six previously unpicked taxa. Count variance of ninety-five individuals. Bray-Curtis similarity index of 95.9%. Biomass on average 3% lighter than Unicomarine Ltd. All three NMBAQCS standards passed.
OS15 – Four taxonomic differences. Three vials contained mixtures of species. Ninety-three individuals not picked from residue, including three previously unpicked taxa. Count variance of one individual. Bray-Curtis similarity index of 92.6%. Biomass on average 93% lighter than Unicomarine Ltd. Estimation of taxa standard failed; estimation of abundance and Bray-Curtis similarity standards passed.
OS16 – Five taxonomic differences. One vial contained a mixture of species. Thirty-eight individuals not picked from residue, including three previously unpicked taxa. Count variance of four individuals. Bray-Curtis similarity index of 91.2%. Biomass on average 18% heavier than Unicomarine Ltd. All three NMBAQCS standards passed.

Overall Own Sample component NMBAQCS standard flag – 'Pass'.

Particle size

PS16 – Data from centralised analysis; No major differences in size distribution curve. NMBAQCS standard passed.
PS17 – Data from centralised analysis; No major differences in size distribution curve. Sediment described as 'mudd'. NMBAQCS standard passed.

Ring Test

RT16 – Four generic and five specific differences. Number of AQC identifications in High group.
RT17 – One generic and two specific differences. Number of AQC identifications in Low group.

Laboratory Reference

Two generic and four specific differences.

Laboratory – LB0702

Macrobenthos

MB08 - Three individuals not picked from residue. Count variance of one individual. Bray-Curtis similarity index of 99.20%. Biomass on average 8% lighter than Unicomarine Ltd. Residue/fauna stained.

Own Sample

OS14 – Count variance of two individuals. Bray-Curtis similarity index of 97.1%. Biomass audit not undertaken due to the condition of the fauna. All three NMBAQCS standards passed.
OS15 – Count variance of eight individuals. Bray-Curtis similarity index of 99.6%. Biomass on average 42% heavier than Unicomarine Ltd. All three NMBAQCS standards passed.
OS16 – One taxonomic difference. One individual not picked from residue. Count variance of twenty individuals. Bray-Curtis similarity index of 98.3%. Biomass audit not undertaken due to the condition of the fauna. All three NMBAQCS standards passed.

Overall Own Sample component NMBAQCS standard flag – 'Pass'.

Particle size

PS16 – Not participating in this component.
PS17 – Not participating in this component.

Ring Test

RT16 – Two specific differences. Number of AQC identifications in Low group.
RT17 – One specific difference. Number of AQC identifications in Low group.

Laboratory Reference

Not participating in this component.

Laboratory – LB0703

Macrobenthos

MB08 - One taxonomic difference. One vial contained a mixture of species. Twenty-three individuals not picked from residue including one previously unpicked taxon (Acariformes). Count variance of twenty-five individuals. Bray-Curtis similarity index of 98.91%. Biomass data not supplied. Residue/fauna stained.

Own Sample

OS14 – One taxonomic difference. Three individuals not picked from residue, including two previously unpicked taxa. Count variance of one individual. Bray-Curtis similarity index of 92.1%. No biomass data supplied. All three NMBAQCS standards passed.
OS15 – Two taxonomic differences. Eight individuals not picked from residue, including one previously unpicked taxon. Count variance of three individuals. Bray-Curtis similarity index of 96.5%. No biomass data supplied. All three NMBAQCS standards passed.
OS16 – One taxonomic difference. Thirteen individuals not picked from residue, including five previously unpicked taxa. Count variance of one individual. Bray-Curtis similarity index of 82.2%. No biomass data supplied. All three NMBAQCS standards failed.

Overall Own Sample component NMBAQCS standard flag – 'Pass'.

Particle size

PS16 - No major differences in size distribution curve. NMBAQCS standard passed.

PS17 – 28% silt/clay recorded, this is below the target range (35.6 – 55.6%). Sediment described as 'very fine sand'. NMBAQCS standard failed.

Ring Test

RT16 – Two generic and three specific differences. Number of AQC identifications in Mid group.
RT17 – Three generic and four specific differences. Number of AQC identifications in Mid group.

Laboratory Reference

Five generic and eight specific differences.

Laboratory – LB0704

Macrobenthos

MB08 - Not participating in this component.

Own Sample

OS14 – Not participating in this component.
OS15 – Not participating in this component.
OS16 – Not participating in this component.

Particle size

PS16 – Data from centralised analysis; No major differences in size distribution curve. NMBAQCS standard passed.
PS17 – Data from centralised analysis; No major differences in size distribution curve. Sediment described as 'mudd'. NMBAQCS standard passed.

Ring Test

RT16 – Not participating in this component.
RT17 – Not participating in this component.

Laboratory Reference

Not participating in this component.

Laboratory – LB0705

Macrobenthos

MB08 - Two taxonomic differences. Fifteen individuals not picked from residue including two previously unpicked taxa (*Cerastoderma edule juv.* and *Hydrobia ulvae*). Count variance of two individuals. Bray-Curtis similarity index of 95.24%. Biomass data not supplied. Residue/fauna stained.

Own Sample

OS14 – Eight taxonomic differences. Four vials contained mixtures of species. Forty individuals not picked from residue, including four previously unpicked taxa. Count variance of ten individuals. Bray-Curtis similarity index of 89.7%. No biomass data supplied. Bray-Curtis similarity standard failed; estimation of taxa and estimation of abundance standards passed.
OS15 - Forty-nine individuals not picked from residue, including two previously unpicked taxa. Count variance of eighteen individuals. Bray-Curtis similarity index of 95.1%. No biomass data supplied. All three NMBAQCS standards passed.
OS16 – Two individuals not picked from residue, these were both previously unpicked taxa. Bray-Curtis similarity index of 98.9%. No biomass data supplied. All three NMBAQCS standards passed.

Overall Own Sample component NMBAQCS standard flag – 'Pass'.

Particle size

PS16 – Not participating in this component.
PS17 – Not participating in this component.

Ring Test

RT16 – Five generic and eight specific differences. Number of AQC identifications in High group.
RT17 – Five generic and eight specific differences. Number of AQC identifications in High group.

Laboratory Reference

Four generic and five specific differences.

Laboratory – LB0706

Macrobenthos

MB08 - Not participating in this component.

Own Sample

OS14 – No sample received. Laboratory in the process of finding new premises.
OS15 – No sample received. Laboratory in the process of finding new premises.
OS16 – No sample received. Laboratory in the process of finding new premises.

Overall Own Sample component NMBAQCS standard flag – 'Deemed Fail'.

Particle size

PS16 – No data received. Laboratory in the process of finding new premises. NMBAQCS standard flag – 'Deemed Fail'.
PS17 – No data received. Laboratory in the process of finding new premises. NMBAQCS standard flag – 'Deemed Fail'.

Ring Test

RT16 – Not participating in this component.
RT17 – Not participating in this component.

Laboratory Reference

No specimens received. Laboratory in the process of finding new premises.

Laboratory – LB0707

Macrobenthos

MB08 - Not participating in this component.

Own Sample

OS14 – Fifteen individuals not picked from residue. Count variance of five individuals. Bray-Curtis similarity index of 99.0%. Biomass on average 5% heavier than Unicomarine Ltd. All three NMBAQCS standards passed.
OS15 – One taxonomic difference. One vial contained a mixture of species. Count variance of four individuals. Bray-Curtis similarity index of 85.2%. Biomass on average 79% heavier than Unicomarine Ltd. Bray-Curtis similarity standard failed; estimation of taxa and estimation of abundance standards passed.
OS16 – Ten taxonomic differences. Eleven vials contained mixtures of species. One thousand one hundred and four individuals not picked from residue, including eleven previously unpicked taxa. Count variance of nine individuals. Bray-Curtis similarity index of 72.2%. Biomass on average 1% heavier than Unicomarine Ltd. All three NMBAQCS standards failed.

Overall Own Sample component NMBAQCS standard flag – 'Fail'.

Particle size

PS16 – Data from centralised analysis; No major differences in size distribution curve. NMBAQCS standard passed.
PS17 – Data from centralised analysis; No major differences in size distribution curve. Sediment described as 'mudd'. NMBAQCS standard passed.

Ring Test

RT16 – Two generic and four specific differences. Number of AQC identifications in Mid group.
RT17 – Two generic and two specific differences. Number of AQC identifications in Low group.

Laboratory Reference

One generic and one specific difference.

Laboratory – LB0708

Macrobenthos

MB08 - Count variance of five individuals. Eight individuals not picked from residue, including two previously unpicked taxa (Cirratulidae juv. and *Glycera sp. juv.*). Bray-Curtis similarity index of 98.54%. Biomass on average 13% lighter than Unicomarine Ltd. Residue/fauna stained.

Own Sample

OS14 – Not participating in this component.
OS15 – Not participating in this component.
OS16 – Not participating in this component.

Particle size

PS16 – No major differences in size distribution curve. NMBAQCS standard passed.
PS17 – 88.6% silt/clay recorded, this is well above the target range (35.6 – 55.6%). No sediment description given. NMBAQCS standard failed.

Ring Test

RT16 – One generic and two specific differences. Number of AQC identifications in the Low group.
RT17 – Six generic and six specific differences. Number of AQC identifications in the Mid group.

Laboratory Reference

One specific difference.

Laboratory – LB0709

Macrobenthos

MB08 - Not participating in this component.

Own Sample

OS14 – Not participating in this component.
OS15 – Not participating in this component.
OS16 – Not participating in this component.

Particle size

PS16 – No major differences in size distribution curve. NMBAQCS standard passed.

PS17 – 25.6% silt/clay recorded, this is below the target range (35.6 – 55.6%). No sediment description given. NMBAQCS standard failed.

Ring Test

RT16 – Not participating in this component.
RT17 – Not participating in this component.

Laboratory Reference

Not participating in this component.

Laboratory – LB0710

Macrobenthos

MB08 - Count variance of two hundred and nineteen individuals. Three vials contained a mixture of species, including two additional taxa. Eighty-five individuals not picked from residue, including two previously unpicked taxa (*Polydora sp.* and *Mytilus edulis juv.*). Bray-Curtis similarity index of 98.01%. Biomass on average 12% lighter than Unicomarine Ltd. Residue/fauna stained.

Own Sample

OS14 – Nine individuals not picked from residue, including two previously unpicked taxa. Count variance of one individual. Bray-Curtis similarity index of 76.9%. Biomass on average 26% heavier than Unicomarine Ltd. Estimation of taxa standard passed; estimation of abundance and Bray-Curtis similarity standards failed.
OS15 – One taxonomic difference. Eleven individuals not picked from residue, including five previously unpicked taxa. Count variance of three individuals. Bray-Curtis similarity index of 92.8%. Biomass on average 25% heavier than Unicomarine Ltd. Estimation of taxa standard failed; estimation of abundance and Bray-Curtis similarity standards passed.
OS16 – Three taxonomic differences. Four vials contained mixtures of species. Thirteen individuals not picked from residue, including six previously unpicked taxa. Count variance of two individuals. Bray-Curtis similarity index of 95.4%. Biomass on average 30% heavier than Unicomarine Ltd. Estimation of taxa standard failed; estimation of abundance and Bray-Curtis similarity standards passed.

Overall Own Sample component NMBAQCS standard flag – 'Fail'.

Particle size

PS16 – No major differences in size distribution curve. NMBAQCS standard passed.
PS17 – No major differences in size distribution curve. Sediment described as 'muddy sand'. NMBAQCS standard passed.

Ring Test

RT16 – One generic and four specific differences. Number of AQC identifications in Mid group.
RT17 – Two generic and three specific differences. Number of AQC identifications in Low group.

Laboratory Reference

Two specific differences.

Laboratory – LB0711

Macrobenthos

MB08 - Two taxonomic differences. Count variance of one individual. Thirty-one individuals not picked from residue, including two previously unpicked taxa (*Tanaissus lilljeborgi* and *Eurydice pulchra*). Bray-Curtis similarity index of 83.08%. Biomass on average 3% heavier than Unicomarine Ltd.

Own Sample

OS14 – Sample received after the deadline – Sample inadmissible.
OS15 – Sample received after the deadline – Sample inadmissible.
OS16 – Sample received after the deadline – Sample inadmissible.

Overall Own Sample component NMBAQCS standard flag – 'Deemed Fail'.

Particle size

PS16 – No major differences in size distribution curve. NMBAQCS standard passed.
PS17 – 29.9% silt/clay recorded, this is below the target range (35.6 – 55.6%). Sediment described as 'fine sand'. NMBAQCS standard failed.

Ring Test

RT16 – One generic and one specific differences. Number of AQC identifications in Low group. Laboratory identification for specimen 07 (*Rissoa labiosa*) marked as correct following a literature review.
RT17 – Three generic and four specific differences. Number of AQC identifications in Mid group.

Laboratory Reference

Two specific differences.

Laboratory – LB0712

Macrobenthos

MB08 - Not participating in this component.

Own Sample

OS14 – Bray-Curtis similarity index of 100%. No biomass data supplied. All three NMBAQCS standards passed.
OS15 – One taxonomic difference. One vials contained a mixture of species. Two individuals not picked from residue, including one previously unpicked taxon. Bray-Curtis similarity index of 82.4%. No biomass data supplied. Estimation of taxa and estimation of abundance standards passed; Bray-Curtis similarity standard failed.
OS16 – One individual not picked from residue, this was a previously unpicked taxon. Bray-Curtis similarity index of 85.7%. No biomass data supplied. Estimation of taxa and estimation of abundance standards passed; Bray-Curtis similarity standard failed.

Overall Own Sample component NMBAQCS standard flag – 'Pass'.

Particle size

PS16 – Not participating in this component.
PS17 – Not participating in this component.

Ring Test

RT16 – Not participating in this component.
RT17 – Not participating in this component.

Laboratory Reference

Not participating in this component.

Laboratory – LB0713

Macrobenthos

MB08 - Not participating in this component.

Own Sample

OS14 – Not participating in this component.
OS15 – Not participating in this component.
OS16 – Not participating in this component.

Particle size

PS16 – Not participating in this component.
PS17 – Not participating in this component.

Ring Test

RT16 – One generic and three specific differences. Number of AQC identifications in Mid group.
RT17 – Three generic and four specific differences. Number of AQC identifications in Mid group.

Laboratory Reference

Not participating in this component.

Laboratory – LB0714

Macrobenthos

MB08 - Count variance of one individual. Twenty-seven individuals not picked from residue, including three previously unpicked taxa (*Macoma balthica, Mesopodopsis slabberi* and *Bathyporeia sarsi*). Bray-Curtis similarity index of 90.85%. Biomass on average 27% heavier than Unicomarine Ltd.

Own Sample

OS14 – Three taxonomic differences. Two vials contained mixtures of species. Two hundred and fifty-six individuals not picked from residue, including thirteen previously unpicked taxa. Count variance of three individuals. Bray-Curtis similarity index of 74.0%. Biomass on average 12% heavier than Unicomarine Ltd. All three NMBAQCS standards failed.
OS15 – Seven taxonomic differences. Two vials contained mixtures of species. Six hundred and seventy individuals not picked from residue, including nine previously unpicked taxa. Count variance of seven individuals. Bray-Curtis similarity index of 81.7%. Biomass on average 17% heavier than Unicomarine Ltd. All three NMBAQCS standards failed.
OS16 – Seven taxonomic differences. One vial contained a mixture of species. Ninety-seven individuals not picked from residue, including seven previously unpicked taxa. Count variance of one individual. Bray-Curtis similarity index of 78.5%. Biomass on average 24% heavier than Unicomarine Ltd. All NMBAQCS standards failed.

Overall Own Sample component NMBAQCS standard flag – 'Fail'.

Particle size

PS16 – Data received after the deadline – Data inadmissible. NMBAQCS standard flag – 'Deemed Fail'.
PS17 – No major differences in size distribution curve. No sediment description given. NMBAQCS standard passed.

Ring Test

RT16 – No results received.
RT17 – Two generic and two specific differences. Number of AQC identifications in Low group.

Laboratory Reference

No specimens received.

Laboratory – LB0715

Macrobenthos

MB08 - Not participating in this component.

Own Sample

OS14 – Count variance of one individual. Bray-Curtis similarity index of 94.1%. Biomass on average 12% lighter than Unicomarine Ltd. All three NMBAQCS standards passed.
OS15 – Count variance of eleven individuals. Bray-Curtis similarity index of 97.4%. Biomass on average 14% lighter than Unicomarine Ltd. All three NMBAQCS standards passed.
OS16 – One vial contained a mixture of species. One individual not picked from residue. Count variance of three individuals. Bray-Curtis similarity index of 98.1%. Biomass on average 17% lighter than Unicomarine Ltd. All three NMBAQCS standards passed.

Overall Own Sample component NMBAQCS standard flag – 'Pass'.

Particle size

PS16 – Data from centralised analysis; No major differences in size distribution curve. NMBAQCS standard passed.
PS17 – Data from centralised analysis; No major differences in size distribution curve. Sediment described as 'mudd'. NMBAQCS standard passed.

Ring Test

RT16 – No results received. Exercise used for training with no submission of results.
RT17 – No results received. Exercise used for training with no submission of results.

Laboratory Reference

Not participating in this component.

Laboratory – LB0716

Macrobenthos

MB08 - Not participating in this component.

Own Sample

OS14 – No samples received. Several reminders circulated. No response received.
OS15 – No samples received. Several reminders circulated. No response received.
OS16 – No samples received. Several reminders circulated. No response received.

Overall Own Sample component NMBAQCS standard flag – 'Deemed Fail'.

Particle size

PS16 – Not participating in this component.
PS17 – Not participating in this component.

Ring Test

RT16 – No results received.
RT17 – Six generic and eleven specific differences. Number of AQC identifications in High group.

Laboratory Reference

No specimens received.

Laboratory – LB0717

Macrobenthos

MB08 - Four taxonomic differences. Count variance of thirty-two individuals. One vial contained a mixture of species. Eleven individuals not picked from residue, including two previously unpicked taxa (Nematoda and *Macoma balthica*). Bray-Curtis similarity index of 87.21%. Biomass on average 30% heavier than Unicomarine Ltd.

Own Sample

OS14 – Nine taxonomic differences. One vial contained a mixture of species. Fourteen individuals not picked from residue. Count variance of one individual. Bray-Curtis similarity index of 72.7%. Biomass on average 26% heavier than Unicomarine Ltd. Estimation of taxa standard passed; estimation of abundance and Bray-Curtis similarity standards failed.
OS15 – Eleven taxonomic differences. Eleven vials contained mixtures of species. Eighteen individuals not picked from residue, including three previously unpicked taxa. Count variance of two individuals. Bray-Curtis similarity index of 89.5%. Biomass on average 32% heavier than Unicomarine Ltd. Estimation of taxa and estimation of abundance standards passed; Bray-Curtis similarity standard failed.
OS16 – Eleven taxonomic differences. Five vials contained mixtures of species. Count variance of three individuals. Bray-Curtis similarity index of 70.9%. Biomass on average 32% heavier than Unicomarine Ltd. Estimation of abundance standard passed; Estimation of taxa and Bray-Curtis similarity standards failed.

Overall Own Sample component NMBAQCS standard flag – 'Fail'.

Particle size

PS16 – No major differences in size distribution curve. NMBAQCS standard passed.
PS17 – No major differences in size distribution curve. No sediment description given. NMBAQCS standard passed.

Ring Test

RT16 – One generic and five specific differences. Number of AQC identifications in High group.
RT17 – Five generic and seven specific differences. Number of AQC identifications in High group.

Laboratory Reference

Three generic and seven specific differences.

Laboratory – LB0718

Macrobenthos

MB08 - Not participating in this component.

Own Sample

OS14 – One taxonomic difference. Bray-Curtis similarity index of 83.6%. Biomass on average 14% lighter than Unicomarine Ltd. Estimation of taxa and estimation of abundance standards passed; Bray-Curtis similarity standard failed.
OS15 – Two taxonomic differences. Two vials contained mixtures of species. Count variance of four individuals. Bray-Curtis similarity index of 77.6%. Biomass on average 9% lighter than Unicomarine Ltd. Estimation of taxa and estimation of abundance standards passed; Bray-Curtis similarity standard failed.
OS16 – One vial contained a mixture of species. Count variance of one individual. Bray-Curtis similarity index of 99.7%. Biomass on average 1% lighter than Unicomarine Ltd. All three NMBAQCS standards passed.

Overall Own Sample component NMBAQCS standard flag – 'Pass'.

Particle size

PS16 – No major differences in size distribution curve. NMBAQCS standard passed.
PS17 – 57.8% silt/clay recorded, this is above the target range (35.6 – 55.6%). Sediment described as 'silt'. NMBAQCS standard failed.

Ring Test

RT16 – No results received.
RT17 – Four generic and five specific differences. Number of AQC identifications in Mid group.

Laboratory Reference

One generic and three specific differences.

Laboratory – LB0719

Macrobenthos

MB08 - Count variance of three individuals. One vial contained a mixture of species, including one additional taxa (*Tanaissus lilljeborgi*). Fifty-six individuals not picked from residue, including two previously unpicked taxa (*Abra tenuis* and *Jaera albifrons agg.*). Bray-Curtis similarity index of 99.17%. Biomass on average 45% lighter than Unicomarine Ltd.

Own Sample

OS14 – Six taxonomic differences. Nine vials contained mixtures of species. Four individuals not picked from residue. Count variance of ten individuals. Bray-Curtis similarity index of 96.7%. Biomass on average 33% heavier than Unicomarine Ltd. All three NMBAQCS standards passed.
OS15 – Four taxonomic differences. Two vials contained mixtures of species. Count variance of one individual. Bray-Curtis similarity index of 98.2%. Biomass on average 38% heavier than Unicomarine Ltd. All three NMBAQCS standards passed.
OS16 – Three taxonomic differences. Two vials contained mixtures of species. Two individuals not picked from residue, these were both previously unpicked taxa. Bray-Curtis similarity index of 97.0%. Biomass on average 29% heavier than Unicomarine Ltd. All three NMBAQCS standards passed.

Overall Own Sample component NMBAQCS standard flag – 'Pass'.

Particle size

PS16 – No major differences in size distribution curve. NMBAQCS standard passed.
PS17 – 100% silt/clay recorded, this is well above the target range (35.6 – 55.6%). No sediment description given. NMBAQCS standard failed.

Ring Test

RT16 – One generic and two specific differences. Number of AQC identifications in Low group.
RT17 – One generic and three specific difference. Number of AQC identifications in Low group.

Laboratory Reference

One generic and two specific difference.

Laboratory – LB0720

Macrobenthos

MB08 - One vial contained a mixture of contents. Thirteen individuals not picked from residue, including three previously unpicked taxa (*Cyathura carinata, Mytilus edulis juv.* and Nematoda). Bray-Curtis similarity index of 95.65%. Biomass on average 56% heavier than Unicomarine Ltd. Residue/fauna stained.

Own Sample

OS14 – Three taxonomic differences. Two vials contained mixtures of species. Thirty-five individuals not picked from residue. Count variance of one individual. Bray-Curtis similarity index of 93.1%. Biomass on average 16% heavier than Unicomarine Ltd. All three NMBAQCS standards passed.
OS15 – Five taxonomic differences. Three vials contained mixtures of species. Four individuals not picked from residue. Count variance of two individuals. Bray-Curtis similarity index of 94.6%. Biomass on average 6% lighter than Unicomarine Ltd. All three NMBAQCS standards passed.
OS16 – Three individuals not picked from residue, including one previously unpicked taxon. Bray-Curtis similarity index of 90.3%. Biomass on average 7% heavier than Unicomarine Ltd. Estimation of taxa and Bray-Curtis similarity standards passed; estimation of abundance standard failed.

Overall Own Sample component NMBAQCS standard flag – 'Pass'.

Particle size

PS16 – No major differences in size distribution curve. NMBAQCS standard passed.
PS17 – 33% silt/clay recorded, this is below the target range (35.6 – 55.6%). Sediment described as 'mud'. NMBAQCS standard failed.

Ring Test

RT16 – Three generic and four specific differences. Number of AQC identifications in Mid group.
RT17 – Two generic and two specific differences. Number of AQC identifications in Low group.

Laboratory Reference

No differences recorded.

Laboratory – LB0721

Macrobenthos

MB08 - Not participating in this component.

Own Sample

OS14 – Fourteen individuals not picked from residue. Count variance of one individual. Bray-Curtis similarity index of 97.0%. Biomass on average 27% lighter than Unicomarine Ltd. All three NMBAQCS standards passed.
OS15 – One taxonomic differences. One vial contained a mixture of species. Fourteen individuals not picked from residue, including one previously unpicked taxon. Count variance of six individuals. Bray-Curtis similarity index of 99.1%. Biomass on average 1% heavier than Unicomarine Ltd. All three NMBAQCS standards passed.
OS16 – Two taxonomic differences. Five vials contained mixtures of species. Eleven individuals not picked from residue. Count variance of twelve individuals. Bray-Curtis similarity index of 98.9%. Biomass on average 26% heavier than Unicomarine Ltd. All three NMBAQCS standards passed.

Overall Own Sample component NMBAQCS standard flag – 'Pass'.

Particle size

PS16 – Data from centralised analysis; No major differences in size distribution curve. NMBAQCS standard passed.
PS17 – Data from centralised analysis; No major differences in size distribution curve. Sediment described as 'mudd'. NMBAQCS standard passed.

Ring Test

RT16 – Four generic and six specific differences. Number of AQC identifications in High group. Specimen 23 (*Harpinia sp.*) dispatched was an intermediate specimen and, upon review, a correct specific identification has been awarded.
RT17 – Six generic and six specific differences. Number of AQC identifications in Mid group.

Laboratory Reference

No differences recorded.

Laboratory – LB0722

Macrobenthos

MB08 - Not participating in this component.

Own Sample

OS14 – One individual not picked from residue, this was a previously unpicked taxon. Bray-Curtis similarity index of 99.2%. Biomass on average 44% heavier than Unicomarine Ltd. All three NMBAQCS standards passed.
OS15 – Two taxonomic differences. Two vials contained mixtures of species. Twenty individuals not picked from residue. Count variance of three individuals. Bray-Curtis similarity index of 91.1%. Biomass on average 40% heavier than Unicomarine Ltd. Estimation of taxa and Bray-Curtis similarity standards passed; estimation of abundance standard failed.
OS16 – One taxonomic difference. Twelve individuals not picked from residue, including one previously unpicked taxon. Count variance of nine individuals. Bray-Curtis similarity index of 96.2%. Biomass on average 53% heavier than Unicomarine Ltd. All three NMBAQCS standards passed.

Overall Own Sample component NMBAQCS standard flag – 'Pass'.

Particle size

PS16 – No major differences in size distribution curve. NMBAQCS standard passed.
PS17 – No major differences in size distribution curve. Sediment described as 'muddy'. NMBAQCS standard passed.

Ring Test

RT16 – One specific difference. Number of AQC identifications in Low group.
RT17 – Two generic and two specific differences. Number of AQC identifications in Low group.

Laboratory Reference

One specific difference.

Laboratory – LB0723

Macrobenthos

MB08 - Count variance of five individuals. Five individuals not picked from residue. Bray-Curtis similarity index of 99.94%. Biomass data not supplied. Residue/fauna stained.

Own Sample

OS14 - Not participating in this component this year.
OS15 – Not participating in this component this year.
OS16 – Not participating in this component this year.

Particle size

PS16 – No major differences in size distribution curve. NMBAQCS standard passed.

PS17 – 25.2% silt/clay recorded, this is below the target range (35.6 – 55.6%). Sediment described as 'very fine sand'. NMBAQCS standard failed.

Ring Test

RT16 – No data received.
RT17 – Eleven generic and thirteen specific differences. Number of AQC identifications in High group.

Laboratory Reference

Two generic and four specific differences.

7. Conclusions and Recommendations

A number of observations may be made of the results of the exercises described above. The following is a summary of the major points of importance.

1. There was considerable variation in the speed with which samples and data were returned by participating laboratories. However, the numbers of laboratories either not submitting data or missing deadlines have reduced this year. This can be attributed partly to the exercise reminders that have been dispatched throughout the scheme year to reminder laboratories of imminent deadlines. Laboratories should endeavour to report within the requested time; this would greatly facilitate the analysis of results and effective feedback. Participating laboratories must give adequate priority to the NMBAQC Scheme components and ensure that they are aware of, and adhere to, the component deadlines circulated at the beginning of each Scheme year.
2. The majority of participating laboratories now use e-mail as their primary means of communication. Only one participating laboratory did not have e-mail capabilities. However, all laboratories participating in Scheme year eight will have e-mail capabilities. E-mail as an option for correspondence facilitates data transfer and its use is strongly recommended where practicable. All primary correspondence for Scheme year eight will be conducted via e-mail; hard copies of data sheets will be provided where appropriate.
3. Laboratories involved in NMMP data submission should endeavour to return data on **ALL** necessary components of the Scheme in the format requested. This will be required to allow the setting of performance "flags". Non-return of data will result in assignment of a "Fail" flag. This deemed "Fail" for no data submission is to be perceived as far worse than a participatory "Fail" flag.
4. A minority of participating laboratories have received 'deemed fail' flags as a result of not informing Unicomarine Ltd. of their intentions to abstain from particular exercises. Participating laboratories must take responsibility for ensuring that the level of their participation in the Scheme is communicated to Unicomarine Ltd.
5. There were continued problems associated with the measurement of biomass for individual species. Further consideration needs to be given to the preparation of a standardised protocol and reporting format. Various methods should be subjected to laboratory trials to ascertain a precise and consistent working protocol for NMMP biomass data. This year several laboratories, despite using blotted wet weight biomass techniques, rendered some of their specimens too damaged to be re-identified. Biomass procedures should not render the specimens indistinguishable; trials should be commissioned to derive the best protocol for the blotted weighing technique.
6. The particle size exercises (PS) showed clear differences in the results obtained by different analytical methods, and therefore, make it essential that the technique employed (*e.g.* Laser, sieve) is stated for each PS submission. PS data indicates that the variance between laser and sieve results is further emphasised by certain sediments characteristics. The overall range of these variances needs to be determined. It is essential that particle size data should be presented with a clear description of the method of analysis used. The participating laboratories provided a wide range of written descriptions for PS17, these ranged from mud to fine sand. The formation of written sediment descriptions, whether utilising particle size analysis summary statistics or not, needs to be examined.
7. The maintenance of a comprehensive reference collection has numerous benefits for improving identification ability, maintaining consistency of identification between surveys and access to

growth series material. The Laboratory Reference exercise (LR) can be used as a means of verifying reference specimens. Laboratories are strongly recommended to implement an in-house reference collection of fauna.

8. Some of the problems with identification, which arose throughout the various components of the scheme, included certain Mollusca. The molluscs distributed in RT16 and RT17 were responsible for 58% and 56% of the generic errors recorded, respectively. This is an area which requires further study to improve laboratory understanding. The use of a growth series and comparative reference specimens / images is imperative when identifying certain molluscs. Molluscs will once again be circulated as primary ring test specimens to clarify the major problem areas.

9. There are still some serious problems of individuals and taxa missed at the sorting stage. The figures for these sorting errors remain as high as in previous years exercises. In the MB exercise up to 3 taxa (21% of the actual total taxa in the sample) were not extracted. On average 1.73 taxa were not extracted from the residue. None of the participating laboratories extracted all the countable individuals from their residues. In the worst instance 27.7% of total individuals in the sample were not extracted. The situation was worse for the OS samples where a maximum of 13 taxa and up to 33% of the taxa were not extracted. In the worst instance 1104 individuals were not picked from the residue and up to 42% of the total individuals remained in the residue. On average for the OS exercise 2.04 taxa were not extracted compared with 1.25, 1.48, 0.45 and 1.39 taxa from last four years data, respectively. Enumeration of sorted individuals is generally good. However, where taxa and individuals are missed during the extraction of fauna from the sediment, laboratories should determine why certain taxa are not extracted. This could be due to the taxon not being recognised as countable or due to problems with the effect of stains upon the specimens. There may also be a problem within certain taxonomic groups (*e.g.* crustaceans floating within sample or molluscs settled within the coarser sediment fractions). Additional training may be required and a review of existing extraction techniques and quality control measures may be beneficial.

10. Earlier in this Scheme year a NMBAQCS Sorting Methods Questionnaire was devised and circulated to all laboratories participating in macrobenthic analysis components (OS & MB). The responses showed that little or no consistency in extraction or identification protocols existed between participating laboratories. The results of this questionnaire have been reported separately to the participating laboratories (Worsfold & Hall, 2001). The report concluded that there is a need for standardisation of extraction protocols, in terms of which fauna are extracted/not extracted. Also a consensus needs to be reached for what constitutes 'countable' individuals and at which taxonomic level specific taxa should be identified. Protocols are to be developed to standardise the approach towards headless and partial specimens. This also has implications for comparing biomass estimations, certain laboratories pick headless portions of specimens from residues and assign them to the relevant taxa for combined biomass measurements. Protocols are to be developed to standardise the faunal groups to be extracted from NMMP samples, and reasonable levels of identification devised for all taxa likely to be encountered.

11. Implementation of an improved learning structure to the scheme through detailed individual exercise reports has been successfully implemented. For the PS, LR, OS and MB exercises, detailed results have been forwarded to each participating laboratory as soon after the exercise deadlines as practicable. After each RT exercise a bulletin was circulated, reviewing the literature used and illustrating the correct identification of the taxa circulated. These ring test bulletins will be set-up as a web page for the next Scheme year. The NMBAQC Scheme website domain been set up. All participants are encouraged to view the website (www.nmbaqcs.org) and provide their comments and suggestions. Currently, not all participating laboratories have day-to-day access to the world wide web, and therefore reporting will continue be conducted in the same manner as for previous years.

12. The current PS 'Flagging' system is unfair and can result in anomalies. The percentage silt/clay present in the sample is the only criterion used to define the pass/fail threshold for this component (See Appendix 2: Description of the Scheme standards for each component). The majority of participating laboratories use laser analysis. These analyses can, with some sediments, give results that are markedly different to those of the sieve analysts. Consequently, the average silt/clay fraction figures used to apply the standards will be biased towards those laboratories using the laser technique. Several laboratories provided incorrect summary statistics for their sediment circulations, notably their statement of %<63μm. This has severe implications upon other participating laboratories because this statistic is used to set the pass/fail target range. A new

scoring system must be devised for the PS component – experienced sedimentologists must be consulted.

13. The current OS 'Flagging' system can result in anomalies. The use of taxa, individual and Bray-Curtis scores combined with a 'six from nine' pass threshold (See Appendix 2: Description of the Scheme standards for each component) could theoretically pass a laboratory which picks and counts all the individuals perfectly but identifies all the species incorrectly. The flagging should reflect the importance of achieving potentially truly representative data (*i.e.* completely picked residues) and also accurately identified taxa. The Own Sample component format and standards were the subjects of a review (Unicomarine, 2001) that suggested an alternative scoring system based solely upon the Bray-Curtis similarity indices on a sample-by-sample basis. Since the introduction of the OS component there have been several recurring concerns raised involving four aspects: standard recording procedures, sample randomisation, the pass/fail criteria, and remedial action. The Own Sample scoring system must be changed, the selection of Own Samples must be randomised, and a facility for tracking and evaluating the remedial action applied to failing samples must be devised.

8. References

Howson, C.M. & Picton, B.E. (eds) (1997) *The species directory of the marine fauna and flora of the British Isles and surrounding seas.* Ulster Museum and The Marine Conservation Society, Belfast and Ross-on-Wye.

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Unicomarine (2001) *National Marine Biological Analytical Quality Control Scheme. Own Sample Format and Standards Review: Current Problems and Proposed Solutions.* Report to the NMBAQC Committee. April 2001.

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Table 1. Results from the analysis of Macrobenthic sample MB08 by the participating laboratories.

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
	Number of Taxa				Number of Individuals				Not extracted			Individuals	Similarity	Taxonomic
LabCode	PL	UM	Diff (n)	%max	PL	UM	Diff (n)	%max	New Taxa	Ind	%ind	Count Error	index	errors
LB0702	15	15	0	0.0	124	126	-2	1.6	0	3	2.4	1	99.20	0
LB0703	17	18	-1	5.6	2209	2207	2	0.1	1	23	1.0	25	98.91	1
LB0705	13	15	-2	13.3	424	437	-13	3.0	2	15	3.4	2	95.24	2
LB0708	14	16	-2	12.5	238	241	-3	1.2	2	8	3.3	5	98.54	0
LB0710	9	13	-4	30.8	3776	3642	134	3.5	2	85	2.3	219	98.01	0
LB0711	11	12	-1	8.3	82	112	-30	26.8	2	31	27.7	1	83.08	2
LB0714	11	14	-3	21.4	139	167	-28	16.8	3	27	16.2	-1	90.85	0
LB0717	11	13	-2	15.4	475	518	-43	8.3	2	11	2.1	-32	87.21	4
LB0719	11	14	-3	21.4	3907	3960	-53	1.3	2	56	1.4	3	99.17	0
LB0720	10	14	-4	28.6	189	202	-13	6.4	3	13	6.4	0	95.65	0
LB0723	14	14	0	0.0	1747	1747	0	0.0	0	5	0.3	5	99.94	0

Key: PL - participating laboratory
UM - Unicomarine Ltd.
See Report, Section 6, for further details.

Table 2. Comparison of the efficiency of extraction of fauna by the participating laboratories for the major taxonomic groups present in sample MB08.

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB0702	UM count	-	38	4	-	77	-	4	3	126
	PL missed	-	0	0	-	2	-	0	1	3
	%missed	-	0.0	0.0	-	2.6	-	0.0	33.3	2.4
LB0703	UM count	-	1968	26	1	186	-	15	11	2207
	PL missed	-	12	5	1	0	-	2	3	23
	%missed	-	0.6	19.2	100.0	0.0	-	13.3	27.3	1.0
LB0705	UM count	-	303	18	-	104	-	8	5	438
	PL missed	-	7	1	-	0	-	4	3	15
	%missed	-	2.3	5.6	-	0.0	-	50.0	60.0	3.4
LB0708	UM count	-	35	6	-	185	-	8	7	241
	PL missed	-	2	0	-	2	-	4	0	8
	%missed	-	5.7	0.0	-	1.1	-	50.0	0.0	3.3
LB0710	UM count	-	3089	10	-	540	-	2	1	3642
	PL missed	-	77	2	-	5	-	1	0	85
	%missed	-	2.5	20.0	-	0.9	-	50.0	0.0	2.3
LB0711	UM count	-	21	2	-	88	-	1	-	112
	PL missed	-	8	1	-	22	-	0	-	31
	%missed	-	38.1	50.0	-	25.0	-	0.0	-	27.7
LB0714	UM count	-	35	1	-	126	-	2	3	167
	PL missed	-	2	0	-	21	-	2	2	27
	%missed	-	5.7	0.0	-	16.7	-	100.0	66.7	16.2
LB0717	UM count	-	246	12	-	257	-	2	1	518
	PL missed	-	5	2	-	2	-	1	1	11
	%missed	-	2.0	16.7	-	0.8	-	50.0	100.0	2.1
LB0719	UM count	-	3563	8	-	384	1	2	2	3960
	PL missed	-	51	0	-	3	0	2	0	56
	%missed	-	1.4	0.0	-	0.8	0.0	100.0	0.0	1.4
LB0720	UM count	-	37	3	-	156	-	5	1	202
	PL missed	-	0	0	-	11	-	1	1	13
	%missed	-	0.0	0.0	-	7.1	-	20.0	100.0	6.4
LB0723	UM count	-	1094	(45)	-	650	-	3	-	1747
	PL missed	-	4	(1)	-	1	-	0	-	5
	%missed	-	0.4	(2.2)	-	0.2	-	0.0	-	0.3

Key: PL - participating laboratory
UM - Unicomarine Ltd.
"-" - No data. See Report, Section 6, for details.

Table 3. Comparison of the estimates of biomass made by the participating laboratories with those made by Unicomarine Ltd. for the major taxonomic groups present in sample MB08. Values are in grams (g).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB0702	PL	-	0.0264	0.0007	-	0.0184	-	1.0852	0.0001	1.1308
	UM	-	0.0468	0.0007	-	0.0343	-	1.1391	0.0001	1.221
	%diff.	-	-77.3	0.0	-	-86.4	-	-5.0	0.0	-8.0
LB0703	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB0705	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB0708	PL	-	0.0142	0.0025	-	0.0475	-	0.1395	0.0001	0.2038
	UM	-	0.0167	0.0026	-	0.0613	-	0.1495	0.0001	0.2302
	%diff.	-	-17.6	-4.0	-	-29.1	-	-7.2	0.0	-13.0
LB0710	PL	-	0.28221	0.00162	-	0.26827	-	-	-	0.5521
	UM	-	0.2887	0.0027	-	0.3244	-	-	-	0.6158
	%diff.	-	-2.3	-66.7	-	-20.9	-	-	-	-11.5
LB0711	PL	-	0.1369	0.0007	-	0.6083	-	0.5325	-	1.2784
	UM	-	0.1115	0.0004	-	0.6027	-	0.5193	-	1.2339
	%diff.	-	18.6	42.9	-	0.9	-	2.5	-	3.5
LB0714	PL	-	0.1515	0.0002	-	0.0601	-	-	0.0001	0.2119
	UM	-	0.1121	0.0001	-	0.0423	-	-	0.0001	0.1546
	%diff.	-	26.0	50.0	-	29.6	-	-	0.0	27.0
LB0717	PL	-	0.06638	0.00185	-	0.1935	-	0.0113	-	0.27303
	UM	-	0.0392	0.0042	-	0.1385	-	0.0097	-	0.1916
	%diff.	-	40.9	-127.0	-	28.4	-	14.2	-	29.8
LB0719	PL	-	0.2101	0.0002	-	0.0736	0.0022	-	0.0001	0.2862
	UM	-	0.2914	0.0009	-	0.1188	0.0035	-	0.0001	0.4147
	%diff.	-	-38.7	-350.0	-	-61.4	-59.1	-	0.0	-44.9
LB0720	PL	-	0.083	0.0008	-	0.0804	-	3.0017	-	3.1659
	UM	-	0.0582	0.0006	-	0.0447	-	1.2791	-	1.3826
	%diff.	-	29.9	25.0	-	44.4	-	57.4	-	56.3
LB0723	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-

Key: PL - participating laboratory
UM - Unicomarine Ltd.
"-" - No data. See Report, Section 6, for details.

Table 4. Variation in faunal content of samples distributed as MB08.

Taxa

LabCode	Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Total taxa
LB0702	0	6	2	0	3	0	3	1	15
LB0703	0	5	2	1	4	0	5	1	18
LB0705	0	6	2	0	2	0	4	1	15
LB0708	0	6	2	0	4	0	3	1	16
LB0710	0	5	2	0	3	0	2	1	13
LB0711	0	5	1	0	5	0	1	0	12
LB0714	0	6	1	0	5	0	1	1	14
LB0717	0	5	3	0	3	0	2	1	14
LB0719	0	4	2	0	5	1	1	1	14
LB0720	0	6	2	0	2	0	3	1	14
LB0723	0	6	2	0	5	0	2	1	16
Mean	0	5	2	0	4	0	2	1	15
Max.	0	6	3	1	5	1	5	1	18
Min.	0	4	1	0	2	0	1	0	12

Individuals

LabCode	Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Total Ind.
LB0702	0	38	4	0	77	0	4	3	126
LB0703	0	1968	26	1	186	0	15	11	2207
LB0705	0	302	18	0	104	0	8	5	437
LB0708	0	35	6	0	185	0	8	7	241
LB0710	0	3089	10	0	540	0	2	1	3642
LB0711	0	21	2	0	88	0	1	0	112
LB0714	0	35	1	0	126	0	2	3	167
LB0717*	0	888	12	0	899	0	2	1	1802
LB0719*	0	3563	8	0	384	1	2	2	3960
LB0720	0	37	3	0	156	0	5	1	202
LB0723	0	1094	46	0	650	0	3	2	1795
Mean	0	1006	12	0	309	0	5	3	1336
Max.	0	3563	46	1	899	1	15	11	3960
Min.	0	21	1	0	77	0	1	0	112

*=subsampled - final multiples given

Table 5. Results from the analysis of Own Samples (OS14 to OS16) supplied by the participating laboratories and re-analysis by Unicomarine.

1		2	3	4	5	6	7	8	9	10	11	12	13	14	15	
		Number of Taxa				Number of Individuals				Not extracted			Count	Similarity	Taxonomic	
LabCode		PL	UM	Diff (n)	%max	PL	UM	Diff (n)	%max	NewTaxa	Ind	%ind	Error	index	Errors	Note
LB0701	OS14	60	62	-2	3.2	3918	4109	-191	4.6	6	286	7.0	95	95.90	5	
LB0701	OS15	16	19	-3	15.8	1462	1554	-92	5.9	3	93	6.0	1	92.57	4	
LB0701	OS16	18	20	-2	10.0	913	955	-42	4.4	3	38	4.0	-4	91.22	5	
LB0702	OS14	15	15	0	0.0	36	34	2	5.6	0	0	0.0	2	97.14	0	Fauna damaged by biomass action
LB0702	OS15	6	6	0	0.0	887	895	-8	0.9	0	0	0.0	-8	99.55	0	Fauna damaged by biomass action
LB0702	OS16	14	13	1	7.1	568	549	19	3.3	0	1	0.2	20	98.30	1	Fauna damaged by biomass action
LB0703	OS14	20	22	-2	9.1	68	70	-2	2.9	2	3	4.3	1	92.09	1	
LB0703	OS15	27	28	-1	3.6	281	292	-11	3.8	1	8	2.7	-3	96.52	2	
LB0703	OS16	18	24	-6	25.0	37	51	-14	27.5	5	13	25.5	-1	82.22	1	
LB0705	OS14	82	87	-5	5.7	676	726	-50	6.9	4	40	5.5	-10	89.73	8	Residue labelled as OS15
LB0705	OS15	34	36	-2	5.6	1845	1876	-31	1.7	2	49	2.6	18	95.06	0	Residue labelled as OS14
LB0705	OS16	27	29	-2	6.9	176	178	-2	1.1	2	2	1.1	0	98.87	0	
LB0706	OS14	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB0706	OS15	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB0706	OS16	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB0707	OS14	12	12	0	0.0	582	592	-10	1.7	0	15	2.5	5	98.98	0	
LB0707	OS15	11	11	0	0.0	79	83	-4	4.8	0	0	0.0	-4	85.19	1	
LB0707	OS16	75	84	-9	10.7	1536	2631	-1095	41.6	11	1104	42.0	9	72.15	10	
LB0710	OS14	5	7	-2	28.6	20	30	-10	33.3	2	9	30.0	-1	76.92	0	
LB0710	OS15	11	16	-5	31.3	173	187	-14	7.5	5	11	5.9	-3	92.82	1	
LB0710	OS16	39	48	-9	18.8	289	300	-11	3.7	6	13	4.3	2	95.43	3	
LB0711	OS14	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB0711	OS15	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB0711	OS16	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB0712	OS14	4	4	0	0.0	4	4	0	0.0	0	0	0.0	0	100.00	0	
LB0712	OS15	4	6	-2	33.3	16	18	-2	11.1	1	2	11.1	0	82.35	1	
LB0712	OS16	2	3	-1	33.3	3	4	-1	25.0	1	1	25.0	0	85.71	0	
LB0714	OS14	57	71	-14	19.7	779	1032	-253	24.5	13	256	24.8	3	74.02	3	
LB0714	OS15	64	74	-10	13.5	2132	2809	-677	24.1	9	670	23.9	-7	81.74	7	
LB0714	OS16	58	66	-8	12.1	319	415	-96	23.1	7	97	23.4	1	78.47	7	
LB0715	OS14	1	1	0	0.0	9	8	1	11.1	0	0	0.0	1	94.12	0	
LB0715	OS15	15	15	0	0.0	216	205	11	5.1	0	0	0.0	11	97.40	0	
LB0715	OS16	9	9	0	0.0	625	623	2	0.3	0	1	0.2	3	98.08	0	
LB0716	OS14	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB0716	OS15	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB0716	OS16	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB0717	OS14	27	27	0	0.0	76	89	-13	14.6	0	14	15.7	1	72.73	9	
LB0717	OS15	56	60	-4	6.7	410	430	-20	4.7	3	18	4.2	-2	89.52	11	
LB0717	OS16	29	26	3	10.3	189	192	-3	1.6	0	0	0.0	-3	70.87	11	

Table 5. Results from the analysis of Own Samples (OS14 to OS16) supplied by the participating laboratories and re-analysis by Unicomarine.

1		2	3	4	5	6	7	8	9	10	11	12	13	14	15	
		Number of Taxa				Number of Individuals				Not extracted			Count	Similarity	Taxonomic	
LabCode		PL	UM	Diff (n)	%max	PL	UM	Diff (n)	%max	NewTaxa	Ind	%ind	Error	index	Errors	Note
LB0718	OS14	15	15	0	0.0	67	67	0	0.0	0	0	0.0	0	83.58	1	
LB0718	OS15	44	44	0	0.0	489	485	4	0.8	0	0	0.0	4	77.62	2	
LB0718	OS16	21	21	0	0.0	169	170	-1	0.6	0	0	0.0	-1	99.71	0	
LB0719	OS14	69	72	-3	4.2	543	537	6	1.1	0	4	0.7	10	96.67	6	
LB0719	OS15	69	71	-2	2.8	250	249	1	0.4	0	0	0.0	1	98.21	4	
LB0719	OS16	38	41	-3	7.3	328	330	-2	0.6	2	2	0.6	0	96.96	3	
LB0720	OS14	55	57	-2	3.5	376	410	-34	8.3	0	35	8.5	1	93.13	3	
LB0720	OS15	39	39	0	0.0	218	224	-6	2.7	0	4	1.8	-2	94.57	5	
LB0720	OS16	7	8	-1	12.5	14	17	-3	17.6	1	3	17.6	0	90.32	0	
LB0721	OS14	11	11	0	0.0	271	286	-15	5.2	0	14	4.9	-1	96.95	0	
LB0721	OS15	26	27	-1	3.7	657	665	-8	1.2	1	14	2.1	6	99.09	1	
LB0721	OS16	51	50	1	2.0	2969	2992	-23	0.8	0	11	0.4	-12	98.95	2	
LB0722	OS14	7	8	-1	12.5	63	64	-1	1.6	1	1	1.6	0	99.21	0	
LB0722	OS15	24	26	-2	7.7	132	149	-17	11.4	0	20	13.4	3	91.10	2	
LB0722	OS16	27	29	-2	6.9	356	359	-3	0.8	1	12	3.3	9	96.22	1	
LB0723	OS14	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Not participating this year
LB0723	OS15	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Not participating this year
LB0723	OS16	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Not participating this year

Key: PL - participating laboratory
UM - Unicomarine Ltd.
"-" - No data. See Report, Section 6, for details.

Table 6. Comparison of the efficiency of extraction of fauna by the participating laboratories for the major taxonomic groups present in Own Samples (OS14-OS16).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB01	UM count	15	3265	421	-	80	1	112	215	4109
OS14	PL missed	1	164	20	-	13	0	21	67	286
	%missed	6.7	5.0	4.8	-	16.3	0.0	18.8	31.2	7.0
LB01	UM count	1	1208	259	-	1	-	16	69	1554
OS15	PL missed	1	30	18	-	1	-	7	36	93
	%missed	100.0	2.5	6.9	-	100.0	-	43.8	52.2	6.0
LB01	UM count	-	824	83	-	-	-	14	34	955
OS16	PL missed	-	22	4	-	-	-	5	7	38
	%missed	-	2.7	4.8	-	-	-	35.7	20.6	4.0
LB02	UM count	-	13	1	-	5	-	15	-	34
OS14	PL missed	-	0	0	-	0	-	0	-	0
	%missed	-	0.0	0.0	-	0.0	-	0.0	-	0.0
LB02	UM count	-	831	3	-	13	-	2	46	895
OS15	PL missed	-	0	0	-	0	-	0	0	0
	%missed	-	0.0	0.0	-	0.0	-	0.0	0.0	0.0
LB02	UM count	-	46	34	-	25	-	440	4	549
OS16	PL missed	-	1	0	-	0	-	0	0	1
	%missed	-	2.2	0.0	-	0.0	-	0.0	0.0	0.2
LB03	UM count	-	16	-	-	14	2	37	1	70
OS14	PL missed	-	0	-	-	3	0	0	0	3
	%missed	-	0.0	-	-	21.4	0.0	0.0	0.0	4.3
LB03	UM count	1	44	-	-	31	1	215	-	292
OS15	PL missed	0	0	-	-	3	0	5	-	8
	%missed	0.0	0.0	-	-	9.7	0.0	2.3	-	2.7
LB03	UM count	1	20	-	-	5	5	15	5	51
OS16	PL missed	1	4	-	-	4	0	2	2	13
	%missed	100.0	20.0	-	-	80.0	0.0	13.3	40.0	25.5
LB05	UM count	2	191	-	-	43.0	55	405	30	726
OS14	PL missed	0	17	-	-	4	1	13	5	40
	%missed	0.0	8.9	-	-	9.3	1.8	3.2	16.7	5.5
LB05	UM count	25	255	-	-	-	45	1541	10	1876
OS15	PL missed	0	4	-	-	-	0	41	4	49
	%missed	0.0	1.6	-	-	-	0.0	2.7	40.0	2.6
LB05	UM count	4	59	-	-	-	21	91	3	178
OS16	PL missed	0	1	-	-	-	0	1	0	2
	%missed	0.0	1.7	-	-	-	0.0	1.1	0.0	1.1
LB06	UM count	-	-	-	-	-	-	-	-	0
OS14	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB06	UM count	-	-	-	-	-	-	-	-	0
OS15	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB06	UM count	-	-	-	-	-	-	-	-	0
OS16	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB07	UM count	-	128	5	-	5	-	454	-	592
OS14	PL missed	-	2	0	-	0	-	13	-	15
	%missed	-	1.6	0.0	-	0.0	-	2.9	-	2.5

Table 6. Comparison of the efficiency of extraction of fauna by the participating laboratories for the major taxonomic groups present in Own Samples (OS14-OS16).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB07	UM count	-	13	-	-	63	-	7	-	83
OS15	PL missed	-	0	-	-	0	-	0	-	0
	%missed	-	0.0	-	-	0.0	-	0.0	-	0.0
LB07	UM count	-	1336	185	6	104	22	63	915	2631
OS16	PL missed	-	323	63	1	22	2	44	649	1104
	%missed	-	24.2	34.1	16.7	21.2	9.1	69.8	70.9	42.0
LB10	UM count	-	15	-	-	1	-	-	14	30
OS14	PL missed	-	9	-	-	0	-	-	0	9
	%missed	-	60.0	-	-	0.0	-	-	0.0	30.0
LB10	UM count	-	25	-	-	3	1	6	152	187
OS15	PL missed	-	5	-	-	3	0	0	3	11
	%missed	-	20.0	-	-	100.0	0.0	0.0	2.0	5.9
LB10	UM count	3	115	-	-	12	2	37	131	300
OS16	PL missed	1	7	-	-	0	0	2	3	13
	%missed	33.3	6.1	-	-	0.0	0.0	5.4	2.3	4.3
LB11	UM count	-	-	-	-	-	-	-	-	0
OS14	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB11	UM count	-	-	-	-	-	-	-	-	0
OS15	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB11	UM count	-	-	-	-	-	-	-	-	0
OS16	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB12	UM count	-	3	-	-	-	-	1	-	4
OS14	PL missed	-	0	-	-	-	-	0	-	0
	%missed	-	0.0	-	-	-	-	0.0	-	0.0
LB12	UM count	-	15	-	-	1	-	2	-	18
OS15	PL missed	-	0	-	-	0	-	2	-	2
	%missed	-	0.0	-	-	0.0	-	100.0	-	11.1
LB12	UM count	-	2	-	-	1	-	1	-	4
OS16	PL missed	-	0	-	-	1	-	0	-	1
	%missed	-	0.0	-	-	100.0	-	0.0	-	25.0
LB14	UM count	1	307	5	-	250	3	441	25	1032
OS14	PL missed	0	28	5	-	4	1	207	11	256
	%missed	0.0	9.1	100.0	-	1.6	33.3	46.9	44.0	24.8
LB14	UM count	-	291	-	-	1597	83	805	33	2809
OS15	PL missed	-	21	-	-	15	16	616	2	670
	%missed	-	7.2	-	-	0.9	19.3	76.5	6.1	23.9
LB14	UM count	-	190	-	12	29	38	124	22	415
OS16	PL missed	-	10	-	1	4	2	78	2	97
	%missed	-	5.3	-	8.3	13.8	5.3	62.9	9.1	23.4
LB15	UM count	-	-	8	-	-	-	-	-	8
OS14	PL missed	-	-	0	-	-	-	-	-	0
	%missed	-	-	0.0	-	-	-	-	-	0.0
LB15	UM count	-	26	175	-	4	-	-	-	205
OS15	PL missed	-	0	0	-	0	-	-	-	0
	%missed	-	0.0	0.0	-	0.0	-	-	-	0.0

Table 6. Comparison of the efficiency of extraction of fauna by the participating laboratories for the major taxonomic groups present in Own Samples (OS14-OS16).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB15	UM count	-	274	338	1	-	-	10	-	623
OS16	PL missed	-	0	0	0	-	-	1	-	1
	%missed	-	0.0	0.0	0.0	-	-	10.0	-	0.2
LB16	UM count	-	-	-	-	-	-	-	-	0
OS14	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB16	UM count	-	-	-	-	-	-	-	-	0
OS15	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB16	UM count	-	-	-	-	-	-	-	-	0
OS16	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB17	UM count	7	55	3	-	5	-	19	-	89
OS14	PL missed	0	0	0	-	0	-	14	-	14
	%missed	0.0	0.0	0.0	-	0.0	-	73.7	-	15.7
LB17	UM count	35	268	-	-	36	20	63	8	430
OS15	PL missed	0	2	-	-	3	9	4	0	18
	%missed	0.0	0.7	-	-	8.3	45.0	6.3	0.0	4.2
LB17	UM count	1	124	8	-	47	-	11	1	192
OS16	PL missed	0	0	0	-	0	-	0	0	0
	%missed	0.0	0.0	0.0	-	0.0	-	0.0	0.0	0.0
LB18	UM count	-	14	-	-	5	2	46	-	67
OS14	PL missed	-	0	-	-	0	0	0	-	0
	%missed	-	0.0	-	-	0.0	0.0	0.0	-	0.0
LB18	UM count	-	362	-	-	53	-	67	3	485
OS15	PL missed	-	0	-	-	0	-	0	0	0
	%missed	-	0.0	-	-	0.0	-	0.0	0.0	0.0
LB18	UM count	-	21	-	-	1	22	126	-	170
OS16	PL missed	-	0	-	-	0	0	0	-	0
	%missed	-	0.0	-	-	0.0	0.0	0.0	-	0.0
LB19	UM count	1	196	-	-	267	9	50	14	537
OS14	PL missed	0	1	-	-	1	0	2	0	4
	%missed	0.0	0.5	-	-	0.4	0.0	4.0	0.0	0.7
LB19	UM count	1	133	-	1	27	15	46	26	249
OS15	PL missed	0	0	-	0	0	0	0	0	0
	%missed	0.0	0.0	-	0.0	0.0	0.0	0.0	0.0	0.0
LB19	UM count	2	96	-	-	200	-	26	6	330
OS16	PL missed	0	0	-	-	1	-	1	0	2
	%missed	0.0	0.0	-	-	0.5	-	3.8	0.0	0.6
LB20	UM count	65	201	1	2	14	44	82	1	410
OS14	PL missed	0	5	0	1	0	1	28	0	35
	%missed	0.0	2.5	0.0	50.0	0.0	2.3	34.1	0.0	8.5
LB20	UM count	9	82	-	-	2	97	21	13	224
OS15	PL missed	0	0	-	-	0	0	3	1	4
	%missed	0.0	0.0	-	-	0.0	0.0	14.3	7.7	1.8
LB20	UM count	-	15	-	-	-	-	2	-	17
OS16	PL missed	-	3	-	-	-	-	0	-	3
	%missed	-	20.0	-	-	-	-	0.0	-	17.6

Table 6. Comparison of the efficiency of extraction of fauna by the participating laboratories for the major taxonomic groups present in Own Samples (OS14-OS16).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB21	UM count	-	61	198	-	-	-	27	-	286
OS14	PL missed	-	4	7	-	-	-	3	-	14
	%missed	-	6.6	3.5	-	-	-	11.1	-	4.9
LB21	UM count	-	298	337	-	17	-	13	-	665
OS15	PL missed	-	7	6	-	0	-	1	-	14
	%missed	-	2.3	1.8	-	0.0	-	7.7	-	2.1
LB21	UM count	5	2011	132	-	70	-	72	701	2991
OS16	PL missed	0	10	1	-	0	-	0	0	11
	%missed	0.0	0.5	0.8	-	0.0	-	0.0	0.0	0.4
LB22	UM count	-	45	18	-	-	-	1	-	64
OS14	PL missed	-	0	0	-	-	-	1	-	1
	%missed	-	0.0	0.0	-	-	-	100.0	-	1.6
LB22	UM count	2	41	-	-	6	5	95	-	149
OS15	PL missed	0	2	-	-	0	0	18	-	20
	%missed	0.0	4.9	-	-	0.0	0.0	18.9	-	13.4
LB22	UM count	2	130	64	-	7	-	156	-	359
OS16	PL missed	0	3	1	-	1	-	7	-	12
	%missed	0.0	2.3	1.6	-	14.3	-	4.5	-	3.3
LB23	UM count	-	-	-	-	-	-	-	-	0
OS14	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB23	UM count	-	-	-	-	-	-	-	-	0
OS15	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB23	UM count	-	-	-	-	-	-	-	-	0
OS16	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-

Key: PL - participating laboratory
UM - Unicomarine Ltd.
"-" - No data. See Report, Section 6, for details.

Table 7. Comparison of the estimates of biomass made by the participating laboratories with those made by Unicomarine for the major taxonomic groups present in samples OS14-OS16.

Sample OS14

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB0701	PL	0.0212	3.3114	0.1792	-	0.2766	0.0007	135.1270	0.0021	138.9182
	UM	0.0191	2.6123	0.2127	-	0.2287	0.0007	140.0501	0.0018	143.1254
	%diff.	9.9	21.1	-18.7	-	17.3	0.0	-3.6	14.3	-3.0
LB0702	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0703	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0705	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0706	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0707	PL	-	0.3185	0.0008	-	0.0123	-	3.7008	-	4.0324
	UM	-	0.2762	0.0003	-	0.0096	-	3.5617	-	3.8478
	%diff.	-	13.3	62.5	-	22.0	-	3.8	-	4.6
LB0710	PL	-	0.0406	-	-	0.0240	-	-	0.1161	0.1807
	UM	-	0.0323	-	-	0.0153	-	-	0.0860	0.1336
	%diff.	-	20.4	-	-	36.3	-	-	25.9	26.1
LB0711	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0712	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0714	PL	0.0012	8.3637	-	-	0.3530	0.2032	20.4723	0.0909	29.4843
	UM	0.0001	5.7795	-	-	0.1749	0.1775	19.7756	0.0517	25.9593
	%diff.	91.7	30.9	-	-	50.5	12.6	3.4	43.1	12.0
LB0715	PL	-	-	0.0049	-	-	-	-	-	0.0049
	UM	-	-	0.0055	-	-	-	-	-	0.0055
	%diff.	-	-	-12.2	-	-	-	-	-	-12.2
LB0716	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0717	PL	0.0173	0.6931	0.0028	-	0.0062	-	0.1143	-	0.8338
	UM	0.0141	0.5114	0.0021	-	0.0047	-	0.0889	-	0.6212
	%diff.	18.5	26.2	26.1	-	24.1	-	22.2	-	25.5

Table 7. Comparison of the estimates of biomass made by the participating laboratories with those made by Unicomarine for the major taxonomic groups present in samples OS14-OS16.

Sample OS14

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB0718	PL	-	0.0412	-	-	-	0.0013	0.0596	-	0.1021
	UM	-	0.0491	-	-	-	0.0016	0.0661	-	0.1168
	%diff.	-	-19.2	-	-	-	-23.1	-10.9	-	-14.4
LB0719	PL	0.0020	1.6280	-	-	0.1570	0.0770	0.7830	0.0020	2.6490
	UM	0.0003	0.9809	-	-	0.0697	0.0484	0.6884	0.0002	1.7879
	%diff.	85.0	39.7	-	-	55.6	37.1	12.1	90.0	32.5
LB0720	PL	0.0400	3.3367	-	0.0001	0.0846	0.9556	2.2348	0.0042	6.6560
	UM	0.0279	2.7489	-	0.0001	0.0127	0.6795	2.1028	0.0033	5.5752
	%diff.	30.3	17.6	-	0.0	85.0	28.9	5.9	21.4	16.2
LB0721	PL	-	0.0935	0.0229	-	-	-	0.0970	-	0.2134
	UM	-	0.1531	0.0245	-	-	-	0.0943	-	0.2719
	%diff.	-	-63.7	-7.0	-	-	-	2.8	-	-27.4
LB0722	PL	-	0.0590	0.0130	-	-	-	-	-	0.0720
	UM	-	0.0332	0.0070	-	-	-	-	-	0.0402
	%diff.	-	43.7	46.2	-	-	-	-	-	44.2
LB0723	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-

Key: PL - participating laboratory
UM - Unicomarine Ltd.
"-" - No data. See Report, Section 6, for details.

Table 7. Comparison of the estimates of biomass made by the participating laboratories with those made by Unicomarine for the major taxonomic groups present in samples OS14-OS16.

Sample OS15

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB0701	PL	-	0.4976	0.0460	-	-	-	0.0905	0.0008	0.6349
	UM	-	1.1098	0.0403	-	-	-	0.0739	0.0006	1.2246
	%diff.	-	-123.0	12.4	-	-	-	18.3	25.0	-92.9
LB0702	PL	-	0.2305	0.0001	-	0.0051	-	0.0003	0.0001	0.2361
	UM	-	0.1286	0.0001	-	0.0060	-	0.0008	0.0012	0.1367
	%diff.	-	44.2	0.0	-	-17.6	-	-166.7	-1100.0	42.1
LB0703	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0705	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0706	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0707	PL	-	0.8990	-	-	0.1464	-	0.0696	-	1.1150
	UM	-	0.0754	-	-	0.0965	-	0.0623	-	0.2342
	%diff.	-	91.6	-	-	34.1	-	10.5	-	79.0
LB0710	PL	-	0.4115	-	-	-	0.0827	0.0945	0.4579	1.0466
	UM	-	0.2817	-	-	-	0.0832	0.0670	0.3494	0.7813
	%diff.	-	31.5	-	-	-	-0.6	29.1	23.7	25.3
LB0711	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0712	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0714	PL	-	9.2064	-	-	0.9131	4.2852	4.7667	5.2813	24.4527
	UM	-	7.0261	-	-	0.5742	4.1178	4.4075	4.1110	20.2366
	%diff.	-	23.7	-	-	37.1	3.9	7.5	22.2	17.2
LB0715	PL	-	0.0175	0.0124	-	0.0018	-	-	-	0.0317
	UM	-	0.0190	0.0152	-	0.0018	-	-	-	0.0360
	%diff.	-	-8.6	-22.6	-	0.0	-	-	-	-13.6
LB0716	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0717	PL	0.0267	0.4862	-	-	0.0106	0.0028	0.0686	0.0050	0.5999
	UM	0.0162	0.3406	-	-	0.0065	0.0030	0.0394	0.0022	0.4079
	%diff.	39.3	29.9	-	-	38.9	-6.8	42.5	56.2	32.0

Table 7. Comparison of the estimates of biomass made by the participating laboratories with those made by Unicomarine for the major taxonomic groups present in samples OS14-OS16.

Sample OS15

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB0718	PL	-	2.0498	-	-	0.0089	-	0.2443	0.3560	2.6590
	UM	-	2.2452	-	-	0.0140	-	0.2288	0.4014	2.8894
	%diff.	-	-9.5	-	-	-57.3	-	6.3	-12.8	-8.7
LB0719	PL	0.0010	0.3260	-	0.0020	0.0730	0.0150	0.4240	0.0100	0.8510
	UM	0.0001	0.1566	-	0.0012	0.0389	0.0070	0.3180	0.0026	0.5244
	%diff.	90.0	52.0	-	40.0	46.7	53.3	25.0	74.0	38.4
LB0720	PL	0.0021	0.9741	-	-	0.0009	6.1164	0.4537	0.0630	7.6102
	UM	0.0020	0.9393	-	-	0.0011	6.6212	0.4603	0.0614	8.0853
	%diff.	4.8	3.6	-	-	-22.2	-8.3	-1.5	2.5	-6.2
LB0721	PL	-	0.0101	0.0286	-	0.0012	-	0.0013	-	0.0412
	UM	-	0.0099	0.0283	-	0.0012	-	0.0015	-	0.0409
	%diff.	-	2.0	1.0	-	0.0	-	-15.4	-	0.7
LB0722	PL	0.0310	0.0600	-	-	0.0040	0.0060	0.0240	-	0.1250
	UM	0.0190	0.0276	-	-	0.0016	0.0085	0.0183	-	0.0750
	%diff.	38.7	54.0	-	-	60.0	-41.7	23.8	-	40.0
LB0723	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-

Key: PL - participating laboratory
UM - Unicomarine Ltd.
"-" - No data. See Report, Section 6, for details.

Table 7. Comparison of the estimates of biomass made by the participating laboratories with those made by Unicomarine for the major taxonomic groups present in samples OS14-OS16.

		Sample OS16								
LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB0701	PL	-	0.8506	0.0204	-	-	-	0.0131	0.0009	0.8850
	UM	-	0.6976	0.0160	-	-	-	0.0100	0.0004	0.7240
	%diff.	-	18.0	21.6	-	-	-	23.7	55.6	18.2
LB0702	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0703	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0705	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0706	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0707	PL	-	7.2182	0.0108	0.0227	0.1874	0.0495	16.6421	0.1188	24.2495
	UM	-	7.0133	0.0075	0.0227	0.1758	0.0470	16.5760	0.1178	23.9601
	%diff.	-	2.8	30.6	0.0	6.2	5.1	0.4	0.8	1.2
LB0710	PL	0.0006	1.0453	-	-	0.0168	0.5285	4.9779	0.5697	7.1388
	UM	0.0008	0.8336	-	-	0.0147	0.4111	3.2821	0.4707	5.0130
	%diff.	-33.3	20.3	-	-	12.4	22.2	34.1	17.4	29.8
LB0711	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0712	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0714	PL	-	1.5718	-	0.0026	0.0304	1.8705	2.7353	6.6510	12.8616
	UM	-	1.0819	-	0.0034	0.0212	1.6967	2.1439	4.8342	9.7813
	%diff.	-	31.2	-	-30.8	30.3	9.3	21.6	27.3	23.9
LB0715	PL	-	0.2127	0.0739	0.0001	-	-	0.0020	-	0.2887
	UM	-	0.2550	0.0816	0.0001	-	-	0.0008	-	0.3375
	%diff.	-	-19.9	-10.4	0.0	-	-	60.0	-	-16.9
LB0716	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0717	PL	0.0015	0.2250	0.0008	-	0.0195	-	0.0052	0.0057	0.2577
	UM	0.0016	0.1559	0.0001	-	0.0117	-	0.0038	0.0009	0.1740
	%diff.	-5.3	30.7	87.0	-	40.1	-	26.8	84.3	32.5

Table 7. Comparison of the estimates of biomass made by the participating laboratories with those made by Unicomarine for the major taxonomic groups present in samples OS14-OS16.

		Sample OS16								
LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB0718	PL	-	0.2228	-	-	0.0019	0.0170	0.5680	-	0.8097
	UM	-	0.2247	-	-	0.0023	0.0211	0.5705	-	0.8186
	%diff.	-	-0.8	-	-	-20.4	-24.1	-0.4	-	-1.1
LB0719	PL	0.0020	1.7940	-	-	0.2010	-	0.7580	-	2.7550
	UM	0.0005	1.2464	-	-	0.0918	-	0.6262	-	1.9649
	%diff.	75.0	30.5	-	-	54.3	-	17.4	-	28.7
LB0720	PL	-	0.3075	-	-	-	-	1.3146	-	1.6221
	UM	-	0.2705	-	-	-	-	1.2305	-	1.5010
	%diff.	-	12.0	-	-	-	-	6.4	-	7.5
LB0721	PL	0.0059	4.6879	0.0387	-	0.1600	-	0.3046	0.8012	5.9983
	UM	0.0056	3.3749	0.0305	-	0.1262	-	0.2916	0.5822	4.4110
	%diff.	5.1	28.0	21.2	-	21.1	-	4.3	27.3	26.5
LB0722	PL	0.0030	0.0890	0.0240	-	0.0050	-	0.0230	-	0.1440
	UM	0.0015	0.0350	0.0145	-	0.0019	-	0.0153	-	0.0682
	%diff.	50.0	60.7	39.6	-	62.0	-	33.5	-	52.6
LB0723	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-

Key: PL - participating laboratory
UM - Unicomarine Ltd.
"-" - No data. See Report, Section 6, for details.

Table 8. Summary of the results of particle size analysis of the replicate samples from sediment circulation PS16.

PS16	% Clay & Silt	Median (phi)	Mean (phi)	Sorting	Skew
PS16 - 34 - laser	0.98	1.01	0.88	0.65	0.02
PS16 - 35 - laser	0.59	1.10	1.03	0.55	0.08
PS16 - 36 - laser	1.35	0.93	0.52	0.96	-0.20
PS16 - 37 - laser	0.49	0.36	0.12	0.95	0.06
PS16 - 38 - laser	0.91	0.97	0.85	0.66	0.03
PS16 - 39 - laser	0.93	0.99	0.81	0.71	-0.02
PS16 - 40 - laser	0.91	1.13	1.06	0.55	0.06
PS16 - 27 - sieve	0.00	1.60	1.57	0.52	-0.07
PS16 - 28 - sieve	0.00	1.53	1.53	0.49	0.00
PS16 - 29 - sieve	0.00	1.58	1.56	0.52	-0.05
PS16 - 30 - sieve	0.00	1.53	1.54	0.50	0.01
PS16 - 31 - sieve	0.00	1.67	1.54	0.51	-0.27
PS16 - 32 - sieve	0.00	1.56	1.55	0.50	-0.02
PS16 - 33 - sieve	0.00	1.54	1.56	0.51	0.04

Table 9. Summary of the results of particle size analysis of the replicate samples from sediment circulation PS17.

PS17	% Clay & Silt	Median (phi)	Mean (phi)	Sorting	Skew
PS17 - 29A - laser	52.23	4.36	3.63	2.72	0.41
PS17 - 30A - laser	53.84	4.65	3.65	2.72	0.32
PS17 - 31A - laser	54.65	4.76	3.62	2.73	0.31
PS17 - 32A - laser	53.74	4.60	3.60	2.71	0.35
PS17 - 33A - laser	58.56	5.26	3.89	2.73	0.20
PS17 - 34A - laser	52.81	4.50	3.64	2.69	0.36
PS17 - 35A - laser	51.09	4.16	3.61	2.68	0.46
PS17 - 36A - sieve	28.76	3.32	4.84	2.06	0.74
PS17 - 37A - sieve	28.41	3.31	4.79	2.01	0.74
PS17 - 38A - sieve	29.41	3.32	4.95	2.17	0.75
PS17 - 39A - sieve	29.60	3.33	4.80	2.01	0.73
PS17 - 40A - sieve	28.42	3.33	4.82	2.02	0.74
PS17 - 41A - sieve	28.95	3.33	4.84	2.03	0.74
PS17 - 42A - sieve	28.88	3.34	4.94	2.14	0.75

Table 10. Summary of the particle size information received from participating laboratories for the sixteenth particle size distribution - PS16.

Lab	Method	%<63µm	Median	Mean	Sort	IGS (SKi)
LB0701*	L	0.36	1.27	1.12	0.56	-0.022
LB0703	DS	0.00	1.56	1.51	0.49	-0.53
LB0704*	L	0.36	1.27	1.12	0.56	-0.02
LB0706	-	-	-	-	-	-
LB0707*	L	0.36	1.27	1.12	0.56	-0.022
LB0708	DS	0.01	-	-	-	-
LB0709	S/P	0.00	1.07	1.12	0.62	-
LB0710	L	0.00	1.14	1.11	0.60	0.000
LB0711	DS/CC	0.58	0.62	-	0.37	0.03
LB0714	-	-	-	-	-	-
LB0715*	L	0.36	1.27	1.12	0.56	-0.022
LB0717	WS/DS/L	0.61	1.25	1.36	0.74	0.06
LB0718	DS	0.10	1.47	1.45	0.49	0.00
LB0719	FD/DS	0.00	1.55	1.55	0.48	-0.05
LB0720	L	0.00	0.99	0.99	0.61	0.00
LB0721*	L	0.36	1.27	1.12	0.56	-0.022
LB0722	S	0.10	1.50	1.50	0.49	-0.03
LB0723	not participating in this component					

Key to methods:

L - Laser analysis DS - Dry sieve CC - Coulter counter
S - Sieve WS - Wet sieve FD - Freeze dried
P - Pipette n/c - not calculated
L* - data for this laboratory not included in calculations below (see text)
"-" - No data. See Report, Section 6, for details.

Summary	%<63µm	Median	Mean	Sort	IGS (SKi)
Number of values	11	10	9	10	9
Mean of laboratories	0.16	1.24	1.30	0.55	-0.06
Mean of 7 replicates (laser)	0.88	0.93	0.75	0.72	0.00
Mean of 7 replicates (sieve)	0.00	1.57	1.55	0.51	-0.05
Laboratory minimum	0.00	0.62	0.99	0.37	-0.53
Laboratory maximum	0.61	1.56	1.55	0.74	0.06

Table 11. Summary of the particle size information received from participating laboratories for the seventeenth particle size distribution - PS17.

Lab	Method	%<63µm	Median	Mean	Sort	IGS (SKi)
LB0701*	L	36.62	3.29	3.02	1.71	0.47
LB0703	DS	28.00	3.33	3.40	0.67	-0.31
LB0704*	L	36.62	3.29	3.02	1.71	0.47
LB0706	-	-	-	-	-	-
LB0707*	L	36.62	3.29	3.02	1.71	0.47
LB0708	DS/L	88.56	-	-	-	-
LB0709	S/P	25.63	2.91	3.34	1.60	-
LB0710	L	41.60	3.47	5.03	2.19	0.60
LB0711	DS/CC	29.89	2.49		1.65	0.98
LB0714	L	40.71	3.24	4.52	2.52	0.700
LB0715*	L	36.62	3.29	3.02	1.71	0.47
LB0717	WS/DS/L	47.48	3.80	5.03	2.63	0.59
LB0718	L	57.78	3.57	3.48	2.24	0.57
LB0719	L	100.00	7.75	7.80	0.55	0.18
LB0720	L	33.03	2.96	4.49	2.20	0.59
LB0721*	L	36.62	3.29	3.02	1.71	0.47
LB0722	L	37.95	3.37	3.31	1.66	0.48
LB0723	DS/L	25.21	-	3.60	moderate	1.71

Key to methods:

L - Laser analysis DS - Dry sieve CC - Coulter counter
S - Sieve WS - Wet sieve FD - Freeze dried
P - Pipette n/c - not calculated
L* - data for this laboratory not included in calculations below (see text)
"-" - No data. See Report, Section 6, for details.

Summary	%<63µm	Median	Mean	Sort	IGS (SKi)
Number of values	13	11	11	11	11
Mean of laboratories	45.57	3.65	4.27	1.78	0.60
Mean of 7 replicates (laser)	53.85	4.61	3.66	2.71	0.34
Mean of 7 replicates (sieve)	28.92	3.33	4.85	2.06	0.74
Laboratory minimum	25.21	2.49	3.02	0.55	-0.31
Laboratory maximum	100.00	7.75	7.80	2.63	1.71

Table 12. The identifications of the fauna made by participating laboratories for RT16. Names are given only where different from the AQC identification.

RT16	Taxon	LB0701	LB0703	LB0707	LB0710	LB0713
RT1601	Caulleriella alata	--	--	--	--	--
RT1602	Malacoceros fuliginosus	--	--	--	--	--
RT1603	Aphelochaeta vivipara	Chaetozone setosa	Tharyx sp. A	--	--	--
RT1604	Bathyporeia elegans	- pelagica	--	--	--	- pelagica
RT1605	Ophelia borealis	--	--	- bicornis	- limacina	--
RT1606	Turtonia minuta	--	--	Mysella bidentata	--	Tellimya ferruginosa
RT1607	Rissoa membranacea	[Rissostomia] -	--	--	- interrupta	--
RT1608	Stenothoe monoculoides	--	--	--	--	--
RT1609	Amphipholis squamata	--	--	--	--	--
RT1610	Amphiura brachiata	--	[Acronida] -	--	--	--
RT1611	Ampharete lindstroemi	--	--	--	--	- baltica
RT1612	Pomatoceros triqueter	--	--	--	--	--
RT1613	Potamopyrgus antipodarum	--	Ventrosia ventrosa	- [jenkinsi]	--	--
RT1614	Hydrobia ulvae	Potamopyrgus antipodarum	--	--	--	--
RT1615	Pisidia longicornis	--	--	--	--	--
RT1616	Nephtys hombergii	- [hombergi]	- [hombergi]	--	--	--
RT1617	Ericthonius punctatus	Jassa falcata	- [punctata]	--	--	--
RT1618	Photis longicaudata	--	--	--	--	--
RT1619	Aphelochaeta marioni	--	--	--	- sp. A	--
RT1620	Heterochaeta costata	--	--	--	--	--
RT1621	Ampelisca spinipes	--	- amoricana	--	--	--
RT1622	Caecum glabrum	--	--	--	--	--
RT1623	Harpinia antennaria	--	--	- pectinata	--	--
RT1624	Potamopyrgus antipodarum	--	--	Ventrosia ventrosa	--	--
RT1625	Trypanosyllis coeliaca	Typosyllis variegata	--	- [coelica]	Syllis sp. F	--

RT16	Taxon	LB0702	LB0705	LB0708	LB0711	LB0714
RT1601	Caulleriella alata	--	--	--	[Cauleriella] -	0 0
RT1602	Malacoceros fuliginosus	--	--	--	- [fulignosa]	0 0
RT1603	Aphelochaeta vivipara	[Aphelochaete] -	--	--	[Aphaelochaeta] -	0 0
RT1604	Bathyporeia elegans	--	--	--	--	0 0
RT1605	Ophelia borealis	--	--	--	--	0 0
RT1606	Turtonia minuta	--	--	--	Mysella bidentata	0 0
RT1607	Rissoa membranacea	--	- parva	--	- [labriosa]	0 0
RT1608	Stenothoe monoculoides	--	Hardametopa nasuta	--	--	0 0
RT1609	Amphipholis squamata	--	Ophiura affinis	--	--	0 0
RT1610	Amphiura brachiata	--	--	- chiajei	--	0 0
RT1611	Ampharete lindstroemi	--	--	--	--	0 0
RT1612	Pomatoceros triqueter	--	--	--	--	0 0
RT1613	Potamopyrgus antipodarum	- [jenkinsi]	Hydrobia neglecta	Hydrobia neglecta	--	0 0
RT1614	Hydrobia ulvae	--	Rissoella diaphana	--	--	0 0
RT1615	Pisidia longicornis	--	--	--	--	0 0
RT1616	Nephtys hombergii	- [hombergi]	--	--	- [hombergi]	0 0
RT1617	Ericthonius punctatus	--	- brasiliensis	--	--	0 0
RT1618	Photis longicaudata	--	--	--	--	0 0
RT1619	Aphelochaeta marioni	- A	--	--	--	0 0
RT1620	Heterochaeta costata	- [costatus]	--	--	--	0 0
RT1621	Ampelisca spinipes	- armoricana	--	--	--	0 0
RT1622	Caecum glabrum	--	--	--	--	0 0
RT1623	Harpinia antennaria	--	- crenulata	--	--	0 0
RT1624	Potamopyrgus antipodarum	- [jenkinsi]	Pusillina inconspicua	--	--	0 0
RT1625	Trypanosyllis coeliaca	--	--	--	--	0 0

Table 12. The identifications of the fauna made by participating laboratories for RT16. Names are given only where different from the AQC identification.

RT16	Taxon	LB0715	LB0717	LB0719	LB0721	LB0723
RT1601	Caulleriella alata	0 0	- -	- -	- -	0 0
RT1602	Malacoceros fuliginosus	0 0	- -	- -	- -	0 0
RT1603	Aphelochaeta vivipara	0 0	- -	- -	- -	0 0
RT1604	Bathyporeia elegans	0 0	- -	- -	- -	0 0
RT1605	Ophelia borealis	0 0	- limacina	- -	- limacina	0 0
RT1606	Turtonia minuta	0 0	Mysella bidentata	- -	- -	0 0
RT1607	Rissoa membranacea	0 0	- -	- -	[Rissostomia] -	0 0
RT1608	Stenothoe monoculoides	0 0	- -	- -	- -	0 0
RT1609	Amphipholis squamata	0 0	- -	- -	- -	0 0
RT1610	Amphiura brachiata	0 0	- -	- -	Ophiactis ballii	0 0
RT1611	Ampharete lindstroemi	0 0	- finmarchica	- finmarchica	- -	0 0
RT1612	Pomatoceros triqueter	0 0	- -	- -	- -	0 0
RT1613	Potamopyrgus antipodarum	0 0	- -	Hydrobia ulvae	Onoba aculeus	0 0
RT1614	Hydrobia ulvae	0 0	- neglecta	- -	- -	0 0
RT1615	Pisidia longicornis	0 0	- -	- -	- -	0 0
RT1616	Nephtys hombergii	0 0	- -	- -	- [hombergi]	0 0
RT1617	Ericthonius punctatus	0 0	- -	- -	- brasiliensis	0 0
RT1618	Photis longicaudata	0 0	- -	- -	- -	0 0
RT1619	Aphelochaeta marioni	0 0	- -	- -	- -	0 0
RT1620	Heterochaeta costata	0 0	- -	- -	[Tubifex] [costatus]	0 0
RT1621	Ampelisca spinipes	0 0	- armoricana	- -	- -	0 0
RT1622	Caecum glabrum	0 0	- -	- -	- -	0 0
RT1623	Harpinia antennaria	0 0	- -	- -	- [pectinata*]	0 0
RT1624	Potamopyrgus antipodarum	0 0	- -	- -	Pusillina sarsi	0 0
RT1625	Trypanosyllis coeliaca	0 0	- -	- -	Syllis amica	0 0

RT16	Taxon	LB0716	LB0718	LB0720	LB0722
RT1601	Caulleriella alata	0 0	0 0	- -	- -
RT1602	Malacoceros fuliginosus	0 0	0 0	- -	- -
RT1603	Aphelochaeta vivipara	0 0	0 0	Chaetozone sp. D?	- -
RT1604	Bathyporeia elegans	0 0	0 0	- -	- -
RT1605	Ophelia borealis	0 0	0 0	- -	- -
RT1606	Turtonia minuta	0 0	0 0	Mysella bidentata	- -
RT1607	Rissoa membranacea	0 0	0 0	- -	- interrupta
RT1608	Stenothoe monoculoides	0 0	0 0	- -	- -
RT1609	Amphipholis squamata	0 0	0 0	Amphiura chiajei	- -
RT1610	Amphiura brachiata	0 0	0 0	- -	- -
RT1611	Ampharete lindstroemi	0 0	0 0	- grubei	- -
RT1612	Pomatoceros triqueter	0 0	0 0	- -	- -
RT1613	Potamopyrgus antipodarum	0 0	0 0	[Pomatopyrgos] -	- -
RT1614	Hydrobia ulvae	0 0	0 0	- -	- -
RT1615	Pisidia longicornis	0 0	0 0	- -	- -
RT1616	Nephtys hombergii	0 0	0 0	- -	- -
RT1617	Ericthonius punctatus	0 0	0 0	- -	- -
RT1618	Photis longicaudata	0 0	0 0	- -	- -
RT1619	Aphelochaeta marioni	0 0	0 0	- -	- -
RT1620	Heterochaeta costata	0 0	0 0	- -	- -
RT1621	Ampelisca spinipes	0 0	0 0	- -	- -
RT1622	Caecum glabrum	0 0	0 0	- -	- -
RT1623	Harpinia antennaria	0 0	0 0	- -	- -
RT1624	Potamopyrgus antipodarum	0 0	0 0	[Pomatopygos] -	- -
RT1625	Trypanosyllis coeliaca	0 0	0 0	- -	- -

Table 13. The identifications of the fauna made by participating laboratories for RT17. Names are given only where different from the AQC identification.

RT17	Taxon	LB0701	LB0703	LB0707	LB0710	LB0713	LB0715
RT1701	Paranais litoralis	--	--	--	--	--	0 0
RT1702	Malacoceros fuliginosus	--	--	--	--	--	0 0
RT1703	Limapontia depressa	--	--	--	--	--	0 0
RT1704	Pygospio elegans	--	--	--	--	--	0 0
RT1705	Tubificoides benedii	--	--	--	--	- [benedeni]	0 0
RT1706	Crepidula fornicata	--	--	Tectura testudinalis	--	--	0 0
RT1707	Fabricia sabella	--	--	--	--	--	0 0
RT1708	Littorina saxatilis	--	--	--	--	--	0 0
RT1709	Tharyx A	--	Chaetozone gibber	--	--	- sp. indet.	0 0
RT1710	Anaitides mucosa	[Phyllodoce] -	--	[Phyllodoce] -	--	--	0 0
RT1711	Abra tenuis	--	--	--	--	--	0 0
RT1712	Mytilus edulis	--	Modiolus modiolus	--	--	--	0 0
RT1713	Melita palmata	--	--	--	--	--	0 0
RT1714	Pycnogonum littorale	--	--	--	--	--	0 0
RT1715	Aphelochaeta vivipara	--	--	--	--	Tharyx sp. indet.	0 0
RT1716	Hydrobia ulvae	--	--	--	- neglecta	--	0 0
RT1717	Cerastoderma edule	--	--	Parvicardium exiguum	--	Parvicardium scabrum	0 0
RT1718	Macoma balthica	--	--	--	--	--	0 0
RT1719	Polydora ciliata	- caeca	- cornuta	--	- [ciliata agg.]	--	0 0
RT1720	Heterochaeta costata	--	--	--	--	--	0 0
RT1721	Streblospio shrubsolii	--	--	--	--	--	0 0
RT1722	Aphelochaeta marioni	--	--	--	--	--	0 0
RT1723	Potamopyrgus antipodarum	--	Ventrosia ventrosa	[Pomatopyrgus] -	Rissoella opalina	Rissoella opalina	0 0
RT1724	Sabella pavonina	Pseudopotamilla reniformis	--	--	--	--	0 0
RT1725	Aphelochaeta marioni	--	--	--	Tharyx killariensis	--	0 0

RT17	Taxon	LB0702	LB0705	LB0708	LB0711	LB0714	LB0716
RT1701	Paranais litoralis	--	--	Tubificoides sp. indet.	--	--	Tubificoides pseudogaster
RT1702	Malacoceros fuliginosus	--	- tetracerus	--	--	--	--
RT1703	Limapontia depressa	--	--	--	- capitata	--	- juv.
RT1704	Pygospio elegans	--	--	--	--	--	--
RT1705	Tubificoides benedii	--	--	--	--	--	--
RT1706	Crepidula fornicata	--	Tectura testudinalis	--	--	--	--
RT1707	Fabricia sabella	--	--	--	--	- [stellaris]	--
RT1708	Littorina saxatilis	- [saxatilis complex]	- littorea	--	- [saxatilis tenebrosa]	- [saxatilis var. rudis]	--
RT1709	Tharyx A	--	- vivipara	Caulleriella zetlandica	--	--	[Thayx] killariensis
RT1710	Anaitides mucosa	[Phyllodoce] -	--	--	--	--	--
RT1711	Abra tenuis	--	--	--	--	--	--
RT1712	Mytilus edulis	--	--	Mytilidae sp. juv.	--	--	Modiolus modiolus
RT1713	Melita palmata	--	--	--	--	--	--
RT1714	Pycnogonum littorale	--	--	--	--	[Pychnogonium] -	--
RT1715	Aphelochaeta vivipara	--	Tharyx A	Caulleriella zetlandica	--	['Tharyx'] -	- sp.
RT1716	Hydrobia ulvae	--	--	--	--	--	--
RT1717	Cerastoderma edule	--	Timoclea ovata	Cardiidae sp. juv.	Parvicardium ovale	Cardiidae juv.	Parvicardium exiguum
RT1718	Macoma balthica	--	--	--	Mactra stultorum	--	--
RT1719	Polydora ciliata	--	--	--	--	--	- caeca
RT1720	Heterochaeta costata	--	--	--	--	--	?Limnodrilus udekemianis?
RT1721	Streblospio shrubsolii	--	--	--	--	--	--
RT1722	Aphelochaeta marioni	--	--	--	--	--	--
RT1723	Potamopyrgus antipodarum	- [jenkinsi]	Paludinella litorina	Hydrobiidae sp. juv.	Hydrobia ulvae	Pseudamnicola confusa	Hydrobia ulvae
RT1724	Sabella pavonina	- spallanzanii	Bispira volutacornis	--	--	--	Pseudopotamilla reniformis
RT1725	Aphelochaeta marioni	--	--	--	--	--	- B

Table 13. The identifications of the fauna made by participating laboratories for RT17. Names are given only where different from the AQC identification.

RT17	Taxon	LB0717	LB0719	LB0721	LB0723
RT1701	Paranais litoralis	- sp.	--	Tubificoides crenecoleus	Oligochaeta spp.
RT1702	Malacoceros fuliginosus	--	--	--	--
RT1703	Limapontia depressa	--	--	--	- spp. juv.
RT1704	Pygospio elegans	--	--	--	--
RT1705	Tubificoides benedii	--	--	- [benedeni]	Oligochaeta spp.
RT1706	Crepidula fornicata	--	--	--	Tectura testitudinalis
RT1707	Fabricia sabella	--	--	- [stellaris]	--
RT1708	Littorina saxatilis	--	--	- [saxatilis saxatilis]	- [neglecta]
RT1709	Tharyx A	Chaetozone setosa	--	Aphelochaeta 'A'	--
RT1710	Anaitides mucosa	--	--	[Phyllodoce] -	--
RT1711	Abra tenuis	Scrobicularia plana	--	--	--
RT1712	Mytilus edulis	--	--	Modiolus modiolus	Mytilidae spp. juv.
RT1713	Melita palmata	--	--	--	Allomelita pellucida
RT1714	Pycnogonum littorale	--	--	--	--
RT1715	Aphelochaeta vivipara	--	- A	--	Chaetozone setosa
RT1716	Hydrobia ulvae	--	--	--	--
RT1717	Cerastoderma edule	--	- glaucum	--	Cardiidae spp. juv.
RT1718	Macoma balthica	--	--	--	--
RT1719	Polydora ciliata	--	--	--	- cornuta
RT1720	Heterochaeta costata	Capitella capitata	--	Tubificoides pseudogaster	Oligochaeta spp.
RT1721	Streblospio shrubsolii	- sp.	--	--	--
RT1722	Aphelochaeta marioni	--	--	--	--
RT1723	Potamopyrgus antipodarum	Hydrobia ulvae	Rissoella opalina	Hydrobia ventrosa	Obtusella intersecta
RT1724	Sabella pavonina	--	--	Demonax brachychona	Branchiomma bombyx
RT1725	Aphelochaeta marioni	Tharyx sp.	--	--	Cirratulidae spp. indet.

RT17	Taxon	LB0718	LB0720	LB0722
RT1701	Paranais litoralis	- [litorales]	- [littoralis]	--
RT1702	Malacoceros fuliginosus	--	--	--
RT1703	Limapontia depressa	--	--	--
RT1704	Pygospio elegans	--	--	--
RT1705	Tubificoides benedii	--	[Tubificoides] -	--
RT1706	Crepidula fornicata	--	--	--
RT1707	Fabricia sabella	--	--	--
RT1708	Littorina saxatilis	--	--	--
RT1709	Tharyx A	--	--	--
RT1710	Anaitides mucosa	--	--	--
RT1711	Abra tenuis	--	Thracia convexa	Scrobicularia plana
RT1712	Mytilus edulis	Modiolula phaseolina	--	--
RT1713	Melita palmata	--	--	--
RT1714	Pycnogonum littorale	--	--	--
RT1715	Aphelochaeta vivipara	--	--	--
RT1716	Hydrobia ulvae	--	--	--
RT1717	Cerastoderma edule	--	--	--
RT1718	Macoma balthica	--	--	--
RT1719	Polydora ciliata	--	--	--
RT1720	Heterochaeta costata	Tubificoides sp.	--	--
RT1721	Streblospio shrubsolii	--	--	--
RT1722	Aphelochaeta marioni	--	--	--
RT1723	Potamopyrgus antipodarum	Ventrosia ventrosa	Hydrobia ulvae	Hydrobia ulvae
RT1724	Sabella pavonina	Pseudopotamilla reniformis	--	--
RT1725	Aphelochaeta marioni	- A	- [marioni?]	--

Table 14. Summary of the results from the identification of specimens supplied by participating laboratories for Laboratory Reference exercise LR05.

	Differences		
LabCode	**Generic**	**Specific**	**Name changes**
LB0701	2	4	2
LB0702	n/p	n/p	n/p
LB0703	5	8	0
LB0705	4	5	0
LB0706	-	-	-
LB0707	1	1	1
LB0708	0	1	0
LB0710	0	2	1
LB0711	0	2	0
LB0714	-	-	-
LB0716	-	-	-
LB0717	3	7	0
LB0718	1	3	0
LB0719	1	2	2
LB0720	0	0	0
LB0721	0	0	0
LB0722	0	1	0
LB0723	2	4	0

Key: "-" - No data.
n/p - Not participating.
See Report, Section 6, for details.

Table 15. Summary of the performance of participating laboratories in the Own Sample (OS) exercises with respect to the NMBAQCS / NMMP standards.

1		2	3	4	5	6	7	8	9	10	11	12	13	14
		Estimation of Taxa			Estimation of Abundance			Estimation of Biomass			Similarity Index			Overall
LabCode		Lab.	Target	Flag	Lab.	Target	Flag	Lab. result	Target	Flag	Target	Lab.	Flag	NMMP Flag
LB0715	OS14	1	-1.0 - 3.0	PASS	9	6.0 - 10.0	PASS	0.0049	0.0044 - 0.0066	*PASS*	90.0	94.12	PASS	
LB0715	OS15	15	13.0 - 17.0	PASS	216	184.5 - 225.5	PASS	0.0317	0.0288 - 0.0432	*PASS*	90.0	97.40	PASS	PASS
LB0715	OS16	9	7.0 - 11.0	PASS	625	560.7 - 685.3	PASS	0.2887	0.2700 - 0.4050	*PASS*	90.0	98.08	PASS	
LB0716	OS14	-	-	-	-	-	-	-	-	-	90.0	-	-	
LB0716	OS15	-	-	-	-	-	-	-	-	-	90.0	-	-	**Fail**
LB0716	OS16	-	-	-	-	-	-	-	-	-	90.0	-	-	
LB0717	OS14	27	24.3 - 29.7	PASS	76	80.1 - 97.9	**Fail**	0.8338	0.4970 - 0.7454	*Fail*	90.0	72.73	**Fail**	
LB0717	OS15	56	54.0 - 66.0	PASS	410	387.0 - 473.0	PASS	0.5999	0.3263 - 0.4895	*Fail*	90.0	89.52	**Fail**	**Fail**
LB0717	OS16	29	23.4 - 28.6	**Fail**	189	172.8 - 211.2	PASS	0.2577	0.1392 - 0.2088	*Fail*	90.0	70.87	**Fail**	
LB0718	OS14	15	13.0 - 17.0	PASS	67	60.3 - 73.7	PASS	0.1021	0.0934 - 0.1402	*PASS*	90.0	83.58	**Fail**	
LB0718	OS15	44	39.6 - 48.4	PASS	489	436.5 - 533.5	PASS	2.6590	2.3115 - 3.4673	*PASS*	90.0	77.62	**Fail**	PASS
LB0718	OS16	21	18.9 - 23.1	PASS	169	153.0 - 187.0	PASS	0.8097	0.6549 - 0.9823	*PASS*	90.0	99.71	PASS	
LB0719	OS14	69	64.8 - 79.2	PASS	543	483.3 - 590.7	PASS	2.6490	1.4303 - 2.1455	*Fail*	90.0	96.67	PASS	
LB0719	OS15	69	63.9 - 78.1	PASS	250	224.1 - 273.9	PASS	0.8510	0.4195 - 0.6293	*Fail*	90.0	98.21	PASS	PASS
LB0719	OS16	38	36.9 - 45.1	PASS	328	297.0 - 363.0	PASS	2.7550	1.5719 - 2.3579	*Fail*	90.0	96.96	PASS	
LB0720	OS14	55	51.3 - 62.7	PASS	376	369.0 - 451.0	PASS	6.6560	4.4602 - 6.6902	*PASS*	90.0	93.13	PASS	
LB0720	OS15	39	35.1 - 42.9	PASS	218	201.6 - 246.4	PASS	7.6102	6.4682 - 9.7024	*PASS*	90.0	94.57	PASS	PASS
LB0720	OS16	7	6.0 - 10.0	PASS	14	15.0 - 19.0	**Fail**	1.6221	1.2008 - 1.8012	*PASS*	90.0	90.32	PASS	
LB0721	OS14	11	9.0 - 13.0	PASS	271	257.4 - 314.6	PASS	0.2134	0.2175 - 0.3263	*Fail*	90.0	96.95	PASS	
LB0721	OS15	26	24.3 - 29.7	PASS	657	598.5 - 731.5	PASS	0.0412	0.0327 - 0.0491	*PASS*	90.0	99.09	PASS	PASS
LB0721	OS16	51	45.0 - 55.0	PASS	2969	2692.8 - 3291.2	PASS	5.9983	3.5288 - 5.2932	*Fail*	90.0	98.95	PASS	
LB0722	OS14	7	6.0 - 10.0	PASS	63	57.6 - 70.4	PASS	0.0720	0.0322 - 0.0482	*Fail*	90.0	99.21	PASS	
LB0722	OS15	24	23.4 - 28.6	PASS	132	134.1 - 163.9	**Fail**	0.1250	0.0600 - 0.0900	*Fail*	90.0	91.10	PASS	PASS
LB0722	OS16	27	26.1 - 31.9	PASS	356	323.1 - 394.9	PASS	0.1440	0.0546 - 0.0818	*Fail*	90.0	96.22	PASS	

Key: "-" - No data. See Report, Section 6, for details.

Table 16. Summary of the performance of participating laboratories in the Particle Size (PS) exercises with respect to the NMBAQC / NMMP standards.

PS16 Target range = 0.0 - 10.2

	PS16	
LabCode	Actual	Flag
LB0701*	0.4	PASS
LB0703	0.0	PASS
LB0704*	0.4	PASS
LB0706	-	Deemed Fail
LB0707*	0.4	PASS
LB0708	0.0	PASS
LB0709	0.0	PASS
LB0710	0.0	PASS
LB0711	0.6	PASS
LB0714	-	Deemed Fail
LB0715*	0.4	PASS
LB0717	0.6	PASS
LB0718	0.1	PASS
LB0719	0.0	PASS
LB0720	0.0	PASS
LB0721*	0.4	PASS
LB0722	0.1	PASS
LB0723	not participating in this component	

PS17 Target range = 35.6 - 55.6

	PS17	
LabCode	Actual	Flag
LB0701*	36.6	PASS
LB0703	28.0	**Fail**
LB0704*	36.6	PASS
LB0706	-	Deemed Fail
LB0707*	36.6	PASS
LB0708	88.6	**Fail**
LB0709	25.6	**Fail**
LB0710	41.6	PASS
LB0711	29.9	**Fail**
LB0714	40.7	PASS
LB0715*	36.6	PASS
LB0717	47.5	PASS
LB0718	57.8	**Fail**
LB0719	100.0	**Fail**
LB0720	33.0	**Fail**
LB0721*	36.6	PASS
LB0722	38.0	PASS
LB0723	25.2	**Fail**

"-" no return and/or data from laboratory. See text, Section 6, for details.
"*" = centralised analysis

Table 17. Comparison of the overall performance of laboratories from 1996/97 to 2000/01 with respect to the NMBAQC / NMMP standards.

Year	Component	Exercise	Pass	Fail	Deemed Fail	% Pass	%Pass (excluding deemed failures)
Yr 03 (1996/97)	OS	02, 03, 04	11	3	9	48	79
Yr 04 (1997/98)	OS	05, 06, 07	12	1	8	57	92
Yr 05 (1998/99)	OS	08, 09, 10	11	3	5	58	79
Yr 06 (1999/00)	OS	11, 12, 13	14	3	2	74	82
Yr 07 (2000/01)	OS	14, 15, 16	11	4	3	61	73
Yr 03 (1996/97)	PS	08, 09	27	1	20	56	96
Yr 04 (1997/98)	PS	10, 11	25	3	22	50	89
Yr 05 (1998/99)	PS	12, 13	21	7	17	47	75
Yr 06 (1999/00)	PS	14, 15	33	2	7	79	94
Yr 07 (2000/01)	PS	16, 17	24	8	3	69	75

Table 18. Comparison of each laboratories performance in the Own Sample exercise in 1996/97, 1997/98, 1998/99, 1999/2000 and 2000/01.

LabCode	Scheme Year 3 **1996/97**	Scheme Year 4 **1997/98**	Scheme Year 5 **1998/99**	Scheme Year 6 **1999/00**	Scheme Year 7 **2000/01**
LB0701	**FAIL**	**Deemed Fail**	PASS	PASS	PASS
LB0702	PASS	PASS	PASS	PASS	PASS
LB0703	n/a	n/p	n/a	n/a	PASS
LB0704	-	n/a	n/a	n/a	n/a
LB0705	PASS	**Deemed Fail**	**Deemed Fail**	PASS	PASS
LB0706	PASS	PASS	n/a	PASS	**Deemed Fail**
LB0707	PASS	PASS	PASS	PASS	**FAIL**
LB0708	-	n/p	n/p	n/p	n/a
LB0709	PASS	PASS	n/a	n/a	n/a
LB0710	PASS	PASS	PASS	PASS	**FAIL**
LB0711	-	-	-	-	**Deemed Fail**
LB0712	-	-	PASS	-	PASS
LB0713	-	-	-	PASS	n/a
LB0714	**Deemed Fail**	PASS	PASS	**FAIL**	**FAIL**
LB0715	**Deemed Fail**	PASS	**FAIL**	PASS	PASS
LB0716	n/p	**Deemed Fail**	**FAIL**	**Deemed Fail**	**Deemed Fail**
LB0717	**Deemed Fail**	**FAIL/Deemed Fail**	**Deemed Fail**	**FAIL**	**FAIL**
LB0718	PASS	PASS	PASS	PASS	PASS
LB0719	**FAIL/Deemed Fail**	PASS	PASS	PASS	PASS
LB0720	PASS	**FAIL**	PASS	**FAIL**	PASS
LB0721	PASS	PASS	PASS	PASS	PASS
LB0722	PASS	PASS	PASS	PASS	PASS
LB0723	n/p	PASS	n/p	n/p	n/p

Key:
n/p - opted not to participate in OS exercise this year
n/a - not applicable (do not subscribe to OS)
"-" - not in scheme this year
Fail/Deemed Fail - insufficient data supplied

Figure 1. Particle size distribution curves resulting from analysis of fourteen replicate samples of sediment distributed as PS16. Seven samples analysed by sieve and seven samples analysed by Laser.

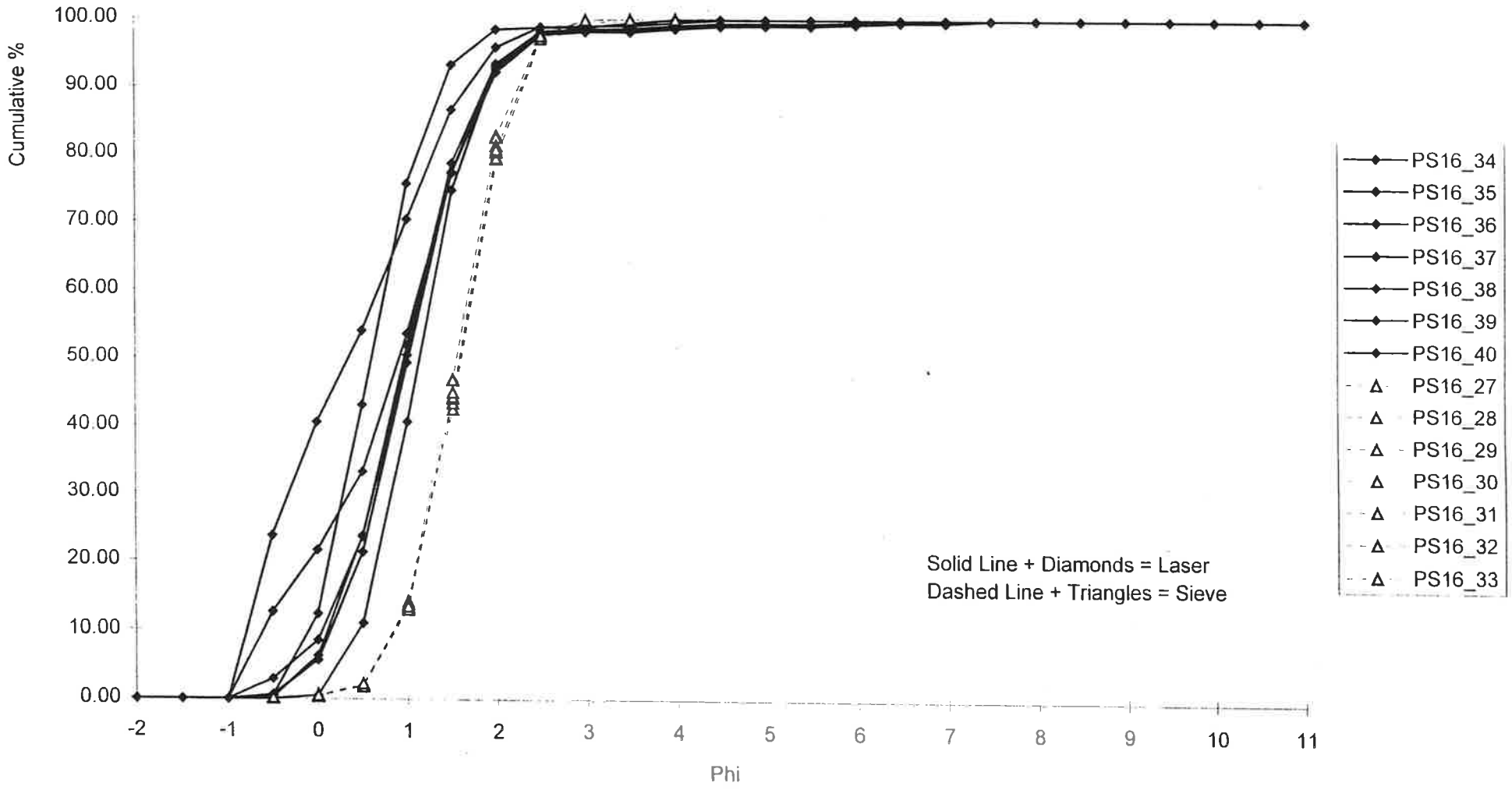


Figure 2. Particle size distribution curves resulting from analysis of fourteen replicate samples of sediment distributed as PS17. Seven samples analysed by sieve and seven samples analysed by Laser.

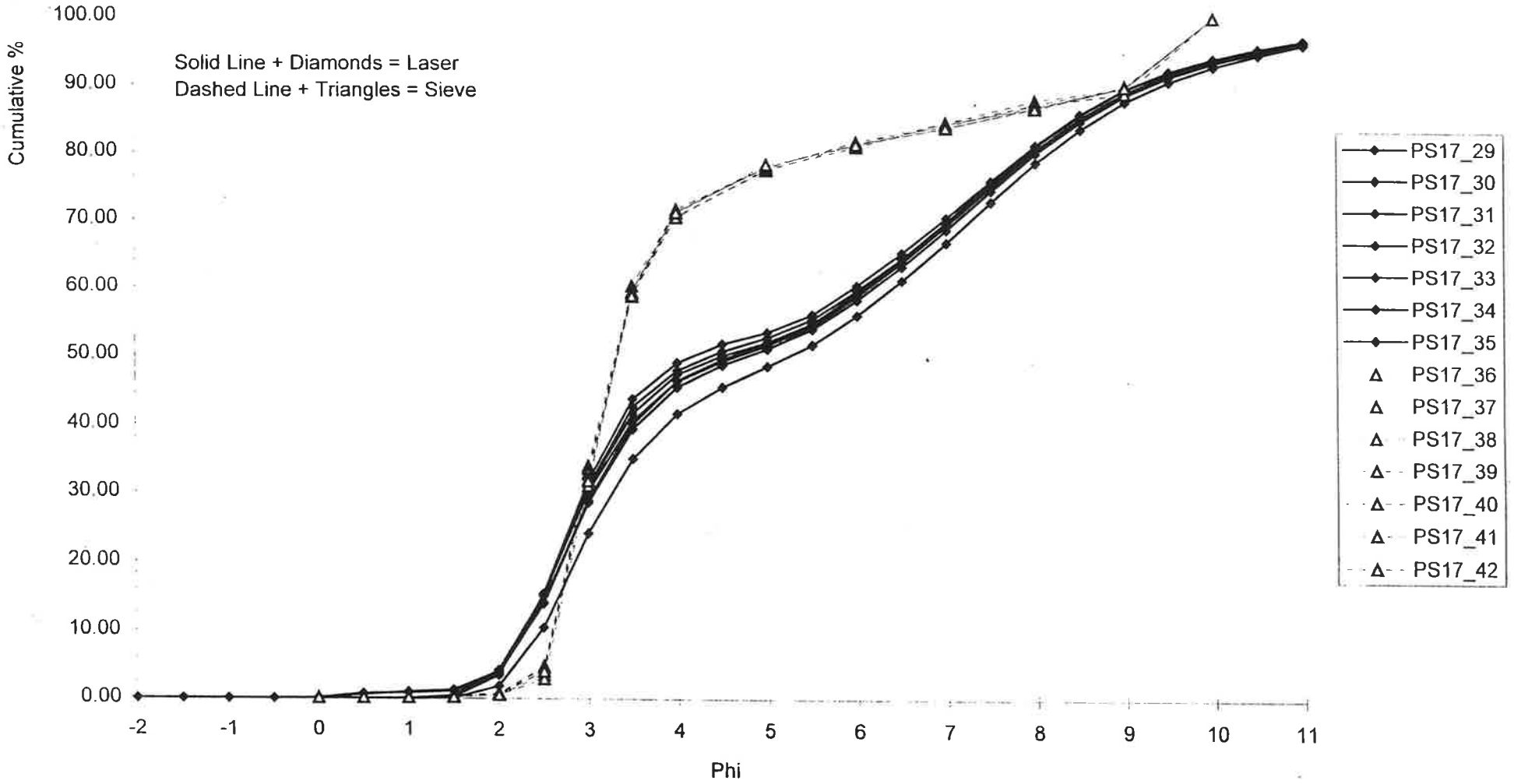


Figure 3. Particle size distribution curves from participating laboratories for sediment samples from PS16. The average values for the AQC analysis of replicates are included.

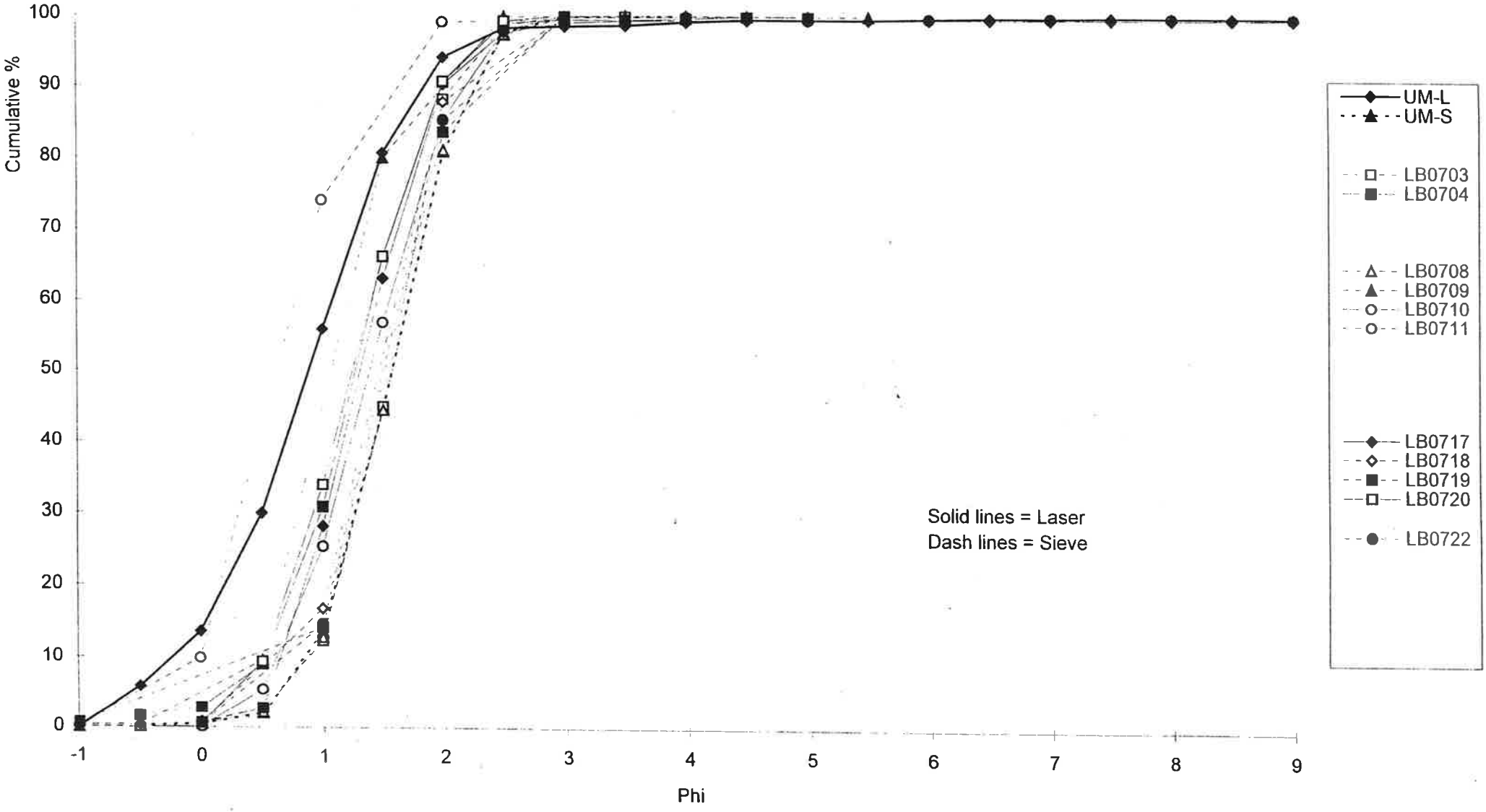


Figure 4. Particle size distribution curves from participating laboratories for sediment samples from PS17. The average values for the AQC analysis of replicates are included.

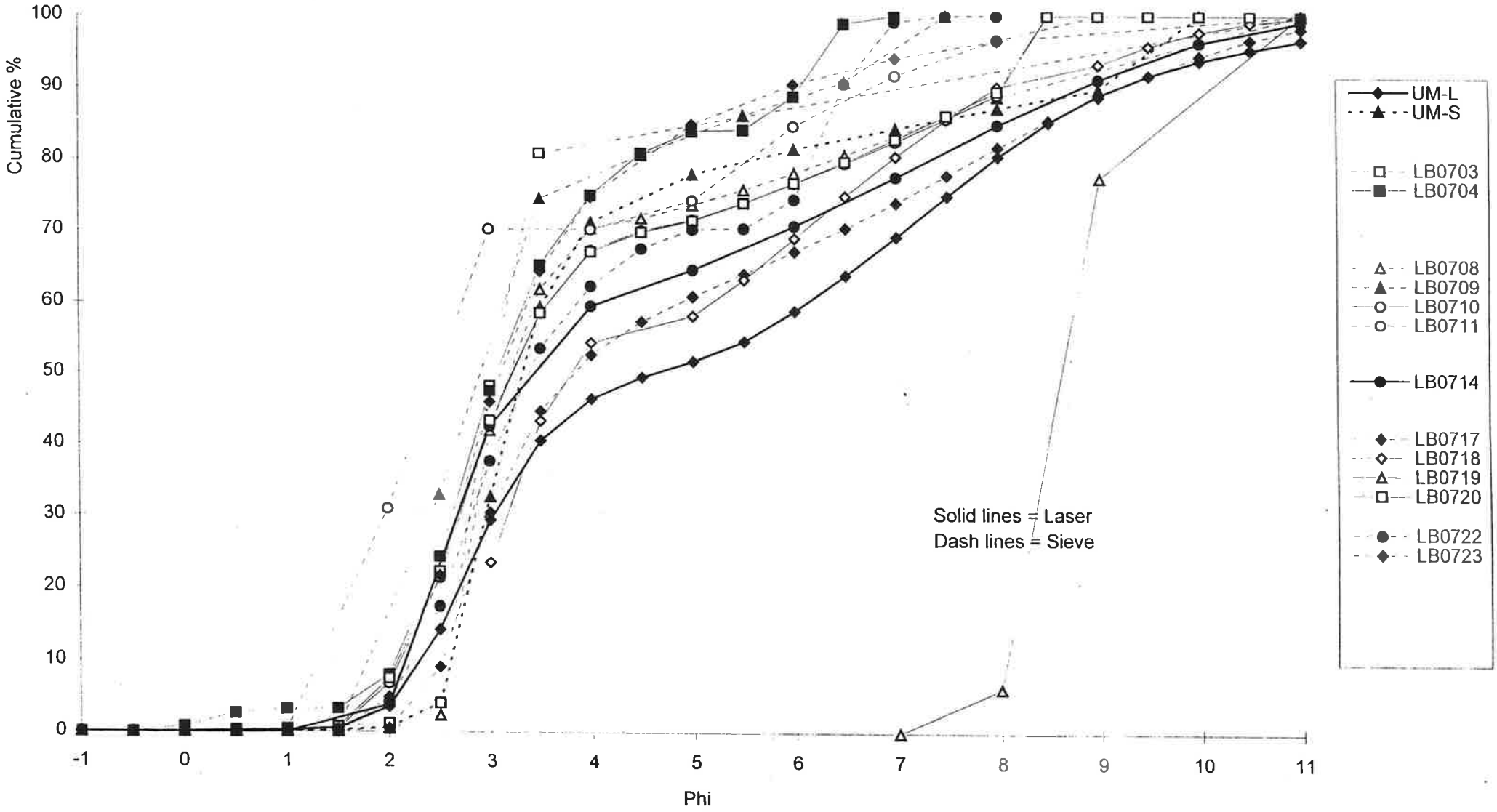


Figure 5. The number of differences from the AQC identification of specimens distributed in RT16 for each of the participating laboratories. Arranged in order of increasing number of differences.

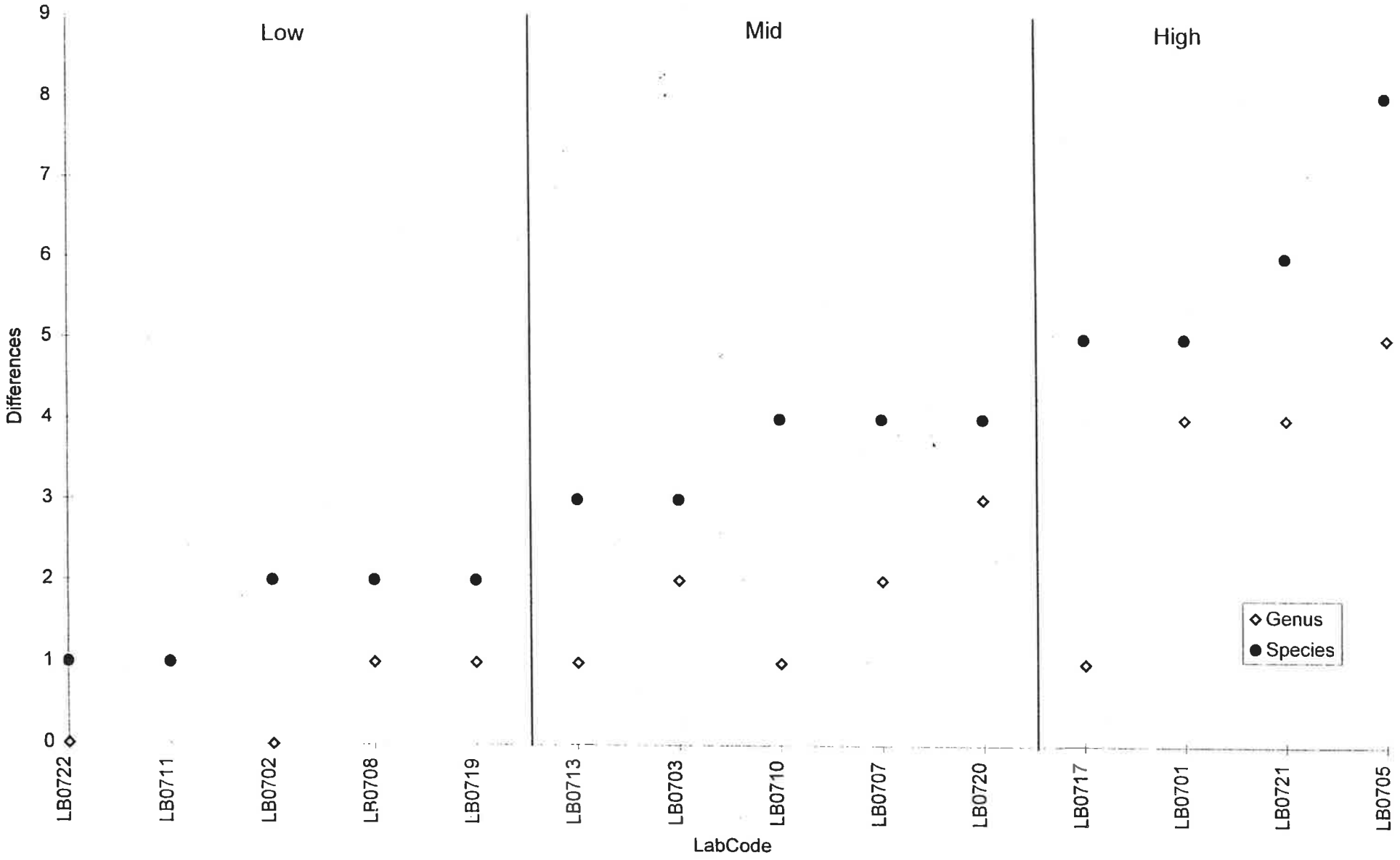
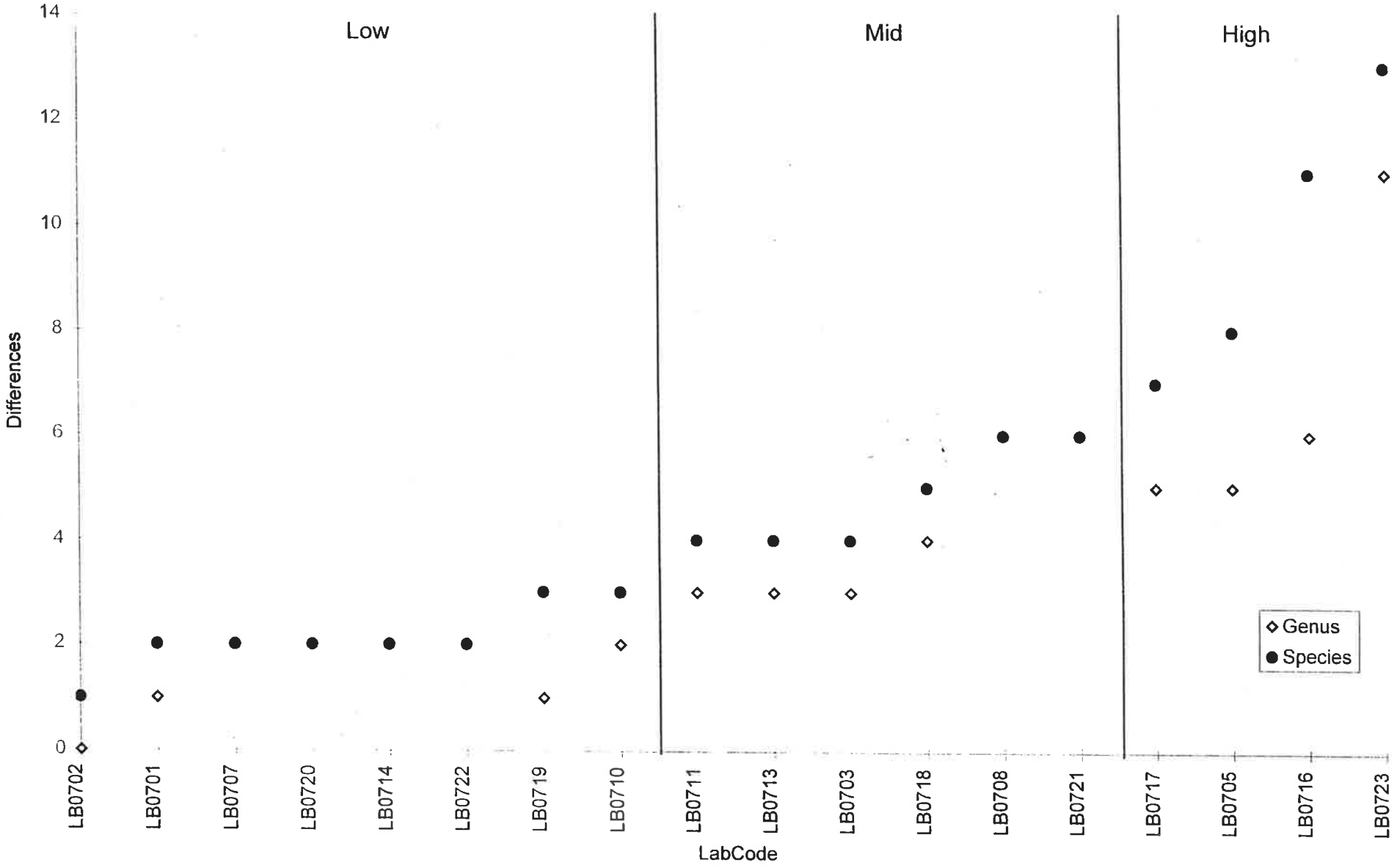


Figure 6. The number of differences from the AQC identification of specimens distributed in RT17 for each of the participating laboratories. Arranged in order of increasing number of differences.



Appendix 1.

National Marine Biological Analytical Quality Control Scheme

Participant Laboratory Reference Collection exercise (LR)

Objective:

To examine the accuracy of identification of fauna recorded in the 'home' area of each participating laboratory. Specifically, to consider the fauna recorded in the NMMP samples. To encourage the assemblage and use of collections of reference specimens for NMMP stations. This exercise will be scored. However, the results are **not** used in the assignment of overall laboratory pass / fail flags.

Protocol:

Please provide twenty-five identified specimens from your laboratory reference material. For NMMP laboratories this should be from samples collected as part of the NMMP programme. A list indicating the major groups we would like to see is given below. You may select the particular species to send but ideally each of the indicated taxonomic groups should be represented. All fauna selected should be from waters around the British Isles. If possible, the species selected should differ from those you sent as part of a previous circulation. If you are unable to supply specimens as specified then alternative specimens can be substituted. Duplicate examples of species can be submitted for the purpose of establishing growth series. Two of the twenty-five specimens requested can be unidentified problem taxa (these specimens must be indicated as such on the data sheet). The specimens received will be identified according to Unicomarine Ltd. standard practice. If there is still disagreement after return of the specimens we will provide full explanations for our identification on request using reference material and images, where necessary. Specimens will be submitted to a third party if a further opinion is required.

Origin of specimens:

Where possible specimens should be selected from samples taken at stations forming part of the NMMP programme, or from the same area. If this is not possible then select from samples which represent your normal area of operation or a particular survey.

Preparation:

All specimens should be supplied in 70% IMS in individually labelled pots. A sheet is provided for entering details of the specimen name, origin, key used and other details. This sheet has labels attached which should be placed in each of the reference pots. All material will be returned when analysis is complete unless you indicate that we may keep material for reference purposes.

Timescale:

Please send specimens to Unicomarine Ltd. by 9th November 2001. Results and specimens will be returned as soon after receipt as practicable.

Problems:

Please call if you have any queries about this exercise.

List of groups from which specimens should be selected

	Major Group	Group	Note
1	Oligochaeta	Participating Laboratory to select	NMMP source (if applicable)
2	Polychaeta	Participating Laboratory to select	NMMP source (if applicable)
3	Polychaeta	Participating Laboratory to select	NMMP source (if applicable)
4	Polychaeta	Participating Laboratory to select	NMMP source (if applicable)
5	Polychaeta	Participating Laboratory to select	NMMP source (if applicable)
6	Polychaeta	Participating Laboratory to select	NMMP source (if applicable)
7	Polychaeta	Participating Laboratory to select	NMMP source (if applicable)
8	Polychaeta	Participating Laboratory to select	NMMP source (if applicable)
9	Polychaeta	Participating Laboratory to select	NMMP source (if applicable)
10	Polychaeta	Participating Laboratory to select	NMMP source (if applicable)
11	Polychaeta	Participating Laboratory to select	NMMP source (if applicable)
12	Polychaeta	Participating Laboratory to select	NMMP source (if applicable)
13	Crustacea	Participating Laboratory to select	NMMP source (if applicable)
14	Crustacea	Participating Laboratory to select	NMMP source (if applicable)
15	Crustacea	Participating Laboratory to select	NMMP source (if applicable)
16	Crustacea	Participating Laboratory to select	NMMP source (if applicable)
17	Crustacea	Participating Laboratory to select	NMMP source (if applicable)
18	Crustacea	Participating Laboratory to select	NMMP source (if applicable)
19	Mollusca	Participating Laboratory to select	NMMP source (if applicable)
20	Mollusca	Participating Laboratory to select	NMMP source (if applicable)
21	Mollusca	Participating Laboratory to select	NMMP source (if applicable)
22	Mollusca	Participating Laboratory to select	NMMP source (if applicable)
23	Mollusca	Participating Laboratory to select	NMMP source (if applicable)
24	Echinodermata	Participating Laboratory to select	NMMP source (if applicable)
25	Other	Participating Laboratory to select	NMMP source (if applicable)

Appendix 2.

Description of Scheme Standards

In the third year of the Scheme (1996/97) required levels of performance were set by the NMBAQC steering committee for the Own Sample and Particle Size Analysis exercises. The flags applied to the various exercises are based on a comparison of the results from sample analysis by Unicomarine Ltd. and those from the laboratory. The OS exercise has several aspects, each with a separate standard. Each of the standards has been calculated independently for the three Own Samples received from each laboratory. The PS standard is based solely upon the determination of the Silt-Clay fraction in the sample and has been calculated independently for the two PS exercises. The process of assigning the flags for each component is described below. The target standards and recommended protocols may be modified in the future. A single standard 'averaged' value calculated across several components was found to be impracticable.

1. Own Sample Standards

1.1 Extraction efficiency - Total Taxa target

This flag relates to the performance of the laboratory with respect to the efficiency with which the animals were extracted from the OS samples. The 'correct' total number of taxa is assumed to be that resulting from re-analysis of the samples by Unicomarine Ltd. To achieve a pass the number of taxa extracted should be within ±10% or ±2 taxa (whichever is greater) of this total.

1.2 Extraction efficiency - Total Individuals target

This flag reflects the efficiency with which the laboratories estimated the number of individuals in the sample. The total should be within ±10% or ±2 individuals (whichever is greater) of the total resulting from re-analysis of the samples by Unicomarine Ltd.

1.3 Total Biomass target

The total value should be within ±20% of the value obtained from re-analysis of the sample.

1.4 Bray-Curtis comparison

Comparison of the two data sets, from re-analysis by Unicomarine Ltd. and by the participating laboratory, should result in a Bray-Curtis similarity index of ≥90%.

1.5 Overall flag

An overall flag for the Scheme has been agreed and set by examining the flags for the individual components. To attain an overall "Pass" flag for the OS exercise on which to base a filtering system for the NMMP data base, it is required that laboratories obtain passes for six of the nine individually flagged exercises *ie.* 3 samples x 3 flagged items (number of taxa, individuals, Bray-Curtis).

Because of the considerable variation in the estimation of biomass (as discussed in earlier reports; (NMBAQC Scheme Annual report 1996/97, Section 3.2.5) the flag for this component has not been included in the determination of the overall flag for the OS exercises. This is the same approach as applied for previous years. Laboratories failing to supply OS or PS data have automatically been assigned a fail flag by default.

2. Particle Size Standards

2.1 Percentage Silt-Clay Fraction target

Only a single aspect of the PS exercises has been considered when preparing the table of flags indicating performance with respect to the Scheme standard. Laboratories are required to determine the silt-clay (<63μm) fraction to within ±10 percentage points of the mean of the results from all laboratories.

In some cases, although returns for the PS exercises were made by laboratories, only data for the production of the particle size distribution curves was provided. A "Deemed fail" flag has been assigned if the required summary statistics were not also provided by the laboratory.

Appendices

APPENDIX 1

NATIONAL MARINE BIOLOGICAL AQC CO-ORDINATING COMMITTEE

Dr. M. Service (Chair)	Department of Agriculture and Rural Development for Northern Ireland
Mrs. E. Hamilton (Secretary)*	SEPA South East
Mrs. A. Henderson (Contract Manager)**	SEPA South West
Dr. M. Elliott	University of Hull
Mr. D. Moore[#]	FRS
Dr. H. Rees	CEFAS
Mr. R. Proudfoot	Environment Agency
Mr. A. Robinson	Environment Agency
Mr. T. Mackie[$]	IRTU/Industrial Science Centre
Mr. D. Connor[+]	JNCC

(* to replace Mrs. A Henderson as Contract Manager - September 2001)

(** resigned from Committee - September 2001)
(to be replaced by Mr. M. O'Reilly - September 2001)

([#] replaced by Mr. M. Robertson - December 2000)

([$] replaced Mrs. E. Hamilton as Secretary - January 2001)

([+] replaced by Dr. J. Davies - February 2001)

APPENDIX 2

ROLE OF THE NATIONAL MARINE BIOLOGICAL ANALYTICAL QUALITY CONTROL (NMBAQC) COMMITTEE

The functions and role of the committee for the marine biological AQC scheme are as follows:

1. Define what services are required with particular reference to the NMP.
2. Interact with Scottish Environmental Protection Agency (SEPA) as managers of the contract.
3. Review other organisations/laboratories that should be approached to join the scheme.
4. Agree and set an annual budget and itemise contributions from individual participants.
5. Agree the funding requirements of SEPA to service the scheme and the committee.
6. Develop all necessary definitions.
7. Develop and document an overall plan for the scheme.
8. Receive and review reports from participating laboratories on any problems arising from internal and external AQC exercises.
9. Receive and review reports from SEPA on the management of the scheme.
10. Establish the frequency and location of committee meetings.
11. Receive and review reports from the tendering organisation on AQC exercises.
12. As necessary, establish ad-hoc groups to address problems as they arise and provide members to chair each sub-group.
13. Produce an annual report which will be presented to MPMMG for information.
14. Establish links and stimulate collaboration with international intercomparison exercises.
15. Encourage accreditation and co-ordinate in-house AQC policy.
16. Make recommendations and receive reports from participating laboratories on in-house AQC.
17. Establish a timetable and dates for reports.

APPENDIX 3

NATIONAL MARINE BIOLOGICAL AQC SCHEME

ROLE OF THE CONTRACT MANAGER

Objectives

1. To establish a managed national marine biological quality control scheme.

2. To recommend quality materials where appropriate.

3. To manage the scheme's finances

Schedule of Work

1. Provide operational support for the National Co-ordinating Committee.

2. Implement the plan of the national AQC scheme.

3. Receive and manage funds donated by participating members of the AQC consortium.

4. Co-ordinate with the Committee the contents of the tender document, issue to relevant laboratories, evaluate tenders, provide a report with recommendations to the Committee and agree the contract.

APPENDIX 4

PARTICIPATING ORGANISATIONS IN NMBAQC 2000/2001

AES Ltd: AstraZeneca Ltd: Centre for Environment, Fisheries and Aquaculture Science (CEFAS): Department of Agriculture Northern Ireland (DANI): Environment Agency: EMU Environmental Ltd: Environmental Resources and Technology Ltd (ERT): Hebog Environmental: Institute of Estuarine and Coastal Sciences (IECS): Industrial Science Centre / Industrial Research and Technology Unit (IRTU Northern Ireland): Institute of Aquaculture, University of Stirling: Queens University Belfast , Marine Laboratory: SEAS Ltd: Scottish Environment Protection Agency (SEPA).

APPENDIX 5

REVIEW OF STANDARDS FOR THE NATIONAL MARINE BIOLOGICAL ANALYTICAL QUALITY CONTROL SCHEME.

By E.I.S. Rees

CONCLUSIONS AND MAIN RECOMMENDATIONS

1. The NMB AQC Scheme has many potential benefits to the ultimate users of benthos data, to those commissioning work and to the various participants. It is well worth continuing the scheme and developing it further.

2. There needs to be a somewhat greater clarity of purpose. At present, different participants, the auditor and even some of the prime movers of the scheme, all appear to place different emphasis on what they want out of the scheme. Some see it narrowly as part of the Quality Assurance filtering for the National Marine Monitoring Plan archive. Others participate for the benefits it may bring through training, access to taxonomic expertise greater than their own and as a way of keeping in touch with taxonomic or technical developments. Yet another interest group see it as a prelude to professional accreditation, so raising the status of benthos monitoring and with it commercial advantage for them over their competitors.

3. There needs to be greater recognition that Standards appropriate for the National Marine Monitoring Plan and/or for full biodiversity surveys may be overly rigorous and hence disproportionately expensive to the aims in some other circumstances. The costs and benefits of achieving greater precision at the laboratory analysis stage need to be measured and considered in the light of the specific objectives of particular surveys / projects.

4. If ecological results are to be really consistent there will be a need to tighten up protocols across the board from survey design, through treatment of samples at sea, to the processing of the data. It will not help just to apply greater precision at the laboratory analysis stage.

5. Discrepancies arising at the laboratory extraction stage in the taking and working up of quantitative benthos samples are, at least in terms of the total numbers of individuals picked from samples, likely to be much less than the usual range of variability found between replicate grabs. This is due to natural patchiness in the environment that cannot be taken into account when sampling remotely and 'blind' from a drifting ship. The NMB AQC Committee may wish to look more closely at what may be the weak links in the chain from survey planning to reporting and to give more attention to those. Demanding very high precision at the laboratory analysis stage may do less to improve survey results than paying greater attention to protocol details at other stages.

6. The >90% extraction of the total numbers of individuals from the samples as proposed by the NMB AQC committee should be treated as a minimum standard except in rare circumstances. Recovery rates between 90 and 95% should be flagged as weak, resulting in failure if there are weaknesses in other measures. (See also earlier comments on damaged specimens)

7. It needs to be acknowledged that the listings of numbers of benthic organisms on data sheets derives as much from "recognition" based on experience, as it does on taxonomic identification in the restricted sense using key characteristics. The 90% standard is reasonable, but allowances need to be made in several ways, such as treatment of damaged specimens, cut off points for juvenile identification, and addition of notes regarding uncertainty.

8. When setting standards, important distinctions need to be made between errors that are recoverable through later checking and those that are not. When aggregating scores for particular components of QC tests this distinction should be taken into account, irredeemable errors being treated as being more serious.

9. Consideration needs to be given to the uses to which the data will be put both in terms of the statistical expressions derived and the aims of the particular survey. Most of the measures used to derive Environmental Quality Standards are quite robust in that misnaming a few species in a one-off survey and will have little effect on the conclusions. That is provided the misnaming is consistent. It is when a discrepancy is erratic or data has to be pooled over time and from different sources that the problems manifest themselves.

10. The standards for passing or failing tests under the NMB AQC scheme should use some sort of scoring to take account of the seriousness of discrepancies between the auditor's opinion and the participating laboratory's results. In particular the scoring should allow for differences between errors recoverable by checking and those that are irredeemable. Allowance also needs to be made where log sheets acknowledge an element of doubt in appended notes. In identification ring trials the scoring needs to have a moderating factor for the difficulties involved even though this may be subjective.

11. The overall marking scheme, where the several different test standards are brought together, to decide whether a laboratory passes or fails, needs to have minimum standards for each as well as an aggregated pass or fail value. A weak result in one measure where the score is 10% under the standard should not result in overall failure, but weakness in two should be flagged as a failure.

12. To confirm whether adjudication on any one trial is reasonable, the frequency distribution of scores could be looked at. If more than 15% of those participating apparently fail, the committee should consider reasons for difficulty with that test and possibly make some adjustment to the cut off point.

13. Informal consultations indicate that there is a divergence of opinion amongst participants over whether they should be allowed to opt out of particular aspects of the trials. Those seeing commercial advantages to their own larger organisations if there were full professional accreditation take a strict line. There may however be more to gain in raising overall standards by acknowledging that there are small laboratories that may not be strong on the identifications of all groups but who will often be getting difficult things cross checked by another organisation. This seems less open to misinterpretations than where large regulatory organisations contract out the processing of samples, and the person writing up a survey report may not have been present either when the samples were taken or when they were processed. On balance I would suggest that the community at large has more to gain if the minor players are encouraged to come up to the AQC scheme standards than if the scheme fosters a cartel ethos.

APPENDIX 6

Final results of NMBAQC Epibiota ring test

Overall Response = 36 Participants

Table 1 Results of individual images used in the Epibiota Ring Test. Correct answers are expressed as a percentage of the total attempted for each species. Overall results for the entire test are given at the end of the table.

Taxonomic Group	Species	% Attempted	% Correct Species	% Correct Family
Porifera	*Clathrina lacunosa*	86.1	67.7	71.0
	Scypha ciliata	100.0	97.2	97.2
	Dercitus bucklandi	83.3	86.7	86.7
	Pachymatisma johnstonia	100.0	97.2	97.2
	Thymosia guernei	97.2	28.6	31.4
	Tethya aurantium	94.4	91.2	91.2
	Polymastia mamillaris	94.4	58.8	64.7
	Axinella infundibuliformis	100.0	91.7	100.0
	Phakellia ventilabrum	80.6	37.9	86.2
	Raspailia ramosa	91.7	84.8	84.8
	Esperiopsis fucorum	94.4	76.5	85.3
	Esperiopsis fucorum	97.2	82.9	82.9
	Hemimycale columella	97.2	97.1	97.1
	Haliclona simulans	100.0	66.7	80.6
Cnidaria	*Corymorpha nutans*	97.2	77.1	77.1
	Tubularia indivisa	100.0	77.8	94.4
	Halecium halecinum	94.4	70.6	73.5
	Gymnangium montagui	94.4	55.9	91.2
	Nemertesia ramosa	83.3	40.0	80.0
	Sertularella gayi	94.4	35.3	88.2
	Sertularia argentea	88.9	46.9	75.0
	Alcyonium glomeratum	100.0	77.8	97.2
	Parerythropodium coralloides	88.9	71.9	90.6
	Swiftia pallida	94.4	94.1	94.1
	Funiculina quadrangularis	97.2	88.6	88.6
	Virgularia mirabilis	97.2	94.3	94.3
	Pachycerianthus multiplicatus	100.0	75.0	97.2
	Epizoanthus couchii	97.2	77.1	85.7
	Parazoanthus anguicomus	100.0	69.4	83.3
	Protanthea simplex	91.7	81.8	84.8
	Anemonia viridis	94.4	97.1	100.0
	Aiptasia mutabilis	91.7	66.7	84.8
	Sagartia elegans	94.4	17.6	55.9
	Actinothoe sphyrodeta	97.2	40.0	94.3
	Amphianthus dohrnii	77.8	60.7	64.3
	Corynactis viridis	97.2	97.1	97.1
Platyhelminthes	*Prostheceraeus vittatus*	100.0	94.4	94.4
Polychaeta	*Anaitides groenlandica*	97.2	17.1	80.0
	Bispira volutacornis	94.4	91.2	97.1
	Myxicola infundibulum	88.9	68.8	96.9
	Protula tubularia	94.4	47.1	50.0

	Salmacina dysteri	94.4	67.6	97.1

Taxonomic Group	Species	% Attempted	% Correct Species	% Correct Family
Crustacea	*Semibalanus balanoides*	94.4	47.1	52.9
	Balanus balanus	91.7	33.3	93.9
	Chthamalus stellatus	88.9	43.8	59.4
	Idotea granulosa	97.2	51.4	91.4
	Pagurus prideaux	97.2	88.6	100.0
	Galathea strigosa	100.0	97.2	100.0
	Munida rugosa	100.0	100.0	100.0
	Pisidia longicornis	100.0	97.2	97.2
	Hyas araneus	100.0	69.4	75.0
	Inachus phalangium	100.0	8.3	91.7
	Atelecyclus rotundatus	97.2	94.3	97.1
	Liocarcinus depurator	100.0	94.4	100.0
Mollusca	*Tonicella marmorea*	100.0	33.3	72.2
	Calliostoma zizyphinum	100.0	97.2	100.0
	Capulus ungaricus	100.0	47.2	50.0
	Trivia monacha	97.2	77.1	100.0
	Buccinum undatum	100.0	100.0	100.0
	Aplysia punctata	100.0	94.4	97.2
	Acanthodoris pilosa	97.2	85.7	97.1
	Diaphorodoris luteocincta	100.0	86.1	94.4
	Polycera quadrilineata	100.0	88.9	91.7
	Coryphella gracilis	97.2	17.1	88.6
	Limaria hians	94.4	97.1	97.1
Brachiopoda	*Terebratula retusa*	91.7	78.8	84.8
	Neocrania anomala	86.1	74.2	74.2
Bryozoa	*Porella compressa*	88.9	56.3	62.5
	Cellepora pumicosa	69.4	60.0	64.0
	Securiflustra securifrons	86.1	41.9	54.8
	Bicellariella ciliata	75.0	51.9	74.1
Phoronida	*Phoronis hippocrepia*	86.1	80.6	100.0
Echinodermata	*Antedon petasus*	97.2	62.9	97.1
	Leptometra celtica	97.2	82.9	97.1
	Crossaster papposus	100.0	100.0	100.0
	Stichastrella rosea	100.0	88.9	91.7
	Ophiothrix fragilis	100.0	91.7	91.7
	Psammechinus miliaris	100.0	94.4	94.4
	Neopentadactyla mixta	94.4	91.2	94.1
	Psolus phantapus	97.2	82.9	85.7

Taxonomic Group	Species	% Attempted	% Correct Species	% Correct Family
Tunicata	*Aplidium nordmanni*	91.7	42.4	60.6
	Aplidium punctum	91.7	72.7	81.8
	Lissoclinum perforatum	94.4	70.6	85.3
	Ciona intestinalis	97.2	91.4	91.4
	Diazona violacea	94.4	73.5	73.5
	Phallusia mammillata	91.7	72.7	87.9
	Polycarpa pomaria	88.9	43.8	75.0
	Stolonica socialis	94.4	58.8	91.2
Pisces	*Scyliorhinus stellaris*	100.0	44.4	88.9
	Phrynorhombus norvegicus	100.0	36.1	88.9
	Trisopterus luscus	100.0	94.4	100.0
	Trisopterus minutus	97.2	71.4	94.3
	Myxocephalus scorpius	100.0	47.2	94.4
	Labrus bergylta	100.0	58.3	97.2
	Labrus mixtus	100.0	88.9	100.0
	Pholis gunnellus	100.0	100.0	100.0
Rhodophyta	*Ptilota gunneri*	83.3	60.0	66.7
Chlorophyta	*Chorda filum*	97.2	91.4	94.3
Phaeophyta	*Laminaria digitata*	97.2	100.0	100.0
	Laminaria hyperborea	100.0	94.4	100.0
	Alaria esculenta	97.2	88.6	94.3
	Total	94.6	72.2	86.6

Table 2 Summary of results of Epibiota Ring Test, analysed to higher taxonomic levels. Correct answers are expressed as a percentage of the total attempted for each taxonomic group.

Taxonomic Group	No. Null Returns	No. Correct Species	% Correct Species	No. Correct Family	% Correct Family
Porifera	30	363	76.6	392	82.7
Cnidaria	46	518	69.4	645	86.5
Platyhelminthes	0	34	94.4	34	94.4
Polychaeta	11	98	58.0	142	84.0
Crustacea	12	291	69.3	372	88.6
Mollusca	5	293	74.9	351	89.8
Brachiopoda	8	49	76.6	51	79.7
Bryozoa	29	60	52.2	73	63.5
Phoronida	5	25	80.6	31	100.0
Echinodermata	5	246	86.9	266	94.0
Tunicata	20	177	66.0	217	81.0
Pisces	1	194	67.6	274	95.5
Rhodophyta	6	18	60.0	20	66.7
Chlorophyta	1	32	91.4	33	94.3
Phaeophyta	2	100	94.3	104	98.1

Table 3 Top 5 Easiest and most difficult taxonomic groups when identified to species level (based on correct answers from those attempted). Taxa are listed in descending order.

Easiest	Most Difficult
Platyhelminthes	Bryozoa
Phaeophyta	Polychaeta
Chlorophyta	Rhodophyta
Echinodermata	Tunicata
Phoronida	Pisces

Table 4 Top 5 Easiest and most difficult taxonomic groups when identified to family level (based on correct answers from those attempted). Taxa are listed in descending order.

Easiest	Most Difficult
Phoronida	Bryozoa
Pisces	Rhodophyta
Platyhelminthes	Brachiopoda
Chlorophyta	Porifera
Echinodermata	Polychaeta

Summary of answers to questionnaire supporting the NMBAQC epibiota ring test

TOTAL PARTICIPANTS = 36

1. How much experience do you have in the identification of marine epibiota? (Circle one option).

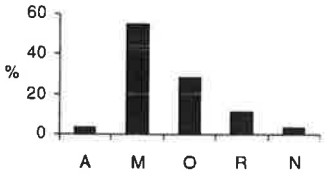
a)	> 5 years	**24**	**(67%)**
b)	1-5 years	**8**	**(22%)**
c)	< 1year	**4**	**(11%)**

2. How regularly do you undertake marine epibiota identification? (Circle one option).

a)	It is a regular aspect of my work	**17**	**(47%)**
b)	It is an occasional aspect of my work	**11**	**(31%)**
c)	I rarely do it as part of my work	**7**	**(19%)**
d)	I never do it as part of my work	**1**	**(3%)**

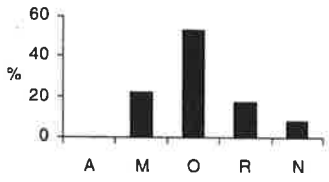
3. How do you identify epibiota? (Mark each option either; Always, Mostly, Occasionally, Rarely, Never).

a) In situ (on shore, by diving or on board ship)

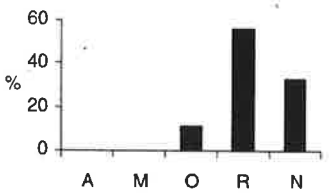


b) From images (photographs or video)

c) From specimens returned to the laboratory for detailed identification



d) Identification by external experts (consultants, museums)



4. How useful an exercise do you feel this ring test has been, in terms of establishing quality procedures in the identification of marine epibiota? (Circle one option).

a)	Very useful	**11**	**(31%)**
b)	Moderately useful	**21**	**(58%)**
c)	Quite useful	**3**	**(8%)**
d)	Not at all useful	**1**	**(3%)**

5. How wide a range of species do you feel was covered by the ring test? (Circle one option).

a)	A wide, diverse range, which covered all the main taxa	**8**	**(22%)**
b)	A fairly wide range, covering most of the main taxa	**24**	**(67%)**
c)	The range covered a few of the more common taxa	**2**	**(5.5%)**
d)	The range was narrow and covered hardly any of the main taxa	**2**	**(5.5%)**

6. How does this ring test cover the epibiotic species you encounter during your own work? (Circle one option).

a)	Yes, I have encountered most of them (>90%)	**12**	**(33%)**
b)	I have encountered more than 50% of them	**8**	**(22%)**
c)	I have encountered less than 50% of them	**15**	**(42%)**
d)	I have encountered very few or none of them (<10%)	**1**	**(3%)**

7. Do you currently participate in any Nationally or laboratory controlled quality assurance/quality control (QA/QC) schemes in your epibiota work? For example, checking a proportion of work by a third party. (Circle one option).

a)	We participate in Nationally and laboratory controlled schemes	**4**	**(11%)**
b)	We participate in Nationally controlled schemes	**1**	**(3%)**
c)	We use our own, laboratory control schemes	**4**	**(11%)**
d)	We do not currently participate in any Nationally or laboratory controlled QA/QC schemes	**24**	**(67%)**

Examples of any schemes currently used;

- Several individuals and organisations currently participate in the NMBAQC scheme, which has so far focused on infauna.
- Some individuals and organisations currently participate in their own in-house QC schemes, involving cross-checking and consultation with experts.

8. Do you feel that this Epibiota Ring Test scheme could be a useful training tool for your organisation? (Circle one option).

a)	Yes	**18**	**(50%)**
b)	Possibly	**16**	**(44%)**
c)	No	**2**	**(5.5%)**

Comments and suggestions received on the current ring test and for developing an epibiota quality assurance scheme can be divided into the following broad categories;

Usefulness of the exercise

- There was a general feeling that there was a definite need for an AQC scheme that covers epibiota.
- The test was enjoyable, informative and interesting to complete, and a high level of interest was expressed in it.
- The test could prove very useful in highlighting species or taxa whose ID in situ or using images could only be regarded as tentative, without detailed examination (many species are too small or problematic to identify with certainty from images, e.g. algae, hydroids, bryozoans).

Problems with the test

- The test was too long and was very time consuming to complete. Had the test been shorter, with less images, more individuals might have participated.
- The images were organised in taxonomic order, which provided clues to species' identities.
- Algae were underrepresented in the study.
- Deeper water species were underrepresented in the study.
- Many of the organisms were virtually impossible to identify to species level, since detailed examination, impossible from images is required for the ID of certain taxa, e.g. sponges and bryozoa.

Suggestions for improvement of the test and for the future development of an epibiota QA scheme

- Information on field characteristics such as habitat/location/water depth/time of year etc would all help in the identification of organisms, since ID from photos is very different from ID in the field.
- Scale bars on the images would be useful.
- More than one view for most organisms would increase accuracy of identification.
- The test could be done at different levels, for example regional/specific taxonomic group versions.
- The production of a comprehensive literature list would be useful for participants.
- An epibiota test such as this would provide a useful pre-survey training/monitoring tool.
- It was generally felt that training should be an important part of any QA scheme.

- Training workshops, as have been organised as part of the infaunal work of the NMBAQC would be very useful. Such workshops might focus on ID skills using a range of techniques including video/photographs along with specimen examination.
- The development of web-based identification guides should be encouraged, specifically using characteristics that can be readily observed in situ.
- A comprehensive CD image or video library would be a useful aid to ID as specialist guides showing colour photos of living specimens do not exist for all taxonomic groups. In the case of the more problematic groups, a specimen-based QA system would be more appropriate.
- It might be useful to develop a test for differing levels of ability of participants, e.g. basic, intermediate and advanced.
- Separate intertidal and subtidal tests might be useful to develop.
- It would be very useful to develop biotope ID QA tests.