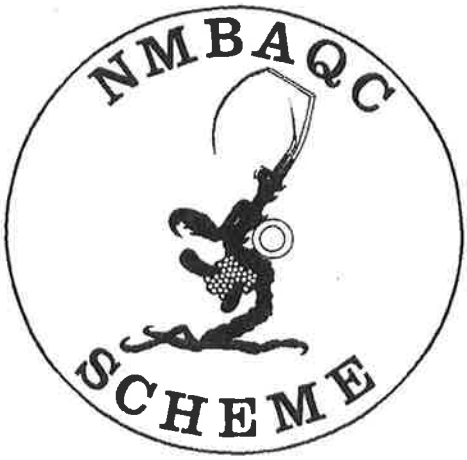

NATIONAL MARINE BIOLOGICAL ANALYTICAL QUALITY CONTROL SCHEME

ANNUAL REPORT

(Year 8)

2001/2002

November 2002
National Marine Biological AQC Coordinating Committee

NATIONAL MARINE BIOLOGICAL ANALYTICAL QUALITY CONTROL SCHEME

Annual Report 2001/2002

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1. OVERALL SUMMARY

- The National Marine Biological AQC Scheme (NMBAQC Scheme) has completed its seventh year in 2001/2002. 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 one laboratories participating. Thirteen of these laboratories submitted data for NMMP and eight were consultants or private contractors. 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.

- **All biomass results should be reported in grams to 4 decimal places.**

- 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.

- The application of the pass / fail criteria for the Own Sample exercise has been altered for this year (scheme year 8). Data flags have been applied on a sample-by-sample basis using a graded system related to the untransformed Bray-Curtis scores. Failed samples have been flagged, along with the other replicates from the same NMMP site. The committee have produced guidelines for the required level of remedial action. Participating labs with failed samples have been informed of the recommended remedial action. Laboratories submitting data to the NMMP data set MUST complete this remedial action and be re-audited. Their data flag will only be removed once a pass has been achieved. Non-NMMP laboratories have the option to complete remedial action. The contract manager will monitor and evaluate the remedial action and inform the committee of progress.

- Using the new pass / fail criteria for the Own Sample exercise 10 samples had a BCSI of less than 90%. Of these 9 samples had a BCSI below 85% and therefore FAILED. **FIVE of these FAILED samples are from NMMP sites.** All relevant labs have been informed of the required / recommended remedial action. Progress is on going.

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

- From scheme year 8 all NMMP laboratories submitting samples for the OS exercise have been required to split their samples to species. As of scheme year 9 **all submissions to the Own Sample exercise must be split to species** or an additional charge will be levied. 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 was suspended in scheme year 8 and the use of z-scores was assessed for full introduction in scheme year 9 (2002/2003).

- The Committee intend to assess the quality of field sediment descriptions by comparing a visual description of the pre-analysed PS21 sediment with a post analysis calculated description, using the Folk TRIANGLE (Folk, 1974).
- 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 was conducted via e-mail. Hard copies were provided where appropriate.

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

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

- A second epibiota ring test will be arranged for scheme year 9.

- The Committee intend to organise two workshops in 2002/2003. One will be on taxonomy and the other will cover epibiota and acoustic methods.
- Fees will be increased in scheme year 10 (2003/2004).
- 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 eighth 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 2001/2002 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 majority of statements made in last year's report hold true for 2001/2002. Amendments have been made to the Own Sample and Particle Size exercises.

- **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 are tackled by the targeted RT and individual feedback. The standard ring test forms 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.

  In addition to the targeted ring test (containing oligochaetes), all participating laboratories were sent a questionnaire on extraction and identification of oligochaetes. The findings from this questionnaire have been reported to the

Committee and participating labs. An extract from the report can be found in Appendix 5. A full copy of the report can be obtained from the contract manager.

- 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 assigned 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 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.

  All biomass results should be reported in grams to 4 decimal places.

- **Own samples**. The OS exercise is seen as a true reflection of local laboratory skills. The scoring of the Own Sample exercise has changed and uses a graded system related to the untransformed Bray-Curtis scores. Data flags will now be applied on a sample-by-sample basis (see Section 3.5 for details). Remedial action has been introduced in to the Scheme this year to improve the quality of data held in the NMMP database.

  In previous scheme years it was apparent that participants gave a lot of weight to these samples and may have selected samples with specimens of which they were confident in order to gain a pass. In an attempt to avoid such selectivity a new, more random, method of sample selection was tested in scheme year 8 and will be fully implemented in year 9 (2002/2003).

  All participating laboratories should familiarise themselves with the revised OS component.

- **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. Most laboratories in this scheme carried out the analysis by one of the two preferred techniques in common use.

As a routine and NMMP determinand, this analysis has previously been assigned a pass / fail standard and must be completed by NMMP labs. The pass / fail criteria was suspended in year 8 and a new scoring system was tested for full implementation in year 9 (see Section 3.5 for details).

All participating laboratories should familiarise themselves with the new scoring system and endeavour to provide all requested statistics.

3.2 Participation

The twenty one participants in 2001/2002 comprised private contractors, university labs and Government labs in Scotland, Northern Ireland, England and Wales. Thirteen 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.**

All primary correspondence for scheme year 9 will be via e-mail. Hard copies of data sheets will be provided where appropriate.

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.**

Thirteen NMMP laboratories are members of the Scheme. Of these four supplied all the data from all the relevant components. The remaining nine 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. One lab failed to complete one of the Ring Tests and one did not complete the PS exercise otherwise both completed all the remaining components.

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.**

Participating laboratories are informed of the timetable of circulations and data deadlines at the beginning of each scheme year. They must give adequate priority to the NMBAQC Scheme components.

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

The Co-ordinating Committee decided to alter the application of the pass / fail criteria for the Own Sample exercise in scheme year 8. Data flags have been applied on a sample-by-sample basis using a graded system related to the untransformed Bray-Curtis scores. The five tier system was 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

Samples not reaching the required standards are flagged, along with the remaining replicates from the same NMMP site.

The NMBAQC Committee has produced guidelines for remedial action, these are detailed in Appendix 6. The Committee will decide on the appropriate remedial action and individual laboratories will be informed of their decision. Those labs submitting data to the NMMP data set MUST complete the remedial action and re-submit samples for audit. **Data flags will only be removed from all the site replicates once a PASS has been achieved.** Non-NMMP laboratories will have remedial action recommended, although completion of such is optional.

Fifteen labs participated in the OS exercise, submitting forty-five samples for audit. The grading of these samples was as follows:

Excellent:	**3 samples**
Good:	**17 samples**
Acceptable:	**15 samples**
Poor:	**1 sample**
Fail:	**9 samples**

Of the above FIVE NMMP samples FAILED and ONE was scored as POOR.

One NMMP laboratory submitted no data for the OS exercise and was deemed to have failed (this is not included in the above summary).

Participating labs with FAILED samples have been informed of the recommended remedial action. The contract manager will monitor and evaluate the remedial action and inform the committee of progress. Where there are continuing disagreements which can not be resolved within the Scheme a third party will be approached by the contract manager.

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

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.

The Committee believe that it is best practice to pot specimens to species level rather than pot whole samples together. NMMP labs have been expected to undertake this action since scheme year 8. As of scheme year 9 **all submissions to the Own Sample exercise must be split to species** or an additional charge will be levied.

Two PS exercises were distributed in 2001/2002. Fourteen laboratories participated in both circulations. The previous pass / fail criteria were suspended for scheme year 8 and a trial assessment using z-scores was applied. The z-score represents the deviation of a result from the mean population of data in units of standard deviation.

The equation for calculating the z-score is as follows:

$$z = \left| \frac{(x_i - A)}{s} \right|$$

Xi = value obtained by the lab

A = true or assigned value from all the samples (mean with outliers removed)

s = population standard deviation (calculated from results excluding outliers)

As the required confidence limits of the data are **95%** then the limits of acceptable values of z are +2 or –2. Z-scores were applied to 5 parameters; percentage silt and clay, median particle size, mean particle size, sorting coefficient and inclusive graphic skewness.

Z-scores will be applied from scheme year 9 (PS21) and will appear on the Statement of Performance for scheme year 8 (trial year). A protocol for applying an overall 'Pass/Fail' flag on the PS exercise is to be devised.
In addition, the formation of written sediment descriptions needs to be examined in detail. These could utilise the PS exercise summary statistics.

4. SCHEME PROPOSAL FOR 2002/2003 (SCHEME YEAR 9)

The core programme for the scheme in the coming year 2002/2003 will contain the following components.

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

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 ALL laboratories will have to be split to species. The NMMP Green Book will be amended accordingly.

Following the suspension of the pass / fail criteria for the PS exercise and trial of the z-score system in year 8, this scoring system will be implemented from year 9. A protocol for applying an overall PS exercise 'pass/fail' flag will be considered by the committee. In an attempt to improve sediment descriptions in the field the Committee intend to introduce the need for a visual description of the sediment before analysis and a calculated one, using the Folk TRIANGLE, post analysis. These will be introduced in PS21. The FOLK sediment description triangle can be found on the British Geological Surveys web site or the reference is Folk, R. L. (1974) The Petrology of Sedimentary Rocks. Hemphill Publishing Co.

During scheme year 9 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 NMMP Green Book will be amended accordingly. This follows on from the Sorting Methods Questionnaire Report completed in August 2001. Appendix 7 contains an extract from this report. Those requiring a full copy of the report should contact the contract manager.

A second Epibiota ring test will be available on the web in early 2003.

All primary correspondence for scheme year 9 will be conducted via e-mail. Hard copies will be provided where appropriate.

The first report on the second phase of the National Marine Monitoring Programme will be published in late 2003. Various committee members will be contributing to this report through 2002/2003.

The Committee intend to organise two workshops in 2002/2003. The first of these will be a taxonomic workshop to be held in Plymouth, England in March 2003. The second will look at epibiota sampling, acoustic methods and AQC of these methods and will be held later in 2003.

5. CO-ORDINATING COMMITTEE ACTIVITIES AND PROJECTS

The scheme is about to enter its ninth year in and remains well supported both by various organisations that contribute committee members and by the participants.

At the start of this reporting period there was concern about the long term financial viability of the scheme which remains self financing. However, thanks to measures taken at the advice of the manager these have been resolved and the future of the scheme assured for the present.

As in previous years committee members have been at the forefront of the development of benthic biology as a monitoring tool by the statutory agencies. The scheme has provided the focus for the development and assessment of benthic indicators to be used in the forthcoming DEFRA State of the Seas Report. Members have also formed part of a sub-group developing benthic Ecological Quality Indicators for the Water Framework Directive.

The core role of the Scheme is to provide the quality measures for the UK NMMP which is due to produce its next report in 2003. Committee members have been actively involved in preparing the benthic data for statistical analysis prior to report writing.

In line with the schemes commitment to the provision of training a workshop on "difficult taxa" was held in Portafery in November 2001 which was attended by more that 30 individuals from a number of different organisations. In the forthcoming year plans are well advanced for a taxonomic workshop to be held in Plymouth in March 2003. Furthermore, in line with development of schemes links with marine SAC monitoring a workshops on acoustic methods and epibenthos are also planned for 2003. This area has also been strengthened by the introduction of a new Internet based epibiota ring test.

It is pleasing to report that NMBAQC has been acknowledged to best model for development of benthic biology AQC on Europe wide basis. It has been proposed that the scheme will take on the role of providing the community biology component of the next phase of BEQUALM(Benthic Effects Quality Assurance in Monitoring Programmes). It is hoped that this will be launched at a one day seminar held alongside the March workshop.

6. FINANCIAL SUMMARY 2001/2002

The eighth year of the scheme has been completed..

Fees in 2001/2002 remained the same as 2000/2001. Non NMMP laboratories were eligible to take advantage of the 'split fee' according to the components required although many elected to participate fully. Fees will be increased in scheme year 10 (2003/2004). This increase will be at the rate of RPI, as published by the Office of National Statistics for March of 2003.

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) South East Area under direction from the AQC committee.

Financial Summary 2000/2001

	INCOME	***EXPENDITURE***
Participant Fees	*£ 58, 358.30*	
Accrued income *Credit note*	*£ 1,653.54* *- £ 3,900.00*	
Interest	*£ 567.48*	
Expenditure *Core project/Additional projects* *Travel/Admin etc.*		 *£ 51,767.37* *0*
Management fee		*£ 3 000.00*
Bank Balance carried forward from 2000/2001	*£ 10, 130.50*	
Balance at year end	***£ 12,042.45***	

Report from the contractor

7. REPORT FROM THE CONTRACTOR

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Appendices

Summary of performance

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

The Scheme consisted of five components:

- Analysis of a single marine 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 seventh 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 91% of comparisons and better than 95% in 82% 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 80.9% and 100% and was better than 90% in 73% of comparisons and better than 95% in 45% of comparisons.

This Scheme year was used for the transition towards 'blind' **Own Sample (OS)** audits. Laboratories were to decide whether to adopt the full data matrices submission (to be compulsory for all participants from Scheme year nine), the old sample code submission, or abstain from the OS exercises for this year to allow auditing in arrears for Scheme year nine. A new flagging system was also introduced, which ascribes flags on a sample by sample basis (See Appendix 2: Description of the Scheme standards for each component). The results for the Own Samples were slightly improved compared to those from the Macrobenthic sample. Agreement between the laboratories and Unicomarine Ltd. was generally very good. Extraction efficiency, irrespective of sorting, was better than 90% in 78% of comparisons and better than 95% in 62% of all comparisons. The Bray-Curtis similarity index was greater than 95% in 44% of comparisons and in most cases (78%) the value of the index was greater than 90%.

The previous 'pass/fail' criterion for the **Particle Size exercises (PS)**, based upon the average percentage silt/clay figure recorded by all participating laboratories, was deemed unreliable and was replaced with the statement of z-scores for the major derived statistics with an acceptable range of ±2 standard deviations (See Appendix 2: Description of the Scheme standards for each component). The influence of analytical technique on the results returned for the PS exercises was marked, especially for the muddy sediment circulated as PS19. As has been previously reported, in most cases there was good agreement between laboratories using the same technique. The first particle size exercise of the scheme year (PS18) resulted in five 'fail' flags and six 'deemed fail' flags (no statistic/data supplied). Four of the five 'fail' flags belonged to one laboratory that supplied data from an incorrect source sediment. The second particle size exercise of the scheme year (PS19) resulted in two 'fail flags' and sixteen 'deemed fail' flags. One of these two 'fail' flags was the result of incorrect processing of the silt-clay fraction.

Two **Ring Tests (RT)** of twenty-five animal specimens were distributed. One set contained general fauna and the other set consisted of twenty-five 'targeted' specimens of 'Oligochaeta and similar fauna'. For the general set of fauna (RT18) 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 2.8 generic errors and 5.2 specific errors, these figures are significantly higher than those of the general ring test from the previous Scheme year. The majority of errors can be attributed to three polychaete and three mollusc taxa. The 'targeted' set (RT19) posed, as expected, far more problems. Several laboratories, possibly at the prospect of receiving twenty-five oligochaetes, decided not to participate in this exercise. On average each participating laboratory recorded 4.2 generic errors and 7.7 specific errors. Seven oligochaete specimens (including three replicated taxa) were responsible for the bulk of these errors (43% of generic and 49% of specific errors). The three non-oligochaete taxa circulated were responsible for 14% of generic and 10% of specific errors. All oligochaete species distributed could be identified without internal examination.

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 eighth year of the Scheme (2001/02) followed the format of the seventh year. A series of exercises involved the distribution of test materials to participating laboratories and the centralised examination of returned data and samples. Twenty-one 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 revised standards were applied to agreed components.

In this report revised 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. These 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 and is encouraged wherever possible as a primary means of communication.

2.1.2 Data returns

Return of data to Unicomarine Ltd. followed the same process as in previous years. Spreadsheet based forms (tailored to the receiving laboratory) were distributed for each circulation (via email) in addition to hard copies. All returned data have been converted to Excel 97 format for storage and analysis. In this and previous Scheme years 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.

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 2001. 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 eight will be recorded as LB0804.

In the present report all references to Laboratory Codes are the post-April 2001 (Scheme Year eight) codes.

2.2 Macrobenthic Samples (MB)

A single unsorted grab sample from marine 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 MB09 was collected from Pegwell Bay, Ramsgate; in an area of muddy sand 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 1.0mm, 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 1.0mm 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 1.0mm 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-one 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. Following a review of the Own Sample exercise (Unicomarine, 2001) several changes were implemented. From Scheme year nine (2002/03) all Own Sample participants must supply their previous years NMMP data matrices, where relevant, for Own Sample selection. This is to ensure that all processing is completed, preventing reworking of the selected Own Samples and enabling samples to be audited earlier in the Scheme year. To enable the transition towards the new Own Sample selection procedure, laboratories were instructed to select whether to adopt the new sample selection system, use the old system, or abstain from the exercise for Scheme year eight. Each participating laboratory was requested to send a list of samples/data matrices 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.

Thirteen weeks were allowed for preparation of the Own Samples selected for reanalysis. 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.

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 2001/02. 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 to ensure sample consistency and illustrate variations in 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 %<63μm, mean, median, sorting and skewness. A written description of the sediment characteristics was to be recorded along with an indication of any peroxide treatment. 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. Approximately **eleven weeks** were allowed for the analysis of each PS sample.

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 2001/02. The first of the year's RT circulations (RT18) was of the same form as for the earlier years - the specimens included representatives of the major phyla and approximately 40% of the taxa were polychaete worms, 28% were crustaceans, and 32% were molluscs. The second circulation (RT 19) 'targeted' specimens of 'Oligochaeta and similar

fauna'. Details of substratum, salinity, depth and geographical location for all RT19 specimens were provided.

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. Where relevant, every effort was made to ensure all specimens of a given species were of the same sex.

For the standard RT (RT18) and the 'targeted' RT (RT19), all specimens were taken from replicate grabs or cores 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. Approximately **eleven weeks** were allowed for the analysis of each RT exercise by the participating laboratories.

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. Participating laboratories were permitted **seventeen weeks** to prepare and submit their reference 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 2001/02 were undertaken, in varying numbers, by twenty-one 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. Sub-contracting by participating laboratories of certain sample analyses also 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 (MB09) was from a marine station in Pegswell Bay, Ramsgate. The samples comprised approximately two litres of muddy sand and shell substratum taken from a depth of approximately four metres. The samples contained an average of twenty-one species and one hundred and thirty-two individuals, covering a variety of phyla. The composite list from all samples was fifty-seven species. Five out of the eleven samples returned had been stained with Rose Bengal during sample processing. Eleven of the twelve laboratories participating in this exercise returned samples and data.

3.1.2 Efficiency of sample sorting

Table 1 presents for sample MB09, 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 13% of the total taxa in the sample) were either not extracted or not recognised within the picked material. On average Unicomarine Ltd. recorded one more taxon 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 three 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 82% of the samples was less than 5% of the true total number in the sample. In the worst instance 27% 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 six. A breakdown of the missed individuals by taxonomic group is presented in Table 2. Oligochaetes and molluscs were the most frequently missed faunal group, on average 25% of the total numbers of oligochaetes present and 10% of the total number of molluscs present were 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. 36% of participating laboratories had no taxonomic differences (Table 1, column 15). In the worst instance eight taxonomic differences were recorded. On average less than two taxonomic differences were 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 variation among laboratories in the values calculated for the index, from 80.9% to 100%, with an average value of 92.9%. The index for the majority of laboratories (6 of 11) was in excess of 95%. Three of the participating laboratories achieved a Bray-Curtis similarity index below 90%, these were 80.9%, 84.3% and 87.3%. One laboratory (LB0816) achieved a Bray-Curtis similarity index of 100%. 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 MB09 circulation is presented in Table 3. Three laboratories did not supply biomass data. The average difference between the two weight values was –14.5%, 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 –76.2% (measurements by laboratory were lighter than those made by Unicomarine Ltd.) to +12.1% (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 the participating laboratories were fairly similar showing only the expected natural variation. The faunal composition of all samples returned was very similar.

3.2 Own Sample (OS)

3.2.1 *General comments*

Following the request to participating laboratories to submit a list of samples or data 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 OS17, OS18 and OS19 on receipt. Two 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 10l of residue. The associated fauna of the samples was also very varied; the number of taxa recorded ranged from 4 to 59, and the number of individuals from 6 to 1283. Overall, of the seventeen laboratories participating in this exercise, fifteen laboratories returned all three Own Samples. One laboratory donated their Own Sample allocation to another laboratory from the same organisation. One laboratory failed to supply Unicomarine Ltd. with a list of samples from which to select their samples, one laboratory decided not to take part in this component for this scheme year. This year allowed for the transition to 'blind' audits (compulsory from the next Scheme year) by permitting two different mechanisms of submitting samples for selection in the OS component. Four laboratories adopted the new selection system and provided data from which their three Own Samples were to be selected. Eleven laboratories used the old, existing system and provided a list of sample codes from which their Own Samples were to be selected.

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, except in instances where the fauna had been damaged and rendered unidentifiable and uncountable. 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 twenty-one taxa and the average difference was two taxa.

The data for the numbers of individuals recorded (columns 6 and 7) shows a range of differences from the value obtained from re-analysis of between 0% and 59%. The average difference is 10% (only twelve samples exceeded this average). Eleven of the samples received showed 100% extraction of fauna from the residue (column 12), and in twelve samples various numbers of individuals (but no new taxa) were missed during sorting (column 11). The remaining twenty-two samples contained taxa in the residue which were not previously extracted, the worst example being twenty-one new taxa found in the residue (column 10). In the worst instance residue was found to contain three hundred and forty-two 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 twenty-nine, 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-one of the forty-five samples received. An average of just under two taxonomic differences per laboratory were recorded; in the worst instance ten 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 56% to 100%, with an average just over the pass/fail margin of 90%. Nine samples from six different laboratories achieved a similarity figure of less than 85%. Three samples gave a similarity figure of 100%, these were submitted by three different laboratories (LB0806, LB0818 and LB0820). The best overall results were achieved by laboratory LB0806, whose results comprised 98.39%, 95.87% and 100%. The worst overall results were achieved by laboratory LB0802, whose results comprised 55.86%, 71.28% and 90.77%. 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 an accurate 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 (two laboratories reported biomass to three decimal places and one laboratory reported at five decimal places). Audit biomass estimations were not calculated for six part samples due to the condition of the fauna received (these were either severely dried or acid treated 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-six 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 +9% difference between the two sets of results (*i.e.* heavier than Unicomarine Ltd.), the range was from –65% to +70%. 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 +0.4% for polychaetes, -2.3% for oligochaetes, -63.3% for nemerteans, -5.1% for crustaceans and +12.6% for molluscs. These figures are markedly different to those produced by this same exercise in each of the previous five 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 PS18, all fourteen participating laboratories returned data (including labs with grouped results). For PS19, thirteen out of the fourteen 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 PS18; 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 1% <63µm). The estimations of <63µm% were clearly different between the two techniques. The average estimation of <63µm% from laser analyses was 1.76%, compared with 0.23% from sieve and pipette analyses. Results for the individual replicates are provided in Table 8 and are displayed in Figure 1.

Sample PS19 was of a muddy sediment (average of 81.57% <63µm) although there was a marked difference in the curves between the two techniques. Once again the estimations of <63µm% were clearly different between the two techniques. The average estimation of <63µm% from laser analyses was 73.92%, compared with 89.22% 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. Figures 5 and 6 show the z-scores for each of the derived statistics.

It should be noted that four laboratories which normally sub-contract particle size analysis to the same two independent laboratories (also participating), elected to utilise the results from these laboratories. These laboratories are indicated in Tables 10 and 11 by an asterisk or pair of asterisks against their LabCode. Accordingly the results from these two sub-contracting laboratories have been used in the Figures and Tables as appropriate. In Figures 3, 4, 5 and 6 only data from the sub-contracting laboratories are displayed, although it also applies to their contracting laboratories. In Tables 10 and 11, which present the summary statistics for PS18 and PS19 respectively, although the results are displayed for all six 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 *Eighteenth distribution - PS18*

There was generally good agreement for PS18 between the results from the analysis of replicates and those from the majority of participating laboratories. The results for a single laboratory (LB0806) were vastly adrift due to the submission of the wrong data. The difference between the analytical techniques was less marked than has been seen for other PS circulations (see Figures 1 and 3).

3.3.3.2 *Nineteenth distribution - PS19*

There was significantly 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 RT18 the species were from a variety of Phyla (as for previous years) while for RT19 twenty-five 'Oligochaeta and similar fauna'

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 seventeen laboratories were distributed with RT18 specimens and eighteen laboratories received RT19 specimens. For RT18, thirteen laboratories returned data; four did not; three specified non-participation for this exercise. For RT19, ten laboratories returned samples and data; eight did not; eight specified non-participation for this exercise.

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. *Nucula turgida* for *Nucula nitidosa*.
- Simple mis-spelling of a name, e.g. *Ptotocirineris* for *Protocirrineris*.

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 RT18 and RT19. 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. A pair of zeros "0 0" in the Tables indicates that the subscribing laboratory did not return data.

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 2000/01 as there was only a single 'standard' exercise (RT18). RT19 was targeted on 'Oligochaeta and similar fauna'. The RT circulations are designed as a learning exercise to discover where particular difficulties lie within specific common taxa. Results were forwarded to the participating laboratories as soon as practicable. Each participant also received a ring test bulletin (RTB18 and RTB19), which outlined the reasons for individual laboratories identification discrepancies. 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 *Eighteenth distribution – RT18*

Table 12 presents the results for the RT18. 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 responsible for the majority of differences and these are described briefly below.

Approximately one third of the ring test comprised mollusc taxa and these caused problems for several laboratories; specifically *Akera bullata, Nucula nucleus* (large specimens) and *Spisula subtruncata* (medium sized specimens). These accounted for 31% of the specific differences recorded. Three of the polychaetes distributed were responsible for 58% of the errors recorded at the generic level. These specimens were *Protocirrineris chrysoderma, Raricirrus beryli* and *Manayunkia aestuarina.* Six of the twenty-five circulated specimens were correctly identified by all participating laboratories (*Branchiomma bombyx, Eudorellopsis deformis, Pseudoprotella phasma, Atylus falcatus, Pseudocuma longicornis* and *Perioculodes longimanus*). Further details and analysis of results can be found in the relevant Ring Test Bulletin (RTB18) which was circulated to each laboratory from which results were received.

3.4.3.2 *Nineteenth distribution – RT19*

RT19 contained twenty-five 'Oligochaeta and similar fauna'. The results from the circulation are presented in Table 13 in the same manner as for the other circulations. Several of taxa were responsible for the majority of differences and these are described briefly below.

The agreement at the generic level was relatively good, forty-two errors were recorded. Agreement at the specific level was fairly poor, seventy-seven errors were recorded. Twenty-two of the twenty-five specimens circulated were oligochaetes; two were capitellids; one was a cirratulid. There were several problem areas for participating laboratories, these can be broadly broken down into the following areas:

- *Psammoryctides barbatus/Tubifex tubifex* – either no access to freshwater keys or a confusion between these species.
- *Tubifioides swirencoides/T. cf. galiciensis/T. amplivasatus* – tubificids with dorsal hair chaetae that rely upon judgements of degrees of banding/papillations and determination of closely applied/widely spaced bifid or simple pointed chaetae.
- *Tubificoides heterochaetus* – probably not encountered by many participating laboratories, difficult to determine amongst large numbers of *T. pseudogaster agg.*

These problem areas accounted for a total of 68% of all specific differences recorded (23%, 38% and 6% respectively). The four *Psammoryctides barbatus* and *Tubifex tubifex* specimens distributed were responsible for 40% of the errors recorded at the generic level.). Two of the twenty-five circulated specimens were correctly identified by all participating laboratories (*Tubificoides benedii* and *T. insularis*). Further details and analysis of results can be found in the relevant Ring Test Bulletin (RTB19) which was circulated to each laboratory from which results were received.

Several laboratories do not routinely identify oligochaetes to species where possible. These laboratories found RT19 significantly difficult and this was reflected in their results. A questionnaire was circulated to qualify RT19 results and gather general information on levels of oligochaete identification. The resultant report (Hall & Worsfold, 2002) details the questionnaire returns and proposes a standard identification policy for NMMP oligochaetes.

3.4.4 *Differences between participating laboratories*

Figures 7 and 8 present the number of differences recorded at the level of genus and species for each of the participating laboratories, for RT circulations RT18 and RT19 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 RT18 were of polychaetes. Ten of the twenty-five specimens circulated were polychaetes and these produced 39% of the generic and 48% of the specific differences

recorded. Molluscs, despite only eight mollusc specimens being circulated, accounted for approximately 39% of the total number of generic differences and 48% of specific differences. Crustacean specimens (seven specimens in total) were responsible for none of generic differences and 6% of the total number 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 seventeen laboratories participating in this exercise, sixteen laboratories returned samples and data; one laboratory gave no indication of their non-participation in this exercise.

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 MB09 comprised a typical inshore muddy sand with shell sample. The extraction of fauna from the sediment was not particularly time consuming due to the nature of the sediment and the medium numbers of individuals (<200) and taxa retained after sieving. The dominant taxa recorded in the majority of samples were *Spiophanes bombyx*, *Nephtys spp.* juv. and *Tubificoides pseudogaster* agg. Only two participating laboratories extracted all the countable material from the residue, however the overall efficiency of faunal extraction is slightly improved compared to the previous year's exercise (MB08). Identification caused various problems for the majority of laboratories, only four laboratories correctly identified all their extracted fauna. Some taxonomic mistakes were noted including *Magelona spp.*, *Abra alba* and *Diastylis bradyi* misidentifications. Three of the eleven returning laboratories attained a Bray-Curtis similarity index less than 90%; one achieved a Bray-Curtis similarity index of 100% (LB0816). The average Bray-Curtis figure of 93% is the second highest recorded for this exercise to date. However, it is still comparable with those recorded for MB08 (95%), MB07 (88%), MB06 (91%), MB05 (85%) and MB04 (82%).

Table 4 shows the variation, by major Phyla, between those samples circulated for the macrobenthic exercise (MB09). The area sampled was fairly uniformed in its faunal composition. All samples were of relatively equal volume, sediment characteristics and species content. Two samples (analysed by LB0807 and LB0811) show an increase in the sandy nature of their sediment, this is denoted by reduced numbers of individuals and very few or no oligochaete individuals recorded.

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; six provided data that was heavier in total than Unicomarine Ltd.; and two supplied data that was lighter than Unicomarine Ltd. estimations. The extremes recorded were 12% lighter (LB0820) and 76% heavier (LB0805) than the Unicomarine Ltd. estimations. Overall the average difference between the values determined by the participating laboratories and Unicomarine Ltd. was –14.6% (*i.e.* laboratory measurements were 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 MB09 was –14.6%, while for MB08 it was +4.9%, 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 MB09 exercise. The average value of the index was 90% for the OS, compared with 93% for MB09. The average values of the other individual measures of processing performance (% of taxa extracted and identified, taxonomic errors) were similar for the MB09 exercise. The most apparent difference between these exercises was the far better extraction of individuals from the residue in the MB09 sample, the average % individuals not extracted from the residues for the OS samples was virtually double that of the MB returns. 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. In summary although the average Bray-Curtis figures between these two exercises are similar, the OS returns had slightly fewer taxonomic differences but contained more missed individuals in their residues compared with the MB09 returns.

There were forty-five samples submitted for this component. This was facilitated by the distribution of timely reminders. The average Bray-Curtis similarity index achieved was 90.45%. Approximately 78% of samples exceeded the 90% Bray-Curtis pass mark and approximately 62% of the samples exceeded 95% Bray-Curtis similarity. This is an improvement upon the previous year's exercises and is similar to results from other previous OS exercises. In the 2000/01 year (OS 14, 15 and 16) the average Bray-Curtis figure was 90.8%, and 67% (of the forty-five samples received) achieved more than 90% Bray-Curtis results. 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 seventy-four samples have been received (OS01-19). The average Bray-Curtis similarity figure is 91.47%. Sixty-nine samples have fallen below the 90% pass mark (25%). Thirty samples have achieved a similarity figure of 100% (11% 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 PS18 appeared from an analysis of replicates (Figure 1) to be very uniform and, with one exception (LB0806), the results from participating laboratories (Figure 3) were closely grouped. Figure 5 shows the z-scores for each of the major statistics supplied by the participating laboratories. The data received from LB0806 were not derived from the circulated PS18 sample and hence the results are clearly displaced.

There was more scatter in the results for PS19 from participating laboratories and a much less clear division between the two analytical methods. Figure 6 shows the z-scores for each of the major statistics supplied by the participating laboratories. The data received from LB0805 indicated a much lower silt-clay fraction compared to other samples. It was deduced that this was the result of coagulation of silt particles (*i.e.* giving them the properties of larger particles) during freeze drying of the whole sample. The separation of <63µm fraction must be performed prior to any drying of the >63µm sediment sample.

Participating laboratories were asked to provide a visual description of the PS18 and PS19 samples. The results varied greatly (Table 16, final column). A standard means of classifying sediments needs to be adopted.

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 the majority of cases laser analysis was used though in a few cases sieve or a mixed technique was employed.

4.4 Ring Test distributions

The results were in general comparable with those from the first seven 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. RT18 identified discrepancies with literature used by some participating laboratories for their identification of the *Pholoe inornata/P. baltica* and *Raricirrus beryli* specimens. All participating laboratories have been made aware of this via the ring test bulletin (RTB18).

The 'targeted' oligochaete ring rest (RT19) and ensuing questionnaire have resulted in a report that suggests a standard approach to oligochaetes encountered in NMMP samples (Hall & Worsfold, 2002). The ring test, although difficult, was felt by participants to be of particular use. Unfortunately this exercise attracted the lowest number of data returns received for a ring test since the beginning of the NMBAQC Scheme. Laboratories should endeavour to participate in all training exercises in order to receive the full benefits of the Scheme.

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 0.8, and in most cases (11 of 16) 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 (9 of 14 laboratories). The average number of specific differences was 2.4. 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 performance target standards were defined for certain Scheme components and applied in Scheme year three (1996/97). These standards were the subject of a recent review (Unicomarine, 2001) and have been altered for the present year; each performance standard is described in detail in Appendix 2: Description of the Scheme standards for each component. 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 exercises.

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 (Columns 4, 13 and 22) 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 87% of the comparisons were considered to have passed the enumeration of taxa standard; 76% exceeded the enumeration of individuals standard and 78% passed the Bray-Curtis comparison standard. Of the sixteen laboratories participating in this component fifteen supplied samples for reanalysis; one laboratory failed to supply samples or indicate their intentions, their samples are to be classified with 'Deemed fail' flags. NMMP sample flags have been applied to each of the Own Sample in accordance with the new performance flagging criteria (Table 15, column 23); nine of the forty-five samples are flagged as 'Fail'; one is flagged as 'Poor'; fourteen are flagged as 'Acceptable'; eighteen are flagged as 'Good'; and three are flagged as 'Excellent' for achieving 100% Bray-Curtis similarity indices.

Performance with respect to the biomass standard was slightly poorer with only 69% of the eligible 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 the requested four, and fauna rendered dry by initial biomass procedures).

Application of the new standards (See Appendix 2: Description of the Scheme standards for each component) to the results for the PS component is shown in Table 16. The upper section of Table 16 shows the results for the PS18 exercise. Three participating laboratories did not submit all five requested statistics, these statistics have been flagged as 'Deemed Fail'. One laboratory (LB0803), which submitted data for IGS(Ski), failed to meet the standard for this statistics; One laboratory (LB0806), which submitted data for all statistics, only met the standard for the IGS(Ski) statistic; ten laboratories submitted data for all statistics and passed all standards, although four of these laboratories were utilising data from centralised sources. The lower section of Table 16 shows the results for the PS19 exercise. One laboratory failed to meet the standards in PS19 due to non-return of data. Four

participating laboratories did not submit all five requested statistics, these statistics have been flagged as 'Deemed Fail'. One laboratory (LB0805), which submitted data for %<63μm, failed to meet the standard for this statistics; One laboratory (LB0802), which submitted data for IGS(Ski), failed to meet the standard for this statistics; seven laboratories submitted data for all statistics and passed all standards, although four of these laboratories were utilising data from centralised sources.

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

Comparisons with previous years' results for NMBAQC Scheme standards will not be conducted due to the introduction of new flagging criteria for both the OS and PS exercises (See Appendix 2: Description of the Scheme standards for each component). Monitoring the situation over a longer period is required before a firm statement about changes in laboratory standards could be made.

5.4 Remedial Action

It is imperative that failing NMMP samples, audited through the Own Sample exercise, are addressed. Remedial action should be conducted upon the remaining NMMP station replicates to improve upon the flagged data. The new NMBAQC Scheme OS standards give clear indications of how to discern what level of remedial action is required (See Appendix 2: Description of the Scheme standards for each component). A failing Own Sample is categorised by the achievement of a Bray-Curtis similarity indices of <90%; ten samples 'failed' in this Scheme year (including five NMMP samples). The performance indicators used to determine what level of remedial action is required are %taxa in residue, %taxonomic errors, %individuals in residue (see Table 15, columns 7, 10 and 16) and %count variance. Any remedial action performed should be examined externally for effectiveness before NMMP data flags are altered.

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 procedures and calculation of statistics

Where possible these are noted for each laboratory listed below.

Also in the comments below, the results for RT18 and RT19 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 four laboratories which normally use two separate centralised sediment analysis centres for the PS exercises, have decided to pool their data from these sub-contracting laboratories. Their data is indicated accordingly in all figures and tables. In the comments below they are termed 'Data from centralised analysis'.

Laboratory – LB0801

Macrobenthos

MB09 - Not participating in this component.

Own Sample

OS17 – Not participating in this component.
OS18 – Not participating in this component.
OS19 – Not participating in this component.

Particle size

PS18 – No major differences in size distribution curve. Sediment described as 'sandy'. All NMBAQCS standards passed.
PS19 – No major differences in size distribution curve. Sediment described as 'muddy'. All NMBAQCS standards passed.

Ring Test

RT18 – Not participating in this component.
RT19 – Not participating in this component.

Laboratory Reference

LR06 - Not participating in this component.

Laboratory – LB0802

Macrobenthos

MB09 – Two taxonomic differences. Thirteen individuals not picked from residue, including two previously unpicked taxa. Count variance of two individuals. Bray-Curtis similarity index of 93.01%. Biomass on average 15% lighter than Unicomarine Ltd.

Own Sample

OS17 – Six taxonomic differences. Count variance of two individuals. Twenty-one individuals not picked from the residue, including six previously unpicked taxa. Bray-Curtis similarity index of 55.9%. %. Biomass on average 7.65% heavier than Unicomarine Ltd. NMBAQCS sample flag – 'Fail'.
OS18 – Ten taxonomic differences. Count variance of one individual. One hundred and fifty-four individuals not picked from the residue, including six previously unpicked taxa. Bray-Curtis similarity index of 71.3%. Biomass on average 2.24% heavier than Unicomarine Ltd. NMBAQCS sample flag – 'Fail'.
OS19 – Nine taxonomic differences. Eight individuals not picked from residue. Count variance of two individuals. Bray-Curtis similarity index of 90.8%. Biomass on average 16.63% heavier than Unicomarine Ltd. NMBAQCS sample flag – 'Acceptable'.

Particle size

PS18 – Size distribution curve slightly below that of the majority of curves. Sediment described as 'very slightly muddy sand'. All NMBAQCS standards passed.
PS19 – No major differences in size distribution curve. Sediment described as 'slightly sandy mud'. NMBAQCS standard for IGS(SKi) failed. All remaining standards passed.

Ring Test

RT18 – Four generic and ten specific differences. Number of AQC identifications in High group.
RT19 – Eighteen generic and twenty-one specific difference. Number of AQC identifications in High group.

Laboratory Reference

LR06 – Three generic and seven specific differences.

Laboratory – LB0803

Macrobenthos

MB09 - Three taxonomic differences. One individual not picked from residue this was a previously unpicked taxon. Count variance of one individual. Bray-Curtis similarity index of 90.8%. Biomass data not supplied. Residue/fauna stained.

Own Sample

OS17 – Not participating in this component.
OS18 – Not participating in this component.
OS19 – Not participating in this component.

Particle size

PS18 -. No major differences in size distribution curve. Sediment described as 'medium sand'. No median statistic given. NMBAQCS standard for IGS(SKi) failed. All remaining standards passed.
PS19 – No major differences in size distribution curve. Sediment described as 'coarse silt'. No median or sorting statistics given. All remaining NMBAQCS standards passed.

Ring Test

RT18 – Two generic and three specific differences. Number of AQC identifications in Low group.
RT19 – Six generic and eleven specific differences. Number of AQC identifications in High group.

Laboratory Reference

LR06 - Two generic and three specific differences.

Laboratory – LB0804

Macrobenthos

MB09 - Two taxonomic differences. Two individuals not picked from residue. Bray-Curtis similarity index of 97.6%. Biomass on average 10.8% lighter than Unicomarine Ltd.

Own Sample

OS17 – Two taxonomic differences. All individuals extracted from the residue. Bray-Curtis similarity index of 71.3%. Biomass on average 16.34% lighter than Unicomarine Ltd. Acid treatment of molluscs limited auditing capabilities. NMBAQCS sample flag – 'Acceptable'.
OS18 – Seven individuals not extracted from residue, including one previously unpicked taxon. Bray-Curtis similarity index of 91.36%. Biomass on average 5.26% heavier than Unicomarine Ltd. Biomass damage limited auditing capabilities. NMBAQCS sample flag – 'Acceptable'.
OS19 – One taxonomic difference. Count variance of nine individuals. Bray-Curtis similarity index of 93.63%. Biomass on average 65.27% lighter than Unicomarine Ltd. Acid treatment of molluscs limited auditing capabilities. NMBAQCS sample flag – 'Acceptable'.

Particle size

PS18 – No major differences in size distribution curve. No sediment description given. No median, mean, sorting or IGS(Ski) statistics given. NMBAQCS %silt/clay standard passed.
PS19 – No major differences in size distribution curve. Sediment described as 'muddy, silty with fine sand'. No median, mean, sorting or IGS(Ski) statistics given. NMBAQCS %silt/clay standard passed.

Ring Test

RT18 – Two generic and three specific differences. Number of AQC identifications in Low group.
RT19 – One generic and five specific differences. Number of AQC identifications in Low group.

Laboratory Reference

LR06 – All specimens correctly identified.

Laboratory – LB0805

Macrobenthos

MB09 - Four taxonomic differences. All individuals picked from residue. Count variance of six individuals. Bray-Curtis similarity index of 96.02%. Biomass on average 76.2% lighter than Unicomarine Ltd. Residue/fauna stained.

Own Sample

OS17 – Four taxonomic differences. Three individuals not picked from residue, including one previously unpicked taxon. Bray-Curtis similarity index of 92.41%. Biomass on average 1.33% heavier than Auditor. NMBAQCS sample flag – 'Acceptable'.
OS18 – Four taxonomic differences. Count variance of five individuals. Bray-Curtis similarity index of 96.74%. Biomass on average 0.26% lighter than Auditor. NMBAQCS sample flag – 'Acceptable'.
OS19 – Three taxonomic differences. Bray-Curtis similarity index of 89.86%. Biomass on average 6.61% heavier than Auditor. NMBAQCS sample flag – 'Poor'.

Particle size

PS18 – No major differences in size distribution curve. No sediment description given. All NMBAQCS standards passed.
PS19 – Size distribution curve to the left of the majority of curves. Sediment described as 'fine sandy mud (black)'. NMBAQCS standard for %silt/clay failed. All remaining standards passed.

Ring Test

RT18 – Not participating in this exercise.
RT19 – Five generic and nine specific differences. Number of AQC identifications in Mid group.

Laboratory Reference

LR06 - Four specific differences.

Laboratory – LB0806

Macrobenthos

MB09 – No data received.

Own Sample

OS17 – Bray-Curtis similarity index of 98.39%. Biomass on average 4.51% lighter than Unicomarine Ltd. NMBAQCS sample flag – 'Good'.
OS18 – One taxonomic difference. Eleven individuals not picked from residue. Count variance of fifty-nine individuals. Bray-Curtis similarity index of 95.87%. Biomass on average 0.30% lighter than Unicomarine Ltd. NMBAQCS sample flag – 'Good'.
OS19 – Bray-Curtis similarity index of 100%. Biomass on average 15.31% lighter than Unicomarine Ltd. NMBAQCS sample flag – 'Excellent'.

Particle size

PS18 – Size distribution curve significantly to the right of all other curves. Sediment described as 'silt'. NMBAQCS standards for %silt/clay, median, mean and sorting failed. NMBAQCS standard for IGS(Ski) passed. Wrong data submitted – later correct submission passed all standards. Participant's in-house procedures/administration have been reviewed in response.
PS19 – Not participating in this exercise.

Ring Test

RT18 – Five generic and six specific differences. Number of AQC identifications in High group.
RT19 – Not participating in this exercise.

Laboratory Reference

LR06 – Two generic and two specific differences.

Laboratory – LB0807

Macrobenthos

MB09 - Eight taxonomic differences. Two individuals not picked from residue, including one previously unpicked taxon. Bray-Curtis similarity index of 80.9%. No biomass data supplied. Residue/fauna stained.

Own Sample

OS17 – Five taxonomic differences. Forty-six individuals not picked from residue, including one previously unpicked taxon. Count variance of one individual. Bray-Curtis similarity index of 93.19%. No biomass data supplied. NMBAQCS sample flag – 'Acceptable'.
OS18 – One taxonomic difference. Two individuals not picked from the residue, including two previously unpicked taxa. Count variance of one individual. Bray-Curtis similarity index of 97.65%. No biomass data supplied. NMBAQCS sample flag – 'Good'.
OS19 – Three taxonomic differences. Nine individuals not picked from residue, including three previously unpicked taxa. Count variance of seven individuals. Bray-Curtis similarity index of 95.95%. No biomass data supplied. NMBAQCS sample flag – 'Good'.

Particle size

PS18 – Not participating in this component.
PS19 – Not participating in this component.

Ring Test

RT18 – Two generic and six specific differences. Number of AQC identifications in Mid group.
RT19 – Not participating in this exercise.

Laboratory Reference

LR06 – All specimens correctly identified.

Laboratory – LB0808

Macrobenthos

MB09 - Not participating in this component.

Own Sample

OS17 – Data not as originally electronically submitted. One individual not picked from residue. Bray-Curtis similarity index of 95.65%. No biomass data supplied. NMBAQCS sample flag – 'Good'.
OS18 – Data not as originally electronically submitted. One taxonomic difference. Three hundred and forty-two individuals not picked from residue, including twenty-one previously unpicked taxa. Count variance of three individuals. Bray-Curtis similarity index of 57.98%. No biomass data supplied. NMBAQCS sample flag – 'Fail'.
OS19 – Data not as originally electronically submitted. Two taxonomic differences. Forty-six individuals not picked from residue, including ten previously unpicked taxa. Bray-Curtis similarity index of 91.20%. No biomass data supplied. NMBAQCS sample flag – 'Acceptable'.

Particle size

PS18 – Data from centralised analysis; No major differences in size distribution curve. Sediment described as 'sandy'. All NMBAQCS standards passed.
PS19 – Data from centralised analysis; No major differences in size distribution curve. Sediment described as 'muddy'. All NMBAQCS standards passed.

Ring Test

RT18 – No data received. No details of non-participation given.
RT19 – Not participating in this exercise.

Laboratory Reference

LR06 - Two specific differences.

Laboratory – LB0809

Macrobenthos

MB09 – One taxonomic difference. Count variance of one individual. Six individuals not picked from residue, including one previously unpicked taxon. Bray-Curtis similarity index of 95.2%. Biomass on average 21% lighter than Unicomarine Ltd.

Own Sample

OS17 – Thirty-one individuals not picked from residue, including two previously unpicked taxa. Count variance of one individual. Bray-Curtis similarity index of 96.89%. Biomass on average 14.55% heavier than Unicomarine Ltd. NMBAQCS sample flag – 'Good'.
OS18 – One hundred and fifty-seven individuals not picked from residue, including one previously unpicked taxon. Count variance of three individuals. Bray-Curtis similarity index of 72.07%. Biomass on average 13.46% lighter than Unicomarine Ltd. NMBAQCS sample flag – 'Fail'.
OS19 – One taxonomic difference. Two hundred and sixty-five individuals not picked from residue, including ten previously unpicked taxa. Count variance of ten individuals. Bray-Curtis similarity index of 56.22%. Biomass on average 4.05% heavier than Unicomarine Ltd. NMBAQCS sample flag – 'Fail'.

Particle size

PS18 – Size distribution curve to the left of the majority of curves. Sediment described as 'medium sand'. No mean statistic given. All remaining NMBAQCS standards passed.
PS19 – No major differences in size distribution curve. Sediment described as 'very fine sand'. No mean statistic given. All remaining NMBAQCS standards passed.

Ring Test

RT18 – One generic and two specific differences. Number of AQC identifications in Low group.
RT19 – Three generic and six specific differences. Number of AQC identifications in Mid group.

Laboratory Reference

LR06 – All specimens correctly identified.

Laboratory – LB0810

Macrobenthos

MB09 - Not participating in this component.

Own Sample

OS17 – Four individuals not picked from residue. Count variance of two individuals. Bray-Curtis similarity index of 96.94%. Biomass audit not possible due to slide mounted oligochaetes and unsplit taxa. NMBAQCS sample flag – 'Good'.

OS18 – Two taxonomic differences. Fourteen individuals not picked from residue, including one previously unpicked taxon. Count variance of thirty individuals. Bray-Curtis similarity index of 95.40%. Biomass audit conducted in part – excluding slide mounted oligochaetes. Biomass on average 24.62% heavier than Unicomarine Ltd. NMBAQCS sample flag – 'Good'.
OS19 – Nine individuals not picked from residue. Count variance of nine individuals. Bray-Curtis similarity index of 98.84%. Biomass audit conducted in part – excluding slide mounted oligochaetes. Biomass on average 3.88% heavier than Unicomarine Ltd. NMBAQCS sample flag – 'Good'.

Particle size

PS18 – Data from centralised analysis; No major differences in size distribution curve. Sediment described as 'sandy'. All NMBAQCS standards passed.
PS19 – Data from centralised analysis; No major differences in size distribution curve. Sediment described as 'muddy'. All NMBAQCS standards passed.

Ring Test

RT18 – Not participating in this exercise. Exercise used for training with no submission of results.
RT19 – Not participating in this exercise. Exercise used for training with no submission of results.

Laboratory Reference

LR06 – One generic and two specific differences.

Laboratory – LB0811

Macrobenthos

MB09 - One individual not picked from residue, including one previously unpicked taxon. Bray-Curtis similarity index of 99.1%. Biomass on average 5.6% lighter than Unicomarine Ltd. Residue/fauna stained.

Own Sample

OS17 – One taxonomic difference. Eight individuals not picked from residue, including one previously unpicked taxon. Count variance of one individual. Bray-Curtis similarity index of 92.68%. Biomass on average 36.6% heavier than Unicomarine Ltd. NMBAQCS sample flag – 'Acceptable'.
OS18 – Four taxonomic differences. Two individuals not picked from residue, including one previously unpicked taxon. Count variance of one individual. Bray-Curtis similarity index of 96.68%. Biomass on average 22.50% heavier than Unicomarine Ltd. NMBAQCS sample flag – 'Good'.
OS19 – Three taxonomic differences. One individual not picked from residue. Bray-Curtis similarity index of 97.43%. Biomass on average 6.84% heavier than Unicomarine Ltd. NMBAQCS sample flag – 'Good'.

Particle size

PS18 – Data from centralised analysis; No major differences in size distribution curve. No sediment description given. All NMBAQCS standards passed.
PS19 – Data from centralised analysis; No major differences in size distribution curve. Sediment described as 'mud'. All NMBAQCS standards passed.

Ring Test

RT18 – Two generic and eight specific differences. Number of AQC identifications in High group.
RT19 – Four generic and nine specific differences. Number of AQC identifications in Mid group.

Laboratory Reference

LR06 - One specific difference.

Laboratory – LB0812

Macrobenthos

MB09 - Not participating in this component.

Own Sample

OS17 – No sample received. No details of non-participation given.
OS18 – No sample received. No details of non-participation given.
OS19 – No sample received. No details of non-participation given.

Particle size

PS18 – Not participating in this component.
PS19 – Not participating in this component.

Ring Test

RT18 – Not participating in this component.
RT19 – Not participating in this component.

Laboratory Reference

LB06 - Not participating in this component.

Laboratory – LB0813

Macrobenthos

MB09 - Not participating in this component.

Own Sample

These three Own Samples were processed by, and are the responsibility of, LB0817. The Own Sample auditing allocations were donated by LB0813 to LB0817.

OS17 – One individual not picked from residue. Bray-Curtis similarity index of 98.99%. Biomass on average 24.95% heavier than Unicomarine Ltd. NMBAQCS sample flag – 'Good'.
OS18 – One taxonomic difference. Two individuals not picked from residue. Bray-Curtis similarity index of 84.62%. Biomass on average 70% heavier than Unicomarine Ltd. NMBAQCS sample flag – 'Fail'.
OS19 – Two taxonomic differences. Ninety-five individuals not picked from residue, including two previously unpicked taxa. Bray-Curtis similarity index of 91.09%. Biomass on average 19.44% heavier than Unicomarine Ltd. NMBAQCS sample flag – 'Acceptable'.

Particle size

PS18 – Not participating in this component.
PS19 – Not participating in this component.

Ring Test

RT18 – Not participating in this exercise.
RT19 – Not participating in this exercise.

Laboratory Reference

LR06 – Two specific differences.

Laboratory – LB0814

Macrobenthos

MB09 – Five taxonomic differences. Eight individuals not picked from residue, including three previously unpicked taxa. Bray-Curtis similarity index of 87.3%. Biomass on average 1.7% heavier than Unicomarine Ltd. Residue/fauna stained.

Own Sample

OS17 – One taxonomic difference. One individual not picked from residue, this was a previously unpicked taxon. Count variance of one individual. Bray-Curtis similarity index of 96.67%. Biomass on average 32.30% heavier than Unicomarine Ltd. NMBAQCS sample flag – 'Good'.
OS18 – One taxonomic difference. Bray-Curtis similarity index of 94.12%. Biomass on average 8.08% heavier than Unicomarine Ltd. NMBAQCS sample flag – 'Acceptable'.
OS19 – Two taxonomic differences. One individual not picked from residue. Count variance of one individual. Bray-Curtis similarity index of 90.39%. Biomass on average 6.42% heavier than Unicomarine Ltd. NMBAQCS sample flag – 'Acceptable'.

Particle size

PS18 – No major differences in size distribution curve. No sediment description given. All NMBAQCS standards passed.
PS19 – No major differences in size distribution curve. Sediment described as 'mud'. All NMBAQCS standards passed.

Ring Test

RT18 – Two generic and four specific differences. Number of AQC identifications in Low group.
RT19 – One generic and five specific differences. Number of AQC identifications in Low group.

Laboratory Reference

LR06 – Three generic and five specific differences.

Laboratory – LB0815

Macrobenthos

MB09 - Not participating in this component.

Own Sample

OS17 – Not participating in this component.
OS18 – Not participating in this component.
OS19 – Not participating in this component.

Particle size

PS18 – Data from centralised analysis; No major differences in size distribution curve. Sediment described as 'sandy'. NMBAQCS standards passed.
PS19 – Data from centralised analysis; No major differences in size distribution curve. Sediment described as 'muddy'. NMBAQCS standards passed.

Ring Test

RT18 – Four generic and eight specific differences. Number of AQC identifications in High group.
RT19 – One generic and two specific differences. Number of AQC identifications in Low group.

Laboratory Reference

LR06 – Three specific differences.

Laboratory – LB0816

Macrobenthos

MB09 – Bray-Curtis similarity index of 100%. No biomass data supplied.

Own Sample

OS17 – One taxonomic difference. Five individuals not picked from residue, including three previously unpicked taxa. Bray-Curtis similarity index of 91.50%. No biomass data supplied. NMBAQCS sample flag – 'Acceptable'.
OS18 – One taxonomic difference. One previously unpicked bryozoan taxon not extracted from the residue. Count variance of one individual. Bray-Curtis similarity index of 99.34%. No biomass data supplied. NMBAQCS sample flag – 'Good'.
OS19 – Three individuals not picked from residue, including two previously unpicked taxa. Bray-Curtis similarity index of 97.22%. No biomass data supplied. NMBAQCS sample flag – 'Good'.

Particle size

PS18 – Not participating in this component.
PS19 – Not participating in this component.

Ring Test

RT18 – Two generic and four specific differences. Number of AQC identifications in Low group.
RT19 – Two specific differences. Number of AQC identifications in Low group.

Laboratory Reference

LR06 – Two generic and five specific differences.

Laboratory – LB0817

Macrobenthos

MB09 - Not participating in this component.

Own Sample

OS17 – Twelve individuals not picked from residue. Count variance of seven individuals. Bray-Curtis similarity index of 99.55%. Biomass on average 7.44% heavier than Unicomarine Ltd. NMBAQCS sample flag – 'Good'.
OS18 – One taxonomic difference. Five individuals not picked from residue. Count variance of three individuals. Bray-Curtis similarity index of 93.98%. Biomass on average 7.02% heavier than Unicomarine Ltd. NMBAQCS sample flag – 'Acceptable'.
OS19 – One individual not picked from residue. Bray-Curtis similarity index of 95.24%. Biomass on average 17.78% heavier than Unicomarine Ltd. NMBAQCS sample flag – 'Good'.

Particle size

PS18 – No major differences in size distribution curve. No sediment description given. All NMBAQCS standards passed.
PS19 – No major differences in size distribution curve. No sediment description given. All NMBAQCS standards passed.

Ring Test

RT18 – Not participating in this component.
RT19 – Not participating in this component.

Laboratory Reference

LR06 – All specimens correctly identified.

Laboratory – LB0818

Macrobenthos

MB09 - Not participating in this component.

Own Sample

OS17 – Six taxonomic differences. Count variance of one individual. Bray-Curtis similarity index of 84.32%. Biomass on average 23.72% heavier than Unicomarine Ltd. NMBAQCS sample flag – 'Fail'.
OS18 – All individuals extracted from residue. Bray-Curtis similarity index of 100%. Biomass on average 27.74% heavier than Unicomarine Ltd. NMBAQCS sample flag – 'Excellent'.
OS19 – Seven taxonomic differences. Twenty individuals not picked from residue, including eleven previously unpicked taxa. Count variance of one individual. Bray-Curtis similarity index of 80.31%. Biomass on average 3.56% heavier than Unicomarine Ltd. NMBAQCS sample flag – 'Fail'.

Particle size

PS18 – Not participating in this component.
PS19 – Not participating in this component.

Ring Test

RT18 – Four generic and five specific differences. Number of AQC identifications in Mid group.
RT19 – Not participating in this exercise.

Laboratory Reference

LR06 - Three specific differences.

Laboratory – LB0819

Macrobenthos

MB09 - Not participating in this component.

Own Sample

OS17 – Not participating in this component.
OS18 – Not participating in this component.
OS19 – Not participating in this component.

Particle size

PS18 – Not participating in this component.
PS19 – Not participating in this component.

Ring Test

RT18 – Three generic and four specific differences. Number of AQC identifications in Mid group.
RT19 – Not participating in this exercise.

Laboratory Reference

LR06 - Not participating in this component.

Laboratory – LB0820

Macrobenthos

MB09 – Eight individuals not picked from residue, including two previously unpicked taxa. Count variance of one individual. Bray-Curtis similarity index of 97.9%. Biomass on average 12.1% heavier than Unicomarine Ltd.

Own Sample

OS17 – One taxonomic difference. Six individuals not picked from residue, including two previously unpicked taxa. Bray-Curtis similarity index of 78.95%. Biomass on average 14.84% heavier than Auditor. NMBAQCS sample flag – 'Fail'.
OS18 – Two taxonomic differences. Six individuals not picked from residue. Count variance of four individuals. Bray-Curtis similarity index of 90.36%. Biomass on average 3.95% lighter than Auditor. NMBAQCS sample flag – 'Acceptable'.
OS19 – All individuals extracted from residue. Bray-Curtis similarity index of 100%. Biomass on average 1.94% heavier than Auditor. NMBAQCS sample flag – 'Excellent'.

Particle size

PS18 – No major differences in size distribution curve. No sediment description given. All NMBAQCS standards passed.
PS19 – No major differences in size distribution curve. Sediment described as 'sandy clayey silt'. All NMBAQCS standards passed.

Ring Test

RT18 – Three generic and four specific differences. Number of AQC identifications in Mid group.
RT19 – Not participating in this exercise.

Laboratory Reference

LR06 - No data received. No details of non-participation received.

Laboratory – LB0821

Macrobenthos

MB09 – Twenty-nine individuals not picked from residue, including three previously unpicked taxa. Bray-Curtis similarity index of 84.3%. Biomass on average 1.3% lighter than Unicomarine Ltd.

Own Sample

OS17 – Not participating in this component.
OS18 – Not participating in this component.
OS19 – Not participating in this component.

Particle size

PS18 – Not participating in this component.
PS19 – Not participating in this component.

Ring Test

RT18 – Not applicable due to late entry into Scheme.
RT19 – Four generic and seven specific differences. Number of AQC identifications in Mid group.

Laboratory Reference

LR06 – Not participating in this component.

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 further 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 Scheme participants now use e-mail as their primary means of communication. All laboratories participating in Scheme year eight had 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 nine 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. In this and the previous Scheme year several laboratories, despite using blotted wet weight biomass techniques, rendered some of their specimens too damaged to be re-identified. One laboratory used acid treatment prior to the biomass of their molluscs, this rendered re-identification virtually impossible. Several laboratories submitted permanent or semi-permanent slides of Oligochaeta, this rendered re-estimations of biomass impossible. The initial processing of an NMMP sample should in no way compromise the effectiveness of an audit. 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. Several laboratories are still not submitting the PS data in the requested format and several are omitting requested statistics. The analysis and presentation of particle size data should both be carried out by persons who fully understand the mechanisms of sediment analysis – all laboratories should be capable of supplying PS data in the simple requested format. Participating laboratories provided a wide range of written descriptions for PS18 and PS19, these were extremely varied. The formation of written sediment descriptions, whether utilising particle size analysis summary statistics or not, needs to be examined in detail.

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 and expand in-house reference collections of fauna. All surveys should have an associated reference collection.

8. Some of the problems with identification, which arose throughout the various components of the scheme, included certain Mollusca. The seven mollusc specimens distributed in RT18 were responsible for 31% of the generic and 43% of the specific errors recorded. 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 (17% of the actual total taxa in the sample) were not extracted. On average 1.27 taxa were

not extracted from the residue. Only two of the participating laboratories extracted all the countable individuals from their residues. In the worst instance 27.1% of total individuals in the sample were not extracted. The situation was worse for the OS samples where a maximum of 21 taxa and up to 58% of the taxa were not extracted. In the worst instance 342 individuals were not picked from the residue and up to 59% of the total individuals remained in the residue. On average for the OS exercise 1.98 taxa were not extracted compared with 2.04, 1.25, 1.48, 0.45 and 1.39 taxa from last five years data, respectively. Enumeration of sorted individuals is generally good. When 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. In Scheme year seven 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. RT19 targeted 'Oligochaeta and similar fauna' and was complimented by a questionnaire regarding oligochaete identification. The ring test and accompanying questionnaire were reported to the participating laboratories (Hall & Worsfold, 2002) and reiterated the need for a standard identification protocol for NMMP samples. A proposal for a standard NMMP approach to oligochaete identification was included in the report. 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. Ring test bulletins for both RT18 and RT19 have been set-up as a web pages during the Scheme year (www.nmbaqcs.org). Participants are encouraged to review their exercise reports and provide feedback concerning content and format wherever appropriate.

12. The new PS 'Flagging' system (See Appendix 2: Description of the Scheme standards for each component) should not result in the previous anomalies. The five major derived statistics are now presented as z-scores with a ±2SD error margin to define 'pass/fail' flags. All participating laboratories should familiarise themselves with the new scoring system and endeavour to provide all requested statistics. A protocol for applying an overall PS exercise 'pass/fail' flag is to be devised.

13. 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 new OS 'Flagging' system should not result in the previous anomalies (See Appendix 2: Description of the Scheme standards for each component). The Own Sample protocol and scoring system has been changed. All participating laboratories should familiarise themselves with the revised OS component. Participating NMMP laboratories should undertake remedial action to address any failing samples. A facility for tracking and evaluating the remedial action applied to failing samples must be devised.

14. The NMMP database should be managed with a clear emphasis upon data quality. A facility for indicating audited samples and flags should be available. All replicates from a failing NMMP site (*e.g.* NMMP2000 site 245 replicates A-E) should be withheld until remedial action has attained a 'pass' flag.

15. As greater emphasis is placed upon remedial action there is need for a comprehensive list of taxonomic experts, to be called upon to offer a third party opinion for taxonomic issues. Prior to any third party intervention the disputing laboratory must provide clear reasons for their disagreement and make every effort to resolve the issue within the Scheme.

8. References

Hall, D. & Worsfold, T.M. (2002) *National Marine Biological Analytical Quality Control Scheme. Oligochaeta Questionnaire Report: Including provisional NMMP standard policy for oligochaete identification.* Report to the NMBAQC Committee and Scheme participants. Unicomarine report NMBAQColigquest, July 2002.

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.

Unicomarine (1995) *National Marine Biological Quality Control Scheme. Annual Report (Year one).* Report to the NMBAQC Committee and Scheme participants. September 1995.

Unicomarine (1996) *National Marine Biological Quality Control Scheme. Annual Report (Year two).* Report to the NMBAQC Committee and Scheme participants. September 1996.

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.

Worsfold, T.M. & Hall, D. (2001) *National Marine Biological Analytical Quality Control Scheme. Sorting Methods Questionnaire.* Report to the NMBAQC Committee and Scheme participants. Unicomarine report NMBAQCsortmeth, August 2001.

Tables

Table 1. Results from the analysis of Macrobenthic sample MB09 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
LB0802	22	22	0	0.0	159	170	-11	6.5	2	13	7.6	2	93.01	2
LB0803	19	19	0	0.0	119	119	0	0.0	1	1	0.8	1	90.76	3
LB0804	25	24	1	4.0	125	127	-2	1.6	0	2	1.6	0	97.62	2
LB0805	24	26	-2	7.7	203	197	6	3.0	0	0	0.0	6	96.02	4
LB0806	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB0807	17	19	-2	10.5	93	95	-2	2.1	1	2	2.1	0	80.85	8
LB0809	21	24	-3	12.5	134	139	-5	3.6	1	6	4.3	1	95.24	1
LB0811	13	14	-1	7.1	58	59	-1	1.7	1	1	1.7	0	99.15	0
LB0814	27	31	-4	12.9	181	189	-8	4.2	3	8	4.2	0	87.33	5
LB0816	16	16	0	0.0	81	81	0	0.0	0	0	0.0	0	100.00	0
LB0820	21	23	-2	8.7	162	169	-7	4.1	2	8	4.7	1	97.89	0
LB0821	15	18	-3	16.7	78	107	-29	27.1	3	29	27.1	0	84.32	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 MB09.

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB0802	UM count	-	123	7	-	21	-	19	-	170
	PL missed	-	6	3	-	1	-	3	-	13
	%missed	-	4.9	42.9	-	4.8	-	15.8	-	7.6
LB0803	UM count	-	77	15	-	11	-	16	-	119
	PL missed	-	0	0	-	0	-	1	-	1
	%missed	-	0.0	0.0	-	0.0	-	6.3	-	0.8
LB0804	UM count	-	97	3	-	15	-	11	1	127
	PL missed	-	2	0	-	0	-	0	0	2
	%missed	-	2.1	0.0	-	0.0	-	0.0	0.0	1.6
LB0805	UM count	-	145	23	-	19	-	10	-	197
	PL missed	-	0	0	-	0	-	0	-	0
	%missed	-	0.0	0.0	-	0.0	-	0.0	-	0.0
LB0806	UM count	-	-	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB0807	UM count	-	75	-	-	6	-	14	-	95
	PL missed	-	0	-	-	1	-	1	-	2
	%missed	-	0.0	-	-	16.7	-	7.1	-	2.1
LB0809	UM count	-	98	16	-	10	-	15	-	139
	PL missed	-	4	1	-	0	-	1	-	6
	%missed	-	4.1	6.3	-	0.0	-	6.7	-	4.3
LB0811	UM count	-	44	1	-	4	-	10	-	59
	PL missed	-	0	1	-	0	-	0	-	1
	%missed	-	0.0	100.0	-	0.0	-	0.0	-	1.7
LB0814	UM count	1	109	38	-	19	-	22	-	189
	PL missed	0	1	1	-	1	-	5	-	8
	%missed	0.0	0.9	2.6	-	5.3	-	22.7	-	4.2
LB0816	UM count	1	62	7	-	6	-	5	-	81
	PL missed	0	0	0	-	0	-	0	-	0
	%missed	0.0	0.0	0.0	-	0.0	-	0.0	-	0.0
LB0820	UM count	-	110	30	-	13	-	16	-	169
	PL missed	-	4	3	-	0	-	1	-	8
	%missed	-	3.6	10.0	-	0.0	-	6.3	-	4.7
LB0821	UM count	-	79	13	-	7	-	7	1	107
	PL missed	-	14	12	-	0	-	3	0	29
	%missed	-	17.7	92.3	-	0.0	-	42.9	0.0	27.1

Key:
PL - participating laboratory
UM - Unicomarine Ltd.
"-" - No data. See Report, Section 6, for details.
n/a - no residue supplied

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 MB09. Values are in grams (g).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB0802	PL	-	0.66852	0.00051	-	0.03821	-	0.19790	-	0.90514
	UM	-	0.7996	0.0004	-	0.0457	-	0.1976	-	1.0433
	%diff.	-	-19.6	21.6	-	-19.6	-	0.2	-	-15.3
LB0803	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB0804	PL	-	0.6619	-	-	0.0304	-	0.0807	0.0004	0.7734
	UM	-	0.7254	-	-	0.0245	-	0.1069	0.0004	0.8572
	%diff.	-	-9.6	-	-	19.4	-	-32.5	0.0	-10.8
LB0805	PL	-	0.3346	0.001	-	0.0032	-	0.0118	-	0.3506
	UM	-	0.5958	0.0011	-	0.0084	-	0.0125	-	0.6178
	%diff.	-	-78.1	-10.0	-	-162.5	-	-5.9	-	-76.2
LB0806	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB0807	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB0809	PL	-	0.3018	0.001	-	0.0239	-	0.1931	-	0.5198
	UM	-	0.4051	0.0006	-	0.0267	-	0.1965	-	0.6289
	%diff.	-	-34.2	40.0	-	-11.7	-	-1.8	-	-21.0
LB0811	PL	-	0.44737	-	-	0.00258	-	0.16116	-	0.61111
	UM	-	0.4854	-	-	0.0031	-	0.1568	-	0.6453
	%diff.	-	-8.5	-	-	-20.2	-	2.7	-	-5.6
LB0814	PL	0.0009	0.8174	-	-	0.0132	-	1.0705	-	1.902
	UM	0.0009	0.828	-	-	0.0135	-	1.0281	-	1.8705
	%diff.	0.0	-1.3	-	-	-2.3	-	4.0	-	1.7
LB0816	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB0820	PL	-	0.8824	0.003	-	0.0243	-	0.7513	-	1.661
	UM	-	0.7207	0.0024	-	0.0172	-	0.7191	-	1.4594
	%diff.	-	18.3	20.0	-	29.2	-	4.3	-	12.1
LB0821	PL	-	0.5154	0.0001	-	0.0242	-	0.0611	0.0001	0.6009
	UM	-	0.523	0.0001	-	0.0253	-	0.0597	0.0004	0.6085
	%diff.	-	-1.5	0.0	-	-4.5	-	2.3	-300.0	-1.3

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 MB09.

Taxa

LabCode	Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Total taxa
LB0802	0	13	1	0	2	0	6	0	22
LB0803	0	8	1	0	4	0	6	0	19
LB0804	0	12	1	0	6	0	4	1	24
LB0805	0	17	1	0	5	0	3	0	26
LB0806	-	-	-	-	-	-	-	-	-
LB0807	0	10	0	0	3	0	6	0	19
LB0809	0	13	1	0	5	0	5	0	24
LB0811	0	7	1	0	2	0	4	0	14
LB0814	1	15	1	0	8	0	5	2	32
LB0816	1	8	1	0	2	0	4	0	16
LB0820	0	11	1	0	6	0	5	0	23
LB0821	0	9	1	0	1	0	6	1	18
Mean	0	11	1	0	4	0	5	0	22
Max	1	17	1	0	8	0	6	2	32
Min	0	7	0	0	1	0	3	0	14

Individuals

LabCode	Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Total Ind.
LB0802	0	123	7	0	21	0	19	0	170
LB0803	0	77	15	0	11	0	16	0	119
LB0804	0	97	3	0	15	0	11	1	127
LB0805	0	145	23	0	19	0	10	0	197
LB0806	-	-	-	-	-	-	-	-	-
LB0807	0	75	0	0	6	0	14	0	95
LB0809	0	98	16	0	10	0	15	0	139
LB0811	0	44	1	0	4	0	10	0	59
LB0814	1	109	38	0	19	0	22	5	194
LB0816	1	66	7	0	2	0	5	0	81
LB0820	0	110	30	0	13	0	16	0	169
LB0821	0	79	13	0	7	0	7	1	107
Mean	0	93	14	0	12	0	13	1	132
Max	1	145	38	0	21	0	22	5	197
Min	0	44	0	0	2	0	5	0	59

Table 5. Results from the analysis of Own Samples (OS17 to OS19) supplied by the participating laboratories and re-analysis by Unicomarine Ltd.

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
LB0802	OS17	20	26	-6	23.1	46	65	-19	29.2	6	21	32.3	2	55.86	6	Biomass 5 d.p.
LB0802	OS18	37	46	-9	19.6	248	403	-155	38.5	6	154	38.2	-1	71.28	10	Biomass 5 d.p.
LB0802	OS19	46	47	-1	2.1	384	394	-10	2.5	0	8	2.0	-2	90.77	9	Biomass 5 d.p.
LB0804	OS17	21	21	0	0.0	82	82	0	0.0	0	0	0.0	0	92.68	2	Biomass acid treatment used
LB0804	OS18	13	14	-1	7.1	37	44	-7	15.9	1	7	15.9	0	91.36	0	Biomass acid treatment used
LB0804	OS19	39	37	2	5.1	138	129	9	6.5	0	0	0.0	9	93.63	1	Biomass acid treatment used
LB0805	OS17	19	20	-1	5.0	68	71	-3	4.2	1	3	4.2	0	92.41	4	External QC
LB0805	OS18	39	40	-1	2.5	402	397	5	1.2	0	0	0.0	5	96.74	4	External QC
LB0805	OS19	36	37	-1	2.7	169	168	1	0.6	0	0	0.0	1	89.86	3	External QC
LB0806	OS17	16	16	0	0.0	62	62	0	0.0	0	0	0.0	0	98.39	0	
LB0806	OS18	13	12	1	7.7	1331	1283	48	3.6	0	11	0.9	59	95.87	1	
LB0806	OS19	13	13	0	0.0	114	114	0	0.0	0	0	0.0	0	100.00	0	
LB0807	OS17	30	32	-2	6.3	498	545	-47	8.6	1	46	8.4	-1	93.19	5	No biomass data
LB0807	OS18	34	37	-3	8.1	105	108	-3	2.8	2	2	1.9	-1	97.65	1	No biomass data
LB0807	OS19	56	59	-3	5.1	362	378	-16	4.2	3	9	2.4	-7	95.95	3	No biomass data
LB0808	OS17	4	4	0	0.0	11	12	-1	8.3	0	1	8.3	0	95.65	0	Data not as originally submitted
LB0808	OS18	15	36	-21	58.3	238	583	-345	59.2	21	342	58.7	-3	57.98	1	Data not as originally submitted
LB0808	OS19	18	29	-11	37.9	256	301	-45	15.0	10	46	15.3	1	91.20	2	Data not as originally submitted
LB0809	OS17	4	6	-2	33.3	498	530	-32	6.0	2	31	5.8	-1	96.89	0	
LB0809	OS18	4	4	0	0.0	200	354	-154	43.5	1	157	44.4	3	72.07	0	
LB0809	OS19	47	49	-2	4.1	181	436	-255	58.5	10	265	60.8	10	56.22	1	
LB0810	OS17	6	6	0	0.0	94	100	-6	6.0	0	4	4.0	-2	96.94	0	Biomass audit in part
LB0810	OS18	16	14	2	12.5	398	382	16	4.0	1	14	3.7	30	95.40	2	Biomass audit in part
LB0810	OS19	12	12	0	0.0	601	601	0	0.0	0	9	1.5	9	98.84	0	Biomass audit in part
LB0811	OS17	11	13	-2	15.4	98	107	-9	8.4	1	8	7.5	-1	92.68	1	
LB0811	OS18	38	42	-4	9.5	316	317	-1	0.3	1	2	0.6	1	96.68	4	
LB0811	OS19	40	42	-2	4.8	312	310	2	0.6	0	1	0.3	3	97.43	3	
LB0812	OS17	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB0812	OS18	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB0812	OS19	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB0813	OS17	12	12	0	0.0	49	50	-1	2.0	0	1	2.0	0	98.99	0	Biomass 3 d.p.
LB0813	OS18	7	6	1	14.3	12	14	-2	14.3	0	2	14.3	0	84.62	1	Biomass 3 d.p.
LB0813	OS19	38	43	-5	11.6	557	655	-98	15.0	2	95	14.5	-3	91.09	2	Biomass 3 d.p.
LB0814	OS17	13	14	-1	7.1	89	91	-2	2.2	1	1	1.1	-1	96.67	1	
LB0814	OS18	7	7	0	0.0	17	17	0	0.0	0	0	0.0	0	94.12	1	
LB0814	OS19	28	30	-2	6.7	103	105	-2	1.9	0	1	1.0	-1	90.39	2	
LB0816	OS17	34	37	-3	8.1	150	155	-5	3.2	3	5	3.2	0	91.50	1	No biomass
LB0816	OS18	12	13	-1	7.7	301	300	1	0.3	1	0	0.0	1	99.34	1	No biomass
LB0816	OS19	26	28	-2	7.1	66	69	-3	4.3	2	3	4.3	0	97.22	0	No biomass
LB0817	OS17	14	14	0	0.0	995	1000	-5	0.5	0	12	1.2	7	99.55	0	Biomass 3 d.p.
LB0817	OS18	11	12	-1	8.3	813	815	-2	0.2	0	5	0.6	3	93.98	1	Biomass 3 d.p.
LB0817	OS19	7	7	0	0.0	10	11	-1	9.1	0	1	9.1	0	95.24	0	Biomass 3 d.p.
LB0818	OS17	32	31	1	3.1	92	93	-1	1.1	0	0	0.0	-1	84.32	6	Some vial labels mixed up
LB0818	OS18	5	5	0	0.0	6	6	0	0.0	0	0	0.0	0	100.00	0	Vial labels mixed up
LB0818	OS19	36	47	-11	23.4	182	203	-21	10.3	11	20	9.9	-1	80.31	7	Some vial labels mixed up
LB0820	OS17	11	13	-2	15.4	16	22	-6	27.3	2	6	27.3	0	78.95	1	External QC
LB0820	OS18	40	40	0	0.0	73	83	-10	12.0	0	6	7.2	-4	90.36	2	External QC
LB0820	OS19	4	4	0	0.0	23	23	0	0.0	0	0	0.0	0	100.00	0	External QC

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 participating laboratories for the major taxonomic groups present in Own Samples (OS17-19).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB0802	UM count	1	48	-	-	7	-	8	1	65
OS17	PL missed	0	14	-	-	2	-	4	1	21
	%missed	0.0	29.2	-	-	28.6	-	50.0	100.0	32.3
LB0802	UM count	5	147	-	-	6	5	191	49	403
OS18	PL missed	2	91	-	-	1	0	19	41	154
	%missed	40.0	61.9	-	-	16.7	0.0	9.9	83.7	38.2
LB0802	UM count	4	162	-	1	36	20	155	16	394
OS19	PL missed	0	0	-	0	0	0	8	0	8
	%missed	0.0	0.0	-	0.0	0.0	0.0	5.2	0.0	2.0
LB0804	UM count	2	37	-	-	4	-	37	2	82
OS17	PL missed	0	0	-	-	0	-	0	0	0
	%missed	0.0	0.0	-	-	0.0	-	0.0	0.0	0.0
LB0804	UM count	-	6	-	-	4	-	3	31	44
OS18	PL missed	-	0	-	-	1	-	0	6	7
	%missed	-	0.0	-	-	25.0	-	0.0	19.4	15.9
LB0804	UM count	6	41	-	-	10	-	55	17	129
OS19	PL missed	0	0	-	-	0	-	0	0	0
	%missed	0.0	0.0	-	-	0.0	-	0.0	0.0	0.0
LB0805	UM count	-	19	7	1	2	-	10	32	71
OS17	PL missed	-	0	0	0	0	-	0	3	3
	%missed	-	0.0	0.0	0.0	0.0	-	0.0	9.4	4.2
LB0805	UM count	-	199	-	-	8	-	159	31	397
OS18	PL missed	-	0	-	-	0	-	0	0	0
	%missed	-	0.0	-	-	0.0	-	0.0	0.0	0.0
LB0805	UM count	-	24	-	-	23	65	38	18	168
OS19	PL missed	-	0	-	-	0	0	0	0	0
	%missed	-	0.0	-	-	0.0	0.0	0.0	0.0	0.0
LB0806	UM count	-	11	-	-	5	1	45	-	62
OS17	PL missed	-	0	-	-	0	0	0	-	0
	%missed	-	0.0	-	-	0.0	0.0	0.0	-	0.0
LB0806	UM count	5	316	9	-	44	-	687	222	1283
OS18	PL missed	0	5	0	-	0	-	6	0	11
	%missed	0.0	1.6	0.0	-	0.0	-	0.9	0.0	0.9
LB0806	UM count	-	33	23	-	4	-	53	1	114
OS19	PL missed	-	0	0	-	0	-	0	0	0
	%missed	-	0.0	0.0	-	0.0	-	0.0	0.0	0.0
LB0807	UM count	1	458	-	-	-	4	59	23	545
OS17	PL missed	0	16	-	-	-	2	12	16	46
	%missed	0.0	3.5	-	-	-	50.0	20.3	69.6	8.4
LB0807	UM count	2	70	-	-	2	8	26	-	108
OS18	PL missed	0	0	-	-	0	0	2	-	2
	%missed	0.0	0.0	-	-	0.0	0.0	7.7	-	1.9
LB0807	UM count	-	73	-	-	19	38	232	16	378
OS19	PL missed	-	3	-	-	0	0	5	1	9
	%missed	-	4.1	-	-	0.0	0.0	2.2	6.3	2.4
LB0808	UM count	-	-	6	-	-	-	6	-	12
OS17	PL missed	-	-	0	-	-	-	1	-	1
	%missed	-	-	0.0	-	-	-	16.7	-	8.3
LB0808	UM count	4	514	4	2	19	-	34	6	583
OS18	PL missed	4	292	4	0	11	-	25	6	342
	%missed	100.0	56.8	100.0	0.0	57.9	-	73.5	100.0	58.7
LB0808	UM count	-	27	3	-	57	-	203	11	301
OS19	PL missed	-	11	1	-	0	-	30	4	46
	%missed	-	40.7	33.3	-	0.0	-	14.8	36.4	15.3

Table 6. Comparison of the efficiency of extraction of fauna by participating laboratories for the major taxonomic groups present in Own Samples (OS17-19).

LB0809	UM count	-	509	-	-	1	-	1	19	530
OS17	PL missed	-	16	-	-	1	-	1	13	31
	%missed	-	3.1	-	-	100.0	-	100.0	68.4	5.8
LB0809	UM count	-	140	-	-	-	-	3	211	354
OS18	PL missed	-	3	-	-	-	-	3	151	157
	%missed	-	2.1	-	-	-	-	100.0	71.6	44.4
LB0809	UM count	27	146	-	-	-	57	180	26	436
OS19	PL missed	9	62	-	-	-	5	178	11	265
	%missed	33.3	42.5	-	-	-	8.8	98.9	42.3	60.8
LB0810	UM count	-	-	96	-	4	-	-	-	100
OS17	PL missed	-	-	4	-	0	-	-	-	4
	%missed	-	-	4.2	-	0.0	-	-	-	4.0
LB0810	UM count	-	180	188	-	-	-	6	8	382
OS18	PL missed	-	10	2	-	-	-	0	2	14
	%missed	-	5.6	1.1	-	-	-	0.0	25.0	3.7
LB0810	UM count	-	399	178	-	6	-	14	4	601
OS19	PL missed	-	3	6	-	0	-	0	0	9
	%missed	-	0.8	3.4	-	0.0	-	0.0	0.0	1.5
LB0811	UM count	-	72	-	-	-	-	20	15	107
OS17	PL missed	-	5	-	-	-	-	2	1	8
	%missed	-	6.9	-	-	-	-	10.0	6.7	7.5
LB0811	UM count	3	142	-	-	10	2	44	116	317
OS18	PL missed	0	2	-	-	0	0	0	0	2
	%missed	0.0	1.4	-	-	0.0	0.0	0.0	0.0	0.6
LB0811	UM count	4	120	-	-	13	3	21	149	310
OS19	PL missed	0	1	-	-	0	0	0	0	1
	%missed	0.0	0.8	-	-	0.0	0.0	0.0	0.0	0.3
LB0812	UM count	-	-	-	-	-	-	-	-	0
OS17	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB0812	UM count	-	-	-	-	-	-	-	-	0
OS18	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB0812	UM count	-	-	-	-	-	-	-	-	0
OS19	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB0813	UM count	-	31	4	-	-	-	15	-	50
OS17	PL missed	-	0	1	-	-	-	0	-	1
	%missed	-	0.0	25.0	-	-	-	0.0	-	2.0
LB0813	UM count	-	-	-	-	9	-	5	-	14
OS18	PL missed	-	-	-	-	0	-	2	-	2
	%missed	-	-	-	-	0.0	-	40.0	-	14.3
LB0813	UM count	9	161	-	-	19	105	346	15	655
OS19	PL missed	4	28	-	-	5	3	55	0	95
	%missed	44.4	17.4	-	-	26.3	2.9	15.9	0.0	14.5
LB0814	UM count	-	78	5	-	5	2	1	-	91
OS17	PL missed	-	0	0	-	0	0	1	-	1
	%missed	-	0.0	0.0	-	0.0	0.0	100.0	-	1.1
LB0814	UM count	-	14	-	-	2	-	1	-	17
OS18	PL missed	-	0	-	-	0	-	0	-	0
	%missed	-	0.0	-	-	0.0	-	0.0	-	0.0
LB0814	UM count	-	25	-	-	1	46	31	2	105
OS19	PL missed	-	0	-	-	0	0	1	0	1
	%missed	-	0.0	-	-	0.0	0.0	3.2	0.0	1.0

Table 6. Comparison of the efficiency of extraction of fauna by participating laboratories for the major taxonomic groups present in Own Samples (OS17-19).

LB0816	UM count	-	18	-	-	32	3	100	2	155
OS17	PL missed	-	0	-	-	2	0	3	0	5
	%missed	-	0.0	-	-	6.3	0.0	3.0	0.0	3.2
LB0816	UM count	1	294	-	-	3	-	2	-	300
OS18	PL missed	0	0	-	-	0	-	0	-	0
	%missed	0.0	0.0	-	-	0.0	-	0.0	-	0.0
LB0816	UM count	-	19	-	-	2	-	41	7	69
OS19	PL missed	-	0	-	-	2	-	1	0	3
	%missed	-	0.0	-	-	100.0	-	2.4	0.0	4.3
LB0817	UM count	-	209	783	-	-	-	8	-	1000
OS17	PL missed	-	2	10	-	-	-	0	-	12
	%missed	-	1.0	1.3	-	-	-	0.0	-	1.2
LB0817	UM count	-	315	494	-	-	-	6	-	815
OS18	PL missed	-	3	1	-	-	-	1	-	5
	%missed	-	1.0	0.2	-	-	-	16.7	-	0.6
LB0817	UM count	-	7	3	-	1	-	-	-	11
OS19	PL missed	-	1	0	-	0	-	-	-	1
	%missed	-	14.3	0.0	-	0.0	-	-	-	9.1
LB0818	UM count	2	62	-	-	2	6	21	-	93
OS17	PL missed	0	0	-	-	0	0	0	-	0
	%missed	0.0	0.0	-	-	0.0	0.0	0.0	-	0.0
LB0818	UM count	-	6	-	-	-	-	-	-	6
OS18	PL missed	-	0	-	-	-	-	-	-	0
	%missed	-	0.0	-	-	-	-	-	-	0.0
LB0818	UM count	-	125	-	-	17	8	53	-	203
OS19	PL missed	-	3	-	-	2	0	15	-	20
	%missed	-	2.4	-	-	11.8	0.0	28.3	-	9.9
LB0820	UM count	4	6	-	-	-	-	10	2	22
OS17	PL missed	0	1	-	-	-	-	4	1	6
	%missed	0.0	16.7	-	-	-	-	40.0	50.0	27.3
LB0820	UM count	4	53	-	-	3	14	4	5	83
OS18	PL missed	0	5	-	-	0	0	0	1	6
	%missed	0.0	9.4	-	-	0.0	0.0	0.0	20.0	7.2
LB0820	UM count	-	23	-	-	-	-	-	-	23
OS19	PL missed	-	0	-	-	-	-	-	-	0
	%missed	-	0.0	-	-	-	-	-	-	0.0

Table 7. Comparison of the estimates of biomass made by the participating laboratories with those made by Unicomarine Ltd. for the major taxonomic groups present in samples OS17-OS19.

Sample OS17

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB0802	PL	0.00008	1.08420	-	-	0.00420	-	0.18914	-	1.2776
	UM	0.0007	1.0270	-	-	0.0061	-	0.1461	-	1.1799
	%diff.	-775.0	5.3	-	-	-45.2	-	22.8	-	7.6
LB0804	PL	0.0048	0.0801	-	-	0.0003	-	0.9770	0.0017	1.06390
	UM	0.0048	0.0953	-	-	0.0004	-	1.1349	0.0023	1.2377
	%diff.	0.0	-19.0	-	-	-33.3	-	-16.2	-35.3	-16.3
LB0805	PL	-	0.2324	0.0003	0.0006	0.0005	-	0.0511	0.0001	0.2850
	UM	-	0.2305	0.0002	0.0004	0.0004	-	0.0496	0.0001	0.2812
	%diff.	-	0.8	33.3	33.3	20.0	-	2.9	0.0	1.3
LB0806	PL	-	0.0123	-	-	0.0043	0.0002	0.6619	-	0.6787
	UM	-	0.0211	-	-	0.0089	0.0002	0.6791	-	0.7093
	%diff.	-	-71.5	-	-	-107.0	0.0	-2.6	-	-4.5
LB0807	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0808	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0809	PL	-	3.9673	-	-	-	-	-	0.0003	3.9676
	UM	-	3.3903	-	-	-	-	-	0.0002	3.3905
	%diff.	-	14.5	-	-	-	-	-	33.3	14.5
LB0810	PL	-	-	-	-	0.0001	-	-	-	0.0001
	UM	-	-	-	-	0.0001	-	-	-	0.0001
	%diff.	-	-	-	-	0.0	-	-	-	0.0
LB0811	PL	-	0.8570	-	-	-	-	0.0648	0.0038	0.9256
	UM	-	0.5249	-	-	-	-	0.0588	0.0034	0.5871
	%diff.	-	38.8	-	-	-	-	9.2	11.2	36.6
LB0812	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0813	PL	-	1.621	0.002	-	-	-	0.011	-	1.634
	UM	-	1.2161	0.0011	-	-	-	0.0091	-	1.2263
	%diff.	-	25.0	45.0	-	-	-	17.3	-	25.0
LB0814	PL	-	0.0753	0.0001	-	1.6303	0.2848	-	-	1.9905
	UM	-	0.0551	0.0001	-	1.0375	0.2548	-	-	1.3475
	%diff.	-	26.8	0.0	-	36.4	10.5	-	-	32.3
LB0816	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0817	PL	-	1.485	1.014	-	-	-	0.005	-	2.504
	UM	-	1.2959	1.0174	-	-	-	0.0043	-	2.3176
	%diff.	-	12.7	-0.3	-	-	-	14.0	-	7.4
LB0818	PL	0.0319	0.9125	-	-	0.0021	0.8674	0.0742	-	1.8881
	UM	0.0257	0.7284	-	-	0.0012	0.6235	0.0615	-	1.4403
	%diff.	19.4	20.2	-	-	42.9	28.1	17.1	-	23.7
LB0820	PL	0.0261	0.0795	-	-	-	-	0.0102	-	0.1158
	UM	0.0222	0.0672	-	-	-	-	0.0092	-	0.0986
	%diff.	14.9	15.5	-	-	-	-	9.8	-	14.9

Table 7. Comparison of the estimates of biomass made by the participating laboratories with those made by Unicomarine Ltd. for the major taxonomic groups present in samples OS17-OS19.

Sample OS18

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB0802	PL	0.06044	0.96602	-	-	0.00544	14.38479	31.49452	0.00240	46.9136
	UM	0.0708	0.8169	-	-	0.0077	12.1755	32.7881	0.0027	45.8617
	%diff.	-17.1	15.4	-	-	-41.5	15.4	-4.1	-12.5	2.2
LB0804	PL	-	0.0019	-	-	0.0008	-	0.0083	0.2305	0.24150
	UM	-	0.0027	-	-	0.0015	-	0.0096	0.2150	0.2288
	%diff.	-	-42.1	-	-	-87.5	-	-15.7	6.7	5.3
LB0805	PL	-	2.5269	-	-	0.0240	-	20.9810	0.9891	24.5210
	UM	-	2.3343	-	-	0.0211	-	21.2060	1.0232	24.5846
	%diff.	-	7.6	-	-	12.1	-	-1.1	-3.4	-0.3
LB0806	PL	0.0015	0.1373	0.0004	-	0.0132	-	17.1528	0.0054	17.3106
	UM	0.0023	0.2344	0.0006	-	0.0275	-	17.0933	0.0052	17.3633
	%diff.	-53.3	-70.7	-50.0	-	-108.3	-	0.3	3.7	-0.3
LB0807	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0808	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0809	PL	-	1.2915	-	-	-	-	-	0.0065	1.2980
	UM	-	1.4692	-	-	-	-	-	0.0035	1.4727
	%diff.	-	-13.8	-	-	-	-	-	46.2	-13.5
LB0810	PL	-	0.0852	-	-	-	-	0.0012	0.0001	0.0865
	UM	-	0.0645	-	-	-	-	0.0006	0.0001	0.0652
	%diff.	-	24.3	-	-	-	-	50.0	0.0	24.6
LB0811	PL	0.0029	1.7500	-	-	0.0256	0.0325	0.3785	0.4387	2.6282
	UM	0.0033	1.2473	-	-	0.0177	0.0302	0.3442	0.3942	2.0369
	%diff.	-12.6	28.7	-	-	30.9	7.1	9.1	10.1	22.5
LB0812	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0813	PL	-	-	-	-	0.004	-	0.003	-	0.007
	UM	-	-	-	-	0.0013	-	0.0008	-	0.0021
	%diff.	-	-	-	-	67.5	-	73.3	-	70.0
LB0814	PL	-	0.0072	-	-	1.2932	-	0.0059	-	1.3063
	UM	-	0.0064	-	-	1.1899	-	0.0044	-	1.2007
	%diff.	-	11.1	-	-	8.0	-	25.4	-	8.1
LB0816	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0817	PL	-	0.071	0.155	-	-	-	0.002	-	0.228
	UM	-	0.0566	0.1546	-	-	-	0.0008	-	0.2120
	%diff.	-	20.3	0.3	-	-	-	60.0	-	7.0
LB0818	PL	-	0.0393	-	-	-	-	-	-	0.0393
	UM	-	0.0284	-	-	-	-	-	-	0.0284
	%diff.	-	27.7	-	-	-	-	-	-	27.7
LB0820	PL	0.3951	0.1190	-	-	0.0007	1.2875	0.0345	0.0008	1.8376
	UM	0.4187	0.1104	-	-	0.0010	1.3707	0.0088	0.0005	1.9101
	%diff.	-6.0	7.2	-	-	-42.9	-6.5	74.5	37.5	-3.9

Table 7. Comparison of the estimates of biomass made by the participating laboratories with those made by Unicomarine Ltd. for the major taxonomic groups present in samples OS17-OS19.

Sample OS19

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB0802	PL	0.01010	1.31714	-	0.00007	0.61725	1.41365	2.37518	0.07629	5.8097
	UM	0.0094	1.1462	-	0.0001	0.5213	1.1830	1.9120	0.0718	4.8438
	%diff.	6.9	13.0	-	-42.9	15.5	16.3	19.5	5.9	16.6
LB0804	PL	0.0034	0.2177	-	-	0.1053	-	0.0174	0.0055	0.34930
	UM	0.0047	0.3715	-	-	0.1698	-	0.0258	0.0055	0.5773
	%diff.	-38.2	-70.6	-	-	-61.3	-	-48.3	0.0	-65.3
LB0805	PL	-	0.1463	-	-	0.0065	0.0125	0.0351	0.0007	0.2011
	UM	-	0.1330	-	-	0.0063	0.0142	0.0340	0.0003	0.1878
	%diff.	-	9.1	-	-	3.1	-13.6	3.1	57.1	6.6
LB0806	PL	-	0.0490	0.0022	-	0.0068	-	0.3731	0.0001	0.4312
	UM	-	0.0802	0.0041	-	0.0134	-	0.3994	0.0001	0.4972
	%diff.	-	-63.7	-86.4	-	-97.1	-	-7.0	0.0	-15.3
LB0807	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0808	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0809	PL	0.1376	6.6086	-	-	-	9.0443	0.7672	0.7369	17.2946
	UM	0.1310	6.8164	-	-	-	8.3424	0.6077	0.6963	16.5938
	%diff.	4.8	-3.1	-	-	-	7.8	20.8	5.5	4.1
LB0810	PL	-	0.4700	-	-	0.0100	-	0.2330	0.0001	0.7131
	UM	-	0.4777	-	-	0.0052	-	0.2024	0.0001	0.6854
	%diff.	-	-1.6	-	-	48.0	-	13.1	0.0	3.9
LB0811	PL	0.0058	1.4498	-	-	0.1439	10.6406	0.3618	0.7137	13.3155
	UM	0.0048	1.1482	-	-	0.0901	10.2848	0.3380	0.5385	12.4044
	%diff.	16.5	20.8	-	-	37.4	3.3	6.6	24.6	6.8
LB0812	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0813	PL	0.276	2.101	-	-	0.006	28.792	0.569	0.684	32.428
	UM	0.2280	2.1422	-	-	0.0032	22.6076	0.5076	0.6338	26.1224
	%diff.	17.4	-2.0	-	-	46.7	21.5	10.8	7.3	19.4
LB0814	PL	-	0.9791	-	-	0.0010	2.0718	0.2948	0.1306	3.4773
	UM	-	0.9627	-	-	0.0008	1.8524	0.2952	0.1431	3.2542
	%diff.	-	1.7	-	-	20.0	10.6	-0.1	-9.6	6.4
LB0816	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0817	PL	-	0.802	0.003	-	0.001	-	-	-	0.806
	UM	-	0.6607	0.0018	-	0.0002	-	-	-	0.6627
	%diff.	-	17.6	40.0	-	80.0	-	-	-	17.8
LB0818	PL	-	1.6269	-	-	0.0282	0.0384	1.4348	-	3.1283
	UM	-	1.5289	-	-	0.0204	0.0303	1.4374	-	3.0170
	%diff.	-	6.0	-	-	27.7	21.1	-0.2	-	3.6
LB0820	PL	-	0.0980	-	-	-	-	-	-	0.0980
	UM	-	0.0961	-	-	-	-	-	-	0.0961
	%diff.	-	1.9	-	-	-	-	-	-	1.9

Table 8. Summary of the results of particle size analysis of the replicate samples from sediment circulation PS18.

PS18	% Clay & Silt	Median (phi)	Mean (phi)	Sorting	Skew
PS18 - 59 - laser	2.37	1.61	1.53	0.55	0.032
PS18 - 60 - laser	0.88	1.60	1.52	0.52	0.013
PS18 - 61 - laser	1.86	1.62	1.52	0.53	0.033
PS18 - 62 - laser	2.20	1.49	1.39	0.55	0.046
PS18 - 63 - laser	0.99	1.51	1.39	0.57	0.003
PS18 - 64 - laser	2.28	1.64	1.55	0.53	0.048
PS18 - 65 - laser	1.73	1.61	1.49	0.53	0.023
PS18 - 66 - sieve	0.23	2.05	2.04	0.36	-0.03
PS18 - 67 - sieve	0.25	2.03	2.02	0.38	-0.04
PS18 - 68 - sieve	0.25	2.05	2.07	0.42	0.04
PS18 - 69 - sieve	0.23	2.06	2.06	0.42	0.00
PS18 - 70 - sieve	0.20	2.04	2.02	0.38	-0.07
PS18 - 71 - sieve	0.23	2.05	2.05	0.37	-0.01
PS18 - 72 - sieve	0.23	2.04	2.02	0.38	-0.07

Table 9. Summary of the results of particle size analysis of the replicate samples from sediment circulation PS19.

PS19	% Clay & Silt	Median (phi)	Mean (phi)	Sorting	Skew
PS19 - 35 - laser	72.70	5.34	3.69	2.61	0.144
PS19 - 36 - laser	73.78	5.61	3.69	2.64	0.062
PS19 - 37 - laser	74.63	5.31	4.10	2.46	0.226
PS19 - 38 - laser	73.94	5.41	4.02	2.53	0.190
PS19 - 39 - laser	74.75	5.34	3.94	2.54	0.240
PS19 - 40 - laser	73.55	5.36	3.74	2.51	0.125
PS19 - 41 - laser	74.07	5.40	3.95	2.51	0.163
PS19 - 42 - sieve	88.83	7.12	-	-	-
PS19 - 43 - sieve	87.35	5.52	-	-	-
PS19 - 44 - sieve	90.03	6.97	-	-	-
PS19 - 45 - sieve	90.73	7.11	-	-	-
PS19 - 46 - sieve	88.44	6.70	-	-	-
PS19 - 47 - sieve	89.47	7.22	-	-	-
PS19 - 48 - sieve	89.66	5.64	-	-	-

Table 10. Summary of the particle size information received from participating laboratories for the eighteenth particle size distribution - PS18.

PS18

Sample	Method	% < 63 micron	Median (phi)	Mean (phi)	Sort	IGS (SKi)
859	L	2.37	1.61	1.53	0.55	0.032
860	L	0.88	1.60	1.52	0.52	0.013
861	L	1.86	1.62	1.52	0.53	0.033
862	L	2.20	1.49	1.39	0.55	0.046
863	L	0.99	1.51	1.39	0.57	0.003
864	L	2.28	1.64	1.55	0.53	0.048
865	L	1.73	1.61	1.49	0.53	0.023
866	S	0.23	2.05	2.04	0.36	-0.03
867	S	0.25	2.03	2.02	0.38	-0.04
868	S	0.25	2.05	2.07	0.42	0.04
869	S	0.23	2.06	2.06	0.42	0.00
870	S	0.20	2.04	2.02	0.38	-0.07
871	S	0.23	2.05	2.05	0.37	-0.01
872	S	0.23	2.04	2.02	0.38	-0.07
	Overall	**1.00**	**1.81**	**1.76**	**0.46**	**0.00**
	Laser	**1.76**	**1.58**	**1.48**	**0.54**	**0.03**
	Sieve	**0.23**	**2.05**	**2.04**	**0.39**	**-0.03**

Lab	Method	%<63µm	Median	Mean	Sort	IGS (SKi)
LB0801*	L	0.79	1.59	1.44	0.55	-0.007
LB0802	WS/DS/L	5.94	1.90	2.15	1.37	0.339
LB0803	DS/L	0.00	-	1.58	0.45	1.490
LB0804	DS	0.31	-	-	-	-
LB0805	FD/DS	0.00	2.00	2.00	0.40	0.000
LB0806	L	85.76	5.43	4.97	1.67	0.232
LB0808*	L	0.79	1.59	1.44	0.55	-0.007
LB0809	DS/CC	0.64	1.22	-	0.42	-0.045
LB0810*	L	0.79	1.59	1.44	0.55	-0.007
LB0811**	L	0	1.39	1.4	0.61	0
LB0814**	L	0.00	1.39	1.40	0.61	0.000
LB0815*	L	0.79	1.59	1.44	0.55	-0.007
LB0817	?	0.87	1.62	1.40	0.59	-0.040
LB0820	L	0.24	1.64	1.63	0.45	-0.040

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)
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	10	8	8	9	9
Mean of laboratories	9.46	2.10	2.07	0.72	0.21
Mean of 7 replicates (laser)	1.76	1.58	1.48	0.54	0.03
Mean of 7 replicates (sieve)	0.23	2.05	2.04	0.39	-0.03
Laboratory minimum	0.00	1.22	1.40	0.40	-0.05
Laboratory maximum	85.76	5.43	4.97	1.67	1.49

Table 11. Summary of the particle size information received from participating laboratories for the nineteenth particle size distribution - PS19.

PS19

Sample	Method	% < 63 micron	Median (phi)	Mean (phi)	Sort	IGS (SKi)
835	L	72.70	5.34	3.69	2.61	0.144
836	L	73.78	5.61	3.69	2.64	0.062
837	L	74.63	5.31	4.10	2.46	0.226
838	L	73.94	5.41	4.02	2.53	0.190
839	L	74.75	5.34	3.94	2.54	0.240
840	L	73.55	5.36	3.74	2.51	0.125
841	L	74.07	5.40	3.95	2.51	0.163
842	S	88.83	7.12	-	-	-
843	S	87.35	5.52	-	-	-
844	S	90.03	6.97	-	-	-
845	S	90.73	7.11	-	-	-
846	S	88.44	6.70	-	-	-
847	S	89.47	7.22	-	-	-
848	S	89.66	5.64	-	-	-
	Overall	**81.57**	**6.00**	**3.88**	**2.54**	**0.16**
	Laser	**73.92**	**5.40**	**3.88**	**2.54**	**0.16**
	Sieve	**89.22**	**6.61**	**n/a**	**n/a**	**n/a**

Lab	Method	%<63µm	Median	Mean	Sort	IGS (SKi)
LB0801*	L	70.66	4.80	4.15	1.41	-0.033
LB0802	WS/DS/L	82.61	5.60	6.10	2.21	-1.516
LB0803	DS/L	54.25	-	4.40	-	0.820
LB0804	DS/L	79.52	-	-	-	-
LB0805	FD/DS	27.60	3.25	3.18	1.32	-0.050
LB0806	-	-	-	-	-	-
LB0808*	L	70.66	4.8	4.15	1.41	-0.033
LB0809	DS	73.98	3.35	-	0.31	-0.040
LB0810*	L	70.66	4.8	4.15	1.41	-0.033
LB0811**	L	74.92	5.26	5.52	2.15	-0.01
LB0814**	L	74.92	5.26	5.52	2.15	-0.010
LB0815*	L	70.66	4.8	4.15	1.41	-0.033
LB0817	?	71.14	4.81	4.21	-	-0.027
LB0820	L	79.03	5.59	5.93	2.47	0.150

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)
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	9	7	7	6	8
Mean of laboratories	68.19	4.67	4.78	1.65	-0.09
Mean of 7 replicates (laser)	73.92	5.40	3.88	2.54	0.16
Mean of 7 replicates (sieve)	89.22	6.61	n/a	n/a	n/a
Laboratory minimum	27.60	3.25	3.18	0.31	-1.52
Laboratory maximum	82.61	5.60	6.10	2.47	0.82

Table 12. The identifications of the fauna made by participating laboratories for RT18. Names are given only where different from the AQC identification.

RT18	Taxon	LB0803	LB0805	LB0807	LB0809	LB0811
RT1801	Akera bullata	Retusa obtusata	0 0	Retusa obtusa	--	--
RT1802	Corbula gibba	--	0 0	--	--	Thracia distorta
RT1803	Protocirrineris chrysoderma	Cirriformia tentaculata	0 0	[Ptotocirineris] -	--	Aphelochaeta sp. A
RT1804	Pholoe inornata	- [baltica]	0 0	--	--	- synophthalmica
RT1805	Branchiomma bombyx	[Branchioma] -	0 0	--	--	--
RT1806	Alvania semistriata	--	0 0	--	--	--
RT1807	Sphaerosyllis tetralix	--	0 0	- sp.	--	--
RT1808	Eudorellopsis deformis	--	0 0	[Eudelloropsis] -	--	--
RT1809	Nucula nucleus	--	0 0	--	- sulcata	- sulcata
RT1810	Pseudoprotella phasma	--	0 0	--	--	--
RT1811	Corophium sextonae	--	0 0	- bonnellii	--	- acutum
RT1812	Nucula nitidosa	--	0 0	--	--	- hanleyi
RT1813	Atylus falcatus	--	0 0	--	--	--
RT1814	Nucula nitidosa	--	0 0	- sulcata	--	--
RT1815	Abra alba	--	0 0	- tenuis	--	--
RT1816	Sphaerosyllis bulbosa	--	0 0	--	--	- hystrix
RT1817	Eudorella truncatula	- emarginata	0 0	--	--	--
RT1818	Syllidia armata	--	0 0	--	--	--
RT1819	Scalibregma inflatum	--	0 0	--	--	--
RT1820	Spisula subtruncata	--	0 0	Nucula nitidosa	--	- elliptica
RT1821	Raricirrus beryli	--	0 0	--	--	--
RT1822	Pseudocuma longicornis	--	0 0	[Pseodocuma] -	--	--
RT1823	Manayunkia aestuarina	[Manyunkia] -	0 0	--	Fabriciola berkeleyi	--
RT1824	Thelepus setosus	[Thelpus] -	0 0	--	--	--
RT1825	Perioculodes longimanus	[Peroculoides] -	0 0	--	--	--

RT18	Taxon	LB0802	LB0804	LB0806	LB0808	LB0810
RT1801	Akera bullata	Haminea navicula	--	Retusa truncatula	0 0	0 0
RT1802	Corbula gibba	--	Bivalvia indet.	--	0 0	0 0
RT1803	Protocirrineris chrysoderma	Cirratulus cirratus	--	Cirriformia tentaculata	0 0	0 0
RT1804	Pholoe inornata	--	- [baltica]	--	0 0	0 0
RT1805	Branchiomma bombyx	[Branchioma] -	--	--	0 0	0 0
RT1806	Alvania semistriata	--	--	Ondina divisa	0 0	0 0
RT1807	Sphaerosyllis tetralix	- bulbosa	--	- magnidentata	0 0	0 0
RT1808	Eudorellopsis deformis	--	--	--	0 0	0 0
RT1809	Nucula nucleus	- sulcata	--	--	0 0	0 0
RT1810	Pseudoprotella phasma	--	--	--	0 0	0 0
RT1811	Corophium sextonae	- acutum	--	--	0 0	0 0
RT1812	Nucula nitidosa	--	--	--	0 0	0 0
RT1813	Atylus falcatus	--	--	--	0 0	0 0
RT1814	Nucula nitidosa	--	--	--	0 0	0 0
RT1815	Abra alba	--	--	--	0 0	0 0
RT1816	Sphaerosyllis bulbosa	- thomasi	--	--	0 0	0 0
RT1817	Eudorella truncatula	--	--	--	0 0	0 0
RT1818	Syllidia armata	--	--	Nereimyra punctata	0 0	0 0
RT1819	Scalibregma inflatum	--	--	--	0 0	0 0
RT1820	Spisula subtruncata	- elliptica	- elliptica	--	0 0	0 0
RT1821	Raricirrus beryli	Monticellina dorsobranchialis	--	Dodecaceria concharum	0 0	0 0
RT1822	Pseudocuma longicornis	--	--	--	0 0	0 0
RT1823	Manayunkia aestuarina	Fabriciola berkeleyi	Fabriciola berkeleyi	--	0 0	0 0
RT1824	Thelepus setosus	- cincinnatus	--	--	0 0	0 0
RT1825	Perioculodes longimanus	--	--	--	0 0	0 0

Table 12. The identifications of the fauna made by participating laboratories for RT18. Names are given only where different from the AQC identification.

RT18	Taxon	LB0813	LB0815	LB0819	LB0821
RT1801	Akera bullata	0 0	Daphana minuta	Diaphana minuta	0 0
RT1802	Corbula gibba	0 0	--	--	0 0
RT1803	Protocirrineris chrysoderma	0 0	Cirriformia tentaculata	Aphelochaeta sp. indet.	0 0
RT1804	Pholoe inornata	0 0	--	--	0 0
RT1805	Branchiomma bombyx	0 0	[Branchioma] -	--	0 0
RT1806	Alvania semistriata	0 0	--	--	0 0
RT1807	Sphaerosyllis tetralix	0 0	- hystrix	--	0 0
RT1808	Eudorellopsis deformis	0 0	--	--	0 0
RT1809	Nucula nucleus	0 0	- sulcata	--	0 0
RT1810	Pseudoprotella phasma	0 0	--	--	0 0
RT1811	Corophium sextonae	0 0	--	--	0 0
RT1812	Nucula nitidosa	0 0	- [turgida]	--	0 0
RT1813	Atylus falcatus	0 0	--	--	0 0
RT1814	Nucula nitidosa	0 0	- [turgida]	--	0 0
RT1815	Abra alba	0 0	- nitida	--	0 0
RT1816	Sphaerosyllis bulbosa	0 0	--	--	0 0
RT1817	Eudorella truncatula	0 0	--	--	0 0
RT1818	Syllidia armata	0 0	--	--	0 0
RT1819	Scalibregma inflatum	0 0	- celticum	--	0 0
RT1820	Spisula subtruncata	0 0	--	- elliptica	0 0
RT1821	Raricirrus beryli	0 0	Cirratulus cirratulus	Dodecaceria concharum	0 0
RT1822	Pseudocuma longicornis	0 0	--	--	0 0
RT1823	Manayunkia aestuarina	0 0	Fabricola berkeleyi	--	0 0
RT1824	Thelepus setosus	0 0	--	--	0 0
RT1825	Perioculodes longimanus	0 0	[Periculodes] -	--	0 0

RT18	Taxon	LB0814	LB0816	LB0818	LB0820
RT1801	Akera bullata	--	Retusa obtusa	[?Akera?] [?bullata?]	Diaphana minuta
RT1802	Corbula gibba	Hiatella arctica	--	--	--
RT1803	Protocirrineris chrysoderma	Aphelochaeta A	Cirriformia tentaculata	Aphelochaeta ?multibranchilis?	--
RT1804	Pholoe inornata	--	--	--	--
RT1805	Branchiomma bombyx	--	--	--	[Branchioma] -
RT1806	Alvania semistriata	--	--	Hydrobia ulvae	--
RT1807	Sphaerosyllis tetralix	--	--	--	[Spaerosyllis] -
RT1808	Eudorellopsis deformis	--	--	--	--
RT1809	Nucula nucleus	- sulcata	- sulcata	--	--
RT1810	Pseudoprotella phasma	--	[Pseodoprotella] -	--	--
RT1811	Corophium sextonae	--	--	--	--
RT1812	Nucula nitidosa	--	--	--	- hanleyi
RT1813	Atylus falcatus	--	--	--	--
RT1814	Nucula nitidosa	--	- hanleyi	--	--
RT1815	Abra alba	--	--	--	--
RT1816	Sphaerosyllis bulbosa	--	--	- [?bulbosa?]	--
RT1817	Eudorella truncatula	--	--	--	--
RT1818	Syllidia armata	--	--	--	--
RT1819	Scalibregma inflatum	--	--	- [?inflatum?]	--
RT1820	Spisula subtruncata	- elliptica	--	- elliptica	--
RT1821	Raricirrus beryli	--	--	Dodecaceria sp. (concharum)	Dodecaceria concharum
RT1822	Pseudocuma longicornis	--	--	--	--
RT1823	Manayunkia aestuarina	--	--	Fabriciola cf. berkeleyi	Fabriciola berkeleyi
RT1824	Thelepus setosus	--	--	--	--
RT1825	Perioculodes longimanus	--	--	--	[Perioculoides] -

Table 13. The identifications of the fauna made by participating laboratories for RT19. Names are given only where different from the AQC identification.

RT19	Taxon	LB0803	LB0805	LB0807	LB0809	LB0811
RT1901	Tubificoides benedii	--	--	0 0	--	--
RT1902	Tubifex tubifex	Tubificoides insularis	Tubificoides aculeatus?	0 0	--	- nerthus
RT1903	Paranais litoralis	- [littoralis]	--	0 0	--	--
RT1904	Tubificoides benedii	--	--	0 0	--	--
RT1905	Nais elinguis	Tubificoides sp.	--	0 0	--	- variabilis
RT1906	Psammoryctides barbatus	Tubifex tubifex	--	0 0	Tubifex tubifex	Tubifex tubifex
RT1907	Heterochaeta costata	--	--	0 0	--	--
RT1908	Tubificoides swirencoides	- sp.	- amplivasatus	0 0	- scoticus	--
RT1909	Tubificoides heterochaetus	Tubificinae sp.	- spp?	0 0	Limnodrilus hoffmeisteri	--
RT1910	Paranais litoralis	- [littoralis]	Chaetogaster spp.	0 0	--	Tubificoides pseudogaster
RT1911	Tubificoides amplivasatus	--	--	0 0	--	--
RT1912	Tubifex tubifex	Tubificoides amplivasatus	Monopylephorus irroratus	0 0	--	Tubificoides aculeatus
RT1913	Tubificoides insularis	--	--	0 0	--	--
RT1914	Tubificoides amplivasatus	- sp.	--	0 0	--	--
RT1915	Psammoryctides barbatus	Tubifex tubifex	--	0 0	Tubifex tubifex	Tubifex tubifex
RT1916	Paranais litoralis	- [littoralis]	--	0 0	--	--
RT1917	Heterochaeta costata	--	--	0 0	--	--
RT1918	Tubificoides swirencoides	- sp.	- cf. galiciensis	0 0	--	- scoticus
RT1919	Tubificoides cf. galiciensis	- swirencoides	--	0 0	- insularis	- swirencoides
RT1920	Tharyx sp. A	--	Chaetozone setosa agg.	0 0	--	--
RT1921	Mediomastus fragilis	--	--	0 0	--	--
RT1922	Capitella capitata	--	- [spp. agg.]	0 0	--	--
RT1923	Nais elinguis	--	Paranais litoralis	0 0	--	--
RT1924	Tubificoides cf. galiciensis	- sp.	- swirencoides?	0 0	- swirencoides	- amplivasatus
RT1925	Heterochaeta costata	--	--	0 0	--	--

RT19	Taxon	LB0802	LB0804	LB0806	LB0808	LB0810
RT1901	Tubificoides benedii	Tubificidae -	--	0 0	0 0	0 0
RT1902	Tubifex tubifex	Paranais sp.	--	0 0	0 0	0 0
RT1903	Paranais litoralis	Tubificoides sp.	--	0 0	0 0	0 0
RT1904	Tubificoides benedii	--	--	0 0	0 0	0 0
RT1905	Nais elinguis	- variabilis	--	0 0	0 0	0 0
RT1906	Psammoryctides barbatus	Tubifex tubifex	--	0 0	0 0	0 0
RT1907	Heterochaeta costata	0 0	--	0 0	0 0	0 0
RT1908	Tubificoides swirencoides	Tubifex tubifex	--	0 0	0 0	0 0
RT1909	Tubificoides heterochaetus	0 0	- pseudogaster	0 0	0 0	0 0
RT1910	Paranais litoralis	- sp.	--	0 0	0 0	0 0
RT1911	Tubificoides amplivasatus	Naididae -	--	0 0	0 0	0 0
RT1912	Tubifex tubifex	Naididae -	Tubificoides indet.	0 0	0 0	0 0
RT1913	Tubificoides insularis	--	--	0 0	0 0	0 0
RT1914	Tubificoides amplivasatus	Tubificidae -	--	0 0	0 0	0 0
RT1915	Psammoryctides barbatus	Tubifex tubifex	--	0 0	0 0	0 0
RT1916	Paranais litoralis	Psammoryctides barbatus	--	0 0	0 0	0 0
RT1917	Heterochaeta costata	Tubificoides amplivasatus	--	0 0	0 0	0 0
RT1918	Tubificoides swirencoides	Clitellio arenarius?	- cf. galiciensis	0 0	0 0	0 0
RT1919	Tubificoides cf. galiciensis	- benedii	- swirencoides	0 0	0 0	0 0
RT1920	Tharyx sp. A	--	- killariensis	0 0	0 0	0 0
RT1921	Mediomastus fragilis	Capitomastus minimus	--	0 0	0 0	0 0
RT1922	Capitella capitata	Tubificoides amplivasatus	--	0 0	0 0	0 0
RT1923	Nais elinguis	Paranais litoralis	--	0 0	0 0	0 0
RT1924	Tubificoides cf. galiciensis	--	--	0 0	0 0	0 0
RT1925	Heterochaeta costata	Tubificoides pseudogaster agg.	--	0 0	0 0	0 0

Table 13. The identifications of the fauna made by participating laboratories for RT19. Names are given only where different from the AQC identification.

RT19	Taxon	LB0813	LB0815	LB0819	LB0821
RT1901	Tubificoides benedii	0 0	--	0 0	--
RT1902	Tubifex tubifex	0 0	--	0 0	--
RT1903	Paranais litoralis	0 0	Tubificoides pseudogaster	0 0	--
RT1904	Tubificoides benedii	0 0	--	0 0	--
RT1905	Nais elinguis	0 0	--	0 0	--
RT1906	Psammoryctides barbatus	0 0	--	0 0	--
RT1907	Heterochaeta costata	0 0	--	0 0	--
RT1908	Tubificoides swirencoides	0 0	--	0 0	--
RT1909	Tubificoides heterochaetus	0 0	--	0 0	--
RT1910	Paranais litoralis	0 0	--	0 0	--
RT1911	Tubificoides amplivasatus	0 0	--	0 0	- insularis
RT1912	Tubifex tubifex	0 0	--	0 0	Eisenella tetraedra
RT1913	Tubificoides insularis	0 0	--	0 0	--
RT1914	Tubificoides amplivasatus	0 0	--	0 0	--
RT1915	Psammoryctides barbatus	0 0	--	0 0	--
RT1916	Paranais litoralis	0 0	--	0 0	--
RT1917	Heterochaeta costata	0 0	--	0 0	--
RT1918	Tubificoides swirencoides	0 0	- cf. galiciensis	0 0	- galiciensis
RT1919	Tubificoides cf. galiciensis	0 0	--	0 0	--
RT1920	Tharyx sp. A	0 0	--	0 0	Chaetozone sp. B
RT1921	Mediomastus fragilis	0 0	--	0 0	0 0
RT1922	Capitella capitata	0 0	--	0 0	0 0
RT1923	Nais elinguis	0 0	--	0 0	--
RT1924	Tubificoides cf. galiciensis	0 0	--	0 0	- benedii
RT1925	Heterochaeta costata	0 0	--	0 0	--

RT19	Taxon	LB0814	LB0816	LB0818	LB0820
RT1901	Tubificoides benedii	--	--	0 0	0 0
RT1902	Tubifex tubifex	--	--	0 0	0 0
RT1903	Paranais litoralis	--	--	0 0	0 0
RT1904	Tubificoides benedii	--	--	0 0	0 0
RT1905	Nais elinguis	- variabilis	--	0 0	0 0
RT1906	Psammoryctides barbatus	--	--	0 0	0 0
RT1907	Heterochaeta costata	--	--	0 0	0 0
RT1908	Tubificoides swirencoides	--	--	0 0	0 0
RT1909	Tubificoides heterochaetus	--	--	0 0	0 0
RT1910	Paranais litoralis	--	--	0 0	0 0
RT1911	Tubificoides amplivasatus	--	--	0 0	0 0
RT1912	Tubifex tubifex	--	--	0 0	0 0
RT1913	Tubificoides insularis	--	--	0 0	0 0
RT1914	Tubificoides amplivasatus	--	- scoticus	0 0	0 0
RT1915	Psammoryctides barbatus	--	--	0 0	0 0
RT1916	Paranais litoralis	--	--	0 0	0 0
RT1917	Heterochaeta costata	--	--	0 0	0 0
RT1918	Tubificoides swirencoides	--	--	0 0	0 0
RT1919	Tubificoides cf. galiciensis	- swirencoides	- scoticus	0 0	0 0
RT1920	Tharyx sp. A	- killariensis?	--	0 0	0 0
RT1921	Mediomastus fragilis	--	--	0 0	0 0
RT1922	Capitella capitata	--	--	0 0	0 0
RT1923	Nais elinguis	- variabilis	--	0 0	0 0
RT1924	Tubificoides cf. galiciensis	- swirencoides?	--	0 0	0 0
RT1925	Heterochaeta costata	--	--	0 0	0 0

Table 14. Summary of the results from the identification of specimens supplied by participating laboratories for Laboratory Reference exercise LR06.

	Differences		
LabCode	Generic	Specific	name changes
LB0802	3	7	0
LB0803	2	3	0
LB0804	0	0	2
LB0805	0	4	0
LB0806	2	2	0
LB0807	0	0	0
LB0808	0	2	1
LB0809	0	0	0
LB0810	1	2	2
LB0811	0	1	0
LB0813	0	2	2
LB0814	3	5	0
LB0815	0	3	5
LB0816	2	5	0
LB0817	0	0	0
LB0818	0	3	0
LB0820	-	-	-

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

Table 15. Results from the Own Samples (OS17-19) with respect to the NMBAQC/NMMP standards.

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
	Estimation of Taxa						Taxonomic Errors			Estimation of Abundance						Estimation of Biomass			Similarity Index			NMMP Sample Flag
LabCode	Lab.	Target	Flag	Missed	% Missed	Remedial Action	Lab.	%	Remedial Action	Lab.	Target	Flag	Missed	% Missed	Remedial Action	Lab.	Target	Flag	Target	Lab.	Flag	
LB0802 OS17	20	23.4 - 28.6	Fail	6	23.1	Reprocess	6	30.0	Reprocess	46	58.5 - 71.5	Fail	21.0	32.3	Reprocess	1.2776	0.9439 - 1.4159	*PASS*	90.0	55.86	Fail	Fail
LB0802 OS18	37	41.4 - 50.6	Fail	6	13.0	Reprocess	10	25.0	Reprocess	248	362.7 - 443.3	Fail	154.0	38.2	Reprocess	46.9136	36.6894 - 55.0340	*PASS*	90.0	71.28	Fail	Fail
LB0802 OS19	46	42.3 - 51.7	PASS	0	0.0	-	9	19.1	-	384	354.6 - 433.4	PASS	8.0	2.0	-	5.8097	3.8750 - 5.8126	*PASS*	90.0	90.77	PASS	Acceptable
LB0804 OS17	21	18.9 - 23.1	PASS	0	0.0	-	2	9.5	-	82	73.8 - 90.2	PASS	0.0	0.0	-	1.0639	0.9902 - 1.4852	*PASS*	90.0	92.68	PASS	Acceptable
LB0804 OS18	13	12.0 - 16.0	PASS	1	7.1	-	0	0.0	-	37	39.6 - 48.4	Fail	7.0	15.9	-	0.2415	0.1830 - 0.2746	*PASS*	90.0	91.36	PASS	Acceptable
LB0804 OS19	39	33.3 - 40.7	PASS	0	0.0	-	1	2.7	-	138	116.1 - 141.9	PASS	0.0	0.0	-	0.3493	0.4618 - 0.6928	*Fail*	90.0	93.63	PASS	Acceptable
LB0805 OS17	19	18.0 - 22.0	PASS	1	5.0	-	4	21.1	-	68	63.9 - 78.1	PASS	3.0	4.2	-	0.2850	0.2250 - 0.3374	*PASS*	90.0	92.41	PASS	Acceptable
LB0805 OS18	39	36.0 - 44.0	PASS	0	0.0	-	4	10.0	-	402	357.3 - 436.7	PASS	0.0	0.0	-	24.5210	19.6677 - 29.5015	*PASS*	90.0	96.74	PASS	Good
LB0805 OS19	36	33.3 - 40.7	PASS	0	0.0	-	3	8.1	Review	169	151.2 - 184.8	PASS	0.0	0.0	-	0.2011	0.1502 - 0.2254	*PASS*	90.0	89.86	Fail	Poor
LB0806 OS17	16	14.0 - 18.0	PASS	0	0.0	-	0	0.0	-	62	55.8 - 68.2	PASS	0.0	0.0	-	0.6787	0.5674 - 0.8512	*PASS*	90.0	98.39	PASS	Good
LB0806 OS18	13	10.0 - 14.0	PASS	0	0.0	-	1	8.3	-	1331	1154.7 - 1411.3	PASS	11.0	0.9	-	17.3106	13.8906 - 20.8360	*PASS*	90.0	95.87	PASS	Good
LB0806 OS19	13	11.0 - 15.0	PASS	0	0.0	-	0	0.0	-	114	102.6 - 125.4	PASS	0.0	0.0	-	0.4312	0.3978 - 0.5966	*PASS*	90.0	100.00	PASS	Excellent
LB0807 OS17	30	28.8 - 35.2	PASS	1	3.1	-	5	16.1	-	498	490.5 - 599.5	PASS	46.0	8.4	-	-	-	-	90.0	93.19	PASS	Acceptable
LB0807 OS18	34	33.3 - 40.7	PASS	2	5.4	-	1	2.9	-	105	97.2 - 118.8	PASS	2.0	1.9	-	-	-	-	90.0	97.65	PASS	Good
LB0807 OS19	56	53.1 - 64.9	PASS	3	5.1	-	3	5.4	-	362	340.2 - 415.8	PASS	9.0	2.4	-	-	-	-	90.0	95.95	PASS	Good
LB0808 OS17	4	2.0 - 6.0	PASS	0	0.0	-	0	0.0	-	11	10.0 - 14.0	PASS	1.0	8.3	-	-	-	-	90.0	95.65	PASS	Good
LB0808 OS18	15	32.4 - 39.6	Fail	21	58.3	Reprocess	1	6.7	Review	238	524.7 - 641.3	Fail	342.0	58.7	Reprocess	-	-	-	90.0	57.98	Fail	Fail
LB0808 OS19	18	26.1 - 31.9	Fail	10	34.5	-	2	10.5	-	256	270.9 - 331.1	Fail	46.0	15.3	-	-	-	-	90.0	91.20	PASS	Acceptable
LB0809 OS17	4	4.0 - 8.0	PASS	2	33.3	-	0	0.0	-	498	477.0 - 583.0	PASS	31.0	5.8	-	3.9676	2.7124 - 4.0686	*PASS*	90.0	96.89	PASS	Good
LB0809 OS18	4	2.0 - 6.0	PASS	1	25.0	Review	0	0.0	-	200	318.6 - 389.4	Fail	157.0	44.4	Reprocess	1.2980	1.1782 - 1.7672	*PASS*	90.0	72.07	Fail	Fail
LB0809 OS19	47	44.1 - 53.9	PASS	10	20.4	Reprocess	1	2.6	-	181	392.4 - 479.6	Fail	265.0	60.8	Reprocess	17.2946	13.2750 - 19.9126	*PASS*	90.0	56.22	Fail	Fail
LB0810 OS17	6	4.0 - 8.0	PASS	0	0.0	-	0	0.0	-	94	90.0 - 110.0	PASS	4.0	4.0	-	0.0001	0.0001 - 0.0001	*PASS*	90.0	96.94	PASS	Good
LB0810 OS18	16	12.0 - 16.0	PASS	1	7.1	-	2	15.4	-	398	343.8 - 420.2	PASS	14.0	3.7	-	0.0865	0.0522 - 0.0782	*Fail*	90.0	95.40	PASS	Good
LB0810 OS19	12	10.0 - 14.0	PASS	0	0.0	-	0	0.0	-	601	540.9 - 661.1	PASS	9.0	1.5	-	0.7131	0.5483 - 0.8225	*PASS*	90.0	98.84	PASS	Good
LB0811 OS17	11	11.0 - 15.0	PASS	1	7.7	-	1	8.3	-	98	96.3 - 117.7	PASS	8.0	7.5	-	0.9256	0.4697 - 0.7045	*Fail*	90.0	92.68	PASS	Acceptable
LB0811 OS18	38	37.8 - 46.2	PASS	1	2.4	-	4	9.8	-	316	285.3 - 348.7	PASS	2.0	0.6	-	2.6282	1.6295 - 2.4443	*Fail*	90.0	96.68	PASS	Good
LB0811 OS19	40	37.8 - 46.2	PASS	0	0.0	-	3	7.1	-	312	279.0 - 341.0	PASS	1.0	0.3	-	13.3155	9.9235 - 14.8853	*PASS*	90.0	97.43	PASS	Good
LB0812 OS17	-	-		-	-	-	-	-	-	-	-		-	-	-	-	-	-	90.0	-		Deemed Fail
LB0812 OS18	-	-		-	-	-	-	-	-	-	-		-	-	-	-	-	-	90.0	-		Deemed Fail
LB0812 OS19	-	-		-	-	-	-	-	-	-	-		-	-	-	-	-	-	90.0	-		Deemed Fail
LB0813 OS17	12	10.0 - 14.0	PASS	0	0.0	-	0	0.0	-	49	45.0 - 55.0	PASS	1.0	2.0	-	1.6340	0.9810 - 1.4716	*Fail*	90.0	98.99	PASS	Good
LB0813 OS18	7	4.0 - 8.0	PASS	0	0.0	-	1	16.7	Review	12	12.0 - 16.0	PASS	2.0	14.3	Review	0.0070	0.0017 - 0.0025	*Fail*	90.0	84.62	Fail	Fail
LB0813 OS19	38	38.7 - 47.3	Fail	2	4.7	-	2	4.9	-	557	589.5 - 720.5	Fail	95.0	14.5	-	32.4280	20.8979 - 31.3469	*Fail*	90.0	91.09	PASS	Acceptable
LB0814 OS17	13	12.0 - 16.0	PASS	1	7.1	-	1	7.7	-	89	81.9 - 100.1	PASS	1.0	1.1	-	1.9905	1.0780 - 1.6170	*Fail*	90.0	96.67	PASS	Good
LB0814 OS18	7	5.0 - 9.0	PASS	0	0.0	-	1	14.3	-	17	15.0 - 19.0	PASS	0.0	0.0	-	1.3063	0.9606 - 1.4408	*PASS*	90.0	94.12	PASS	Acceptable
LB0814 OS19	28	27.0 - 33.0	PASS	0	0.0	-	2	6.7	-	103	94.5 - 115.5	PASS	1.0	1.0	-	3.4773	2.6034 - 3.9050	*PASS*	90.0	90.39	PASS	Acceptable
LB0816 OS17	34	33.3 - 40.7	PASS	3	8.1	-	1	2.9	-	150	139.5 - 170.5	PASS	5.0	3.2	-	-	-	-	90.0	91.50	PASS	Acceptable
LB0816 OS18	12	11.0 - 15.0	PASS	1	7.7	-	1	8.3	-	301	270.0 - 330.0	PASS	0.0	0.0	-	-	-	-	90.0	99.34	PASS	Good
LB0816 OS19	26	25.2 - 30.8	PASS	2	7.1	-	0	0.0	-	66	62.1 - 75.9	PASS	3.0	4.3	-	-	-	-	90.0	97.22	PASS	Good
LB0817 OS17	14	12.0 - 16.0	PASS	0	0.0	-	0	0.0	-	995	900.0 - 1100.0	PASS	12.0	1.2	-	2.5040	1.8541 - 2.7811	*PASS*	90.0	99.55	PASS	Good
LB0817 OS18	11	10.0 - 14.0	PASS	0	0.0	-	1	8.3	-	813	733.5 - 896.5	PASS	5.0	0.6	-	0.2280	0.1696 - 0.2544	*PASS*	90.0	93.98	PASS	Acceptable
LB0817 OS19	7	5.0 - 9.0	PASS	0	0.0	-	0	0.0	-	10	9.0 - 13.0	PASS	1.0	9.1	-	0.8060	0.5302 - 0.7952	*Fail*	90.0	95.24	PASS	Good
LB0818 OS17	32	27.9 - 34.1	PASS	0	0.0	-	6	19.4	Reprocess	92	83.7 - 102.3	PASS	0.0	0.0	-	1.8881	1.1522 - 1.7284	*Fail*	90.0	84.32	Fail	Fail
LB0818 OS18	5	3.0 - 7.0	PASS	0	0.0	-	0	0.0	-	6	4.0 - 8.0	PASS	0.0	0.0	-	0.0393	0.0227 - 0.0341	*Fail*	90.0	100.00	PASS	Excellent
LB0818 OS19	36	42.3 - 51.7	Fail	11	23.4	Reprocess	7	19.4	Reprocess	182	182.7 - 223.3	Fail	20.0	9.9	Review	3.1283	2.4136 - 3.6204	*PASS*	90.0	80.31	Fail	Fail
LB0820 OS17	11	11.0 - 15.0	PASS	2	15.4	Review	1	9.1	Review	16	19.8 - 24.2	Fail	6.0	27.3	Reprocess	0.1158	0.0789 - 0.1183	*PASS*	90.0	78.95	Fail	Fail
LB0820 OS18	40	36.0 - 44.0	PASS	0	0.0	-	2	5.0	-	73	74.7 - 91.3	Fail	6.0	7.2	-	1.8376	1.5281 - 2.2921	*PASS*	90.0	90.36	PASS	Acceptable
LB0820 OS19	4	2.0 - 6.0	PASS	0	0.0	-	0	0.0	-	23	20.7 - 25.3	PASS	0.0	0.0	-	0.0980	0.0769 - 0.1153	*PASS*	90.0	100.00	PASS	Excellent

Table 16. Z-score results for the derived statistics supplied by participating laboratories for the Particle Size (PS) exercises - PS18 and PS19 - NMBAQC/NMMP standards applied.

PS18

Lab	%<63µm	z-score	Flag	Median	z-score	Flag	Mean	z-score	Flag	Sort	z-score	Flag	IGS (SKi)	z-score	Flag	Description
LaserRepAv	1.76	-0.26	PASS	1.58	-0.38	PASS	1.48	-0.49	PASS	0.54	-0.32	PASS	0.028	-0.32	PASS	-
SieveRepAv	0.23	-0.32	PASS	2.05	0.00	PASS	2.04	0.03	PASS	0.39	-0.67	PASS	-0.026	-0.44	PASS	-
LB0801*	0.79	-0.30	PASS	1.59	-0.37	PASS	1.44	-0.53	PASS	0.55	-0.29	PASS	-0.007	-0.40	PASS	Sandy
LB0802	5.9	-0.09	PASS	1.90	-0.12	PASS	2.15	0.13	PASS	1.37	1.62	PASS	0.339	0.36	PASS	Very slightly muddy sand
LB0803	0.0	-0.33	PASS	-	-	Deemed Fail	1.58	-0.40	PASS	0.45	-0.53	PASS	1.490	2.90	Fail	Medium sand
LB0804	0.3	-0.32	PASS	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-
LB0805	0.0	-0.33	PASS	2.00	-0.03	PASS	2.00	-0.01	PASS	0.40	-0.64	PASS	0.000	-0.39	PASS	-
LB0806	85.8	3.17	Fail	5.43	2.78	Fail	4.97	2.75	Fail	1.67	2.31	Fail	0.232	0.12	PASS	Silt
LB0808*	0.79	-0.30	PASS*	1.59	-0.37	PASS*	1.44	-0.53	PASS*	0.55	-0.29	PASS*	-0.007	-0.40	PASS*	Sandy
LB0809	0.64	-0.30	PASS	1.22	-0.67	PASS	-	-	Deemed Fail	0.42	-0.61	PASS	-0.045	-0.49	PASS	Medium sand
LB0810*	0.79	-0.30	PASS*	1.59	-0.37	PASS*	1.44	-0.53	PASS*	0.55	-0.29	PASS*	-0.007	-0.40	PASS*	Sandy
LB0811**	0	-0.33	PASS**	1.39	-0.54	PASS**	1.4	-0.57	PASS**	0.61	-0.15	PASS**	0	-0.39	PASS**	-
LB0814**	0.00	-0.33	PASS	1.39	-0.54	PASS	1.40	-0.57	PASS	0.61	-0.15	PASS	0.000	-0.39	PASS	-
LB0815*	0.79	-0.30	PASS*	1.59	-0.37	PASS*	1.44	-0.53	PASS*	0.55	-0.29	PASS*	-0.007	-0.40	PASS*	Sandy
LB0817	0.87	-0.29	PASS	1.62	-0.35	PASS	1.40	-0.57	PASS	0.59	-0.20	PASS	-0.040	-0.48	PASS	-
LB0820	0.24	-0.32	PASS	1.64	-0.33	PASS	1.63	-0.35	PASS	0.45	-0.53	PASS	-0.040	-0.48	PASS	-

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

PS19

Lab	%<63µm	z-score	Flag	Median	z-score	Flag	Mean	z-score	Flag	Sort	z-score	Flag	IGS (SKi)	z-score	Flag	Description
LaserRepAv	73.92	0.20	PASS	5.40	0.40	PASS	3.88	-0.76	PASS	2.54	0.96	PASS	0.164	0.37	PASS	-
SieveRepAv	89.22	1.11	PASS	6.61	1.52	PASS	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-
LB0801*	70.66	0.00	PASS	4.80	-0.15	PASS	4.15	-0.49	PASS	1.41	-0.45	PASS	-0.033	0.04	PASS	Muddy
LB0802	82.61	0.72	PASS	5.60	0.59	PASS	6.10	1.36	PASS	2.21	0.54	PASS	-1.516	-2.38	Fail	Slightly sandy mud
LB0803	54.25	-0.98	PASS	-	-	Deemed Fail	4.40	-0.26	PASS	-	-	Deemed Fail	0.820	1.44	PASS	Coarse silt
LB0804	79.52	0.53	PASS	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	Muddy, silty with fine sand
LB0805	27.60	-2.57	Fail	3.25	-1.58	PASS	3.18	-1.42	PASS	1.32	-0.56	PASS	-0.050	0.02	PASS	Fine sandy mud(black)
LB0806	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-
LB0808*	70.66	0.00	PASS*	4.8	-0.15	PASS*	4.15	-0.49	PASS*	1.41	-0.45	PASS*	-0.033	0.04	PASS*	Muddy
LB0809	73.98	0.20	PASS	3.35	-1.49	PASS	-	-	Deemed Fail	0.31	-1.82	PASS	-0.040	0.03	PASS	Very fine sand
LB0810*	70.66	0.00	PASS*	4.8	-0.15	PASS*	4.15	-0.49	PASS*	1.41	-0.45	PASS*	-0.033	0.04	PASS*	Muddy
LB0811**	74.92	0.26	PASS**	5.26	0.27	PASS**	5.52	0.81	PASS**	2.15	0.47	PASS**	-0.01	0.08	PASS**	Mud
LB0814**	74.92	0.26	PASS	5.26	0.27	PASS	5.52	0.81	PASS	2.15	0.47	PASS	-0.010	0.08	PASS	Mud
LB0815*	70.66	0.00	PASS*	4.8	-0.15	PASS*	4.15	-0.49	PASS*	1.41	-0.45	PASS*	-0.033	0.04	PASS*	Muddy
LB0817	71.14	0.03	PASS	4.81	-0.14	PASS	4.21	-0.44	PASS	-	-	Deemed Fail	-0.027	0.05	PASS	-
LB0820	79.03	0.50	PASS	5.59	0.58	PASS	5.93	1.20	PASS	2.47	0.87	PASS	0.150	0.34	PASS	Sandy clayey silt

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

Figures

Figure 1. Particle size distribution curves resulting from analysis of fourteen replicate samples of sediment distributed as PS18. Seven samples analysed by sieve and seven samples analysed by Laser.

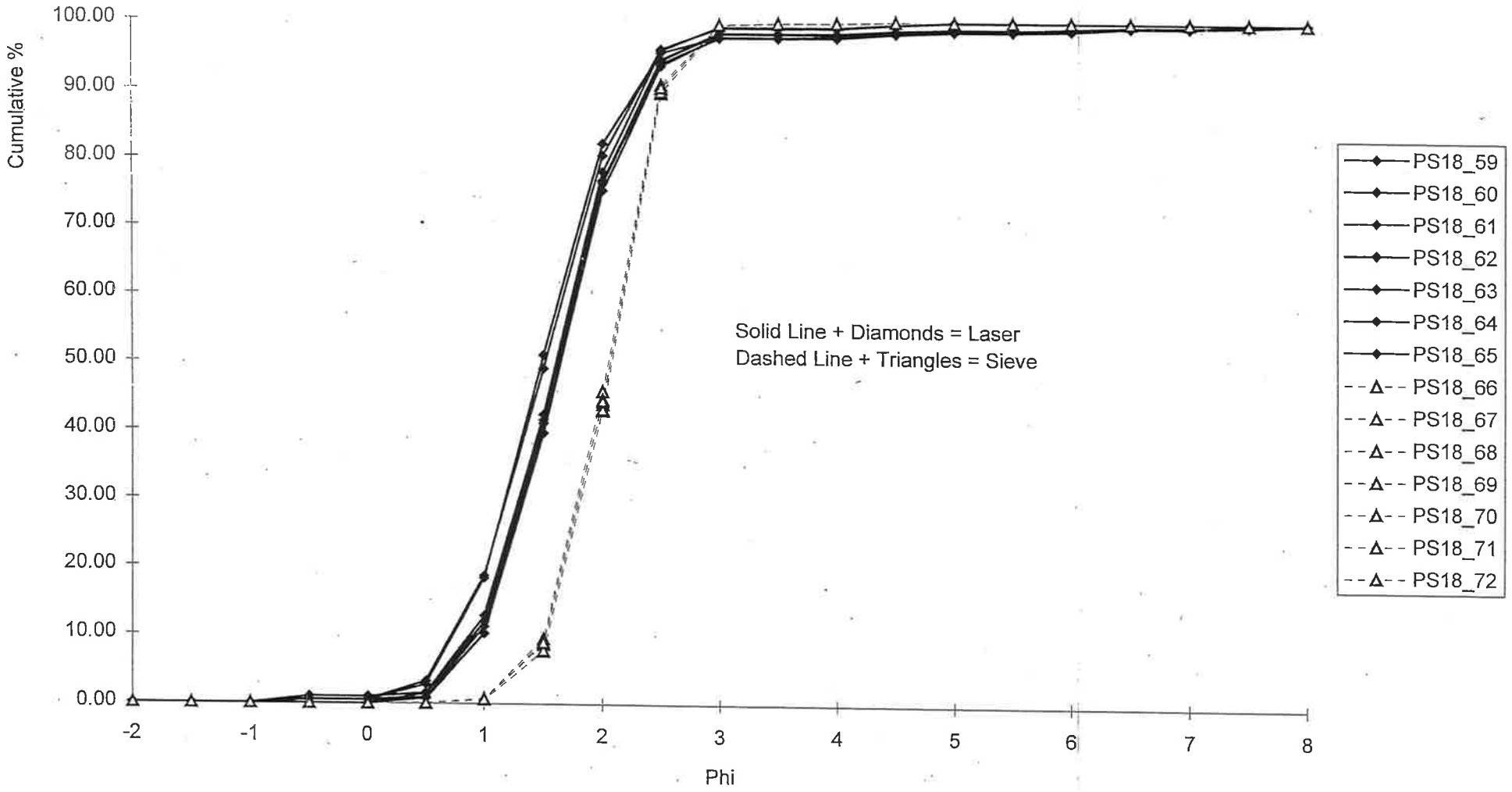


Figure 2. Particle size distribution curves resulting from analysis of fourteen replicate samples of sediment distributed as PS19. Seven samples analysed by sieve and seven samples analysed by Laser.

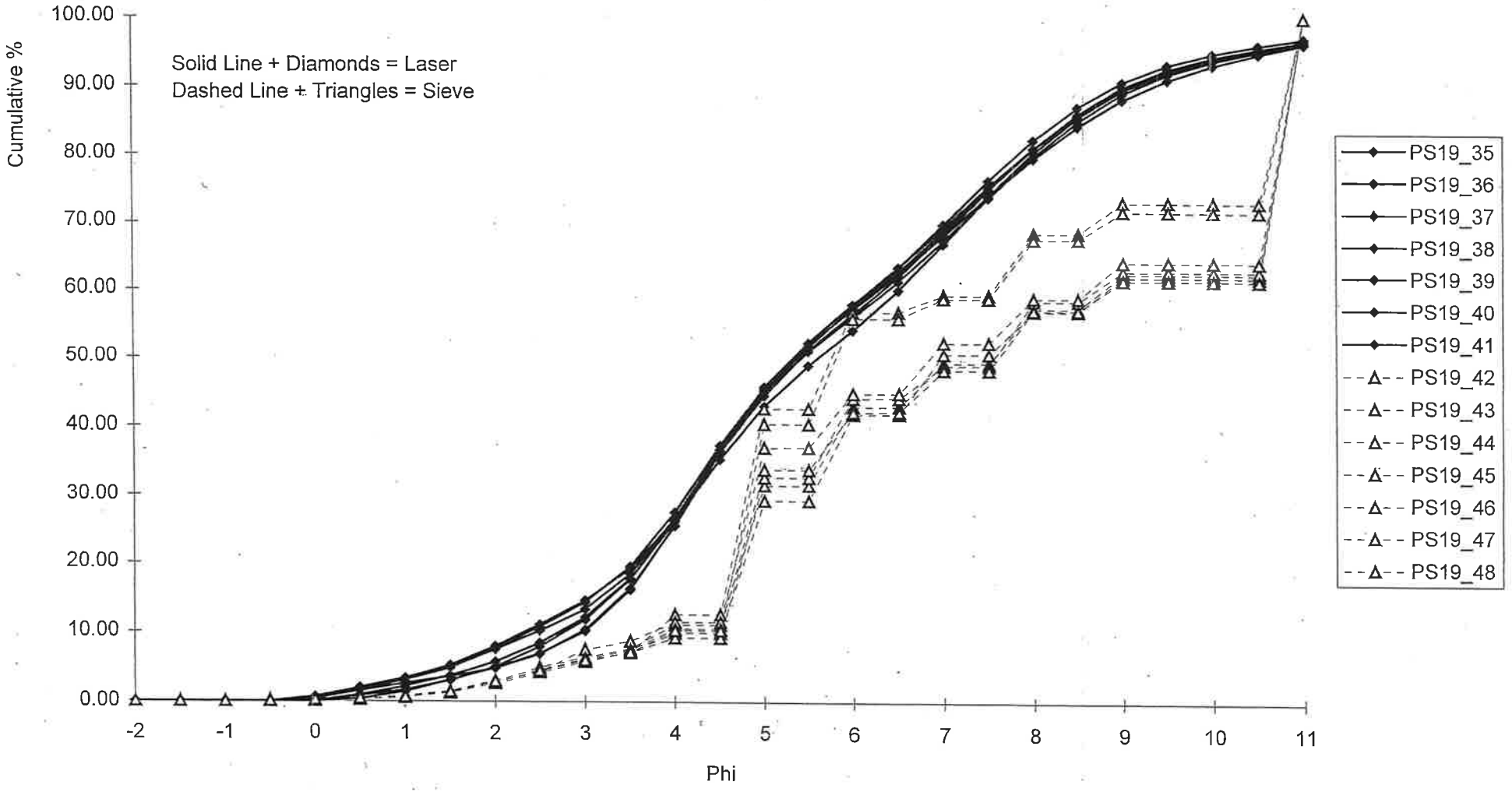


Figure 3. Particle size distribution curves from participating laboratories for sediment samples from PS18. The average values for the AQC analysis of replicates are included.

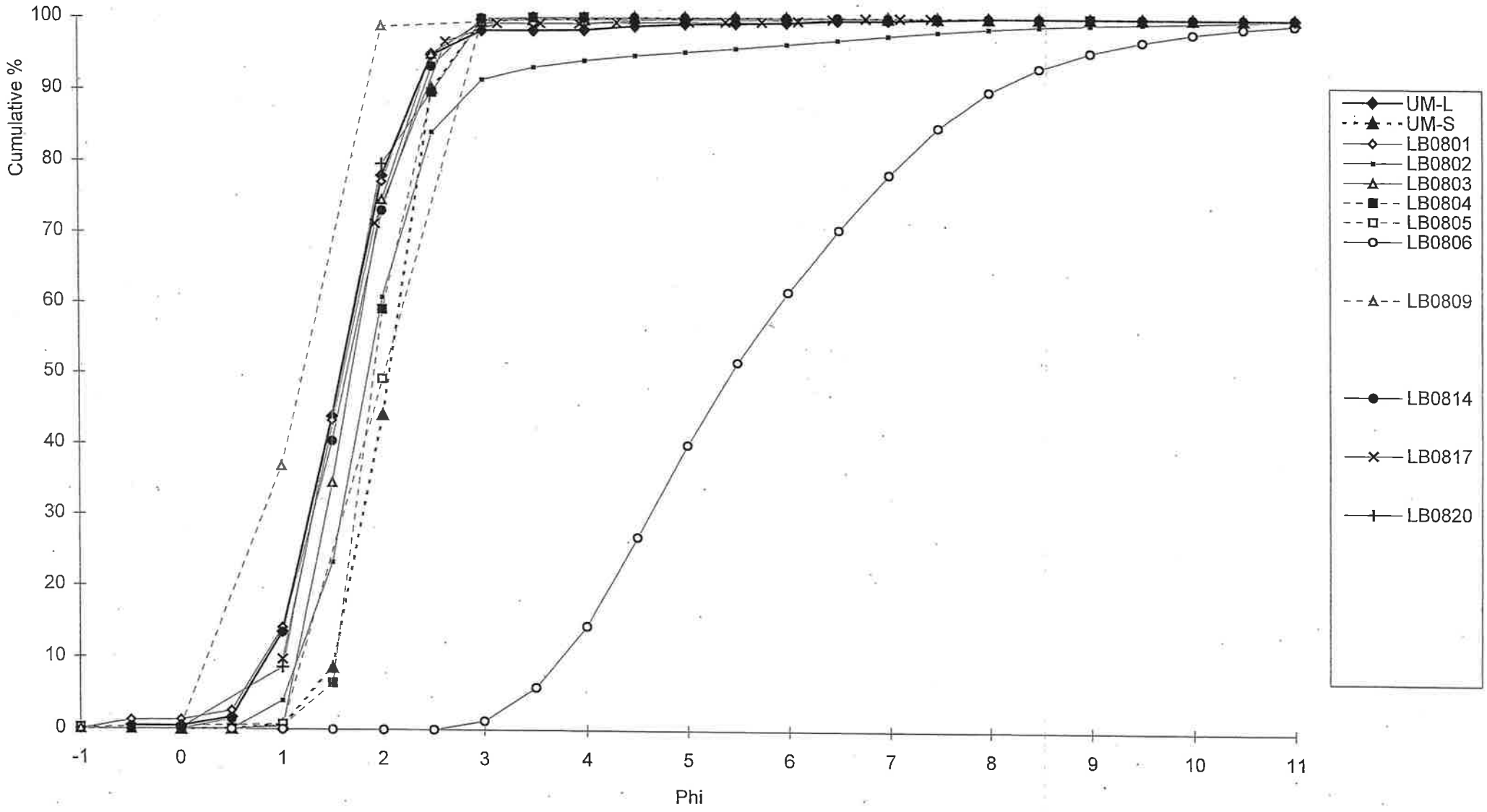


Figure 4. Particle size distribution curves from participating laboratories for sediment samples from PS19. The average values for the AQC analysis of replicates are included.

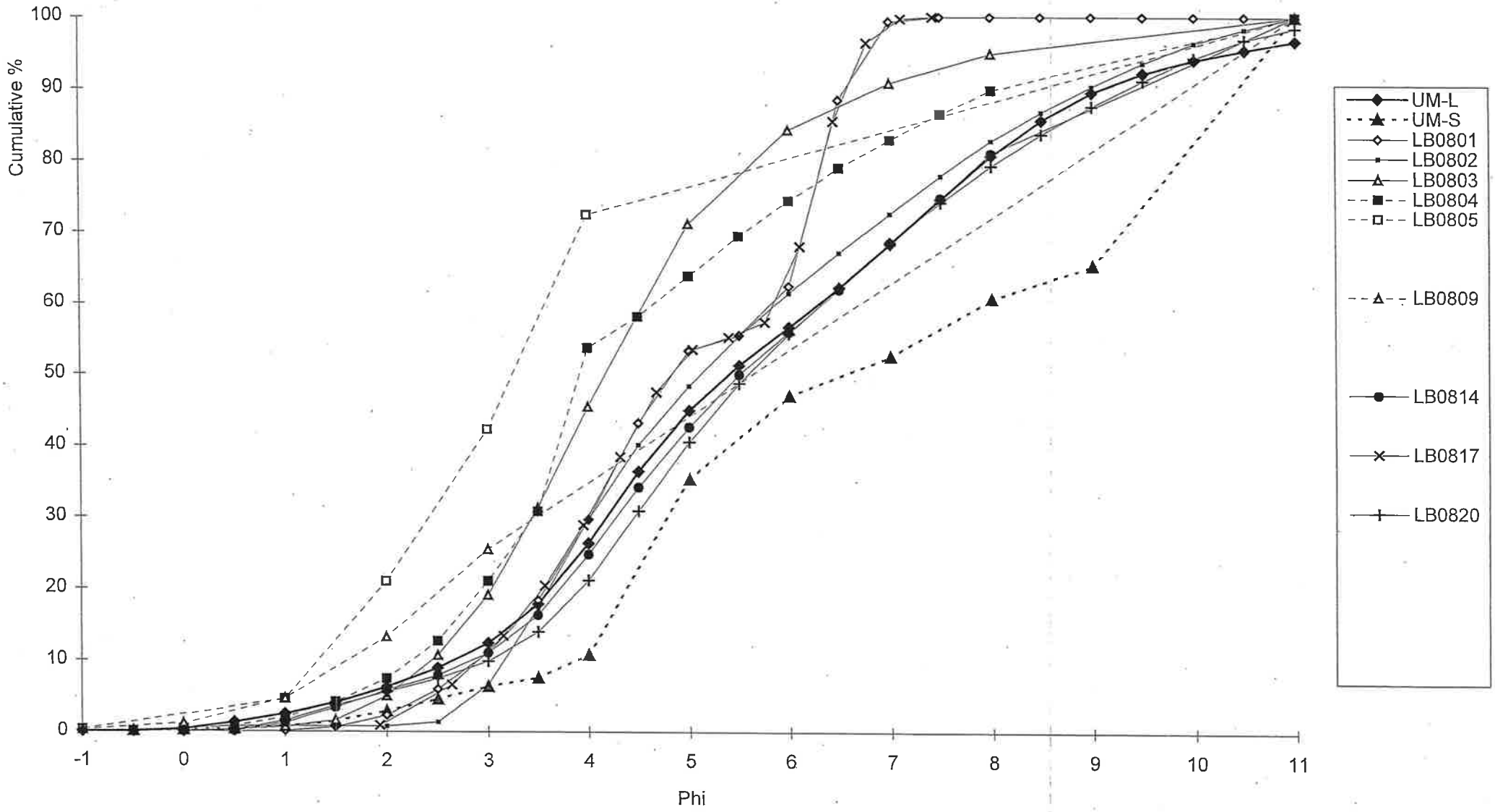


Figure 5. Z-scores for PS18 derived statistics (replicated data not displayed).

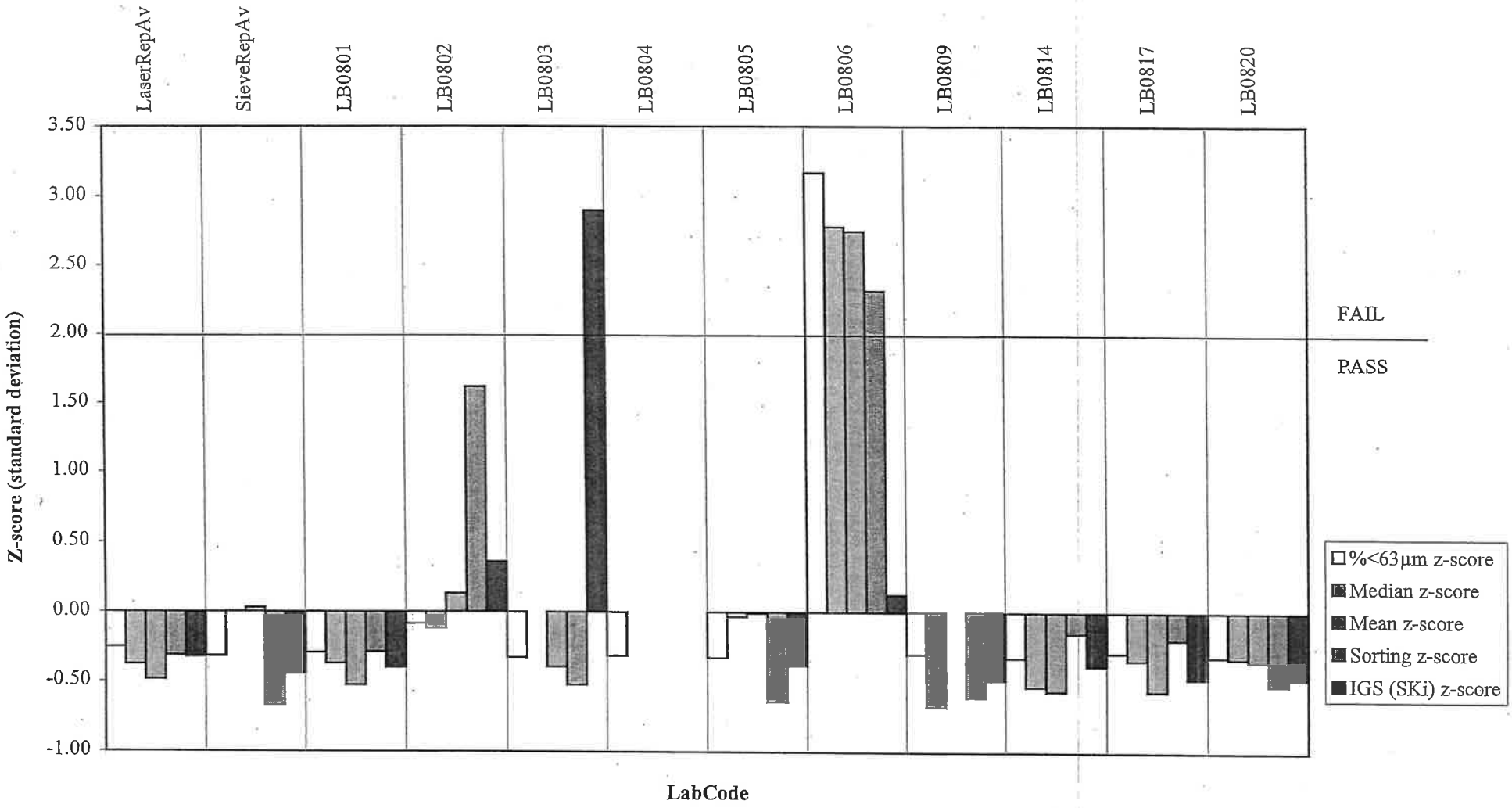


Figure 6. Z-scores for PS19 derived statistics (replicated data not displayed).

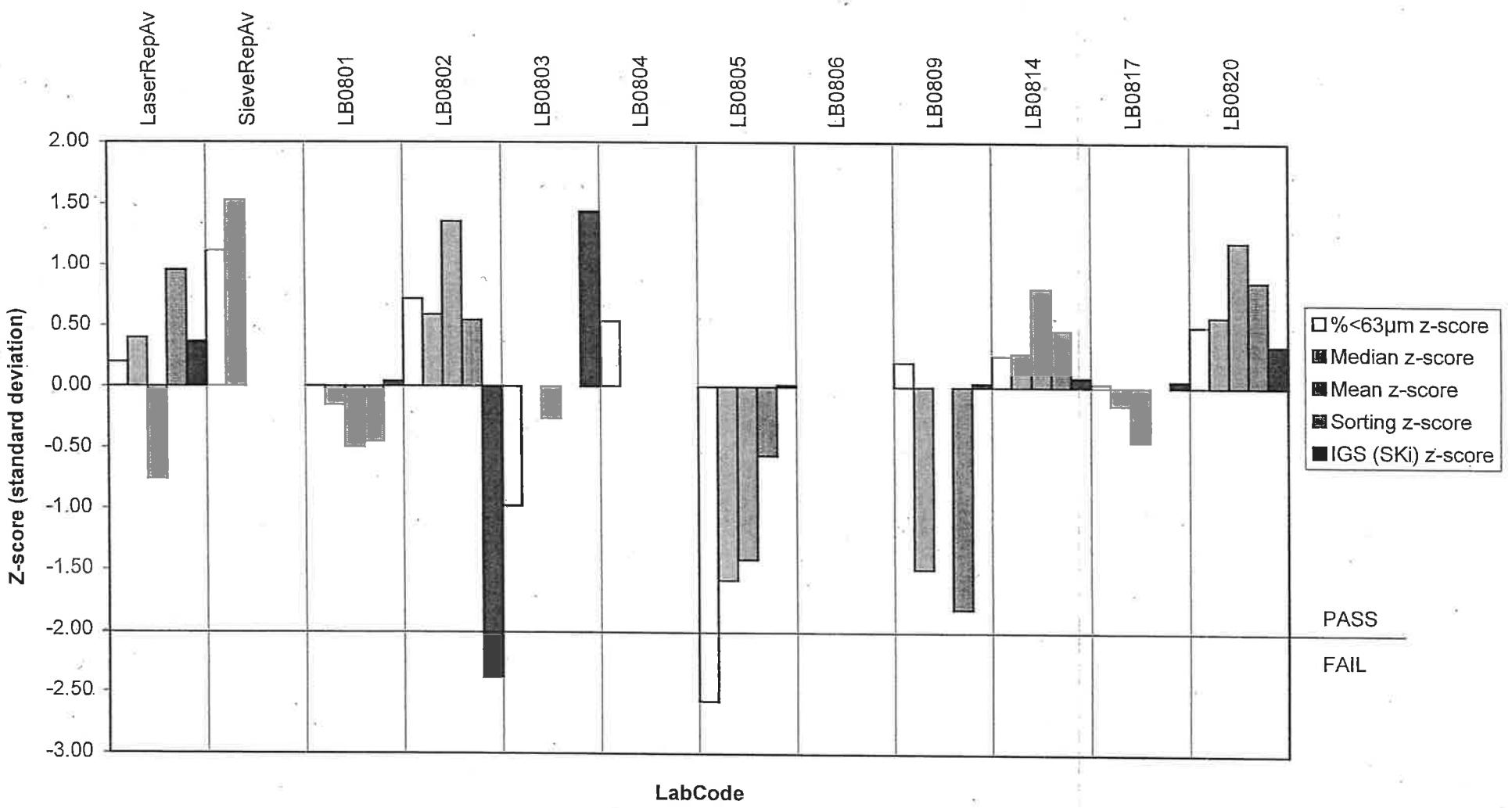


Figure 7. The number of differences from the AQC identification of specimens distributed in RT18 for each of the participating laboratories. Arranged in order of increasing number of differences.

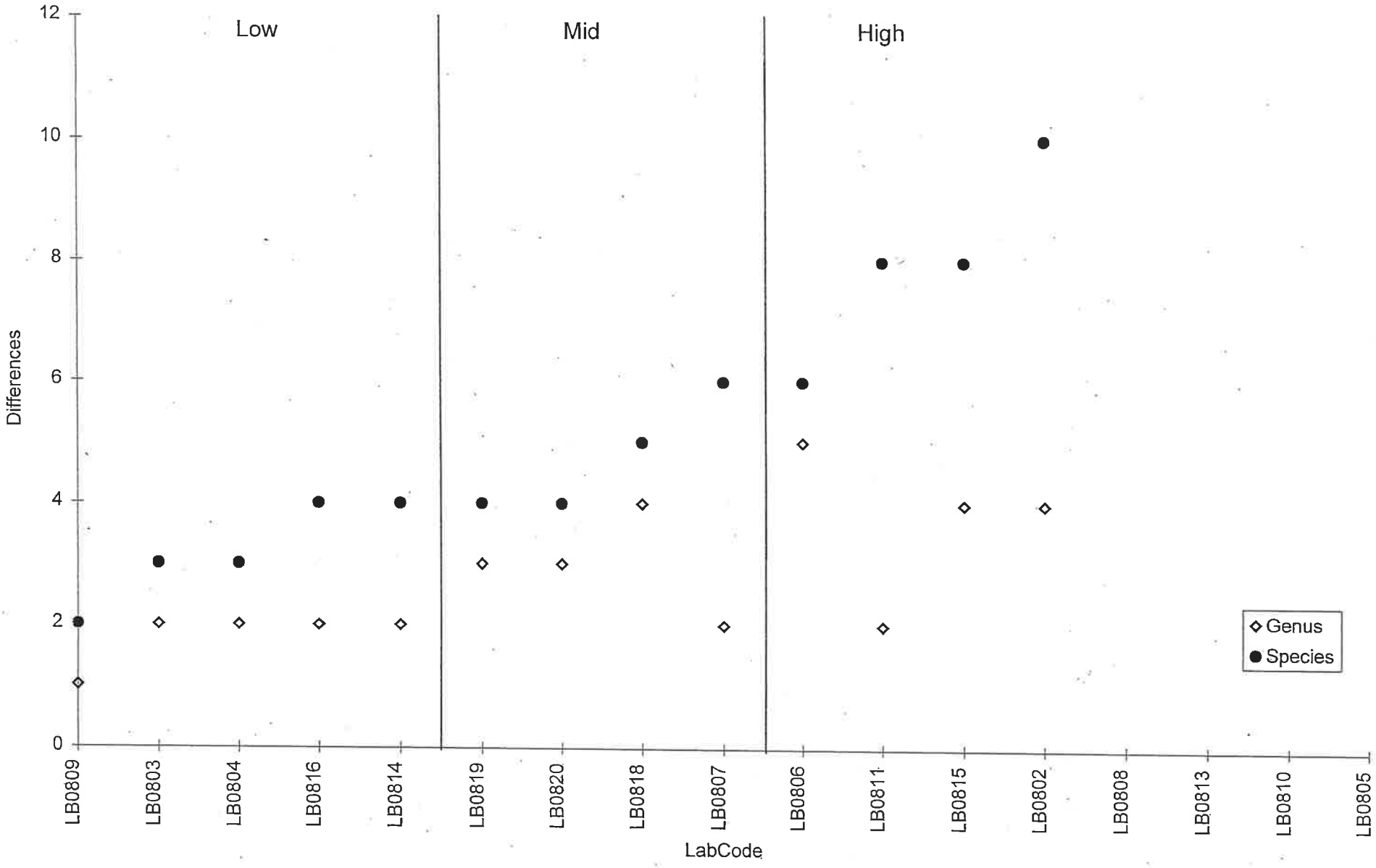
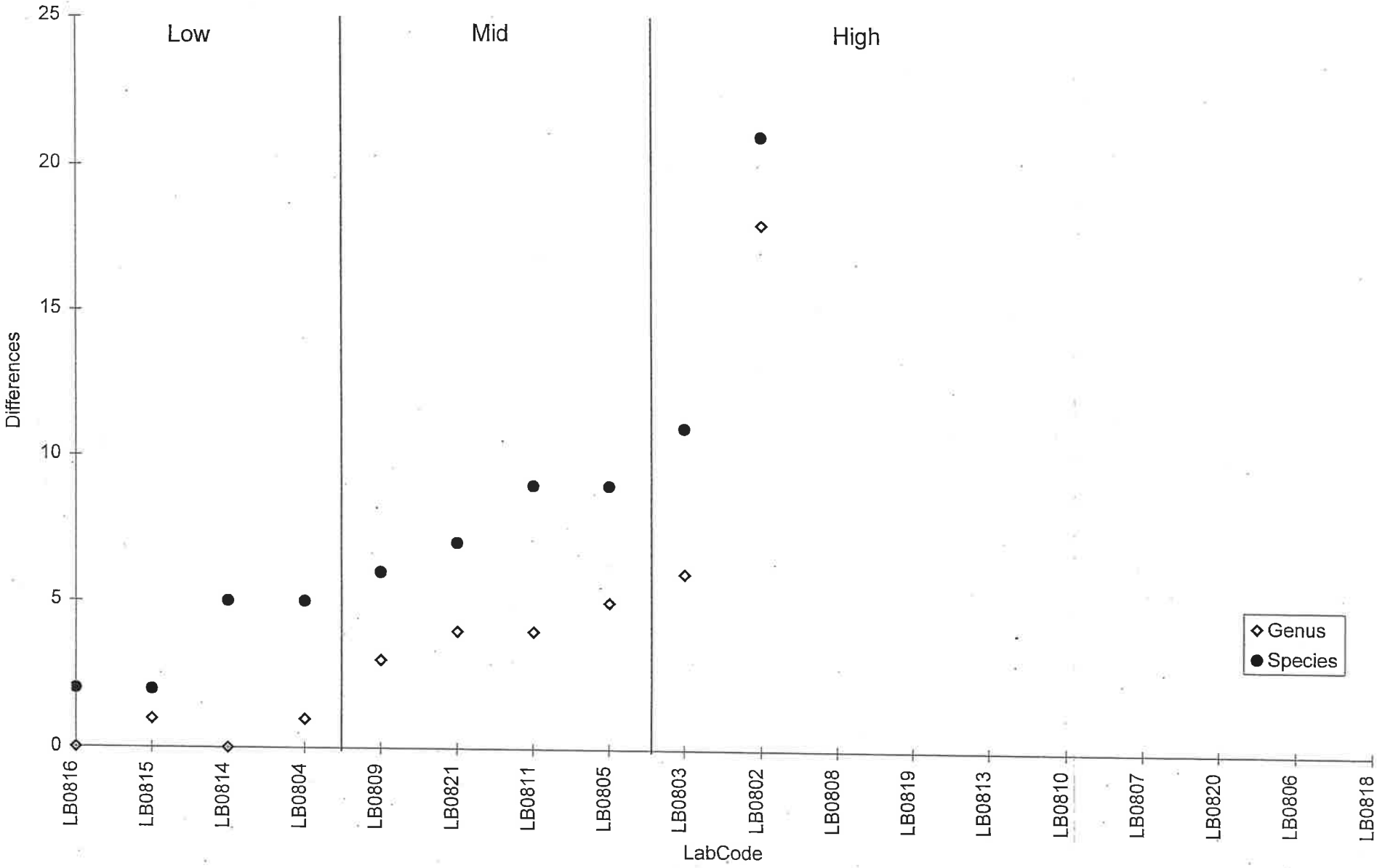


Figure 8. The number of differences from the AQC identification of specimens distributed in RT19 for each of the participating laboratories. Arranged in order of increasing number of differences.



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 should 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.

1. Description of Scheme Standards

In the third year of the NMBAQC Scheme (1996/97) required levels of performance were set by the NMBAQC steering committee for the Own Sample (OS) and Particle Size analysis (PS) exercises and flags were placed upon the results. The flags applied are based on a comparison of the results from sample analysis by Unicomarine Ltd. and those from the laboratory. The Own Sample flagging criteria were reviewed during the seventh Scheme year (2000/01) a new set of NMBAQC standards and exercise protocols were devised (Unicomarine, 2001) and introduced in Scheme year eight (2001/02).

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 was also altered in Scheme year eight and is no longer based solely upon the determination of the Silt-Clay fraction in the samples. Each particle size sample is now given z-scores for each of the major derived statistics.

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.

1.1 Own Sample Standards

Protocol changes introduced in Scheme year eight (2001/02):

- NMMP data to be audited one year in arrears.
- Own Samples to be selected from completed data matrices.
- Remedial Action to be encouraged to improve upon 'fail' flags.

1.1.1 Primary Performance Targets

These targets are stated for all Own Samples and give a clear indication of the samples performance.

1.1.1.1 Extraction/Sorting efficiency - Total taxa target

This flag relates to the performance of the laboratory with respect to the efficiency with which the animals were extracted and sorted 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 total number of taxa recorded should be within ±10% or ±2 taxa (whichever is greater) of this total.

1.1.1.2 Extraction/Sorting/Enumeration efficiency - Total individuals target

This flag reflects the efficiency with which the laboratory estimated the total 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.

1.1.1.3 Biomass estimation accuracy - Total biomass target

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

1.1.1.4 Bray-Curtis comparison target

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%.

1.1.2 Secondary Performance Targets

These targets are analysed to determine specific areas of processing for remedial action.

1.1.2.1 Extraction efficiency - Taxa in residue target

This flag relates to the performance of the laboratory with respect to the efficiency with which the animals were extracted from the sample residue. The total number of taxa is assumed to be that resulting from re-analysis of the fauna and residue by Unicomarine Ltd. To achieve a 'pass' the number of taxa not extracted should be <10% or <2 taxa (whichever is greater) of this total.

1.1.2.2 Identification accuracy – Taxonomic errors target

This flag relates to the performance of the laboratory with respect to the identification of the animals extracted from the sample residue by the participating laboratory. The 'correct' identification is assumed to be that resulting from re-analysis of the sample by Unicomarine Ltd. (following any appeals). To achieve a 'pass' the number of taxa incorrectly identified should be <10% or <2 taxa (whichever is greater) of the number of taxa extracted by the participating laboratory.

1.1.2.3 Extraction efficiency - Individuals in residue target

This flag reflects the efficiency with which the laboratory extracted the individuals from the sample residue. The number of individuals not extracted from the residue should be <10% or <2 individuals (whichever is greater) of the total resulting from re-analysis of the fauna and residue by Unicomarine Ltd.

1.1.2.4 Enumeration efficiency – Enumeration of extracted individuals target

This flag reflects the efficiency with which the laboratory has enumerated the individuals extracted by the participating laboratory. The count variance should be ±10% or 2 individuals (whichever is greater) of the total resulting from re-enumeration of the fauna by Unicomarine Ltd.

1.1.3 Overall Sample Flag

Each Own Sample is assigned an individual flag based upon their Bray-Curtis similarity indices. A five tier system of classifying individual Own Samples is used:

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

If an Own Sample achieves a BCSI of less than 90% remedial action is required. The nature of this remedial action can be ascertained by examining the secondary performance targets (See 1.1.2). A remedial action guidance table is utilised to structure any resultant action:

	<5%	5 – 10%	>10% & < or = 2 units	>10% & > 2 units
Individuals missed in residue	-	Review Extraction	Review Extraction	Reprocess – Resort Residues
Taxa missed in residue	-	Review Extraction	Review Extraction	Reprocess – Resort Residues
Taxonomic errors in extracted fauna	-	Review Identification	Review Identification	Reprocess – Reanalyse Fauna
Count variance	-	Review Enumeration	Review Enumeration	Reprocess – Recount Fauna

Version 1.1 Remedial Action Protocol August 2002

Considerable variation in the estimation of biomass (as discussed in earlier reports; (NMBAQC Scheme Annual report, 1996/97, Section 3.2.5) has led to the flag for this component being excluded from the determination of the overall sample flag for the OS exercises. Laboratories failing to supply OS data have automatically been assigned a fail flag by default.

1.2 Particle Size Standards

1.2.1 Percentage Silt-Clay Fraction target

The derived statistics of %silt-clay, mean particle size, median particle size, sorting and IGS(Ski) are expressed as z-scores based upon all data returned from participating laboratories and the average results obtained from the laser and sieve replicates (analysed by Unicomarine Ltd. to examine sample conformity). The z-scores must fall within ±2SD of the mean for each statistic to achieve a pass:

% silt-clay	**±2SD of all data**
Mean particle size	**±2SD of all data**
Median particle size	**±2SD of all data**
Sorting	**±2SD of all data**
IGS(Ski)	**±2SD of all data**

A "Deemed fail" flag is to be assigned when the required summary statistics are not 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 (Contract Manager)*	SEPA South East
Mr. T. Mackie (Secretary)[$]	Environment & Heritage Service, Northern Ireland
Dr. M. Elliott**	University of Hull
Mr. M. Robertson	FRS
Dr. H. Rees	CEFAS
Mr. R. Proudfoot	Environment Agency
Mr. A. Robinson	Environment Agency , Wales
Dr. J. Davies[#]	JNCC
Mr. M. O'Reilly*	SEPA South West

([$] as of January 2001)

(* as of September 2001)

(** resigned from the Committee – February 2002)
(Replaced by Mr. N. Proctor - February 2002)

([#] as of 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

AstraZeneca Ltd: Centre for Environment, Fisheries and Aquaculture Science (CEFAS): Department of Agriculture and Rural Development for Northern Ireland (DARDNI): Environment Agency: Environment & Heritage Service , Water Management Unit (Northern Ireland): EMU Environmental Ltd: ERT (Scotland) Ltd: Hebog Environmental: Institute of Estuarine and Coastal Sciences (IECS): Institute of Aquaculture, University of Stirling: SEAS Ltd: Scottish Environment Protection Agency (SEPA): Svitzer Ltd.

APPENDIX 5

Extract from the Oligochaeta Questionnaire Report: Including Provisional NMMP Standard Policy for Oligochaete Identification.

Introduction

The exercises of the National Marine Biological Analytical Quality Control (NMBAQC) Scheme conducted over the past eight years have shown that there is little or no consistency in recording between laboratories (Worsfold & Hall, 2001). Oligochaetes are identified to a variety of taxonomic levels by the participants and standardisation is required. Ring test nineteen (RT19) was selected to target 'oligochaetes and similar fauna' and assess comparative levels of identification. In addition to the ring test, all participating laboratories were sent a questionnaire to enable the ring test results to be qualified and to gather general information on levels of oligochaete identification.

RT19 comprised twenty-five single specimens and was distributed to eighteen ring test participant laboratories on 17th January 2002. One cirratulid and two capitellid species were included in the ring test due to their oligochaete-like features. Nine Tubificidae species were distributed, including repeated taxa. They accounted for seventeen of the twenty-two oligochaetes. The remaining five oligochaete specimens were repetitions of two Naididae species. All oligochaetes distributed within RT19 were readily identifiable on gross morphological features. Unfortunately the original intention to send oligochaetes from a variety of habitats was hindered as no external expert could be appointed within the timescale required. This meant that the expert help required to assist in the compilation of enchytraeids and *Tubificoides pseudogaster* aggregate species was lacking. The three non-oligochaete ring test specimens were included to highlight the problems associated with laboratories that do not routinely identify oligochaetes beyond class and the potential problems of these laboratories not being able to distinguish between oligochaetes and some polychaetes. Habitat notes were provided for each specimen (sediment, salinity, depth and geographical location). The participating laboratories were given ten weeks to complete RT19. Results were received from ten of the eighteen participants.

This report reviews the questionnaire returns to give an overview of current approaches to oligochaete identification amongst the NMBAQC Scheme participants. Reference is made, where relevant, to the RT19 results. Recommendations for National Marine Monitoring Plan (NMMP) standardisation are given, where appropriate, as a precursor to standard operating procedures (SOPs). SOPs in marine biological sample collection and analysis were reviewed for the NMBAQC Scheme by Cooper & Rees (2000). However, that report focussed primarily on sampling methods and safety and did not deal with all issues concerning the fundamental requirements of processing of macrobenthos samples (Worsfold & Hall, 2001).

Few agencies or other organisations that commission samples for analysis of macrobenthos give clear guidelines as to the required treatment of samples. Laboratories that carry out sample analysis generally develop their own in-house practices. The practices are often not explicitly written down but become established through tradition. As the agencies requiring data do not give clear guidelines and as they often subcontract their sample analysis to more than one laboratory, it is important to evolve and maintain consistency of practice between laboratories.

Consistency is particularly important where data collected by different organisations are to be used for comparative purposes, as with the NMMP (Worsfold & Hall, 2001).

Discussion

The questionnaire data shows that all NMBAQC Scheme ring test subscribing laboratories encounter oliochaetes in their macrobenthic samples and that the majority of these laboratories attempt to identify most oliochaetes to species. However, a number of laboratories showed variations in their identification policies towards tubificids, naids and enchytraeids. These variations, although minor in many cases, when examined as combined data from all laboratories would result in a significant loss of specific detail. Two laboratories that normally would not identify their oligochaetes beyond class, achieved the lowest number of correct identifications for RT19. One such laboratory identified the *Capitella capitata* specimen as *Tubificoides amplivasatus*. Under normal macrobenthic processing conditions how many specimens could potentially be assigned to the wrong class? Such problems can arise when entire faunal groups are not examined or understood in sufficient detail. Gaps in faunal knowledge must be bridged to achieve data comparability. A major problem confronting analysts of combined data from several laboratory sources is that of having to reduce each taxon to the lowest common denominator (i.e. highest taxonomic level). For example, an entry of 'Tubificidae' could result in all tubificids being lumped to family. However the Tubificidae specimen could have simply been in poor condition with no discernible features beyond the family level. A recording system should be agreed to counter the discrepancy. Identification consistency is important if data from different laboratories is to be compared, as is the case with NMMP data. There is a need for a standard policy for NMMP oligochaete identification.

There was an overwhelming indication that RT19 was found by participants to be very challenging although most achieved better results than they expected. Single oligochaete specimens are rarely easy to identify. This, coupled with many laboratories' discomfort with oligochaete identification, was reflected in their difficulty ranking for this exercise. This lack of confidence with oligochaete identification was reiterated by the participants' low predictions of their RT19 scores. Those laboratories that do not routinely encounter or identify oligochaetes must be commended for their participation in RT19. Several supposedly more experienced laboratories decided not to participate. The inexperienced laboratories invariably achieved the lowest RT19 scores. They are, however, very likely to have achieved disproportionate gains in knowledge, as compared with more experienced laboratories, particularly those that did not participate. The majority (six out of ten) of laboratories provided RT19 data produced by solitary workers. The practice of solitary identifiers is not recommended. Even experienced staff function much better with an additional staff member with which to discuss their identifications. An element of quality control / assurance can be achieved by such practice.

The habitat notes appear to have been of limited use, primarily due to a lack of available ecological information. Records of habitats need to be kept for verified oligochaete taxa in order to build a better understanding of specific requirements and distributions.

The results sheet for RT19 required laboratories to list any items of literature that were consulted for identification of each specimen. Several sources of oligochaete literature were noted in the data received. These were Brinkhurst (1971, 1982 &

1985), Brinkhurst and Jamieson (1971), Erséus (1975) and the 1994 Oligochaete workshop notes (which contained several Tubificidae papers and a Tubificidae features table). Some laboratories utilised just a single text which, in most instances, greatly reduced their capability to identify specimens correctly. The majority of questionnaire respondents commented upon the inadequacy of oligochaete literature. Several laboratories stated that the literature was too subjective. The comments can be summarised as a majority desire for a single Oligochaeta text containing marine, estuarine and freshwater taxa, which includes whole animal diagrams and / or images, comparative diagrams of chaetae, detailed descriptions, ecological notes and less reliance upon internal anatomy for identification.

The use of reference material to aid identification is universally understood by participants of the NMBAQC Scheme to be best practice. However, many laboratories have either no or very limited reference collections of oligochaete taxa. A positive correlation between the amount of reference material available and each laboratory's performance was evident in RT19. Those laboratories with little or no reference specimens invariably achieved the lowest number of correct identifications. It must also be noted that laboratories with larger oligochaete reference specimens are likely to be more familiar with identifying oligochaetes and are consequently capable of relatively high ring test scores.

The majority of laboratories identify their oligochaetes using gross morphological features and temporary slide preparations for chaetal examination. Several laboratories stated that they do not find the clearing of oligochaetes to be an efficient use of time and the use of Ammans Lactophenol also raises health and safety (COSHH) issues. Four laboratories use permanent cleared mounts for the examination of internal oligochaete anatomy. The method is rarely performed upon all specimens encountered and usually a 10% subsample is selected for identification to species by this method. One laboratory stated that the expert opinion was that oligochaetes could not be identified reliably to species without the internal anatomical examination of adult specimens, which influenced oligochaete identification policy significantly. Laboratories may identify their oligochaetes to higher taxonomic levels because they believe that without clearing oligochaetes species identification is unachievable and / or the process of clearing all oligochaetes is not economically viable. The net result is reduction in oligochaete data and a dismissive attitude towards uncleared oligochaetes identified to species.

The ring test has proven that, with experience, several common species, including most sexually immature specimens, can be identified consistently without resorting to internal examination. The clearing of oligochaetes, aside from COSHH concerns, is not conducive to full sample audits. Secondary biomass calculations cannot be conducted and initial biomass records, as well as abundance records, are commonly estimated from proportions attained from an examined subsample. Random subsampling of oligochaetes prior to detailed examination is not recommended, as less abundant taxa are often overlooked and bias towards larger specimens and hence species often occurs. All RT19 oligochaete specimens were identifiable without examination of internal anatomy. Hence, only 1% of the RT19 specimens were cleared for identification by the participating laboratories. Clearing is often used as a final identification tool in instances where other external features are inconclusive. Intertidal estuarine macrobenthic samples often contain a large proportion of juvenile (sexually immature) oligochaete individuals. Clearing techniques would not classify such specimens to species. However, with experience and an understanding of growth series and gross morphological features, many such individuals can be identified to species and a far greater quality of ecological data acquired.

When asked to give their opinions of the importance of oligochaete identification, several laboratories gave surprising questionnaire responses. Many laboratories directly related oligochaete identification importance to relative oligochaete abundance. One laboratory rated oligochaete species identification of little importance because of its limited interpretative use. The interpretative use of oligochaetes would undoubtedly improve if more comprehensive literature and records were available. Greater levels of identification expertise would, in turn, lead to better ecological knowledge. One laboratory, with a relatively high degree of oligochaete identification experience in comparison with most laboratories, described oligochaete identification as extremely important. They added that Oligochaeta are dominant fauna at several of their stations and estimates of species diversity can be seriously skewed by failure to include diversity within the Oligochaeta. Oligochaeta show species partitioning on salinity, sediment, habitat, depth and organic enrichment (pollution) characteristics. Some laboratories persist in suggesting the short-sighted 'horses for courses' approach of only processing according to perceived immediate objectives. Such an approach has been dismissed for NMMP data (Worsfold & Hall, 2001). The knowledge and understanding of oligochaetes will improve with time unless ill-conceived 'horses for courses' policies are allowed to prevail. The cost and damage caused by environmental surveys necessitates that the resultant data be transferable, used to their full potential, and not processed according to imagined short-term objectives.

The RT19 scores achieved by participating laboratories were very good considering that only single specimens were available for examination and many laboratories had limited experience. Two laboratories achieved very high scores with only two taxonomic differences recorded. The poorest results were achieved by laboratories that encounter few oligochaetes of limited diversity, which they do not routinely identify beyond class or family. Hopefully, such laboratories, given training and better literature, will be capable of raising the standard of their oligochaete knowledge to meet the proposed NMMP oligochaete identification requirements, discussed later.

Differences in the taxonomic levels to which animals are identified reduce the comparability of data. Current quality control procedures (NMBAQC Scheme Own Sample audits) do not highlight the problems as identifications to higher taxonomic levels are taken to be correct. Reduction of data to the lowest common denominator (i.e. highest taxonomic level) is a poor short-term solution to the use of the data that will not ensure maximum benefit (Worsfold & Hall, 2001). Therefore a SOP for NMMP oligochaetes is proposed (Appendix III), to be posted on the Scheme web site (www.nmbaqcs.org). Comments are invited. The SOP has been devised using ring test and macrobenthic data studied over the duration of the NMBAQC Scheme coupled with the questionnaire data. Essentially, the SOP advocates the best identification possible for oligochaete taxa without resorting to clearing and internal examination. It is the first version and is subject to change should subsequent studies enable greater taxonomic detail using gross morphological features. A laboratory adopting the NMMP oligochaete SOP (Ver.1.1) can qualify their data as such and greatly improve the comparative value of their data. For example, 'Tubificidae' recorded by such a laboratory (due to poor condition or recognition of an unfamiliar taxon) should not cause all tubificid species to be combined to family.

Implementation of the oligochaete SOP must be accompanied by sufficient training opportunities to enable all NMMP laboratories to achieve the required standard of expertise. Scheme participants may use the Laboratory Reference (LR) exercise to verify their NMMP oligochaetes, if necessary.

Conclusion

Three proposals are given for the improvement of Oligochaeta records for the NMMP. These are the development of an Oligochaeta SOP, additional training and improved literature. Initiatives for these proposals are detailed.

1. Development of an Oligochaeta SOP.

- Adoption of an NMMP standard policy for oligochaete identification.

  - **NMMP Oligochaeta SOP Version 1.1 (provisional) – Appendix III.**

2. Additional Training.

- Use of NMBAQC Scheme taxonomic workshop and Laboratory Reference (LR) exercise to improve and disseminate knowledge of oligochaetes.

  - **NMBAQC Scheme workshop (provisionally March 2003, MBA Plymouth) to include Oligochaeta. NMBAQC Scheme LR exercise is now free form to allow submission of any UK taxa.**

3. Improved Literature.

- Improved oligochaete literature covering marine, estuarine and freshwater taxa, including diagrams / images of whole specimens and details of ecological preferences. Ongoing literature search on taxonomy regularly submitted to NMBAQC (required for all taxonomic groups – NMBAQC funding required).

  - **Literature updates and ecological notes to be distributed at NMBAQC Scheme workshop (provisionally March 2003, MBA Plymouth).**

Oligochaetes, like many faunal groups, first all appear alike (probably none more so than oligochaetes). However, with experience and training, differences in gross morphological features can be observed and habitat details recorded to improve our understanding. In truth, the economics of clearing has long been a convenient excuse for many laboratories not attempting to identify the oligochaetes encountered. Methods in pure taxonomy require great attention to detail but it is essential that practical (e.g. ecological) outlets for taxonomic research be considered. The logical progression from the anatomically verifiable definition of a species is to find pragmatic means of quickly recognising it to provide ecological information. The present report and provisional SOP represent progress to that end.

APPENDIX 6

Guidance for NMMP Remedial Action

If an Own Sample achieves either a 'Poor' or a 'Fail' NMBAQCS flag (i.e. <90% BCSI) then the sample is reviewed by the NMBAQC Committee to ascertain whether any remedial action needs to be applied to the remaining NMMP replicates.

The remedial action required is then based upon the samples performance in the following criteria:

	<5%	5 - 10%	>10% & < or = 2 units*	>10% & >2 units*
Individuals missed in residue	-	Review Extraction	Review Extraction	Reprocess - Resort Residues
Taxa missed in residue	-	Review Extraction	Review Extraction	Reprocess - Resort Residues
xonomic errors in extracted fauna	-	Review Identification	Review Identification	Reprocess - Reanalyse Fauna
Count variance	-	Review Enumeration	Review Enumeration	Reprocess - Recount Fauna

*Note that allowances are made for small samples in which single errors can represent significant percentage errors. If the % error is greater than 10% but the number of error units (i.e. missed individuals, missed taxa or taxonomic errors) is less than or equal to 2, a review of the failing category is suggested rather than reprocessing.

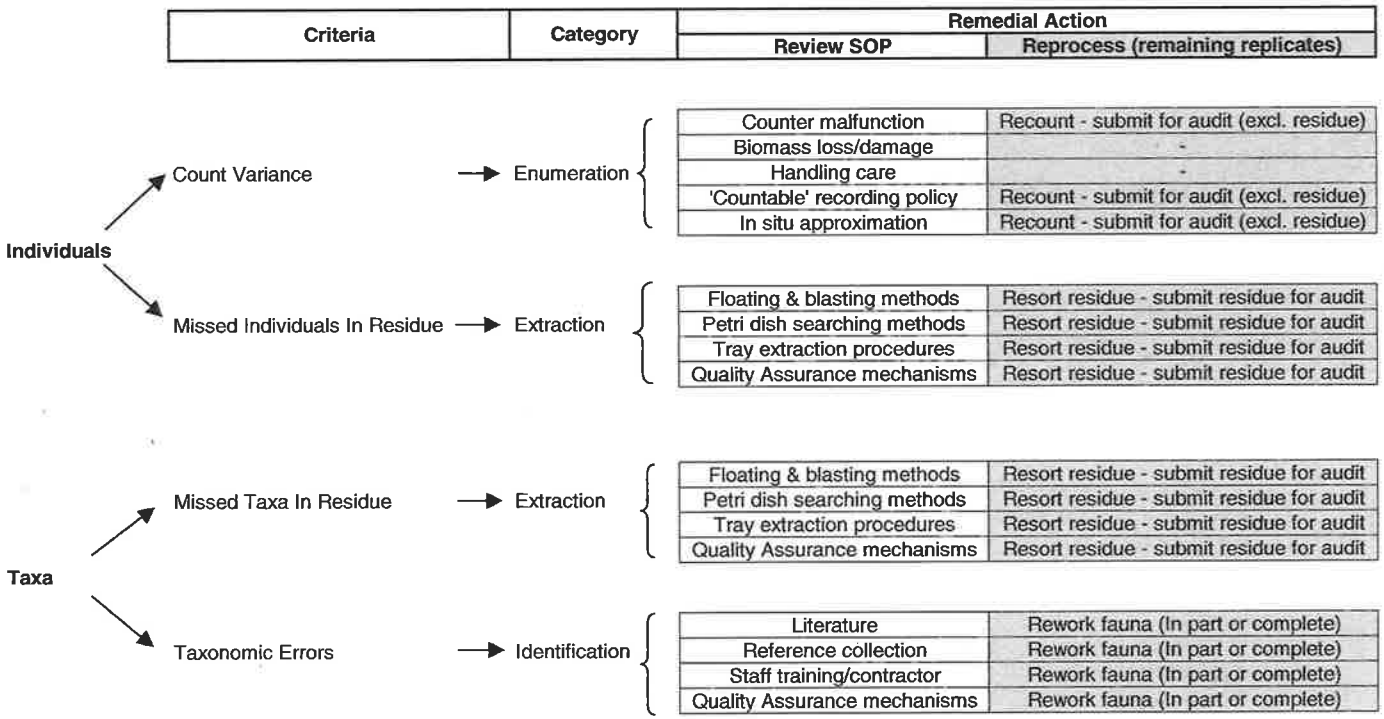
NMBAQC Scheme year 8 examples:

Shaded cells with bold type represent a failing category in need of reprocessing (i.e. data and/or residue to be reaudited following remedial action).
Bold type represent a category in need of review by participant (i.e data to be altered in-house prior to submission to the client).

	% - Units shown in brackets				
LabCode; OS Code (%BCSI)	ndividuals missed in residu	Taxa missed in residue	axonomic errors in extracted faun	Count Variance	Remedial Action
LB08XX; OSXX (55.86%)	32.3% (21)	23.1% (6)	30% (6)	3.1% (2)	Reanalyse remaining replicates
LB08XX; OSXX (89.86%)	0% (0)	0% (0)	8.1% (3)	0.6% (1)	Review identification
LB08XX; OSXX (57.98%)	58.7% (342)	58.3% (21)	6.7% (1)	0.5% (3)	Resort remaining residues; Review identification
LB08XX; OSXX (72.07%)	44.4% (157)	25% (1)	0% (0)	0.8% (3)	Resort remaining residues
LB08XX; OSXX (84.62%)	14.3% (2)	0% (0)	16.7% (1)	0% (0)	Review extraction; Review identification
LB08XX; OSXX (84.32%)	0% (0)	0% (0)	19.4% (6)	1.1% (1)	Reanalyse remaining fauna
LB08XX; OSXX (80.31%)	9.9% (20)	23.4% (11)	19.4% (7)	0.5% (1)	Reanalyse remaining replicates
LB08XX; OSXX (78.95%)	27.3% (6)	15.4% (2)	9.1% (1)	0% (0)	Resort remaining residues; Review identification

APPENDIX 6 (Cont.)

NMBAQC Scheme Action Protocol for NMMP Own Samples



Criteria	Category	Remedial Action	
		Review SOP	Reprocess (remaining replicates)
Individuals → Count Variance	→ Enumeration	Counter malfunction	Recount - submit for audit (excl. residue)
		Biomass loss/damage	-
		Handling care	-
		'Countable' recording policy	Recount - submit for audit (excl. residue)
		In situ approximation	Recount - submit for audit (excl. residue)
Individuals → Missed Individuals In Residue	→ Extraction	Floating & blasting methods	Resort residue - submit residue for audit
		Petri dish searching methods	Resort residue - submit residue for audit
		Tray extraction procedures	Resort residue - submit residue for audit
		Quality Assurance mechanisms	Resort residue - submit residue for audit
Taxa → Missed Taxa In Residue	→ Extraction	Floating & blasting methods	Resort residue - submit residue for audit
		Petri dish searching methods	Resort residue - submit residue for audit
		Tray extraction procedures	Resort residue - submit residue for audit
		Quality Assurance mechanisms	Resort residue - submit residue for audit
Taxa → Taxonomic Errors	→ Identification	Literature	Rework fauna (In part or complete)
		Reference collection	Rework fauna (In part or complete)
		Staff training/contractor	Rework fauna (In part or complete)
		Quality Assurance mechanisms	Rework fauna (In part or complete)

APPENDIX 7

Extract from the Sorting Methods Questionnaire (August 2001)

INTRODUCTION

Standard operating procedures (SOPs) in marine biological sample collection and analysis were reviewed for the National Marine Biological Analytical Quality Control Scheme (NMBAQCS) by Cooper & Rees (2000). However, that report focussed primarily on sampling methods and safety and did not deal with all issues concerning the fundamental requirements of processing of macrobenthos samples.

Few agencies or other organisations that commission samples for analysis of macrobenthos give clear guidelines as to the required treatment of samples. Laboratories that carry out sample analysis generally develop their own in-house practices. The practices are often not explicitly written down but become established through tradition. As the agencies requiring data do not give clear guidelines and as they often subcontract their sample analysis to more than one laboratory, it is important to ascertain the consistency of practice between laboratories. Consistency is particularly important where data collected by different organisations are to be used for comparative purposes, as with the National Marine Monitoring Plan (NMMP).

METHODS

On 20th October 2000, a questionnaire (Appendix 1) was sent to twenty participants of the NMBAQC Scheme. Reminders for outstanding questionnaires were circulated on 26th January 2001. The purpose was to evaluate the consistency of sample processing and, consequently, of data quality between different laboratories that carry out NMMP macrobenthos sample analysis. The questions were designed to highlight areas of likely discrepancy between different laboratory practices that had been noticed during examination of data sets submitted through the NMBAQC Scheme. The ordering of the questions on the questionnaire was random but here the most basic sample handling issues are dealt with first, followed by more detailed issues of specimen identification and enumeration. The questions from the questionnaire (Appendix 1) are quoted in the text below with question numbers in brackets.

Sample collection

There are many issues relating to the sampling process itself that are beyond the scope of this report. The design of the sampling grid, numbers of replicate samples, sampling type and methodology all have a great impact on the value of the final data set. They must be considered elsewhere. Some aspects of sampling, however, have a more direct impact on the nature of the samples themselves, as received for further analysis. The type and nature of the preservative have a great affect upon the quality of the samples and specimens contained within them. Factors include formaldehyde concentration and the addition of buffers such as borax. The nature of the sediment affects the effectiveness of preservation. The amount of water contained within sediment changes the concentration of added preservative. Coarse sediments with many empty shells need less buffer (for preventing the decomposition of mollusc shells) than soft muds. The degree and style of any processing (e.g. sieving) before

preservation affects the condition of preserved biota. There is also a need for clear labelling of samples. These issues were considered by Cooper & Rees (2000).

One of the questions on the form (stated below) was concerned with the addition of stain to the samples. Stains are generally added at the same time as the preservative as part of the sample collection process.

> "Do you routinely use any form of staining in your sample processing? If so give details and reasons for use" (Q.7)

Initial sample processing

Most of this report is concerned with laboratory processing. Generally, samples for macrofaunal analyses arrive at the laboratory (which may or may not be directly connected to the organisation that originally collected the samples) contained in watertight containers with a volume of sediment and associated biota preserved in formaldehyde. The required remit is generally no more precise than e.g. extraction, identification and enumeration of macrofauna to the lowest taxonomic level possible. Instructions for biomass, reference collections and return of specimens and residues are often provided but there is much room for different interpretations with most of the other requirements. We asked laboratories to describe their methods for a hypothetical complex sample:

> "If your samples contained stones with *Pomatoceros* tubes, *Sabellaria* reefs, barnacles, hydroids and encrusting bryozoans attached, how would you proceed with the sorting?" (Q.5)

Samples with very large volumes of sediment are not generally searched in their entirety due to time (cost) restraints. It is therefore necessary to ask how different laboratories subsample such sediments:

> "If your samples contained several litres of 0.5-1mm and 1-4mm sediment fractions, how would you process these fractions?" (Q.6)

Extraction of fauna

Extraction of fauna may seem to be a simple requirement. However, the title has already assumed that plant material need not be extracted or recorded. Plants may be an important aspect of the biology within certain samples. Many laboratories also assume that only benthic animals need be extracted, some assume only macrofauna should be recorded and some assume that only infauna are required. The assumptions are not consistent and are rarely defined in protocols. In addition, the terms benthic, macrofauna and infauna are not clearly defined and interpretations have been known to vary between laboratories. The following questions were asked of participating laboratories. Some examples of problem taxa were provided (see Appendix 1).

> "Which of the following do you routinely extract and record:"
> "List any additional taxa that you would not record:" (Q. 4A & 4B)

In addition to macrofauna, some laboratories extract, or require extraction of, anthropogenic items or seeds. Protocols are usually more clear with such requirements but routines were investigated with the following question:

"List any additional materials (non-faunal) that you record" (Q.4C)

Recording of fauna

The issues considered so far concern only the basic processes of extracting animals from a sample. Greater discrepancies might be expected with the actual recording and identification. One of the simplest issues is how to record fragmented animals.

"What constitutes a countable individual for the following taxa:" (Q.2)

Identification involves many more sources of inconsistency and error than those connected with whether or not a particular identification is "correct". The usual requirement of "lowest taxonomic level possible" appears not to recognise the fact that different levels of identification are possible for different laboratories. Individual laboratories may have established traditions of identification levels for different taxa at different sizes but they may not be consistent between laboratories. Small individuals are often recorded as juveniles. We attempted to test the consistency of recording of juveniles in different taxa and the sizes at which they were considered to be juveniles:

"Please list all taxa that you separate into adults and juveniles" (Q.1)

Laboratory traditions concerned with taxa that are considered too difficult to identify to species were compared by the following question:

"List all taxa which you would normally identify at a higher taxonomic level than species:" (Q.3)

Finally, we asked for participating laboratories to provide any further comments that might be relevant to the study:

"If you have any further comments please use the reverse of this sheet". (Q.8)

CONCLUSIONS

It is clear from the results of the questionnaire that there is little or no consistency in recording criteria between different laboratories participating in the NMBAQC Scheme. Recording consistency is important if data from different laboratories is to be compared, as is the case with NMMP data.

Some of the differences in practice, such as staining and different extraction procedures, would only be a problem if they affected the quality of sample sorting, which could be tested by quality control procedures. However, as NMBAQCS results show that sorting efficiency is often poor, it may be necessary to suggest a common approach.

Inconsistencies in recording policies are a more serious problem. Currently, sample quality control operates on the individual laboratories' procedures such that, for

example, hydroids will not be recorded if the participant did not record them. Unfortunately, this means that results from different laboratories are not truly comparable. It is important that a standard approach be developed as soon as possible so that maximum benefit can be derived from the data. Standardised extraction and recording procedures should be produced through the NMBAQC Scheme.

Differences in the taxonomic levels to which animals are identified also reduce the comparability of data. Current quality control procedures, again, do not highlight the problems as identifications to higher taxonomic levels are taken to be correct. Reduction of data to the lowest common denominator (i.e. highest taxonomic level) is a poor short-term solution to the use of the data that will not ensure maximum benefit. It would be difficult to standardise definitions for juveniles and required taxonomic levels for identification, as they would necessarily differ for different species and higher taxa. However, such a system is necessary for adequate quality control and some priority should be given to its development. It is suggested that representatives from the organisations involved in NMMP processing and individuals with relevant taxonomic expertise (museum staff, etc.) should be tasked with producing an NMMP extraction and recording protocol.

Development of the standard approaches suggested above should be applied firstly, and most urgently, to NMMP data. A comprehensive set of protocols for all laboratories processing the samples must be produced. Ideally, the same protocols should then be applied to all sampling, so that data from a variety of sources can be used in many ways.

REFERENCES

Cooper, K., & Rees, H., 2000. Review of standard operating procedures (SOPs). NMBAQC. National Marine Biological Analytical Quality Control Scheme.