NATIONAL MARINE BIOLOGICAL ANALYTICAL QUALITY CONTROL SCHEME

ANNUAL REPORT

(Year 9)

2002/2003

March 2004
National Marine Biological AQC Coordinating Committee

NATIONAL MARINE BIOLOGICAL ANALYTICAL QUALITY CONTROL SCHEME

Annual Report 2002/2003

Year 9

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Appendices

1. OVERALL SUMMARY

- The National Marine Biological AQC Scheme (NMBAQC Scheme) has completed its ninth year in 2002/2003. The background to the scheme is described in previous annual reports.

- Components of the scheme continue to be based on: a whole MacroBenthic sample (MB), Own Samples (OS), Ring Tests (RT), and a Laboratory Reference (LR) for biological determinands, plus Particle Size (PS) tests.

- Participation in the scheme remained high with a total of twenty-two laboratories participating. Thirteen of these laboratories submitted data for NMMP and nine were consultants or private contractors. Only five labs undertook all scheme components. Seven labs sent grouped results for the particle size tests. Other labs opted not to participate in some components: own samples (4 labs), macrobenthos sample (10 labs), ring tests (3 labs), and lab reference (3 labs). Individual laboratories are responsible for communicating their level of participation to the contractor, Unicomarine Ltd. **It is mandatory for NMMP labs to participate in all biological components. Some NMMP labs are failing to participate fully in all relevant components.**

- As of this scheme year 9, pre-submission of electronic data sets for random selection of the OS samples and splitting all own samples to individual species vials was mandatory.

- Detailed results of the circulations are presented in the contractors report (Section 6) 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 still needs to address the issue of biomass determination.** Trials are required to derive the best method for the "blotted technique". Consideration needs to be given to the preparation of a standardised protocol and reporting format.

- **Serious problems still persist in sorting accuracy.** Laboratories should assess their own procedures with reference to the recommendations now provided by the NMBAQC Review of Standard Operating Procedures (Cooper & Rees, 2002*).

- In year 9, fifteen labs submitted 44 own samples. Overall performance was very similar to year 8 with around **three-quarters of samples achieving acceptable grades (or better).**

- Failed own samples have been flagged, along with the other replicates from the same NMMP site. Participating labs with failed samples have been informed of the required or recommended remedial action. **NMMP laboratories must complete remedial action and be re-audited. Only 2 NMMP samples were unacceptable. The remedial action on the relevant replicate batches has now been successfully completed.**

- **A protocol for applying an overall 'Pass/Fail' flag on the Particle Size (PS) exercise remains to be devised. In addition, the formation of written sediment descriptions needs to be examined in detail. It is of concern that in the first request to apply post analysis sediment description using the**

Folk triangle, only 5 labs returned a description, and 4 different descriptions were presented for what should be identical replicates!

- A second epibiota ring test will be arranged for scheme year 10 (2003/2004).
- The Committee intended to organise two workshops (on taxonomy and on acoustic methods) in 2002/2003. Both workshops were unavoidably delayed and will take place in the autumn of 2003 (year 10).
- Fees are to 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.

* Ref:. Cooper K.M. & Rees, H.L. (2002). National Marine Biological Control Scheme (NMBAQC): Review of Standard Operating Procedures. NMBAQC/CEFAS Science Series, Aquatic Environment Protection: Analytical Methods No.13. 57pp.

2. SCOPE OF THE SCHEME

The aims of the scheme include improving laboratory skills, improving the consistency and quality of marine biological benthic data, and screening data for the UK NMMP programme.
The ninth year of the scheme followed previous years with the emphasis on assessment of participant analytical performance on "own samples" of macrobenthos, along with contractor supplied ring test sets of faunal specimens and sediments. In total fourteen participants supplied macrobenthic own samples and have now been judged against the NMBAQC standards (derived in 1996/97) as modified in 2001/02.

Scheduled circulations:

a) 1 contractor supplied MacroBenthic sample (MB).

b) 3 participant supplied macrobenthic Own Samples (OS) to be (re)analysed by Unicomarine.

c) 2 contractor supplied Particle Size (PS) sediment samples.

d) Ring Tests (RT) as follows;
1 contractor supplied ring test of twenty five diverse species.
1 contractor supplied ring test targeted at "problem taxa".

e) 1 participant supplied Lab Reference (LR) set of 25 different reference specimens.

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 for Year 9, are contained in the contractors report in Section 7.

3. ISSUES ARISING

3.1 The composition and aims of the scheme.

MacroBenthic Sample: This exercise was designed to examine sample processing skills, in addition to taxonomic skills, based on a sample from a geographical location unfamiliar to participants. The MB component is considered by many labs to be irrelevant or too time consuming. Some labs opt not to participate in this exercise.

It became apparent in Year 8 that a few labs had some serious problems overlooking a number of taxa in addition to many others overlooking some specimens. These difficulties persisted in Year 9 and indicate that **some labs may need to review their procedures**. 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.

Similarly difficulties also persist with determining biomass, although this procedure is not routinely carried out by many of the laboratories. Although biomass determination is a requirement for NMMP labs, no standard has been set by the AQC Committee, because of these procedural problems. **The derivation of a standardised effective protocol and reporting format requires addressing by the committee.**

Own Samples: The OS exercise is seen as a true reflection of local laboratory skills. 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 more randomised method of sample selection was tested in scheme Year 8 and has now been fully implemented in Year 9.

The scoring of the Own Sample exercise also changed in Year 8 and now uses a graded system related to the untransformed Bray-Curtis scores. Data flags are now applied on a sample-by-sample basis. Remedial action was introduced into the scheme in Year 8 and continues in Year 9 in order to improve the quality of data held in the NMMP database. **Completion of remedial action is now mandatory for labs submitting data to the NMMP database and is strongly encouraged for non-NMMP labs.**

Particle Size: The particle size determinands 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 either laser granulometry or dry sieving.

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, while a new scoring system was tested. This has been fully implemented in Year 9 and a new set of pass/fail criteria introduced, along with an attempt to standardise sediment descriptions using the Folk triangle. The new criteria appear to work well although return of sediment statistics was incomplete in a number of cases resulting in deemed fails. Only 5 of the 10 analytical labs provided a description based on the Folk triangle. It appears that some procedural inconsistencies which may affect analytical results are not being detailed by labs. **It is clear that further guidance on procedural documentation as well as presentation and interpretation of particle size data would be beneficial.**

Ring Tests: Aim to improve taxonomic skills. Where difficulties emerge with particular faunal groups these can be tackled by the targeted RTs 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.

Laboratories generally achieved good results both on the standard ring test and the targeted ring test on Spionida. Minor issue raised in relation to literature used for identificaton of the oligochaete *Stylaria lacustris* and the polychaete *Raricirrus beryli.* **The provision of a standard literature database would help avoid such problems.**

Laboratory Reference: The initial aim of this component was to encourage labs to establish marine voucher collections from NMMP sites and apply quality control to these 'own specimens'. Assessment of performance in this exercise is difficult as

there is not always a clear distinction between specimens already assigned to a reference collection, with confident identifications, and difficult specimens, provisionally put forward, pending a second opinion from an external consultant. Participants have been permitted to include up to 2 uncertain taxa within their submission. The average number of specific differences, at 3.4 (= 13.6%) would be relatively high for a voucher collection, but is not such a problem if it is assumed that each participant includes 2 (or more?) difficult taxa. Although the LR exercise is not assigned a pass / fail standard, **it might be beneficial if participants clarified the status of their submitted specimens and if more detailed feedback was cascaded to all participants in relation to identification discrepancies raised**.

3.2 Participation

The twenty-two participants in 2002/2003 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 database. 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 opt to undertake only those components that they regard as compatible with their commercial interests, budgets or time constraints. **However, all laboratories submitting data to the NMMP database must complete all components and are required to carry out remedial actions if needed to achieve a "pass" standard.**

All primary correspondence for the scheme is now via e-mail. Hard copies of data sheets will only be provided where appropriate.

3.3 Submission of data

Participating laboratories are responsible for informing Unicomarine Ltd. of their level of participation in the Scheme. There has been a further 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. 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.

Eleven NMMP laboratories are members of the Scheme. Of these four supplied data from all the components. Of the remaining labs, six had indicated at the beginning of the scheme year that they would not participate in the MB exercise. One lab indicated it would receive Ring Tests but not return data. Two labs completed only one of the Ring Tests and three did not complete either Ring Test. Four labs did not undertake the Lab Reference exercise. One lab did not undertake the PS exercise and one completed only one of the PS tests.

It remains of concern that some "NMMP labs" which ought to be undertaking all components are not participating in, or not completing, some components. 'Fail flags' which are applied when no data is submitted are perceived as far worse than a participatory 'fail flag'.

3.4 Data feedback

As in previous years some 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 are now applied on a sample-by-sample basis using a graded system related to the untransformed Bray-Curtis scores. The five tier system is 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 5. Specific details of appropriate remedial action for individual laboratories will be approved by the Committee. 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-four samples for audit. The grading of the samples in Year 9 was quite similar to Year 8 though more have attained Good rather than Acceptable as shown below:

	Yr.9	**Yr.8**	
Excellent:	**2**	**3**	**samples**
Good:	**23**	**17**	**samples**
Acceptable:	**8**	**15**	**samples**
Poor:	**2**	**1**	**sample(s)**
Fail:	**9**	**9**	**samples**

Of the above Year 9 samples, one NMMP sample was graded FAIL and one was graded as POOR. Remedial action has now been carried out on the relevant NMMP sample batches.

One NMMP laboratory submitted only 2 samples for the OS exercise and was deemed to have failed on the third (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. If there are continuing disagreements which cannot be resolved within the Scheme a third party will be approached by the contract manager.

Selection of samples for the OS exercise has been randomised from Scheme year 9. All participating laboratories must submit their previous years completed NMMP data set (or other appropriate data set) prior to sample selection. 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 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 it has been mandatory for all submissions to the Own Sample exercise to be split to species, otherwise an additional charge will be levied.

Two PS exercises (PS20 & PS21) were distributed in Year 9. Fourteen laboratories participated in PS20 but only thirteen returned data for PS21. The previous pass / fail criteria were suspended in 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 have been applied in scheme year 9 (PS21) and appear on the Statement of Performance in same way as for year 8 (trial year). **A protocol for applying an overall 'Pass/Fail' flag on the PS exercise remains 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 or the Folk Triangle. It is of concern that in the first request to apply post analysis sediment description using the Folk triangle, only 5 labs returned a description and 4 of these were different for what should be identical replicates!** 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.

4. SCHEME PROPOSAL FOR 2003/2004 (SCHEME YEAR 10)

From Year 10 the Scheme will operate within the auspices of the European BEQUALM (Benthic Effects Quality Assurance in Monitoring) programme and will aim to include participants from other european countries.

Management of the scheme finances will be transferred from the Scottish Environment Protection Agency to the Environmental Agency. This should facilitate fund flow flexibility, and will enable considerable saving to be made on VAT costs.

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

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

Pre-submission of Own Sample data sets for random sample selection will be mandatory. Splitting of samples to species level will be mandatory.

A protocol for applying an overall PS exercise 'pass/fail' flag will be considered by the committee. (This task is outstanding from Year 9).

Pre and post analysis sediment descriptions will continue to be requested using visual observation and the Folk Triangle.

The Committee will continue to develop a protocol 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 exercise commenced in Year 9 follows on from the NMBAQC Review of Standard Operating Procedures (Cooper & Rees, 2002).

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

All primary correspondence for scheme year 10 will be conducted via e-mail

The first report on the second phase of the National Marine Monitoring Programme will be drafted in 2003. Committee members will be contribute to this report throughout 2003 in preparation for its publication (in early 2004).

The Committee intend to sponsor two workshops in Year 10. (See Section 5 below).

5. CO-ORDINATING COMMITTEE ACTIVITIES AND PROJECTS

A review of Standard Operating Procedures was published in conjunction with CEFAS (see Cooper & Rees, 2002*). This covered both benthic field sampling methodology and laboratory analysis and was undertaken on behalf of the NMBAQC Committee as part of its remit to improve the quality of benthos data generated from sampling programmes in UK estuaries and Coastal waters. Twenty-three procedures submitted by NMBAQC scheme participants were reviewed. The report identified examples of good practice as well as cases of inconsistency with the aim of improving procedures and promoting harmonisation between laboratories.

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 2004. Committee members have been actively involved in analysis and interpretation of the Phase 2 (99-2001) NMMP benthic data and preparation of the benthos section of the forthcoming NMMP report.

In line with the schemes commitment to the provision of training a workshop on "difficult taxa" plans were well advanced for a taxonomic workshop to be held in Plymouth in March 2003. However, due to various logistical problems both the venue and time of the intended workshop have had to be changed. The benthic invertebrate taxonomic workshop will now take place at the Dove Marine Laboratory, Newcastle in November 2003 (see appendix 6 for proposed programme.) In addition to this, a workshop on acoustic methods and epibenthos is also planned. This is a joint workshop on Acoustic Ground Discrimination methods to be held in September 2003 at the Dunstaffnage Marine Laboratory. Other sponsors of this workshop include JNCC, DARD, and Marine Microsystems and the hosts will be SAMS (Scottish Association of Marine Science). A detailed rationale and programme is shown in appendix 7.

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. Committee Members have formed part of a Benthic Invertebrate Component sub-group of the Marine & Transitional Waters Classification Scheme for the Water Framework Directive. The project is being undertaken by the Environment Agency and involves testing classification tools appropriate for the ecological status assessment of benthic invertebrate communities for the purposes of the Water Framework Directive (WFD). An overview of the aims and approach of this study is provided in appendix 8.

* Ref:. Cooper K.M. & Rees, H.L. (2002). National Marine Biological Control Scheme (NMBAQC): Review of Standard Operating Procedures. NMBAQC/CEFAS Science Series, Aquatic Environment Protection: Analytical Methods No.13. 57pp.

Section 6

Report from the Contractor:

(NB Pagination differs from Sections 1-5)

6. REPORT FROM THE CONTRACTOR

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Summary of Performance

List of Tables, Figures and Appendices

Tables

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Appendices

Summary of Performance

This report presents the findings of the ninth 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 eighth 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 good however the results are markedly lower than those achieved in this exercise in the previous Scheme year. The samples did pose some problems associated with faunal extraction from vegetation and incorrect identifications of the more abundant taxa. Extraction efficiency, irrespective of sorting, was on average 92%, however four laboratories failed to extract 90% of the individuals from the residue. 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 70.4% and 98.1% and was better than 90% in just 55% of comparisons and better than 95% in only 27% of comparisons.

This Scheme year marked the full introduction of 'blind' **Own Sample (OS)** audits. Laboratories were to submit full completed data matrices from their previous year's UK NMMP sampling programme (or alternative sampling programmes if not responsible for UK NMMP samples). The new OS flagging system, introduced in Scheme year eight, was continued (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 89% of comparisons and better than 95% in 66% of all comparisons. The Bray-Curtis similarity index ranged from 43% to 100% with an average figure of 92%. The Bray-Curtis similarity index was greater than 95% in 57% of comparisons and in most cases (75%) 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. This was replaced in the last Scheme year 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 evident, especially for the muddy sediment circulated as PS21. As has been previously reported, in most cases there was good agreement between laboratories, especially those using the same technique. The first particle size exercise of the Scheme year (PS20) resulted in three 'fail' flags and three 'deemed fail' flags (no statistic/data supplied). Two of the three 'fail' flags belonged to one laboratory whose results indicated significantly more silt/clay than all the other laboratories. The second particle size exercise of the Scheme year (PS21) resulted in three 'fail flags' and five 'deemed fail' flags. All three 'fail' flags belonged to one laboratory and were the result of incorrect processing of the silt-clay fraction (air-drying prior to the

separation of the silt/clay fraction resulting in silt/clay particles sticking together to form artificially larger particles).

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 belonging to the polychaete order Spionida. For the general set of fauna (RT20) 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 5.1 generic errors and 6.1 specific errors, these figures are higher than those of the general ring test from the previous Scheme year. The majority of errors can be attributed to one oligochaete, three crustacean and four mollusc taxa. The 'targeted' ring test (RT21 - Spionida) posed far fewer problems. On average each participating laboratory recorded 1.4 generic errors and 3.5 specific errors. Cirratulid specimens were responsible for the bulk of these errors (55% of all generic and 57% of all specific errors recorded).

The identification of a set of twenty-five species selected and supplied 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 UK National Marine Monitoring Programme (UK NMMP) 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 ninth year of the Scheme (2002/03) followed the format of the eighth year. A series of exercises involved the distribution of test materials to participating laboratories and the centralised examination of returned data and samples. Twenty-two laboratories participated in the Scheme.

As in previous years, some laboratories elected to be involved in limited aspects of the Scheme. UK NMMP laboratories were required to participate in all components and standards were applied to agreed components.

In this report performance targets have been applied for the OS and PS components only (See Appendix 2: Description of the Scheme standards for each component). These targets have been applied to the results from laboratories (See Section 5: Application of NMBAQC Scheme standards) and "Pass" or "Fail" flags assigned accordingly. As these data have been deemed the basis for quality target assessment, where laboratories failed to fulfil these components through not returning the data, a "Fail" flag has been assigned. 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). Email has become the primary means of communication for all participating laboratories. This has considerably reduced the amount of paper required for the administration of the Scheme.

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 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 2002. 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 nine will be recorded as LB0904.

In the present report all references to Laboratory Codes are the post-April 2002 codes (Scheme year nine).

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 MB10 was collected from the Blackwater Estuary; in an area of mud and vegetation with some grit sediment. A set of forty samples was collected using a 0.1m² Day Grab. Sampling was carried out while at anchor and samples for distribution were collected within a five hour period. All grabs taken were equal in size. Sieving was carried out on-board using a mesh of 0.5mm, followed by fixing in buffered formaldehyde solution. Samples were mixed after a week in the fixative. Prior to distribution to the participating laboratories the samples were washed over a 0.5mm sieve and transferred to 70% IMS.

2.2.2 Analysis required

Each participating laboratory was required to carry out sorting, identification, enumeration and biomass estimations of the macrobenthic fauna contained in the sample. Precise protocols were not provided, other than the use of a 0.5mm sieve mesh; participating laboratories were instructed to employ their normal methods. The participating laboratories were required to complete a Macrobenthic Sample Details Form, which specified their processing methodology (for example, nematodes and copepods not extracted). The extracted fauna was to be separated, identified 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 each participating laboratory's 'home' area. Following a review of the Own Sample exercise (Unicomarine, 2001) several changes were implemented in Scheme year eight. A transition period was permitted, however and from Scheme year nine all participants must meet the new Own Sample requirements. Own Sample participants must supply their previous years UK 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. 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. UK NMMP laboratories were advised to use UK 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.

Eleven 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 2002/03. 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 two circulations was collected from two different locations covering a range of sediment types. A minimum of 30 litres of sediment was removed from a small visually uniform area for each circulation. This material 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 (pre-processing and post-processing using the Folk Triangle) 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 2002/03. The first of the year's RT circulations (RT20) was of the same form as for the earlier years - the specimens included representatives of the major phyla and approximately 36% of the taxa were molluscs, 28% were polychaete worms, 24% were crustaceans, 8% were oligochaete worms and 4% were echinoderms. The second circulation (RT 21) 'targeted' specimens of the order Spionida. Details of substratum, salinity, depth and geographical location for all ring test 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 (RT20) and the 'targeted' RT (RT21), 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 UK 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 **fifteen 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 2002/03 were undertaken, in varying numbers, by twenty-two 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 (-). In some instances, laboratories had elected not to participate in a particular component of the Scheme despite originally subscribing to the component.

To avoid unnecessary detail in the Tables described below the reasons for the dashes are 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 macrobenthic sample (MB10) was from an estuarine intertidal station in the Blackwater Estuary. The samples comprised approximately half a litre of mud with vegetation taken from a depth of approximately one metre. The samples contained on average twenty-two species and three thousand three hundred individuals, covering a variety of phyla. The composite list from all samples was thirty-six species. Five out of the eleven samples returned had been stained with Rose Bengal during sample processing. Two laboratories subsampled their residues. One laboratory accidentally processed the sample using the wrong sieve mesh (LB0915). 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 MB10, 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 fauna missed by each participating laboratory. The subsampling technique used by one laboratory (LB0913) rendered the auditing of the sorted residue impossible, due to the combination of sorted and unsorted fractions.

3.1.2.1 Number of Taxa

Table 1 (column 5) shows that there was considerable variation between laboratories in the percentage of taxa identified in the samples. Up to three taxa (and 15% 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. However the majority of laboratories only missed one taxon in their residues, and in the worst instance just two 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 60% of the samples was less than 10% of the true total number in the sample. In the worst instance 17% 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 one hundred and forty-seven. A breakdown of the missed individuals by taxonomic group is presented in Table 2. 'Others' (predominantly nematodes) and molluscs were the most frequently missed faunal groups, on average 29% of the total number of 'others' present and 27% 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. Only one of participating laboratories had no taxonomic differences (Table 1, column 15). In the worst instances four taxonomic differences were recorded. On average over two and a half 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 70.4% to 98.1%, with an average value of 87.9%. The index for the majority of laboratories (6 of 11) was in excess of 90%. Five of the participating laboratories achieved a Bray-Curtis similarity index below 90%, these were 70.4, 79.3% 80.6%, 81.9% and 83.2%. It must be noted that the sample processing details varied greatly between participants. Four out of the eleven participants did not extract or enumerate nematodes; three omitted copepods; two omitted aquatic insects. Two laboratories (LB0905 & LB0913) subsampled their macrobenthic residues. The subsampling technique used by one laboratory (LB0913) rendered the residue extraction audit impossible, therefore the Bray-Curtis similarity figure achieved by this laboratory could be artificially high. One laboratory (LB0915) processed the macrobenthic sample using the wrong sieve mesh (1mm instead of 0.5mm), this laboratory achieved the highest Bray-Curtis similarity score possibly due to the ease of extracting far fewer and larger specimens from their sample residue. 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 MB10 circulation is presented in Table 3. Three laboratories did not supply biomass data. The average difference between the two weight values was –13.3%, 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 –42.7% (measurements by laboratory were lighter than those made by Unicomarine Ltd.) to +17.2% (measurements by laboratory were greater than those made by Unicomarine Ltd.). The average difference between estimations varied greatly between faunal groups, ranging from –5.9% to –65.7% (from molluscs to 'others' predominantly nematodes, respectively)

3.1.5 *Uniformity of samples*

The faunal content of the samples distributed as MB10 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 data of suitable samples for re-analysis, forty-two selected samples were received from fourteen laboratories, together with descriptions of their origin and the collection and analysis procedures employed. Samples were identified as OS20, OS21 and OS22 and labelled with LabCodes. The nature of the samples varied considerably. Samples were received from estuarine and marine locations, both intertidal and subtidal. The sediment varied from mud to gravel and from 20ml to 7l of residue. The associated fauna of the samples was also very varied; the number of taxa recorded ranged from 1 to 103, and the number of individuals from 6 to 3237. Overall, of the seventeen laboratories participating in this exercise, fourteen laboratories returned all three Own Samples and one laboratory submitted two samples. Two laboratories decided not to take part in this component for this Scheme year.

3.2.2 *Efficiency of sample sorting*

Table 5 displays a summary of the data obtained from the analysis of the Own Sample exercise. All taxa identified and enumerated by the participating laboratory were included in the analysis, except in instances where the fauna had been damaged and rendered unidentifiable and uncountable. In twenty cases (45% of the comparisons) the number of taxa recorded by the participating laboratories was identical to that obtained by Unicomarine Ltd. (column 4). In the twenty-four exceptions, the difference was at most twenty-three 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 37%. The average difference was 4.9% (sixteen samples exceeded this average). Twelve of the samples received showed 100% extraction of fauna from the residue (column 12), and in sixteen samples various numbers of individuals (but no new taxa) were missed during sorting (column 11). The remaining sixteen samples contained taxa in the residue which were not previously extracted, the worst example being sixteen new taxa found in the residue (column 10). In the worst instance residue was found to contain five hundred and forty-six 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 thirty-three, and the average number of missed taxa was less than two.

3.2.3 *Uniformity of identification*

Taxonomic differences between participating laboratory and Unicomarine Ltd. results were found in twenty-five of the forty-four samples received. An average of just under two and a half taxonomic differences per laboratory were recorded; in the worst instance fourteen 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 43% to 100%, with an average figure of 92%. Nine samples from six different laboratories achieved a similarity figure of less than 85%. Two samples gave a similarity figure of 100%, these were submitted by a single laboratory (LB0919). The best overall results were achieved by laboratory LB0910, whose results comprised 99.37%, 99.24% and 98.67%. The worst overall results were achieved by laboratory LB0904, whose results comprised 88.89%, 43.32% and 83.72%. 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; one laboratory reported biomass to three decimal places; one laboratory reported at five decimal places; one provided data only to major taxonomic group; one laboratory provided partial biomass data. Table 7 shows the comparison of the participating laboratory and Unicomarine Ltd. biomass figures by major taxonomic groups. Twenty-eight 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 +3% difference between the two sets of results (*i.e.* heavier than Unicomarine Ltd.), the range was from –41% to +28%. 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 +3.3% for polychaetes, -18.6% for oligochaetes, -71.5% for nemerteans, +0.5% for crustaceans, -11.5% for echinoderms, +13% for molluscs and –5.4% for all remaining faunal groups. These figures are different to those produced by this same exercise in each of the previous six 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 PS20, fourteen out of sixteen participating laboratories returned data (including labs with grouped results); two laboratories decided not to participate. For PS21, thirteen out of the sixteen participating laboratories returned data; three laboratories decided not to participate.

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 initial exercise 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 the sandy sediment circulated as PS20; the shape of the distribution curves was similar for the two analytical techniques and they were closely grouped with the sieve curves displaced to the right of the laser curves. This sample had a very low percentage of sediment in the fine fraction (average of 0.05% <63μm). The derived statistic for median particle size (ϕ) were markedly different between the two techniques. The average median particle size from laser analyses was 0.26ϕ, compared with 0.57ϕ from sieve and pipette analyses. Results for the individual *replicates* are provided in Table 8 and are displayed in Figure 1.

Sample PS21 was of a muddy sediment (average of 88.02% <63μm) and the cumulative distribution curves differed between the two techniques. The sieve technique showed a larger component of sands compared to the laser technique. 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 five laboratories which normally sub-contract particle size analysis to the same two independent laboratories (also participating), elected to utilise the results from these laboratories for PS20. One further laboratory adopted centralised results for PS21. 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 PS20 and PS21 respectively, although the results are displayed for all participating laboratories the replicated data supplied by the centralised laboratories (sub-contractors) have 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 Twentieth distribution – PS20

There was generally good agreement for PS20 between the results from the analysis of replicates and those from the majority of participating laboratories. The results for a single laboratory (LB0919) were adrift due to a higher estimation of the silt/clay fraction. 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 *Twenty-first distribution – PS21*

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 again evident in the *replicate* samples analysed by Unicomarine Ltd. However this was not clear in the data supplied by the participating laboratories (see Figures 2 and 4). One laboratory (LB0918) incorrectly prepared their sample for dry sieving, causing silt/clay particles to adhere to each other and consequently produce a vast underestimation of the silt/clay proportion.

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. This Scheme year both circulations were accompanied by details of each specimens habitat details (depth, salinity, substratum, and geographical location). A number of labs use this part of the Scheme as a training exercise and have selected it preferentially over other components. UK 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 RT20 the species were from a variety of Phyla while for RT21 twenty-five specimens belonging to the order Spionida were 'targeted' for circulation. Other aspects of the two circulations, in particular the method of scoring results, were the same as for previous circulations. Overall nineteen laboratories were distributed with RT20 specimens and nineteen laboratories received RT21 specimens. For RT20, fifteen laboratories returned data; four specified non-participation for this exercise. For RT21, fourteen laboratories returned samples and data; five 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. *Polydora ligni* for *Polydora cornuta*.
- Simple mis-spelling of a name, e.g. *Calliostoma zizphinum* for *Calliostoma zizyphinum*.

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 RT20 and RT21. 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 2001/02 as there was only a single 'standard' exercise (RT20). RT21 was targeted on the order Spionida. 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 (RTB20 and RTB21), 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 *Twentieth distribution – RT20*

Table 12 presents the results for the RT20. The agreement at the generic level was relatively poor, seventy-six errors were recorded from the fifteen participating laboratories. Agreement at the specific level was also fairly poor, ninety-one errors were recorded. For approximately half of the distributed taxa there was good agreement between participating laboratories and the identification made by Unicomarine Ltd. The remaining taxa were responsible for the majority of differences, some are described briefly below.

Approximately one third of the ring test comprised mollusc taxa and these caused problems for several laboratories; specifically *Fabulina fabula* (small specimens), *Ventrosia ventrosa* (large specimens), *Buccinum undatum* (juvenile specimens), *Tellimya ferruginosa* (small specimens) and *Leptochiton asellus* (large specimens). These accounted for 46% of the generic and 38% of the specific differences recorded. Three of the twenty-five circulated specimens were correctly identified by all participating laboratories (*Calliostoma zizyphinum*, *Barnea candida* and *Scalibregma inflatum*). Further details and analysis of results can be found in the relevant Ring Test Bulletin (RTB20) which was circulated to each laboratory from which results were received.

3.4.3.2 *Twenty-first distribution – RT21*

RT21 contained twenty-five specimens belonging to the order Spionida. The results from the circulation are presented in Table 13 in the same manner as for the other circulations. Only a few of the taxa were responsible for the majority of differences and these are described briefly below.

The agreement at the generic level was relatively very good, only twenty errors were recorded from the fourteen participating laboratories. Agreement at the specific level was relatively good, forty-nine errors were recorded. Eleven of the twenty-five specimens circulated were Spionidae specimens; nine were Cirratulidae specimens; four were Magelonidae specimens; one was a Poecilochaetidae specimen. The bulk of the errors recorded could be attributed to the Cirratulidae specimens. These cirratulids accounted for a total of 55% of all generic and 57% of all the specific differences recorded. Nine of the twenty-five circulated specimens were correctly identified by all participating laboratories (*Poecilochaetus serpens*, *Streblospio shrubsolii*, *Cirriformia tentaculata*, *Magelona alleni*, *Caulleriella alata*, *Spio martinensis*, *Scolelepis squamata*, *Minuspio* cf. *multibranchiata* and *Polydora cornuta*). Further details and analysis of results can be found in the relevant Ring Test Bulletin (RTB21) which was circulated to each laboratory from which results were received.

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 RT20 and RT21 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 RT20 were of molluscs. Seven of the twenty-five specimens circulated were polychaetes and these produced 22% of the generic and 20% of the specific differences recorded. Molluscs, despite only nine mollusc specimens being circulated, accounted for approximately 49% of the total number of generic differences and 41% of specific differences. Crustacean specimens (six specimens in total) were responsible for 13% of generic differences and 26% of the total number of specific differences. Oligochaete specimens (two specimens) were responsible for 14% of generic differences and 12% of specific differences. The single echinoderm specimen circulated produced 1% of the generic and specific differences recorded.

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 nineteen laboratories participating in this exercise, fourteen laboratories returned samples and data; five laboratories decided not to participate.

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 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 MB10 comprised a typical estuarine mud sample. The extraction of fauna from the sediment was particularly time consuming due to the nature of the sediment and the high numbers of individuals (<2000 individuals on average) retained after sieving. The dominant taxa recorded in the majority of samples were *Tubificoides benedii*, *Manayunkia aestuarina* and Nematoda. None of the participating laboratories extracted all the countable material from the residue, consequently the overall efficiency of faunal extraction is reduced compared to the previous year's exercise (MB09). Identification caused various problems for the majority of laboratories, only one laboratory (LB0908) correctly identified all their extracted fauna. Some taxonomic mistakes were noted including *Tharyx* Type A, *Macoma balthica/Scrobicularia plana/Abra tenuis* juveniles, *Ampharete grubei* and *Polydora cornuta* misidentifications. Five of the eleven returning laboratories attained a Bray-Curtis similarity index less than 90%. The highest Bray-Curtis similarity index achieved was 98.12% (LB0915), however this laboratory used a 1mm sieve mesh instead of the instructed 0.5mm sieve mesh. The average Bray-Curtis figure of 88% is somewhat poor for these typical estuarine samples. However, it is still comparable with those recorded for MB09 (93%), 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 (MB10). The area sampled was uniform in its faunal composition. All samples were of relatively equal volume, sediment characteristics and species content.

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 lighter in total than Unicomarine Ltd.; two supplied data that was heavier than Unicomarine Ltd.

estimations. The extremes recorded were 43% lighter (LB0903) and 17% heavier (LB0912) than the Unicomarine Ltd. estimations. Overall the average difference between the values determined by the participating laboratories and Unicomarine Ltd. was –13.3% (*i.e.* laboratory measurements were lighter than those made by Unicomarine Ltd.), this figure is similar to that of the previous Scheme year's MB exercise (MB09).

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 MB10 exercise. The average value of the index was 92% for the OS, compared with 88% for MB10. The average values of the other individual measures of processing performance (% of taxa extracted and identified, taxonomic errors) were similar for the MB10 exercise. The most apparent difference between these exercises was the far better extraction of individuals from the residue in the Own Samples, the average % individuals not extracted from the residues for the MB10 samples was almost double that of the OS returns. This is the complete opposite to these exercises in the previous Scheme year, where the MB09 samples showed far better extraction efficiency figures than the Own Samples (OS17-19). 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 the average Bray-Curtis figure for the Own Samples is four percentage points higher than the MB10 samples, due to the OS returns containing slightly fewer taxonomic differences and far fewer missed individuals in their residues compared with the MB10 returns.

There were forty-four samples submitted for this component. This was facilitated by the distribution of timely reminders. The average Bray-Curtis similarity index achieved was 92%. Approximately 75% of samples exceeded the 90% Bray-Curtis pass mark and approximately 57% of the samples exceeded 95% Bray-Curtis similarity. These figures are similar to results from previous OS exercises. In the 2001/02 year (OS 17, 18 and 19) the average Bray-Curtis figure was 90.5%, and 78% (of the forty-five samples received) achieved more than 90% Bray-Curtis results. 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 three hundred and eighteen samples have been received (OS01-22). The average Bray-Curtis similarity figure is 91.54%. Eighty samples have fallen below the 90% pass mark (25%). Thirty-two samples have achieved a similarity figure of 100% (10% of all returns). 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 evident in the results from the analysis of the replicates samples and from those from the participating laboratories. The sample distributed as PS20 appeared from an analysis of replicates (Figure 1) to be very uniform and 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 LB0919 indicated a much higher proportion of silt/clay than the other data returns for PS20 and hence the results are displaced.

There was far more scatter in the results for PS21 from participating laboratories. Figure 6 shows the z-scores for each of the major statistics supplied by the participating laboratories. The data received from LB0918 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 air 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 PS20 and PS21 samples. The results varied greatly (Table 16, final column). Participating laboratories were instructed to describe the PS21 sediment using the Folk triangle. Data were provided by only five laboratories, one of which described the sediment as 'slightly gravely sandy mud'. All PS samples are pre-sieved at either 2 or 1mm prior to circulation therefore the description of gravel particles (>2mm) is extremely unlikely. It appears that guidance upon the use and interpretation of particle size data would be very valuable to the biology specialists that have to report the raw sediment data.

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 eight 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), which detail specifically the reasons for any identification errors, have further emphasised the learning aspect of this component. RT20 identified discrepancies with literature used by some participating laboratories for their identification of the *Stylaria lacustris* and *Raricirrus beryli* specimens. All participating laboratories have been made aware of this via the ring test bulletin (RTB20).

The 'targeted' Spionida ring rest (RT21) resulted in very good agreement with identifications. Generally the Spionidae were very well identified, the majority of errors were a result of the Cirratulidae specimens. This has previously been highlighted as a problem polychaete family and a revision to the literature and possible a further targeted ring test are planned.

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 2.1, and in many cases (6 of 14) laboratories had no differences or only a single difference at the generic level.

The situation was similar for identification at the level of species where the majority of laboratories achieved at most three differences in identification (8 of 14 laboratories). The average number of specific differences was 3.4. 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 UK National Marine Monitoring Programme. 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 were altered in Scheme year eight; 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 UK National Marine Monitoring Programme.

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. 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 82% of the comparisons were considered to have passed the enumeration of taxa standard; 86% exceeded the enumeration of individuals standard and 75% passed the Bray-Curtis comparison standard. Of the seventeen laboratories participating in this component fourteen supplied samples for reanalysis; two laboratories decided not to participate in this component for this Scheme year. UK NMMP sample flags have been applied to each of the Own Sample in accordance with the performance flagging criteria introduced in the last Scheme year (Table 15, column 23); nine of the forty-four samples are flagged as 'Fail'; two are flagged as 'Poor'; eight are flagged as 'Acceptable'; twenty-three are flagged as 'Good'; and two are flagged as 'Excellent' for achieving 100% Bray-Curtis similarity indices.

Performance with respect to the biomass standard was slightly poorer with only 75% 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, introduced in the last Scheme year, (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 PS20 exercise. Two participating laboratories did not submit all five requested statistics, these statistics have been flagged as 'Deemed Fail'. One laboratory (LB0919), which submitted data for %<63μm, failed to meet the standard for this statistic; one laboratory (LB0905), which submitted data for median (ϕ), failed to meet the standard for this statistic; one laboratory (LB0919), which submitted data for IGS(Ski), failed to meet the standard for this statistics. Eleven laboratories submitted data for all statistics and passed all standards, although five of these laboratories were utilising data from centralised sources. The lower section of Table 16 shows the results for the PS21 exercise. One participating laboratory did not submit all five requested statistics, these statistics have been flagged as 'Deemed Fail'. One laboratory (LB0918) failed to meet the standard required for the %<63μm, median (ϕ) and mean (ϕ) statistics. Eleven laboratories submitted data for all statistics and passed all standards, although six of these laboratories were utilising data from centralised sources.

5.2 Statement of Performance

Each participating laboratory has 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 in the previous Scheme year 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 any statement concerning changes in laboratory standards can be reliably deduced.

5.4 Remedial Action

It is imperative that failing UK NMMP samples, audited through the Own Sample exercise, are addressed. Remedial action should be conducted upon the remaining UK NMMP station replicates to improve upon the flagged data. The NMBAQC Scheme OS standards, introduced in the previous Scheme year, 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%; eleven samples 'failed' in this Scheme year (including two UK 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 UK NMMP data flags are altered.

The recommended remedial action for two 'failing' Own Samples from two laboratories (LB0905-OS20 and LB0917-OS20) has been conducted and externally audited. These samples have now been awarded 'pass' flags. These samples were both from UK NMMP sampling stations and therefore the station data flag can now be amended and the 'fail' flag removed.

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 RT20 and RT21 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 six 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. One of these laboratories provided independent data for PS20 but utilised their sub-contractor's data for PS21. Their data is indicated accordingly in all figures and tables. In the comments below they are termed 'Data from centralised analysis'.

If an exercise contains the comment 'not participating in this component' then the laboratory has not subscribed to the component. If an exercise contains the comment 'not participating in this exercise' then the laboratory, despite subscribing to this component, has decided not to submit data for the exercise.

Laboratory – LB0901

Macrobenthos (Training Component)

MB10 - Not participating in this component.

Ring Test (Training Component)

RT20 – Two generic and three specific differences. Number of AQC identifications in Low group.
RT21 – Two specific differences. Number of AQC identifications in Low group.

Laboratory Reference (Training Component)

LR07 - Not participating in this exercise.

Own Sample (Quality Control Component with Pass/Fail NMBAQC Standards)

OS20 – Not participating in this component.
OS21 – Not participating in this component.
OS22 – Not participating in this component.

Particle Size (Quality Control Component with Pass/Fail NMBAQC Standards)

PS20 – Not participating in this component.
PS21 – Not participating in this component.

Laboratory – LB0902

Macrobenthos (Training Component)

MB10 – Not participating in this component.

Ring Test (Training Component)

RT20 – Four generic and four specific differences. Number of AQC identifications in Mid group.
RT21 – One generic and four specific differences. Number of AQC identifications in Mid group.

Laboratory Reference (Training Component)

LR07 – All specimens correctly identified.

Own Sample (Quality Control Component with Pass/Fail NMBAQC Standards)

OS20 – NMBAQCS sample flag – 'Good'.
Count variance of twenty individuals. Six individuals not picked from the residue. Bray-Curtis similarity index of 99.1%. Biomass in the wrong format (stated to 3 decimal places). Biomass on average 23.4% heavier than Unicomarine Ltd.
OS21 – NMBAQCS sample flag – 'Good'.
Count variance of four individuals. Five individuals not picked from the residue. Bray-Curtis similarity index of 96.7%. Biomass in the wrong format (stated to 3 decimal places). Biomass on average 10.5% heavier than Unicomarine Ltd.
OS22 – NMBAQCS sample flag – 'Good'.
Count variance of six individuals. Two individuals not picked from residue. Bray-Curtis similarity index of 98.1%. Biomass in the wrong format (stated to 3 decimal places). Biomass on average 24.1% heavier than Unicomarine Ltd.

Particle Size (Quality Control Component with Pass/Fail NMBAQC Standards)

PS20 – All NMBAQCS standards passed.
No major differences in size distribution curve. No sediment description given.
PS21 – All NMBAQCS standards passed.
Data from centralised analysis; Size distribution curve to the left of the majority of curves. Sediment described as 'muddy'.

Laboratory – LB0903

Macrobenthos (Training Component)

MB10 - Four taxonomic differences. One hundred and eleven individuals not picked from the residue. Count variance of twenty-two individuals. Bray-Curtis similarity index of 70.4%. Biomass on average 42.7% lighter than Unicomarine Ltd. Residue/fauna stained.

Ring Test (Training Component)

RT20 – Five generic and seven specific differences. Number of AQC identifications in High group.
RT21 – Two generic and four specific differences. Number of AQC identifications in Mid group.

Laboratory Reference (Training Component)

LR07 - Three generic and six specific differences.

Own Sample (Quality Control Component with Pass/Fail NMBAQC Standards)

OS20 – NMBAQCS sample flag – 'Good'.
Eight taxonomic differences. Five individuals not picked from the residue, including one previously unpicked taxon. Bray-Curtis similarity index of 96.9%. Biomass on average 1.9% lighter than Unicomarine Ltd.
OS21 – NMBAQCS sample flag – 'Acceptable'.
Six taxonomic differences. Count variance of three individuals. Six individuals not picked from the residue. Bray-Curtis similarity index of 93.7%. Biomass on average 3.7% lighter than Unicomarine Ltd.
OS22 – NMBAQCS sample flag – 'Acceptable'.
Fourteen taxonomic differences. Count variance of eight individuals. Two hundred and fourteen individuals not picked from residue, including three previously unpicked taxa. Bray-Curtis similarity index of 91.2%. No biomass data supplied.

Particle Size (Quality Control Component with Pass/Fail NMBAQC Standards)

PS20 - All NMBAQCS standards passed.
Data from centralised analysis; No major differences in size distribution curve. Sediment described as 'gritty sand'.
PS21 – All NMBAQCS standards passed.

Data from centralised analysis; No major differences in size distribution curve. Sediment described as 'sandy mud'.

Laboratory – LB0904

Macrobenthos (Training Component)

MB10 - Four taxonomic differences. One hundred and twenty individuals not picked from the residue, including one previously unpicked taxon. Count variance of twenty-eight individuals. Bray-Curtis similarity index of 83.2%. Biomass on average 11.5% lighter than Unicomarine Ltd.

Ring Test (Training Component)

RT20 – Three generic and four specific differences. Number of AQC identifications in Mid group.
RT21 – Two generic and four specific differences. Number of AQC identifications in Mid group.

Laboratory Reference (Training Component)

LR07 – All specimens correctly identified.

Own Sample (Quality Control Component with Pass/Fail NMBAQC Standards)

OS20 – NMBAQCS sample flag – 'Poor'.
Three taxonomic differences. All individuals extracted from the residue. Count variance of two individuals. Bray-Curtis similarity index of 88.9%. Biomass estimations provided by major group.
OS21 – NMBAQCS sample flag – 'Fail'.
Two taxonomic differences. All individuals extracted from the residue. Count variance of two individuals. Bray-Curtis similarity index of 43.3%. Biomass estimations provided by major group.
OS22 – NMBAQCS sample flag – 'Fail'.
Two taxonomic differences. All individuals extracted from the residue. Count variance of one individual. Bray-Curtis similarity index of 83.7%. Biomass estimations provided by major group.

Particle Size (Quality Control Component with Pass/Fail NMBAQC Standards)

PS20 – Not participating in this component.
PS21 – Not participating in this component.

Laboratory – LB0905

Macrobenthos (Training Component)

MB10 - Four taxonomic differences. Two hundred and four individuals not picked from the residue, including two previously unpicked taxa. Count variance of twenty individuals. Bray-Curtis similarity index of 80.6%. Biomass on average 1.9% heavier than Unicomarine Ltd. Fauna subsampled.

Ring Test (Training Component)

RT20 – Seven generic and eight specific differences. Number of AQC identifications in High group.
RT21 – Two generic and six specific differences. Number of AQC identifications in High group.

Laboratory Reference (Training Component)

LR07 - Four generic and eight specific differences.

Own Sample (Quality Control Component with Pass/Fail NMBAQC Standards)

OS20 – NMBAQCS sample flag – 'Fail'. Remedial action has subsequently been successfully performed upon the remaining replicates from this station.

Seven taxonomic differences. All individuals extracted from the residue. Bray-Curtis similarity index of 72.6%. Biomass expressed to five decimal places not four as requested. Biomass on average 27.7% heavier than Unicomarine Ltd.

OS21 – NMBAQCS sample flag – 'Good'.

One taxonomic difference. All individuals extracted from the residue. Count variance of one individual. Biomass expressed to five decimal places not four as requested. Bray-Curtis similarity index of 98.6%. Biomass on average 17.9% heavier than Unicomarine Ltd.

OS22 – NMBAQCS sample flag – 'Good'.

All individuals extracted from the residue. Count variance of two individuals. Bray-Curtis similarity index of 99.6%. Biomass expressed to five decimal places not four as requested. Biomass on average 18.8% heavier than Unicomarine Ltd.

Particle Size (Quality Control Component with Pass/Fail NMBAQC Standards)

PS20 – NMBAQCS standard for median failed. All remaining standards passed.

No major differences in size distribution curve. Sediment described as 'sand'.

PS21 – All NMBAQCS standards passed.

No major differences in size distribution curve. Sediment described as 'slightly gravely sand mud'.

Laboratory – LB0906

Macrobenthos (Training Component)

MB10 - Two taxonomic differences. Three hundred and eighteen individuals not picked from the residue, including one previously unpicked taxon. Count variance of one hundred and twenty-three individuals. Bray-Curtis similarity index of 79.2%. No biomass data supplied. Residue/fauna stained.

Ring Test (Training Component)

RT20 – Seven generic and nine specific differences. Number of AQC identifications in High group.

RT21 – Three specific differences. Number of AQC identifications in Low group.

Laboratory Reference (Training Component)

LR07 – Two generic and three specific differences.

Own Sample (Quality Control Component with Pass/Fail NMBAQC Standards)

OS20 – NMBAQCS sample flag – 'Good'.

Original data differs from submitted sample. One taxonomic difference. One individual not picked from the residue. Bray-Curtis similarity index of 95.1%. No biomass data supplied.

OS21 – NMBAQCS sample flag – 'Acceptable'.

Original data differs from submitted sample. Fourteen individuals not picked from residue, including five previously unpicked taxa. Count variance of one individual. Bray-Curtis similarity index of 93.2%. No biomass data supplied.

OS22 – NMBAQCS sample flag – 'Fail'.

Original data differs from submitted sample. Six taxonomic differences. Thirty-four individuals not picked from residue, including five previously unpicked taxa. Count variance of one individual. Bray-Curtis similarity index of 84.0%. No biomass data supplied.

Particle Size (Quality Control Component with Pass/Fail NMBAQC Standards)

PS20 – Not participating in this component.

PS21 – Not participating in this component.

Laboratory – LB0907

Macrobenthos (Training Component)

MB10 – Not participating in this component.

Ring Test (Training Component)

RT20 – Not participating in this exercise. Exercise used for training without submission of results.
RT21 – Not participating in this exercise. Exercise used for training without submission of results.

Laboratory Reference (Training Component)

LR07 – Two generic and five specific differences.

Own Sample (Quality Control Component with Pass/Fail NMBAQC Standards)

OS20 – Not participating in this exercise.
OS21 – Not participating in this exercise.
OS22 – Not participating in this exercise.

Particle Size (Quality Control Component with Pass/Fail NMBAQC Standards)

PS20 – All NMBAQCS standards passed.
Data from centralised analysis; No major differences in size distribution curve. Sediment described as 'coarse sand'.
PS21 – All NMBAQCS standards passed.
Data from centralised analysis; Size distribution curve to the left of the majority of curves. Sediment described as 'muddy'.

Laboratory – LB0908

Macrobenthos (Training Component)

MB10 - Seventy-eight individuals not picked from the residue, including one previously unpicked taxon. Count variance of eighty-eight individuals. Bray-Curtis similarity index of 97.1%. Biomass on average 25.6% lighter than Unicomarine Ltd.

Ring Test (Training Component)

RT20 – Two generic and two specific differences. Number of AQC identifications in Low group.
RT21 – One generic and three specific differences. Number of AQC identifications in Low group.

Laboratory Reference (Training Component)

LR07 - One specific difference.

Own Sample (Quality Control Component with Pass/Fail NMBAQC Standards)

OS20 – NMBAQCS sample flag – 'Good'.
Two taxonomic differences. Five individuals not picked from residue, including six new taxa (colonial taxa not enumerated). Count variance of one individual. Bray-Curtis similarity index of 98.7%. Biomass data not comprehensive. Biomass on average 1.2% lighter than Unicomarine Ltd.
OS21 – NMBAQCS sample flag – 'Good'.
Five taxonomic differences. All individuals extracted from the residue. Count variance of two individuals. Bray-Curtis similarity index of 96.4%. Biomass data not comprehensive. Biomass on average 0.3% heavier than Unicomarine Ltd.
OS22 – NMBAQCS sample flag – 'Acceptable'.
Two taxonomic differences. Fourteen individuals not picked from residue, including nine previously unpicked taxa. Count variance of three individuals. Bray-Curtis similarity index of 92.5%. Biomass data not comprehensive. Biomass on average 3.8% lighter than Unicomarine Ltd.

Particle Size (Quality Control Component with Pass/Fail NMBAQC Standards)

PS20 – All NMBAQCS standards passed.
No major differences in size distribution curve. Sediment described as 'sand'.

PS21 – All NMBAQCS standards passed.
No major differences in size distribution curve. Sediment described as 'mud'.

Laboratory – LB0909

Macrobenthos (Training Component)

MB10 – Two taxonomic differences. Nineteen individuals not picked from residue. Count variance of seven individuals. Bray-Curtis similarity index of 94.3%. No biomass data supplied.

Ring Test (Training Component)

RT20 – Two generic and four specific differences. Number of AQC identifications in Mid group.
RT21 – Two generic and five specific differences. Number of AQC identifications in High group.

Laboratory Reference (Training Component)

LR07 – Four generic and six specific differences.

Own Sample (Quality Control Component with Pass/Fail NMBAQC Standards)

OS20 – NMBAQCS sample flag – 'Fail'.
Ten taxonomic differences. Twenty-five individuals not picked from residue, including four previously unpicked taxa. Count variance of one individual. Bray-Curtis similarity index of 84.9%. No biomass data supplied.
OS21 – NMBAQCS sample flag – 'Fail'.
Five taxonomic differences. Eight individuals not picked from residue, including three previously unpicked taxa. Bray-Curtis similarity index of 76.9%. No biomass data supplied.
OS22 – NMBAQCS sample flag – 'Fail'.
Three taxonomic differences. One individual not picked from residue. Bray-Curtis similarity index of 80.5%. No biomass data supplied.

Particle Size (Quality Control Component with Pass/Fail NMBAQC Standards)

PS20 – Not participating in this component.
PS21 – Not participating in this component.

Laboratory – LB0910

Macrobenthos (Training Component)

MB10 - Not participating in this component.

Ring Test (Training Component)

RT20 – Fifteen generic and sixteen specific differences. Number of AQC identifications in High group.
RT21 – Not participating in this exercise.

Laboratory Reference (Training Component)

LR07 – Not participating in this exercise.

Own Sample (Quality Control Component with Pass/Fail NMBAQC Standards)

OS20 – NMBAQCS sample flag – 'Good'.
Sample audited by the Scheme's External Auditor due to Unicomarine Ltd. being responsible for the initial processing. One individual not picked from residue. Count variance of thirteen individuals. Bray-Curtis similarity index of 99.4%. Biomass on average 4.2% heavier than the Auditor.
OS21 – NMBAQCS sample flag – 'Good'.
Sample audited by the Scheme's External Auditor due to Unicomarine Ltd. being responsible for the initial processing. One individual not picked from residue. Count variance of twelve

individuals. Bray-Curtis similarity index of 99.2%. Biomass on average 9.2% lighter than the Auditor.

OS22 – NMBAQCS sample flag – 'Good'.
Sample audited by the Scheme's External Auditor due to Unicomarine Ltd. being responsible for the initial processing. Three individuals not picked from residue. Count variance of thirty-two individuals. Bray-Curtis similarity index of 98.7%. Biomass on average 3.11% lighter than the Auditor.

Particle Size (Quality Control Component with Pass/Fail NMBAQC Standards)

PS20 – All NMBAQCS standards passed.
Data from centralised analysis; No major differences in size distribution curve. Sediment described as 'coarse sand'.

PS21 – All NMBAQCS standards passed.
Data from centralised analysis; Size distribution curve to the left of the majority of curves. Sediment described as 'muddy'.

Laboratory – LB0911

Macrobenthos (Training Component)

MB10 - Three taxonomic differences. One hundred and fifty-nine individuals not picked from the residue, including one previously unpicked taxon. Count variance of forty-nine individuals. Bray-Curtis similarity index of 92.1%. Biomass on average 2.9% lighter than Unicomarine Ltd. Residue/fauna stained.

Ring Test (Training Component)

RT20 – Three generic and five specific differences. Number of AQC identifications in Mid group.

RT21 – Three generic and four specific differences. Number of AQC identifications in Mid group.

Laboratory Reference (Training Component)

LR07 - One generic and one specific difference.

Own Sample (Quality Control Component with Pass/Fail NMBAQC Standards)

OS20 – NMBAQCS sample flag – 'Acceptable'.
One taxonomic difference. Ten individuals not picked from residue, including one previously unpicked taxon. Count variance of one individual. Bray-Curtis similarity index of 94.3%. Biomass on average 3.6% lighter than Unicomarine Ltd.

OS21 – NMBAQCS sample flag – 'Good'.
One taxonomic difference. All individuals extracted from the residue. Bray-Curtis similarity index of 96.4%. Biomass on average 0.2% heavier than Unicomarine Ltd.

OS22 – NMBAQCS sample flag – 'Good'.
One individual not picked from residue. Bray-Curtis similarity index of 96.8%. Biomass on average 21.3% heavier than Unicomarine Ltd.

Particle Size (Quality Control Component with Pass/Fail NMBAQC Standards)

PS20 – All NMBAQCS standards passed.
No major differences in size distribution curve. Sediment described as 'gritty sand'.

PS21 – All NMBAQCS standards passed.
No major differences in size distribution curve. Sediment described as 'sandy mud'.

Laboratory – LB0912

Macrobenthos (Training Component)

MB10 – Two taxonomic differences. One hundred and ninety-two individuals not picked from the residue. Count variance of one hundred and three individuals. Bray-Curtis similarity index of 93.5%. Biomass on average 17.2% heavier than Unicomarine Ltd.

Ring Test (Training Component)

RT20 – Not participating in this component.
RT21 – Not participating in this component.

Laboratory Reference (Training Component)

LB07 - Not participating in this component.

Own Sample (Quality Control Component with Pass/Fail NMBAQC Standards)

OS20 – Not participating in this component.
OS21 – Not participating in this component.
OS22 – Not participating in this component.

Particle Size (Quality Control Component with Pass/Fail NMBAQC Standards)

PS20 – Not participating in this component.
PS21 – Not participating in this component.

Laboratory – LB0913

Macrobenthos (Training Component)

MB10 – Four taxonomic differences. Count variance of four individuals. Faunal extraction efficiency could not be measured due to the subsampling method used by the participating laboratory. Bray-Curtis similarity index of 96.1%. No biomass data supplied. Fauna/residue stained. Fauna subsampled.

Ring Test (Training Component)

RT20 – Five generic and five specific differences. Number of AQC identifications in Mid group.
RT21 – One generic and four specific differences. Number of AQC identifications in Mid group.

Laboratory Reference (Training Component)

LR07 – Seven generic and eight specific differences.

Own Sample (Quality Control Component with Pass/Fail NMBAQC Standards)

OS20 – Not participating in this component.
OS21 – Not participating in this component.
OS22 – Not participating in this component.

Particle Size (Quality Control Component with Pass/Fail NMBAQC Standards)

PS20 – No data supplied for sorting and IGS(SKi) standards. All remaining NMBAQCS standards passed.
No major differences in size distribution curve. Sediment described as 'coarse sand'.
PS21 – No data supplied for sorting and IGS(SKi) standards. All remaining NMBAQCS standards passed.
Size distribution curve to the left of the majority of curves. No sediment description given.

Laboratory – LB0914

Macrobenthos (Training Component)

MB10 – Not participating in this component.

Ring Test (Training Component)

RT20 – Not participating in this exercise.
RT21 – One specific difference. Number of AQC identifications in Low group.

Laboratory Reference (Training Component)

LR07 – Not participating in this exercise.

Own Sample (Quality Control Component with Pass/Fail NMBAQC Standards)

OS20 – Not participating in this exercise.
OS21 – Not participating in this exercise.
OS22 – Not participating in this exercise.

Particle Size (Quality Control Component with Pass/Fail NMBAQC Standards)

PS20 – Not participating in this exercise.
PS21 – Not participating in this exercise.

Laboratory – LB0915

Macrobenthos (Training Component)

MB10 – Sample processed using the wrong sieve mesh (1mm), therefore comparisons with results from other laboratories are limited. One taxonomic difference. Twenty-nine individuals not picked from the residue. Count variance of four individuals. Bray-Curtis similarity index of 98.1%. Biomass on average 5.6% lighter than Unicomarine Ltd.

Ring Test (Training Component)

RT20 – Two generic and two specific differences. Number of AQC identifications in Low group.
RT21 – One specific difference. Number of AQC identifications in Low group.

Laboratory Reference (Training Component)

LR07 – All specimens correctly identified.

Own Sample (Quality Control Component with Pass/Fail NMBAQC Standards)

OS20 – Not participating in this component.
OS21 – Not participating in this component.
OS22 – Not participating in this component.

Particle Size (Quality Control Component with Pass/Fail NMBAQC Standards)

PS20 – Not participating in this exercise.
PS21 – Not participating in this exercise.

Laboratory – LB0916

Macrobenthos (Training Component)

MB10 – Not participating in this exercise.

Ring Test (Training Component)

RT20 – Not participating in this exercise.
RT21 – Not participating in this exercise.

Laboratory Reference (Training Component)

LR07 – Not participating in this exercise.

Own Sample (Quality Control Component with Pass/Fail NMBAQC Standards)

OS20 – NMBAQCS sample flag – 'Fail'.
Six taxonomic differences. One hundred and sixty-six individuals not picked from residue, including fifteen previously unpicked taxa. Count variance of eleven individuals. Bray-Curtis similarity index of 70.3%. No biomass data supplied.
OS21 – NMBAQCS sample flag – 'Acceptable'.
Five taxonomic differences. Two hundred and sixty-two individuals not picked from residue, including sixteen previously unpicked taxa. Count variance of eight individuals. Bray-Curtis similarity index of 94.7%. No biomass data supplied.
OS22 – NMBAQCS sample flag – 'Fail'.
Two taxonomic differences. One individual not picked from residue, this was a previously unpicked taxon. Count variance of one individual. Bray-Curtis similarity index of 78.6%. No biomass data supplied.

Particle Size (Quality Control Component with Pass/Fail NMBAQC Standards)

PS20 – All NMBAQCS standards passed.
Size distribution curve slightly to the left of the majority of curves. Sediment described as 'sand'.
PS21 – Not participating in this exercise.

Laboratory – LB0917

Macrobenthos (Training Component)

MB10 - Not participating in this component.

Ring Test (Training Component)

RT20 – Three generic and three specific differences. Number of AQC identifications in Low group.
RT21 – Two generic and three specific differences. Number of AQC identifications in Low group.

Laboratory Reference (Training Component)

LR07 – Two generic and three specific differences.

Own Sample (Quality Control Component with Pass/Fail NMBAQC Standards)

OS20 – NMBAQCS sample flag – 'Poor'. Remedial action has subsequently been successfully performed upon the remaining replicates from this station.
Twelve taxonomic differences. Five hundred and forty-six individuals not picked from residue, including three previously unpicked taxa. Count variance of five individuals. Bray-Curtis similarity index of 86.2%. Biomass on average 8.0% heavier than Unicomarine Ltd.
OS21 – NMBAQCS sample flag – 'Good'.
One individual not picked from residue. Count variance of three individuals. Bray-Curtis similarity index of 98.4%. Biomass on average 8.8% lighter than Unicomarine Ltd.
OS22 – NMBAQCS sample flag – 'Good'.
Forty-three individuals not picked from residue. Bray-Curtis similarity index of 96.8%. Biomass on average 0.6% heavier than Unicomarine Ltd.

Particle Size (Quality Control Component with Pass/Fail NMBAQC Standards)

PS20 – All NMBAQCS standards passed.
Data from centralised analysis; No major differences in size distribution curve. Sediment described as 'coarse sand'.
PS21 – All NMBAQCS standards passed.
Data from centralised analysis; Size distribution curve to the left of the majority of curves. Sediment described as 'muddy'.

Laboratory – LB0918

Macrobenthos (Training Component)

MB10 – Four taxonomic differences. Two hundred and forty individuals not picked from residue, including one previously unpicked taxon. Count variance of one hundred and three individuals. Bray-Curtis similarity index of 81.9%. Biomass on average 37.3% lighter than Unicomarine Ltd. Fauna/residue stained.

Ring Test (Training Component)

RT20 – Not participating in this exercise.
RT21 – Not participating in this exercise.

Laboratory Reference (Training Component)

LR07 – All specimens correctly identified.

Own Sample (Quality Control Component with Pass/Fail NMBAQC Standards)

OS20 – NMBAQCS sample flag – 'Good'.
Sample audited by the Scheme's External Auditor due to Unicomarine Ltd. being responsible for the initial processing. One taxonomic difference. Nine individuals not picked from residue. Count variance of fifty-six individuals. Bray-Curtis similarity index of 98.5%. Biomass on average 6.7% heavier than the Auditor.
OS21 – NMBAQCS sample flag – 'Good'.
Sample audited by the Scheme's External Auditor due to Unicomarine Ltd. being responsible for the initial processing. Two individuals not picked from the residue. Count variance of four individuals. Bray-Curtis similarity index of 98.2%. Biomass on average 20% lighter than the Auditor.
OS22 – NMBAQCS sample flag – 'Good'.
Sample audited by the Scheme's External Auditor due to Unicomarine Ltd. being responsible for the initial processing. Two individuals not picked from residue, these belonged to a previously unpicked taxon. Count variance of two individuals. Bray-Curtis similarity index of 99.5%. Biomass on average 3.0% lighter than the Auditor.

Particle Size (Quality Control Component with Pass/Fail NMBAQC Standards)

PS20 – All NMBAQCS standards passed.
No major differences in size distribution curve. Sediment described as 'coarse sand/gravel'.
PS21 – NMBAQCS standards for %silt/clay, median and mean failed. Sorting and IGS(SKi) standards passed.
Size distribution curve significantly to the left of the majority of curves. Sediment described as 'muddy sand'.

Laboratory – LB0919

Macrobenthos (Training Component)

MB10 - Not participating in this component.

Ring Test (Training Component)

RT20 – Five generic and seven specific differences. Number of AQC identifications in High group.
RT21 – Four generic and five specific differences. Number of AQC identifications in High group.

Laboratory Reference (Training Component)

LR07 – Five generic and six specific differences.

Own Sample (Quality Control Component with Pass/Fail NMBAQC Standards)

OS20 – NMBAQCS sample flag – 'Excellent'.

All individuals extracted from residue. Bray-Curtis similarity index of 100%. Biomass on average 15.4% lighter than Unicomarine Ltd.
OS21 – NMBAQCS sample flag – 'Excellent'.
All individuals extracted from residue. Bray-Curtis similarity index of 100%. Biomass on average 7.9% lighter than Unicomarine Ltd.
OS22 – NMBAQCS sample flag – 'Good'.
Two individuals not picked from residue, these were two previously unpicked taxa. Bray-Curtis similarity index of 95.2%. Biomass on average 41.0% lighter than Unicomarine Ltd.

Particle Size (Quality Control Component with Pass/Fail NMBAQC Standards)

PS20 – NMBAQCS standards for %silt/clay and IGS(SKi) failed. No data received for sorting. All remaining standards passed.
Size distribution curve below that of the majority of curves. Sediment described as 'sand'.
PS21 – All NMBAQCS standards passed.
No major differences in size distribution curve. Sediment described as 'mud'.

Laboratory – LB0920

Macrobenthos (Training Component)

MB10 – Not participating in this component.

Ring Test (Training Component)

RT20 – Not participating in this component.
RT21 – Not participating in this component.

Laboratory Reference (Training Component)

LR07 - Not participating in this component.

Own Sample (Quality Control Component with Pass/Fail NMBAQC Standards)

OS20 – Not participating in this component.
OS21 – Not participating in this component.
OS22 – Not participating in this component.

Particle Size (Quality Control Component with Pass/Fail NMBAQC Standards)

PS20 – All NMBAQCS standards passed.
No major differences in size distribution curve. Sediment described as 'coarse sand'.
PS21 – All NMBAQCS standards passed.
Size distribution curve to the left of the majority of curves. Sediment described as 'muddy'.

Laboratory – LB0921

Macrobenthos (Training Component)

MB10 – Not participating in this component.

Ring Test (Training Component)

RT20 – Not participating in this component.
RT21 – Not participating in this component.

Laboratory Reference (Training Component)

LR07 – Not participating in this component.

Own Sample (Quality Control Component with Pass/Fail NMBAQC Standards)

OS20 – NMBAQCS sample flag – 'Good'.
Two taxonomic difference. Twenty-five individuals not picked from residue, including one previously unpicked taxon. Count variance of one individual. Bray-Curtis similarity index of 97.5%. No biomass data supplied.

OS21 – NMBAQCS sample flag – 'Good'.
Two individuals not picked from residue. Count variance of twenty-four individuals. Bray-Curtis similarity index of 99.4%. No biomass data supplied.
OS22 – NMBAQCS sample flag – 'Acceptable'.
One taxonomic difference. All individuals extracted from residue. Bray-Curtis similarity index of 92.9%. No biomass data supplied.

Particle Size (Quality Control Component with Pass/Fail NMBAQC Standards)

PS20 – Not participating in this component.
PS21 – Not participating in this component.

Laboratory – LB0922

Macrobenthos (Training Component)

MB10 – Not participating in this component.

Ring Test (Training Component)

RT20 – Eleven generic and twelve specific differences. Number of AQC identifications in High group.
RT21 – Not participating in this exercise.

Laboratory Reference (Training Component)

LR07 – Not participating in this exercise.

Own Sample (Quality Control Component with Pass/Fail NMBAQC Standards)

OS20 – NMBAQCS sample flag – 'Good'.
Twenty-two individuals not picked from residue. Count variance of seven individuals. Bray-Curtis similarity index of 98.1%. Biomass on average 15.3% heavier than Unicomarine Ltd.
OS21 – NMBAQCS sample flag – 'Acceptable'.
Twenty-eight individuals not picked from residue. Count variance of eight individuals. Bray-Curtis similarity index of 94.4%. Biomass on average 27.1% lighter than Unicomarine Ltd.
OS22 – Sample not received.

Particle Size (Quality Control Component with Pass/Fail NMBAQC Standards)

PS20 – All NMBAQCS standards passed.
Data from centralised analysis; No major differences in size distribution curve. Sediment described as 'coarse sand'.
PS21 – All NMBAQCS standards passed.
Data from centralised analysis; Size distribution curve to the left of the majority of curves. Sediment described as 'muddy'.

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 nine had e-mail capabilities. E-mail capabilities must be made a prerequisite for participation in the Scheme. All primary correspondence for Scheme year

ten will continue to be conducted via e-mail; hard copies of data sheets will be provided only 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. Some laboratories submitted permanent or semi-permanent slides of oligochaetes, 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 unidentifiable; trials should be commissioned to derive the best protocol for the blotted weighing technique.
6. The particle size exercises (PS) once again show 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. Some laboratories are still not submitting the PS data in the requested format and some 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 PS20 and PS21, these were extremely varied. Guidance/training should be provided for all biologists that have to report upon raw sediment data.
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 nine mollusc specimens distributed in RT20 were responsible for 49% of the generic and 41% 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. Differences in the literature used for identification of invertebrates have been highlighted by the RT, MB and OS exercises. Funding should be made available for the collation of identification literature into a searchable database for use by Scheme participants. Unpublished keys from workshops, etc could be posted of the Scheme's website.
10. 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 (16% of the actual total taxa in the sample) were either not extracted or not distinguished from other extracted taxa. On average 0.70 taxa were not extracted from the residue. None of the participating laboratories extracted all the countable individuals from their residues. In the worst instance 17.5% of total individuals in the sample were not extracted. The situation was worse for the OS samples where a maximum of 16 taxa and up to 29% of the taxa were not extracted. In the worst instance 546 individuals were not picked from the residue and up to 35% of the total

individuals remained in the residue. On average for the OS exercise 1.73 taxa were not extracted compared with 1.98, 2.04, 1.25, 1.48, 0.45 and 1.39 taxa from last six 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.

11. 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. In the previous Scheme year 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.
12. 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. Participants are encouraged to review their exercise reports and provide feedback concerning content and format wherever appropriate.
13. The NMMP database should be managed with a clear emphasis upon data quality. A facility for indicating audited samples and flags should be available. In the event of an NMMP Own Sample failing to attain a 'pass' flag all replicates from the NMMP site should be upheld a 'failing' until remedial action upon the remaining replicates has attained a 'pass' flag. A facility for tracking and evaluating the remedial action applied to failing samples must be devised.
14. 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.
15. Funding should be provided for the development and maintenance of the Scheme's website (www.nmbaqcs.org). The site is along way short of it's full potential. The current website was designed and is maintained free of charge. Provisions should be made for accessing online results/reports.

8. References

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

Section 6 Contd.

Contractor Report -Tables:

Table 1. Results from the analysis of Macrobenthic sample MB10 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
LB0903	20	21	-1	4.8	2390	2479	-89	3.6	0	111	4.5	22	70.41	4
LB0904	16	17	-1	5.9	954	1102	-148	13.4	1	120	10.9	-28	83.17	4
LB0905	16	18	-2	11.1	1247	1431	-184	12.9	2	204	14.3	20	80.58	4
LB0906	16	19	-3	15.8	1377	1818	-441	24.3	1	318	17.5	-123	79.25	2
LB0908	18	19	-1	5.3	1842	1832	10	0.5	1	78	4.3	88	97.06	0
LB0909	22	20	2	9.1	1616	1628	-12	0.7	0	19	1.2	7	94.27	2
LB0911	18	19	-1	5.3	1512	1622	-110	6.8	1	159	9.8	49	92.09	3
LB0912	17	20	-3	15.0	2596	2685	-89	3.3	0	192	7.2	103	93.51	2
LB0913	16	17	-1	5.9	3296	3300	-4	0.1	n/a	n/a	n/a	-4	96.06	4
LB0915	25	22	3	12.0	1288	1313	-25	1.9	0	29	2.2	4	98.12	1
LB0918	17	18	-1	5.6	1817	2160	-343	15.9	1	240	11.1	-103	81.87	4

Key:
PL - participating laboratory.
UM - Unicomarine Ltd.
Shaded data - processed using 1mm sieve mesh (all other data >0.5mm).
n/a - data not available due to subsample method preventing audit.
See Annual 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 MB10.

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB0903	UM count	-	1035	723	-	8	-	339	374	2479
	PL missed	-	2	0	-	0	-	80	29	111
	%missed	-	0.2	0.0	-	0.0	-	23.6	7.8	4.5
LB0904	UM count	-	440	386	-	20	-	140	116	1102
	PL missed	-	33	0	-	0	-	24	63	120
	%missed	-	7.5	0.0	-	0.0	-	17.1	54.3	10.9
LB0905	UM count	-	764	452	-	11	-	204	-	1431
	PL missed	-	97	44	-	0	-	63	-	204
	%missed	-	12.7	9.7	-	0.0	-	30.9	-	14.3
LB0906	UM count	-	785	533	-	11	-	96	393	1818
	PL missed	-	87	3	-	0	-	76	152	318
	%missed	-	11.1	0.6	-	0.0	-	79.2	38.7	17.5
LB0908	UM count	1	869	379	-	17	-	175	391	1832
	PL missed	0	9	3	-	2	-	46	18	78
	%missed	0.0	1.0	0.8	-	11.8	-	26.3	4.6	4.3
LB0909	UM count	2	790	629	-	17	-	190	-	1628
	PL missed	0	10	2	-	0	-	7	-	19
	%missed	0.0	1.3	0.3	-	0.0	-	3.7	-	1.2
LB0911	UM count	-	851	472	-	21	-	278	-	1622
	PL missed	-	9	0	-	1	-	149	-	159
	%missed	-	1.1	0.0	-	4.8	-	53.6	-	9.8
LB0912	UM count	-	1135	467	-	12	-	478	593	2685
	PL missed	-	26	1	-	0	-	31	134	192
	%missed	-	2.3	0.2	-	0.0	-	6.5	22.6	7.2
LB0913	UM count	-	-	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB0915	UM count	-	452	475	-	13	-	166	207	1313
	PL missed	-	5	0	-	0	-	18	6	29
	%missed	-	1.1	0.0	-	0.0	-	10.8	2.9	2.2
LB0918	UM count	-	1238	479	-	18	-	174	251	2160
	PL missed	-	9	0	-	0	-	43	188	240
	%missed	-	0.7	0.0	-	0.0	-	24.7	74.9	11.1

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

Table 3. Comparison of the estimates of biomass made by the participating laboratories with those made by Unicomarine Ltd. for the major taxonomic groups present in sample MB10. Values are in grams (g).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB0903	PL	-	0.24506	0.17833	-	0.0025	-	0.31192	0.011	0.74881
	UM	-	0.3335	0.2728	-	0.003	-	0.45	0.009	1.0683
	%diff.	-	-36.1	-53.0	-	-20.0	-	-44.3	18.2	-42.7
LB0904	PL	-	0.1175	0.141	-	0.0404	-	0.2691	0.0034	0.5714
	UM	-	0.1548	0.1589	-	0.0412	-	0.2793	0.0031	0.6373
	%diff.	-	-31.7	-12.7	-	-2.0	-	-3.8	8.8	-11.5
LB0905	PL	-	0.41	0.1832	-	0.0129	-	0.2345	-	0.8406
	UM	-	0.4248	0.1544	-	0.0146	-	0.2305	-	0.8243
	%diff.	-	-3.6	15.7	-	-13.2	-	1.7	-	1.9
LB0906	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB0908	PL	0.0151	0.1037	0.0759	-	0.0089	-	0.2959	0.0056	0.5051
	UM	0.0215	0.1859	0.122	-	0.0122	-	0.2864	0.0063	0.6343
	%diff.	-42.4	-79.3	-60.7	-	-37.1	-	3.2	-12.5	-25.6
LB0909	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB0911	PL	-	0.1485	0.1465	-	0.0251	-	0.533	-	0.8531
	UM	-	0.1752	0.1727	-	0.0245	-	0.5054	-	0.8778
	%diff.	-	-18.0	-17.9	-	2.4	-	5.2	-	-2.9
LB0912	PL	-	0.4059	0.248	-	0.023	-	5.4187	0.01	6.1056
	UM	-	0.2126	0.1928	-	0.0081	-	4.6312	0.0109	5.0556
	%diff.	-	47.6	22.3	-	64.8	-	14.5	-9.0	17.2
LB0913	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB0915	PL	-	0.1217	0.1794	-	0.0066	-	0.386	0.0083	0.702
	UM	-	0.1293	0.1819	-	0.0069	-	0.4171	0.0062	0.7414
	%diff.	-	-6.2	-1.4	-	-4.5	-	-8.1	25.3	-5.6
LB0918	PL	-	0.0352	0.0397	-	0.0063	-	0.3804	0.0004	0.462
	UM	-	0.0834	0.0939	-	0.0161	-	0.439	0.0021	0.6345
	%diff.	-	-136.9	-136.5	-	-155.6	-	-15.4	-425.0	-37.3

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

Table 4. Variation in faunal content of samples distributed as MB10.

Taxa*

LabCode	Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Total taxa
LB0903	0	10	3	0	1	0	6	1	21
LB0904	0	8	2	0	1	0	4	2	17
LB0905	0	11	2	0	2	0	4	1	20
LB0906	0	11	2	0	1	0	4	1	19
LB0908	1	10	2	0	2	0	3	1	19
LB0909	1	10	2	0	2	0	5	1	21
LB0911	0	10	3	0	2	0	4	1	20
LB0912	0	12	2	0	1	0	4	1	20
LB0913	1	11	2	0	2	0	5	2	23
LB0915	0	12	2	0	1	0	5	2	22
LB0918	0	10	2	0	2	0	3	1	18
Mean	0	11	2	0	2	0	4	1	20
Max	1	12	3	0	2	0	5	2	23
Min	0	8	2	0	1	0	3	1	17

*UM data used for all faunal groups. Shaded data derived using 1mm sieve mesh - all other data 0.5mm.

Individuals*

LabCode	Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Total Ind.
LB0903	0	1035	723	0	8	0	339	374	2479
LB0904	0	440	386	0	20	0	140	116	1102
LB0905	0	677	463	0	12	0	294	438	1884
LB0906	0	785	533	0	11	0	96	393	1818
LB0908	1	869	379	0	17	0	175	391	1832
LB0909	2	790	629	0	17	0	190	187	1815
LB0911	0	851	472	0	21	0	278	287	1909
LB0912	0	1135	467	0	12	0	478	593	2685
LB0913	1	1375	765	0	27	0	340	880	3388
LB0915	0	452	475	0	13	0	166	207	1313
LB0918	0	1238	479	0	18	0	174	251	2160
Mean	0	877	525	0	16	0	243	374	2035
Max	2	1375	765	0	27	0	478	880	3388
Min	0	440	379	0	8	0	96	116	1102

*UM data used for all faunal groups. Shaded data derived using 1mm sieve mesh - all other data 0.5mm.

Table 5. Results from the analysis of Own Samples (OS20 to OS22) 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
LB0902	OS20	13	13	0	0.0	1188	1174	14	1.2	0	6	0.5	20	99.07	0	Biomass 3 dp
LB0902	OS21	7	7	0	0.0	403	412	-9	2.2	0	5	1.2	-4	96.69	0	Biomass 3 dp
LB0902	OS22	13	13	0	0.0	379	375	4	1.1	0	2	0.5	6	98.14	0	Biomass 3 dp
LB0903	OS20	99	103	-4	3.9	911	916	-5	0.5	1	5	0.5	0	96.91	8	
LB0903	OS21	35	36	-1	2.8	404	407	-3	0.7	0	6	1.5	3	93.74	6	
LB0903	OS22	75	82	-7	8.5	1756	1962	-206	10.5	3	214	10.9	8	91.23	14	No biomass data
LB0904	OS20	10	9	1	10.0	37	35	2	5.4	0	0	0.0	2	88.89	3	Biomass by major group
LB0904	OS21	19	18	1	5.3	100	98	2	2.0	0	0	0.0	2	43.32	2	Biomass by major group
LB0904	OS22	9	9	0	0.0	21	22	-1	4.5	0	0	0.0	-1	83.72	2	Biomass by major group
LB0905	OS20	30	26	4	13.3	62	62	0	0.0	0	0	0.0	0	72.58	7	Biomass 5 dp
LB0905	OS21	34	34	0	0.0	174	173	1	0.6	0	0	0.0	1	98.56	1	Biomass 5 dp
LB0905	OS22	32	31	1	3.1	258	256	2	0.8	0	0	0.0	2	99.61	0	Biomass 5 dp
LB0906	OS20	18	18	0	0.0	60	61	-1	1.6	0	1	1.6	0	95.08	1	No biomass; Data differs from submission
LB0906	OS21	17	22	-5	22.7	102	117	-15	12.8	5	14	12.0	-1	93.15	0	No biomass; Data differs from submission
LB0906	OS22	61	66	-5	7.6	368	403	-35	8.7	5	34	8.4	-1	84.05	6	No biomass; Data differs from submission
LB0908	OS20	52	58	-6	10.3	782	786	-4	0.5	6	5	0.6	1	98.66	2	Biomass data not comprehensive
LB0908	OS21	52	51	1	1.9	254	252	2	0.8	0	0	0.0	2	96.44	5	Biomass data not comprehensive
LB0908	OS22	35	44	-9	20.5	199	210	-11	5.2	9	14	6.7	3	92.46	2	Biomass data not comprehensive
LB0909	OS20	44	50	-6	12.0	282	308	-26	8.4	4	25	8.1	-1	84.94	10	No biomass
LB0909	OS21	20	23	-3	13.0	35	43	-8	18.6	3	8	18.6	0	76.92	5	No biomass
LB0909	OS22	19	19	0	0.0	41	42	-1	2.4	0	1	2.4	0	80.46	3	No biomass
LB0910	OS20	35	35	0	0.0	961	949	12	1.2	0	1	0.1	13	99.37	0	
LB0910	OS21	48	47	1	2.1	2969	2958	11	0.4	0	1	0.0	12	99.24	0	
LB0910	OS22	39	39	0	0.0	1323	1294	29	2.2	0	3	0.2	32	98.67	0	
LB0911	OS20	31	32	-1	3.1	109	118	-9	7.6	1	10	8.5	1	94.27	1	
LB0911	OS21	11	12	-1	8.3	28	28	0	0.0	0	0	0.0	0	96.43	1	
LB0911	OS22	5	5	0	0.0	15	16	-1	6.3	0	1	6.3	0	96.77	0	
LB0916	OS20	57	80	-23	28.8	302	479	-177	37.0	15	166	34.7	-11	70.25	6	No biomass data
LB0916	OS21	71	89	-18	20.2	2585	2839	-254	8.9	16	262	9.2	8	94.68	5	No biomass data
LB0916	OS22	8	10	-2	20.0	27	29	-2	6.9	1	1	3.4	-1	78.57	2	No biomass data
LB0917	OS20	75	79	-4	5.1	2602	3153	-551	17.5	3	546	17.3	-5	86.15	12	
LB0917	OS21	7	7	0	0.0	128	126	2	1.6	0	1	0.8	3	98.43	0	
LB0917	OS22	16	16	0	0.0	739	782	-43	5.5	0	43	5.5	0	96.78	0	
LB0918	OS20	91	92	-1	1.1	3284	3237	47	1.4	0	9	0.3	56	98.54	1	
LB0918	OS21	19	19	0	0.0	109	107	2	1.8	0	2	1.9	4	98.20	0	
LB0918	OS22	51	52	-1	1.9	424	424	0	0.0	1	2	0.5	2	99.54	0	
LB0919	OS20	1	1	0	0.0	6	6	0	0.0	0	0	0.0	0	100.00	0	
LB0919	OS21	4	4	0	0.0	21	21	0	0.0	0	0	0.0	0	100.00	0	
LB0919	OS22	5	7	-2	28.6	20	22	-2	9.1	2	2	9.1	0	95.24	0	
LB0921	OS20	26	26	0	0.0	651	677	-26	3.8	1	25	3.7	-1	97.52	2	No biomass data
LB0921	OS21	22	22	0	0.0	3148	3126	22	0.7	0	2	0.1	24	99.43	0	No biomass data
LB0921	OS22	7	7	0	0.0	13	13	0	0.0	0	0	0.0	0	92.86	1	No biomass data
LB0922	OS20	7	7	0	0.0	352	367	-15	4.1	0	22	6.0	7	98.06	0	
LB0922	OS21	4	4	0	0.0	306	342	-36	10.5	0	28	8.2	-8	94.44	0	
LB0922	OS22	-	-	-	-	-	-	-	-	-	-	-	-	-	-	

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

Table 6. Comparison of the efficiency of extraction of fauna by the participating laboratories for the major taxonomic groups present in Own Samples (OS20-22).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB0902	UM count	-	875	285	-	-	-	14	-	1174
OS20	PL missed	-	6	0	-	-	-	0	-	6
	%missed	-	0.7	0.0	-	-	-	0.0	-	0.5
LB0902	UM count	-	187	223	-	-	-	2	-	412
OS21	PL missed	-	3	2	-	-	-	0	-	5
	%missed	-	1.6	0.9	-	-	-	0.0	-	1.2
LB0902	UM count	-	48	318	-	-	-	8	1	375
OS22	PL missed	-	1	1	-	-	-	0	0	2
	%missed	-	2.1	0.3	-	-	-	0.0	0.0	0.5
LB0903	UM count	21	401	-	-	60	52	169	213	916
OS20	PL missed	0	0	-	-	0	0	5	0	5
	%missed	0.0	0.0	-	-	0.0	0.0	3.0	0.0	0.5
LB0903	UM count	-	114	45	-	-	6	111	131	407
OS21	PL missed	-	1	0	-	-	0	4	1	6
	%missed	-	0.9	0.0	-	-	0.0	3.6	0.8	1.5
LB0903	UM count	-	610	-	1	35	34	1264	18	1962
OS22	PL missed	-	121	-	0	1	0	82	10	214
	%missed	-	19.8	-	0.0	2.9	0.0	6.5	55.6	10.9
LB0904	UM count	-	15	-	-	-	-	20	-	35
OS20	PL missed	-	0	-	-	-	-	0	-	0
	%missed	-	0.0	-	-	-	-	0.0	-	0.0
LB0904	UM count	1	3	-	-	2	1	89	2	98
OS21	PL missed	0	0	-	-	0	0	0	0	0
	%missed	0.0	0.0	-	-	0.0	0.0	0.0	0.0	0.0
LB0904	UM count	-	15	-	-	-	-	7	-	22
OS22	PL missed	-	0	-	-	-	-	0	-	0
	%missed	-	0.0	-	-	-	-	0.0	-	0.0
LB0905	UM count	1	32	-	-	11	-	18	-	62
OS20	PL missed	0	0	-	-	0	-	0	-	0
	%missed	0.0	0.0	-	-	0.0	-	0.0	-	0.0
LB0905	UM count	-	57	-	-	4	7	102	3	173
OS21	PL missed	-	0	-	-	0	0	0	0	0
	%missed	-	0.0	-	-	0.0	0.0	0.0	0.0	0.0
LB0905	UM count	-	97	-	-	5	3	137	14	256
OS22	PL missed	-	0	-	-	0	0	0	0	0
	%missed	-	0.0	-	-	0.0	0.0	0.0	0.0	0.0
LB0906	UM count	-	26	-	-	-	6	27	2	61
OS20	PL missed	-	0	-	-	-	0	1	0	1
	%missed	-	0.0	-	-	-	0.0	3.7	0.0	1.6
LB0906	UM count	1	29	-	-	8	4	71	4	117
OS21	PL missed	1	1	-	-	0	0	10	2	14
	%missed	100.0	3.4	-	-	0.0	0.0	14.1	50.0	12.0
LB0906	UM count	14	239	-	-	4	68	36	42	403
OS22	PL missed	0	10	-	-	2	2	9	11	34
	%missed	0.0	4.2	-	-	50.0	2.9	25.0	26.2	8.4

Table 6. Comparison of the efficiency of extraction of fauna by the participating laboratories for the major taxonomic groups present in Own Samples (OS20-22).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB0908	UM count	1	670	15	-	76	-	20	4	786
OS20	PL missed	0	1	0	-	0	-	4	0	5
	%missed	0.0	0.1	0.0	-	0.0	-	20.0	0.0	0.6
LB0908	UM count	-	85	4	1	41	9	81	31	252
OS21	PL missed	-	0	0	0	0	0	0	0	0
	%missed	-	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
LB0908	UM count	-	57	-	-	124	1	12	16	210
OS22	PL missed	-	3	-	-	0	0	11	0	14
	%missed	-	5.3	-	-	0.0	0.0	91.7	0.0	6.7
LB0909	UM count	33	216	-	-	8	7	38	6	308
OS20	PL missed	1	14	-	-	0	0	9	1	25
	%missed	3.0	6.5	-	-	0.0	0.0	23.7	16.7	8.1
LB0909	UM count	5	27	-	-	2	4	4	1	43
OS21	PL missed	4	2	-	-	0	0	2	0	8
	%missed	80.0	7.4	-	-	0.0	0.0	50.0	0.0	18.6
LB0909	UM count	-	28	-	-	1	3	9	1	42
OS22	PL missed	-	1	-	-	0	0	0	0	1
	%missed	-	3.6	-	-	0.0	0.0	0.0	0.0	2.4
LB0910	UM count	3	267	185	-	53	-	36	405	949
OS20	PL missed	0	1	0	-	0	-	0	0	1
	%missed	0.0	0.4	0.0	-	0.0	-	0.0	0.0	0.1
LB0910	UM count	4	1445	332	-	44	-	650	483	2958
OS21	PL missed	0	0	1	-	0	-	0	0	1
	%missed	0.0	0.0	0.3	-	0.0	-	0.0	0.0	0.0
LB0910	UM count	1	841	295	-	131	-	19	7	1294
OS22	PL missed	0	2	1	-	0	-	0	0	3
	%missed	0.0	0.2	0.3	-	0.0	-	0.0	0.0	0.2
LB0911	UM count	5	62	-	-	6	2	42	1	118
OS20	PL missed	0	2	-	-	0	0	8	0	10
	%missed	0.0	3.2	-	-	0.0	0.0	19.0	0.0	8.5
LB0911	UM count	-	10	-	-	2	2	14	-	28
OS21	PL missed	-	0	-	-	0	0	0	-	0
	%missed	-	0.0	-	-	0.0	0.0	0.0	-	0.0
LB0911	UM count	-	13	-	-	3	-	-	-	16
OS22	PL missed	-	0	-	-	1	-	-	-	1
	%missed	-	0.0	-	-	33.3	-	-	-	6.3
LB0916	UM count	4	201	-	1	30	35	140	68	479
OS20	PL missed	2	83	-	0	4	9	17	51	166
	%missed	50.0	41.3	-	0.0	13.3	25.7	12.1	75.0	34.7
LB0916	UM count	2	324	-	2	51	13	2374	73	2839
OS21	PL missed	0	104	-	0	10	6	105	37	262
	%missed	0.0	32.1	-	0.0	19.6	46.2	4.4	50.7	9.2
LB0916	UM count	-	20	1	-	-	-	8	-	29
OS22	PL missed	-	0	1	-	-	-	0	-	1
	%missed	-	0.0	100.0	-	-	-	0.0	-	3.4

Table 6. Comparison of the efficiency of extraction of fauna by the participating laboratories for the major taxonomic groups present in Own Samples (OS20-22).

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB0917	UM count	7	2144	26	4	198	-	303	471	3153
OS20	PL missed	1	281	6	4	20	-	100	134	546
	%missed	14.3	13.1	23.1	100.0	10.1	-	33.0	28.5	17.3
LB0917	UM count	-	-	125	-	-	-	-	1	126
OS21	PL missed	-	-	1	-	-	-	-	0	1
	%missed	-	-	0.8	-	-	-	-	0.0	0.8
LB0917	UM count	-	395	334	-	-	-	31	22	782
OS22	PL missed	-	7	8	-	-	-	14	14	43
	%missed	-	1.8	2.4	-	-	-	45.2	63.6	5.5
LB0918	UM count	-	1580	3	-	398	1	1106	149	3237
OS20	PL missed	-	6	0	-	0	0	3	0	9
	%missed	-	0.4	0.0	-	0.0	0.0	0.3	0.0	0.3
LB0918	UM count	-	26	45	-	1	-	35	-	107
OS21	PL missed	-	0	2	-	0	-	0	-	2
	%missed	-	0.0	4.4	-	0.0	-	0.0	-	1.9
LB0918	UM count	13	72	1	-	29	219	86	4	424
OS22	PL missed	0	0	0	-	0	0	0	2	2
	%missed	0.0	0.0	0.0	-	0.0	0.0	0.0	50.0	0.5
LB0919	UM count	-	-	-	-	6	-	-	-	6
OS20	PL missed	-	-	-	-	0	-	-	-	0
	%missed	-	-	-	-	0.0	-	-	-	0.0
LB0919	UM count	-	1	-	-	20	-	-	-	21
OS21	PL missed	-	0	-	-	0	-	-	-	0
	%missed	-	0.0	-	-	0.0	-	-	-	0.0
LB0919	UM count	1	4	-	-	15	-	1	1	22
OS22	PL missed	1	0	-	-	0	-	1	0	2
	%missed	100.0	0.0	-	-	0.0	-	100.0	0.0	9.1
LB0921	UM count	-	408	247	-	8	-	13	1	677
OS20	PL missed	-	16	9	-	0	-	0	0	25
	%missed	-	3.9	3.6	-	0.0	-	0.0	0.0	3.7
LB0921	UM count	-	2084	1027	-	2	-	3	10	3126
OS21	PL missed	-	1	1	-	0	-	0	0	2
	%missed	-	0.0	0.1	-	0.0	-	0.0	0.0	0.1
LB0921	UM count	-	9	-	-	4	-	-	-	13
OS22	PL missed	-	0	-	-	0	-	-	-	0
	%missed	-	0.0	-	-	0.0	-	-	-	0.0
LB0922	UM count	-	270	2	-	8	-	87	-	367
OS20	PL missed	-	15	1	-	2	-	4	-	22
	%missed	-	5.6	50.0	-	25.0	-	4.6	-	6.0
LB0922	UM count	-	10	330	-	2	-	-	-	342
OS21	PL missed	-	1	27	-	0	-	-	-	28
	%missed	-	10.0	8.2	-	0.0	-	-	-	8.2

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 OS20-OS22.

Sample OS20

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB0902	PL	-	0.1600	0.1200	-	-	-	0.0060	-	0.2860
	UM	-	0.1156	0.1001	-	-	-	0.0034	-	0.2191
	%diff.	-	27.8	16.6	-	-	-	43.3	-	23.4
LB0903	PL	0.2231	2.3307	-	-	0.0204	1.0732	7.9309	0.0515	11.6298
	UM	0.2417	2.4023	-	-	0.0186	0.8738	8.2778	0.0338	11.8480
	%diff.	-8.3	-3.1	-	-	8.8	18.6	-4.4	34.4	-1.9
LB0904	PL	-	-	-	-	-	-	-	-	0.00000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0905	PL	0.00629	0.09514	-	-	0.21716	-	0.51177	-	0.83036
	UM	0.0008	0.0677	-	-	0.1282	-	0.4039	-	0.6006
	%diff.	87.3	28.8	-	-	41.0	-	21.1	-	27.7
LB0906	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0908	PL	0.0012	1.3361	0.0011	-	0.0274	-	0.5449	4.2652	6.1759
	UM	0.0017	1.6233	0.0015	-	0.0453	-	0.5310	4.0493	6.2521
	%diff.	-41.7	-21.5	-36.4	-	-65.3	-	2.6	5.1	-1.2
LB0909	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0910	PL	0.0002	0.8419	0.0203	-	0.0025	-	0.0561	0.8898	1.8108
	UM	0.0003	0.8509	0.0208	-	0.0024	-	0.0559	0.8051	1.7354
	%diff.	-50.0	-1.1	-2.5	-	4.0	-	0.4	9.5	4.2
LB0911	PL	0.0013	1.3175	-	-	0.0070	0.0789	1.9411	2.2447	5.5905
	UM	0.0012	1.4014	-	-	0.0052	0.0773	1.8429	2.4615	5.7895
	%diff.	7.7	-6.4	-	-	25.7	2.0	5.1	-9.7	-3.6
LB0916	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0917	PL	0.0287	6.2123	0.0010	-	0.0453	-	38.4589	0.0033	44.7495
	UM	0.0162	3.9842	0.0029	-	0.0699	-	37.0913	0.0048	41.1693
	%diff.	43.6	35.9	-190.0	-	-54.3	-	3.6	-45.5	8.0
LB0918	PL	0.0018	4.9200	0.0009	-	0.4061	0.0008	1.3548	6.9414	13.6258
	UM	0.0014	4.6920	0.0009	-	0.3778	0.0007	1.3033	6.3366	12.7127
	%diff.	22.2	4.6	0.0	-	7.0	12.5	3.8	8.7	6.7
LB0919	PL	-	-	-	-	0.0013	-	-	-	0.0013
	UM	-	-	-	-	0.0015	-	-	-	0.0015
	%diff.	-	-	-	-	-15.4	-	-	-	-15.4
LB0921	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0922	PL	-	0.1957	0.0008	-	0.0187	-	2.3094	-	2.5246
	UM	-	0.1538	0.0004	-	0.0147	-	1.9686	-	2.1375
	%diff.	-	21.4	50.0	-	21.4	-	14.8	-	15.3

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 OS20-OS22.

Sample OS21

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB0902	PL	-	0.0580	0.0680	-	-	-	0.0020	-	0.1280
	UM	-	0.0401	0.0739	-	-	-	0.0005	-	0.1145
	%diff.	-	30.9	-8.7	-	-	-	75.0	-	10.5
LB0903	PL	-	8.1926	0.0020	-	-	0.0001	0.3637	-	8.5584
	UM	-	8.4993	0.0024	-	-	0.0002	0.3724	-	8.8743
	%diff.	-	-3.7	-20.0	-	-	-100.0	-2.4	-	-3.7
LB0904	PL	-	-	-	-	-	-	-	-	0.00000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0905	PL	-	0.76248	-	-	0.04086	40.04897	9.38272	0.00670	50.24173
	UM	-	0.5133	-	-	0.0251	31.7240	8.9573	0.0095	41.2292
	%diff.	-	32.7	-	-	38.6	20.8	4.5	-41.8	17.9
LB0906	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0908	PL	-	4.8329	0.0003	-	0.0157	0.1180	0.8461	0.0060	5.8190
	UM	-	4.8191	0.0006	-	0.0201	0.1207	0.8359	0.0062	5.8026
	%diff.	-	0.3	-100.0	-	-28.0	-2.3	1.2	-3.3	0.3
LB0909	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0910	PL	0.0012	3.8738	0.0898	-	0.1687	-	0.2713	0.3394	4.7442
	UM	0.0010	3.5637	0.0810	-	0.1763	-	0.2571	1.1027	5.1818
	%diff.	16.7	8.0	9.8	-	-4.5	-	5.2	-224.9	-9.2
LB0911	PL	-	0.3542	-	-	1.9173	0.4213	2.0458	-	4.7386
	UM	-	0.4036	-	-	1.8643	0.3943	2.0666	-	4.7288
	%diff.	-	-13.9	-	-	2.8	6.4	-1.0	-	0.2
LB0916	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0917	PL	-	-	0.0499	-	-	-	-	0.0001	0.050
	UM	-	-	0.0543	-	-	-	-	0.0001	0.0544
	%diff.	-	-	-8.8	-	-	-	-	0.0	-8.8
LB0918	PL	-	0.1525	0.0072	-	0.0002	-	0.0278	-	0.1877
	UM	-	0.1922	0.0069	-	0.0001	-	0.0260	-	0.2252
	%diff.	-	-26.0	4.2	-	50.0	-	6.5	-	-20.0
LB0919	PL	-	0.0005	-	-	0.0033	-	-	-	0.0038
	UM	-	0.0003	-	-	0.0038	-	-	-	0.0041
	%diff.	-	40.0	-	-	-15.2	-	-	-	-7.9
LB0921	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0922	PL	-	0.0624	0.0515	-	0.0016	-	-	-	0.1155
	UM	-	0.0488	0.0341	-	0.0013	-	-	-	0.0842
	%diff.	-	21.8	33.8	-	18.8	-	-	-	27.1

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 OS20-OS22.

Sample OS22

LabCode		Nemertea	Polychaeta	Oligochaeta	Chelicerata	Crustacea	Echinodermata	Mollusca	Other	Overall
LB0902	PL	-	0.0150	0.1070	-	-	-	0.0050	0.0010	0.1280
	UM	-	0.0088	0.0876	-	-	-	0.0006	0.0001	0.0971
	%diff.	-	41.3	18.1	-	-	-	88.0	90.0	24.1
LB0903	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0904	PL	-	-	-	-	-	-	-	-	0.00000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0905	PL	-	0.29600	-	-	0.06410	0.01006	6.34540	0.05618	6.77174
	UM	-	0.1635	-	-	0.0262	0.0099	5.2659	0.0299	5.4954
	%diff.	-	44.8	-	-	59.1	1.6	17.0	46.8	18.8
LB0906	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0908	PL	-	0.0170	-	-	0.2351	0.0073	0.1650	0.0035	0.4279
	UM	-	0.0250	-	-	0.2449	0.0128	0.1574	0.0039	0.4440
	%diff.	-	-47.1	-	-	-4.2	-75.3	4.6	-11.4	-3.8
LB0909	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0910	PL	0.0001	0.7357	0.0616	-	0.3926	-	22.9319	0.0002	24.1221
	UM	0.0001	1.1453	0.1202	-	0.6966	-	22.9100	0.0002	24.8724
	%diff.	0.0	-55.7	-95.1	-	-77.4	-	0.1	0.0	-3.1
LB0911	PL	-	0.5469	-	-	1.1877	-	-	-	1.7346
	UM	-	0.5139	-	-	0.8519	-	-	-	1.3658
	%diff.	-	6.0	-	-	28.3	-	-	-	21.3
LB0916	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0917	PL	-	0.0715	0.1431	-	-	-	2.7398	0.0003	2.955
	UM	-	0.0776	0.1238	-	-	-	2.7349	0.0002	2.9365
	%diff.	-	-8.5	13.5	-	-	-	0.2	33.3	0.6
LB0918	PL	0.0042	0.1738	0.0002	-	0.0058	0.7896	0.0514	0.0018	1.0268
	UM	0.0375	0.1755	0.0002	-	0.0055	0.7847	0.0530	0.0015	1.0579
	%diff.	-792.9	-1.0	0.0	-	5.2	0.6	-3.1	16.7	-3.0
LB0919	PL	-	0.0007	-	-	0.0031	-	-	0.0001	0.0039
	UM	-	0.0012	-	-	0.0042	-	-	0.0001	0.0055
	%diff.	-	-71.4	-	-	-35.5	-	-	0.0	-41.0
LB0921	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB0922	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-

Table 8. Summary of the results of particle size analysis of the replicate samples from sediment circulation PS20.

PS20	% Clay & Silt	Median (phi)	Mean (phi)	Sorting	Skew
PS20 - 42 - laser	0.07	0.25	0.30	0.77	0.150
PS20 - 43 - laser	0.11	0.26	0.31	0.78	0.150
PS20 - 44 - laser	0.05	0.24	0.28	0.76	0.140
PS20 - 45 - laser	0.08	0.24	0.29	0.77	0.150
PS20 - 46 - laser	0.08	0.28	0.33	0.77	0.140
PS20 - 47 - laser	0.08	0.26	0.31	0.77	0.140
PS20 - 48 - laser	0.11	0.27	0.33	0.76	0.160
PS20 - 35 - sieve	0.03	0.59	0.62	0.66	0.04
PS20 - 36 - sieve	0.03	0.58	0.63	0.66	0.08
PS20 - 37 - sieve	0.00	0.58	0.59	0.65	0.01
PS20 - 38 - sieve	0.00	0.58	0.61	0.68	0.04
PS20 - 39 - sieve	0.03	0.59	0.68	0.67	0.13
PS20 - 40 - sieve	0.00	0.55	0.59	0.65	0.05
PS20 - 41 - sieve	0.03	0.53	0.61	0.66	0.12

Table 9. Summary of the results of particle size analysis of the replicate samples from sediment circulation PS21.

PS21	% Clay & Silt	Median (phi)	Mean (phi)	Sorting	Skew
PS21 - 42 - laser	88.35	6.43	6.53	2.20	0.090
PS21 - 43 - laser	87.99	6.42	6.49	2.17	0.080
PS21 - 44 - laser	87.65	6.43	6.46	2.14	0.040
PS21 - 45 - laser	88.65	6.49	6.55	2.17	0.060
PS21 - 46 - laser	88.34	6.46	6.53	2.17	0.070
PS21 - 47 - laser	87.90	6.43	6.46	2.12	0.050
PS21 - 48 - laser	88.33	6.48	6.51	2.14	0.050
PS21 - 35 - sieve	89.11	7.01	-	-	-
PS21 - 36 - sieve	89.26	6.20	-	-	-
PS21 - 37 - sieve	88.92	6.81	-	-	-
PS21 - 38 - sieve	85.04	6.63	-	-	-
PS21 - 39 - sieve	86.26	6.52	-	-	-
PS21 - 40 - sieve	88.99	6.52	-	-	-
PS21 - 41 - sieve	87.53	6.29	-	-	-

Table 10. Summary of the particle size information received from participating laboratories for the twentieth particle size distribution - PS20.

Lab	Method	%<63µm	Median	Mean	Sort	IGS (SKi)
LB0902	L	0.51	0.33	0.25	0.69	0.135
LB0903**	L	0.00	0.21	0.24	0.71	0.080
LB0905	WS/DS/L	0.00	0.90	0.95	0.71	0.110
LB0907*	L	0.00	0.33	0.28	0.65	0.173
LB0908	DS	0.02	0.55	0.63	0.81	0.143
LB0910*	L	0.00	0.33	0.28	0.65	0.173
LB0911**	L	0.00	0.21	0.24	0.71	0.080
LB0913	L	0.00	0.46	0.50	-	-
LB0914	L	-	-	-	-	-
LB0915	L	-	-	-	-	-
LB0916	L	0.05	0.19	0.22	0.78	0.11
LB0917*	L	0.00	0.33	0.28	0.65	0.173
LB0918	DS	0.00	0.50	0.53	0.63	0.15
LB0919	S/L	2.20	0.59	0.74	-	1.76
LB0920*	L	0.00	0.33	0.28	0.65	0.173
LB0922*	L	0.00	0.33	0.28	0.65	0.173

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	9	9	7	8
Mean of laboratories	0.31	0.45	0.48	0.71	0.33
Mean of 7 replicates (laser)	0.08	0.26	0.31	0.77	0.15
Mean of 7 replicates (sieve)	0.02	0.57	0.62	0.66	0.07
Laboratory minimum	0.00	0.19	0.22	0.63	0.08
Laboratory maximum	2.20	0.90	0.95	0.81	1.76

Table 11. Summary of the particle size information received from participating laboratories for the twenty-first particle size distribution - PS21.

Lab	Method	%<63µm	Median	Mean	Sort	IGS (SKi)
LB0902*	L	79.52	5.98	4.57	1.28	-0.618
LB0903**	L	84.72	6.15	5.86	1.88	-0.210
LB0905	WS/DS/L	86.74	6.06	6.14	2.05	0.080
LB0907*	L	79.52	5.98	4.57	1.28	-0.618
LB0908	?	84.53	6.34	6.19	1.87	-0.200
LB0910*	L	79.52	5.98	4.57	1.28	-0.618
LB0911**	L	84.72	6.15	5.86	1.88	-0.210
LB0913	DS/L	75.70	3.95	5.28	-	-
LB0914	L	-	-	-	-	-
LB0915	L	-	-	-	-	-
LB0916	L	-	-	-	-	-
LB0917*	L	79.52	5.98	4.57	1.28	-0.618
LB0918	Air Dry/DS	31.30	3.05	3.10	1.73	0.070
LB0919	L	92.09	6.30	5.41	1.86	0.113
LB0920*	L	79.52	5.98	4.57	1.28	-0.618
LB0922*	L	79.52	5.98	4.57	1.28	-0.618

Key to methods:

L - Laser analysis
S - Sieve
P - Pipette
DS - Dry sieve
WS - Wet sieve
CC - Coulter counter
FD - Freeze dried
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	7	7	7	6	6
Mean of laboratories	76.37	5.40	5.22	1.78	-0.13
Mean of 7 replicates (laser)	88.17	6.45	6.50	2.16	0.06
Mean of 7 replicates (sieve)	87.87	6.57	n/a	n/a	n/a
Laboratory minimum	31.30	3.05	3.10	1.28	-0.62
Laboratory maximum	92.09	6.34	6.19	2.05	0.11

Table 12. The identifications of the fauna made by participating laboratories for RT20. Names are given only where different from the AQC identification.

RT20	Taxon	LB0901	LB0903	LB0905	LB0908	LB0910	LB0913	LB0917	LB0922
RT2001	Calliostoma zizyphinum	--	- [zizphinum]	--	--	--	--	[Callistoma] -	--
RT2002	Urothoe poseidonis	--	- pulchella	--	--	0 0	--	--	--
RT2003	Psammoryctides barbatus	--	--	Tubificoides amplivasatus	--	Tubificoides amplivasatus	Tubifex tubifex	--	Tubifex tubifex
RT2004	Eusyllis blomstrandi	--	--	Typosyllis sp.	--	Trypanosyllis coeliaca	--	--	Syllis prolifera
RT2005	Barnea candida	--	--	--	--	--	--	--	--
RT2006	Fabulina fabula	--	Moerella pygmaea	--	Tellinacea sp. juv.	0 0	Moerella pygmaea	--	--
RT2007	Ophiothrix fragilis	--	--	--	--	--	--	--	--
RT2008	Owenia fusiformis	--	--	--	--	0 0	--	--	--
RT2009	Parapleustes assimilis	--	--	Tritaeta gibbosa	--	Pleusymtes glaber	Pleusymtes glaber	--	Gitanopsis bispinosa
RT2010	Monticellina dorsobranchialis	--	--	Aphelochaeta marioni	--	Aphelochaeta marioni	--	[Monticella] -	Aphelochaeta marioni
RT2011	Bathyporeia guilliamsoniana	--	- pelagica	- pelagica	--	--	--	--	- pelagica
RT2012	Stylaria lacustris	--	--	--	--	0 0	--	Nais elinguis	0 0
RT2013	Raricirrus beryli	--	--	Caulleriella A	--	0 0	--	Cirratulus juv.	Ctenodrillina 0
RT2014	Caprella linearis	- septentrionalis	--	--	--	- sp.	--	--	Aeginina longicornis
RT2015	Hiatella arctica	--	--	--	--	0 0	--	--	--
RT2016	Gnathia oxyuraea	--	--	--	--	--	--	--	- [oxyaraea]
RT2017	Ventrosia ventrosa	--	Hydrobia ulvae	Onoba aculeus	--	[Hydrobia] -	Hydrobia sp.	[Hydrobia] -	Potamopyrgus antopodarum
RT2018	Tharyx killariensis	--	Chaetozone setosa	--	--	0 0	--	--	--
RT2019	Buccinum undatum	Liomesus ovum	--	Colus jeffreysianus	Colus jeffreysianus	Buccinidae juv.	Buccinidae sp. juv.	--	Colus jeffreysianus
RT2020	Tritaeta gibbosa	--	--	--	--	0 0	--	--	--
RT2021	Tellimya ferruginosa	Lutraria lutraria	Mysella bidentata	--	--	0 0	--	Veneroida juv.	--
RT2022	Nucella lapillus	--	--	--	--	--	--	--	Buccinum humphreysianum
RT2023	Pomatoceros lamarcki	--	--	--	--	--	--	--	--
RT2024	Scalibregma inflatum	--	--	--	--	--	--	--	--
RT2025	Leptochiton asellus	--	Callochiton septemvalvis	--	--	0 0	--	--	Tonocella rubra

RT20	Taxon	LB0902	LB0904	LB0906	LB0909	LB0911	LB0915	LB0919
RT2001	Calliostoma zizyphinum	--	--	--	--	- [ziziyphinum]	--	--
RT2002	Urothoe poseidonis	--	--	--	- elegans	--	--	--
RT2003	Psammoryctides barbatus	Tubifex tubifex	--	--	Tubifex tubifex	--	--	Nais elinguis
RT2004	Eusyllis blomstrandi	--	--	--	- [blomstrandii]	--	--	Syllis armillaris
RT2005	Barnea candida	--	--	--	--	--	--	--
RT2006	Fabulina fabula	--	Moerella pygmaea	Moerella pygmaea	--	Angulus tenuis	--	--
RT2007	Ophiothrix fragilis	--	--	Ophiocomina nigra	--	--	--	--
RT2008	Owenia fusiformis	--	--	--	--	--	--	--
RT2009	Parapleustes assimilis	--	--	0 0	--	Apherusa jurinei	--	--
RT2010	Monticellina dorsobranchialis	--	--	--	--	--	--	Aphelochaeta marioni
RT2011	Bathyporeia guilliamsoniana	--	--	- pelagica	- pelagica	- pelagica	--	--
RT2012	Stylaria lacustris	--	--	--	Paranais litoralis	--	--	--
RT2013	Raricirrus beryli	--	--	--	--	--	--	Dodecaceria diceria
RT2014	Caprella linearis	--	--	- acanthifera	--	- tuberculata	--	- septentrionalis
RT2015	Hiatella arctica	--	--	--	--	--	--	--
RT2016	Gnathia oxyuraea	--	--	--	--	--	--	- maxillaris
RT2017	Ventrosia ventrosa	Hydrobia ulvae	--	Hydrobia ulvae	--	Hydrobia ulvae	Hydrobia neglecta	[Hydrobia] -
RT2018	Tharyx killariensis	--	Chaetozone setosa 'C'	--	--	--	--	--
RT2019	Buccinum undatum	Buccinidae juv.	--	Trivia sp.	--	--	Nucella lapillus	Liomesus ovum
RT2020	Tritaeta gibbosa	--	Apherusa jurinei	--	--	--	--	--
RT2021	Tellimya ferruginosa	Montacutidae -	--	Mysella bidentata	--	--	--	--
RT2022	Nucella lapillus	--	--	--	--	--	--	--
RT2023	Pomatoceros lamarcki	--	- triqueter	--	--	--	--	--
RT2024	Scalibregma inflatum	--	--	--	--	--	--	--
RT2025	Leptochiton asellus	--	--	Lepidochitona cinereus	--	--	- [assellus]	--

Table 13. The identifications of the fauna made by participating laboratories for RT21. Names are given only where different from the AQC identification.

RT21	Taxon	LB0901	LB0903	LB0905	LB0908	LB0911	LB0914	LB0917
RT2101	Poecilochaetus serpens	--	--	--	--	--	--	--
RT2102	Streblospio shrubsolii	--	--	--	--	--	--	--
RT2103	Magelona johnstoni	--	- mirabilis	- mirabilis	--	--	--	--
RT2104	Tharyx A	--	Aphelochaeta marioni	--	--	Aphelochaeta sp. A	--	--
RT2105	Boccardiella ligerica	--	[Boccardia] [redeki]	--	--	Polydora cornuta	--	--
RT2106	Cirriformia tentaculata	--	--	--	--	--	--	--
RT2107	Magelona alleni	--	--	--	--	--	--	--
RT2108	Aphelochaeta marioni	--	--	--	--	--	--	--
RT2109	Prionospio fallax	--	--	- cirrifera	--	--	--	--
RT2110	Magelona minuta	--	--	--	--	--	--	--
RT2111	Polydora caulleryi	--	--	--	--	--	--	--
RT2112	Magelona filiformis	--	--	--	--	--	--	Pygospio elegans
RT2113	Polydora quadrilobata	--	--	--	--	--	--	--
RT2114	Tharyx killariensis	--	--	--	--	--	--	--
RT2115	Chaetozone gibber	--	--	--	--	--	--	--
RT2116	Caulleriella zetlandica	--	--	--	--	[Chaetozone] -	--	Pygospio elegans
RT2117	Pseudopolydora cf. paucibranchiata	- antennata	- [paucibranchiata]	Pygospio elegans	--	- [paucibranchiata]	--	--
RT2118	Polydora ciliata	--	--	- flava	- caeca	--	--	[Procirrinereis] -
RT2119	Protocirrineris chrysoderma	--	Cirratulus cirratus (juv)	Cirriformia norvegica	Cirriformia tentaculata	Aphelochaeta vivipara	--	--
RT2120	Caulleriella alata	--	--	--	--	--	--	--
RT2121	Spio martinensis	--	--	--	--	--	--	--
RT2122	Scolelepis squamata	--	--	--	--	--	--	--
RT2123	Chaetozone christiei	- setosa	- setosa	- setosa agg.	- setosa	- setosa	- setosa	- setosa
RT2124	Minuspio cf. multibranchiata	--	- [multibranchiata]	[Prionospio] [multibranchiata]	--	[Prionospio] [multibranchiata]	--	[Prionospio] [multibranchiata]
RT2125	Polydora cornuta	--	--	--	--	--	--	--

RT21	Taxon	LB0902	LB0904	LB0906	LB0909	LB0913	LB0915	LB0919
RT2101	Poecilochaetus serpens	--	--	--	--	--	--	--
RT2102	Streblospio shrubsolii	--	--	--	--	--	--	--
RT2103	Magelona johnstoni	- mirabilis	--	--	- mirabilis	--	--	--
RT2104	Tharyx A	--	--	--	Chaetozone gibber	--	--	Polydora ciliata
RT2105	Boccardiella ligerica	--	--	--	--	--	--	--
RT2106	Cirriformia tentaculata	--	--	--	--	--	--	--
RT2107	Magelona alleni	--	--	--	--	- sp.	--	--
RT2108	Aphelochaeta marioni	--	- A	[Aphelochaete] A	--	--	--	--
RT2109	Prionospio fallax	--	--	--	--	--	--	--
RT2110	Magelona minuta	- filiformis	--	--	--	--	--	Pseudopolydora antennata
RT2111	Polydora caulleryi	- flava	--	--	--	--	--	--
RT2112	Magelona filiformis	--	- equilamellae	--	--	Pseudopolydora antennata	--	Pseudopolydora antennata
RT2113	Polydora quadrilobata	--	--	--	--	- sp.	--	--
RT2114	Tharyx killariensis	--	Aphelochaeta sp.	- A	--	--	--	--
RT2115	Chaetozone gibber	--	--	- D	--	--	--	--
RT2116	Caulleriella zetlandica	Chaetozone christiei	--	--	--	--	--	--
RT2117	Pseudopolydora cf. paucibranchiata	- [paucibranchiata]	--	- [paucibranchiata]	--	--	--	--
RT2118	Polydora ciliata	--	Pseudopolydora pulchra	- [limicola]	- caeca agg.	--	--	Aphelochaeta A
RT2119	Protocirrineris chrysoderma	- [sp.]	--	[cf. Protocirrineris] -	Cirriformia tentaculata	--	--	--
RT2120	Caulleriella alata	--	--	--	--	--	--	--
RT2121	Spio martinensis	--	--	--	--	--	--	--
RT2122	Scolelepis squamata	--	--	--	--	--	--	--
RT2123	Chaetozone christiei	--	--	- [B]	- setosa agg.	- setosa	- setosa agg.	- setosa agg.
RT2124	Minuspio cf. multibranchiata	- [multibranchiata]	[Prionospio] [multibranchiata]	[Prionospio] [multibranchiata]	--	--	--	--
RT2125	Polydora cornuta	--	--	- [ligni]	--	--	--	--

Table 14. Summary of the results from the identification of specimens supplied by participating laboratories for Laboratory Reference exercise LR07.

	Differences		
LabCode	Generic	Specific	name changes
LB0902	0	0	0
LB0903	3	6	0
LB0904	0	0	0
LB0905	4	8	1
LB0906	2	3	0
LB0907	2	5	1
LB0908	0	1	2
LB0909	4	6	1
LB0911	1	1	1
LB0913	7	8	1
LB0915	0	0	1
LB0917	2	3	0
LB0918	0	0	1
LB0919	5	6	0

Key: "-" - No data.

np - Not participating.

See Report, Section 6, for details.

Table 15. Summary of the performance of participating laboratories in the Own Sample exercises (OS20-22) with respect to the NMBAQC / UK 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			NMBAQCS/NMMP
LabCode		Lab.	Target	Flag	Missed	% Missed	Remedial Action	Lab.	%	Remedial Action	Lab.	Target	Flag	Missed	% Missed	Remedial Action	Lab.	Target	Flag	Target	Lab.	Flag	Sample Flag
LB0902	OS20	13	11.0 - 15.0	PASS	0	0.0	-	0	0.0	-	1188	1056.6 - 1291.4	PASS	6	0.5	-	0.2860	0.1753 - 0.2629	*Fail*	90.0	99.07	PASS	Good
LB0902	OS21	7	5.0 - 9.0	PASS	0	0.0	-	0	0.0	-	403	370.8 - 453.2	PASS	5	1.2	-	0.1280	0.0916 - 0.1374	*PASS*	90.0	96.69	PASS	Good
LB0902	OS22	13	11.0 - 15.0	PASS	0	0.0	-	0	0.0	-	379	337.5 - 412.5	PASS	2	0.5	-	0.1280	0.0777 - 0.1165	*Fail*	90.0	98.14	PASS	Good
LB0903	OS20	99	92.7 - 113.3	PASS	1	1.0	-	8	7.8	-	911	824.4 - 1007.6	PASS	5	0.5	-	11.6298	9.4784 - 14.2176	*PASS*	90.0	96.91	PASS	Good
LB0903	OS21	35	32.4 - 39.6	PASS	0	0.0	-	6	16.7	-	404	366.3 - 447.7	PASS	6	1.5	-	8.5584	7.0994 - 10.6492	*PASS*	90.0	93.74	PASS	Acceptable
LB0903	OS22	75	73.8 - 90.2	PASS	3	3.7	-	14	17.7	-	1756	1765.8 - 2158.2	**Fail**	214	10.9	-	-	-	-	90.0	91.23	PASS	Acceptable
LB0904	OS20	10	7.0 - 11.0	PASS	0	0.0	-	3	33.3	Reprocess	37	31.5 - 38.5	PASS	0	0.0	-	-	-	-	90.0	88.89	**Fail**	Poor
LB0904	OS21	19	16.0 - 20.0	PASS	0	0.0	-	2	11.1	Review	100	88.2 - 107.8	PASS	0	0.0	-	-	-	-	90.0	43.32	**Fail**	**Fail**
LB0904	OS22	9	7.0 - 11.0	PASS	0	0.0	-	2	22.2	Review	21	19.8 - 24.2	PASS	0	0.0	-	-	-	-	90.0	83.72	**Fail**	**Fail**
LB0905	OS20	30	23.4 - 28.6	**Fail**	0	0.0	-	7	26.9	Reprocess	62	55.8 - 68.2	PASS	0	0.0	-	0.8304	0.4805 - 0.7207	*Fail*	90.0	72.58	**Fail**	**Fail**
LB0905	OS21	34	30.6 - 37.4	PASS	0	0.0	-	1	2.9	-	174	155.7 - 190.3	PASS	0	0.0	-	50.2417	32.9834 - 49.4750	*Fail*	90.0	98.56	PASS	Good
LB0905	OS22	32	27.9 - 34.1	PASS	0	0.0	-	0	0.0	-	258	230.4 - 281.6	PASS	0	0.0	-	6.7717	4.3963 - -	*PASS*	90.0	99.61	PASS	Good
LB0906	OS20	18	16.0 - 20.0	PASS	0	0.0	-	1	5.6	-	60	54.9 - 67.1	PASS	1	1.6	-	-	-	-	90.0	95.08	PASS	Good
LB0906	OS21	17	19.8 - 24.2	**Fail**	5	22.7	-	0	0.0	-	102	105.3 - 128.7	**Fail**	14	12.0	-	-	-	-	90.0	93.15	PASS	Acceptable
LB0906	OS22	61	59.4 - 72.6	PASS	5	7.6	Review	6	9.8	Review	368	362.7 - 443.3	PASS	34	8.4	Review	-	-	-	90.0	84.05	**Fail**	**Fail**
LB0908	OS20	52	52.2 - 63.8	**Fail**	6	10.3	-	2	3.8	-	782	707.4 - 864.6	PASS	5	0.6	-	6.1759	5.0017 - 7.5025	*PASS*	90.0	98.66	PASS	Good
LB0908	OS21	52	45.9 - 56.1	PASS	0	0.0	-	5	9.8	-	254	226.8 - 277.2	PASS	0	0.0	-	5.8190	4.6421 - 6.9631	*PASS*	90.0	96.44	PASS	Good
LB0908	OS22	35	39.6 - 48.4	**Fail**	9	20.5	-	2	5.7	-	199	189.0 - 231.0	PASS	14	6.7	-	0.4279	0.3552 - 0.5328	*PASS*	90.0	92.46	PASS	Acceptable
LB0909	OS20	44	45.0 - 55.0	**Fail**	4	8.0	Review	10	21.7	Reprocess	282	277.2 - 338.8	PASS	25	8.1	Review	-	-	-	90.0	84.94	**Fail**	**Fail**
LB0909	OS21	20	20.7 - 25.3	**Fail**	3	13.0	Reprocess	5	25.0	Reprocess	35	38.7 - 47.3	**Fail**	8	18.6	Reprocess	-	-	-	90.0	76.92	**Fail**	**Fail**
LB0909	OS22	19	17.0 - 21.0	PASS	0	0.0	-	3	15.8	Reprocess	41	37.8 - 46.2	PASS	1	2.4	-	-	-	-	90.0	80.46	**Fail**	**Fail**
LB0910	OS20	35	31.5 - 38.5	PASS	0	0.0	-	0	0.0	-	961	854.1 - 1043.9	PASS	1	0.1	-	1.8108	1.3883 - 2.0825	*PASS*	90.0	99.37	PASS	Good
LB0910	OS21	48	42.3 - 51.7	PASS	0	0.0	-	0	0.0	-	2969	2662.2 - 3253.8	PASS	1	0.0	-	4.7442	4.1454 - 6.2182	*PASS*	90.0	99.24	PASS	Good
LB0910	OS22	39	35.1 - 42.9	PASS	0	0.0	-	0	0.0	-	1323	1164.6 - 1423.4	PASS	3	0.2	-	24.1221	19.8979 - 29.8469	*PASS*	90.0	98.67	PASS	Good
LB0911	OS20	31	28.8 - 35.2	PASS	1	3.1	-	1	3.2	-	109	106.2 - 129.8	PASS	10	8.5	-	5.5905	4.6316 - 6.9474	*PASS*	90.0	94.27	PASS	Acceptable
LB0911	OS21	11	10.0 - 14.0	PASS	0	0.0	-	1	8.3	-	28	25.2 - 30.8	PASS	0	0.0	-	4.7386	3.7830 - 5.6746	*PASS*	90.0	96.43	PASS	Good
LB0911	OS22	5	3.0 - 7.0	PASS	0	0.0	-	0	0.0	-	15	14.0 - 18.0	PASS	1	6.3	-	1.7346	1.0926 - 1.6390	*Fail*	90.0	96.77	PASS	Good
LB0916	OS20	57	72.0 - 88.0	**Fail**	15	18.8	Reprocess	6	9.2	Review	302	431.1 - 526.9	**Fail**	166	34.7	Reprocess	-	-	-	90.0	70.25	**Fail**	**Fail**
LB0916	OS21	71	80.1 - 97.9	**Fail**	16	18.0	-	5	6.8	-	2585	2555.1 - 3122.9	PASS	262	9.2	-	-	-	-	90.0	94.68	PASS	Acceptable
LB0916	OS22	8	8.0 - 12.0	PASS	1	10.0	-	2	22.2	Review	27	26.1 - 31.9	PASS	1	3.4	-	-	-	-	90.0	78.57	**Fail**	**Fail**
LB0917	OS20	75	71.1 - 86.9	PASS	3	3.8	-	12	15.8	Reprocess	2602	2837.7 - 3468.3	**Fail**	546	17.3	Reprocess	44.7495	32.9354 - 49.4032	*PASS*	90.0	86.15	**Fail**	Poor
LB0917	OS21	7	5.0 - 9.0	PASS	0	0.0	-	0	0.0	-	128	113.4 - 138.6	PASS	1	0.8	-	0.0500	0.0435 - 0.0653	*PASS*	90.0	98.43	PASS	Good
LB0917	OS22	16	14.0 - 18.0	PASS	0	0.0	-	0	0.0	-	739	703.8 - 860.2	PASS	43	5.5	-	2.9547	2.3492 - 3.5238	*PASS*	90.0	96.78	PASS	Good
LB0918	OS20	91	82.8 - 101.2	PASS	0	0.0	-	1	1.1	-	3284	2913.3 - 3560.7	PASS	9	0.3	-	13.6258	10.1702 - 15.2552	*PASS*	90.0	98.54	PASS	Good
LB0918	OS21	19	17.0 - 21.0	PASS	0	0.0	-	0	0.0	-	109	96.3 - 117.7	PASS	2	1.9	-	0.1877	0.1802 - 0.2702	*PASS*	90.0	98.20	PASS	Good
LB0918	OS22	51	46.8 - 57.2	PASS	1	1.9	-	0	0.0	-	424	381.6 - 466.4	PASS	2	0.5	-	1.0268	0.8463 - 1.2695	*PASS*	90.0	99.54	PASS	Good
LB0919	OS20	1	-1.0 - 3.0	PASS	0	0.0	-	0	0.0	-	6	4.0 - 8.0	PASS	0	0.0	-	0.0013	0.0012 - 0.0018	*PASS*	90.0	100.00	PASS	Excellent
LB0919	OS21	4	2.0 - 6.0	PASS	0	0.0	-	0	0.0	-	21	18.9 - 23.1	PASS	0	0.0	-	0.0038	0.0033 - 0.0049	*PASS*	90.0	100.00	PASS	Excellent
LB0919	OS22	5	5.0 - 9.0	PASS	2	28.6	-	0	0.0	-	20	19.8 - 24.2	PASS	2	9.1	-	0.0039	0.0044 - 0.0066	*Fail*	90.0	95.24	PASS	Good
LB0921	OS20	26	23.4 - 28.6	PASS	1	3.8	-	2	8.0	-	651	609.3 - 744.7	PASS	25	3.7	-	-	-	-	90.0	97.52	PASS	Good
LB0921	OS21	22	19.8 - 24.2	PASS	0	0.0	-	0	0.0	-	3148	2813.4 - 3438.6	PASS	2	0.1	-	-	-	-	90.0	99.43	PASS	Good
LB0921	OS22	7	5.0 - 9.0	PASS	0	0.0	-	1	14.3	-	13	11.0 - 15.0	PASS	0	0.0	-	-	-	-	90.0	92.86	PASS	Acceptable
LB0922	OS20	7	5.0 - 9.0	PASS	0	0.0	-	0	0.0	-	352	330.3 - 403.7	PASS	22	6.0	-	2.5246	1.7100 - 2.5650	*PASS*	90.0	98.06	PASS	Good
LB0922	OS21	4	2.0 - 6.0	PASS	0	0.0	-	0	0.0	-	306	307.8 - 376.2	**Fail**	28	8.2	-	0.1155	0.0674 - 0.1010	*Fail*	90.0	94.44	PASS	Acceptable
LB0922	OS22	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	90.0	-	-	-

Table 16. Z-score results for the derived statistics supplied by participating laboratories for the Particle Size (PS) exercises - PS20 and PS21- NMBAQC / UK NMMP standards applied.

PS20

Lab	%<63µm	z-score	Flag	Median	z-score	Flag	Mean	z-score	Flag	Sort	z-score	Flag	IGS (SKi)	z-score	Flag	Description
LaserRepAv	0.08	-0.27	PASS	0.26	-0.89	PASS	0.31	-0.71	PASS	0.77	0.89	PASS	0.147	-0.27	PASS	n/a
SieveRepAv	0.02	-0.37	PASS	0.57	0.61	PASS	0.62	0.58	PASS	0.66	-0.81	PASS	0.067	-0.43	PASS	n/a
LB0902	0.5	0.38	PASS	0.33	-0.54	PASS	0.25	-0.95	PASS	0.69	-0.36	PASS	0.135	-0.29	PASS	-
LB0903**	0.00	-0.40	PASS**	0.21	-1.12	PASS**	0.24	-0.99	PASS**	0.71	-0.04	PASS**	0.080	-0.40	PASS**	gritty sand**
LB0905	0.0	-0.40	PASS	0.90	2.17	Fail	0.95	1.96	PASS	0.71	-0.04	PASS	0.110	-0.34	PASS	sand
LB0907*	0.00	-0.40	PASS*	0.33	-0.54	PASS*	0.28	-0.82	PASS*	0.65	-0.99	PASS*	0.173	-0.22	PASS*	coarse sand*
LB0908	0.02	-0.37	PASS	0.55	0.50	PASS	0.63	0.63	PASS	0.81	1.60	PASS	0.143	-0.28	PASS	sand
LB0910*	0.00	-0.40	PASS*	0.33	-0.54	PASS*	0.28	-0.82	PASS*	0.65	-0.99	PASS*	0.173	-0.22	PASS*	coarse sand*
LB0911**	0.00	-0.40	PASS	0.21	-1.12	PASS	0.24	-0.99	PASS	0.71	-0.04	PASS	0.080	-0.40	PASS	gritty sand
LB0913	0.00	-0.40	PASS	0.46	0.07	PASS	0.50	0.09	PASS	-	-	Deemed Fail	-	-	Deemed Fail	coarse sand
LB0916	0.05	-0.32	PASS	0.19	-1.21	PASS	0.22	-1.07	PASS	0.78	1.07	PASS	0.110	-0.34	PASS	sand
LB0917*	0.00	-0.40	PASS*	0.33	-0.54	PASS*	0.28	-0.82	PASS*	0.65	-0.99	PASS*	0.173	-0.22	PASS*	coarse sand*
LB0918	0.00	-0.40	PASS	0.50	0.27	PASS	0.53	0.21	PASS	0.63	-1.31	PASS	0.150	-0.27	PASS	coarse sand/gravel
LB0919	2.20	2.94	Fail	0.59	0.69	PASS	0.74	1.08	PASS	-	-	Deemed Fail	1.760	2.84	Fail	sand
LB0920*	0.00	-0.40	PASS	0.33	-0.54	PASS	0.28	-0.82	PASS	0.65	-0.99	PASS	0.173	-0.22	PASS	coarse sand
LB0922*	0.00	-0.40	PASS*	0.33	-0.54	PASS*	0.28	-0.82	PASS*	0.65	-0.99	PASS*	0.173	-0.22	PASS*	coarse sand*

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

PS21

Lab	%<63µm	z-score	Flag	Median	z-score	Flag	Mean	z-score	Flag	Sort	z-score	Flag	IGS (SKi)	z-score	Flag	Description Pre/Post Analysis
LaserRepAv	88.17	0.50	PASS	6.45	0.64	PASS	6.50	1.01	PASS	2.16	1.16	PASS	0.063	0.61	PASS	-
SieveRepAv	87.87	0.48	PASS	6.57	0.73	PASS	-	-	Deemed Fail	-	-	Deemed Fail	-	-	Deemed Fail	-
LB0902*	79.52	0.03	PASS*	5.98	0.26	PASS*	4.57	-0.73	PASS*	1.28	-1.97	PASS*	-0.618	-1.95	PASS*	Muddy/-
LB0903**	84.72	0.31	PASS**	6.15	0.40	PASS**	5.86	0.43	PASS**	1.88	0.17	PASS**	-0.210	-0.41	PASS**	-
LB0905	86.74	0.42	PASS	6.06	0.33	PASS	6.14	0.68	PASS	2.05	0.77	PASS	0.080	0.68	PASS	Sandy mud + shell frag./Slightly gravelly sandy mud
LB0907*	79.52	0.03	PASS*	5.98	0.26	PASS*	4.57	-0.73	PASS*	1.28	-1.97	PASS*	-0.618	-1.95	PASS*	Muddy/-
LB0908	84.53	0.30	PASS	6.34	0.55	PASS	6.19	0.73	PASS	1.87	0.13	PASS	-0.200	-0.38	PASS	Fine silt-mud/Mud
LB0910*	79.52	0.03	PASS*	5.98	0.26	PASS*	4.57	-0.73	PASS*	1.28	-1.97	PASS*	-0.618	-1.95	PASS*	Muddy/-
LB0911**	84.72	0.31	PASS	6.15	0.40	PASS	5.86	0.43	PASS	1.88	0.17	PASS	-0.210	-0.41	PASS	Black sticky mud/Sandy mud
LB0913	75.70	-0.18	PASS	3.95	-1.36	PASS	5.28	-0.09	PASS	-	-	Deemed Fail	-	-	Deemed Fail	-
LB0917*	79.52	0.03	PASS*	5.98	0.26	PASS*	4.57	-0.73	PASS*	1.28	-1.97	PASS*	-0.618	-1.95	PASS*	Muddy/-
LB0918	31.30	-2.57	Fail	3.05	-2.08	Fail	3.10	-2.06	Fail	1.73	-0.37	PASS	0.070	0.64	PASS	Sandy Mud/inS
LB0919	92.09	0.71	PASS	6.30	0.52	PASS	5.41	0.03	PASS	1.86	0.10	PASS	0.113	0.80	PASS	Silty mud/Mud
LB0920*	79.52	0.03	PASS	5.98	0.26	PASS	4.57	-0.73	PASS	1.28	-1.97	PASS	-0.618	-1.95	PASS	Muddy/-
LB0922*	79.52	0.03	PASS*	5.98	0.26	PASS*	4.57	-0.73	PASS*	1.28	-1.97	PASS*	-0.618	-1.95	PASS*	Muddy/-

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

Section 6 Contd.

Contractor Report - Figures:

Figure 1. Particle size distribution curves resulting from analysis of fourteen replicate samples of sediment distributed as PS20. Seven samples analysed by sieve and seven samples analysed by Laser.

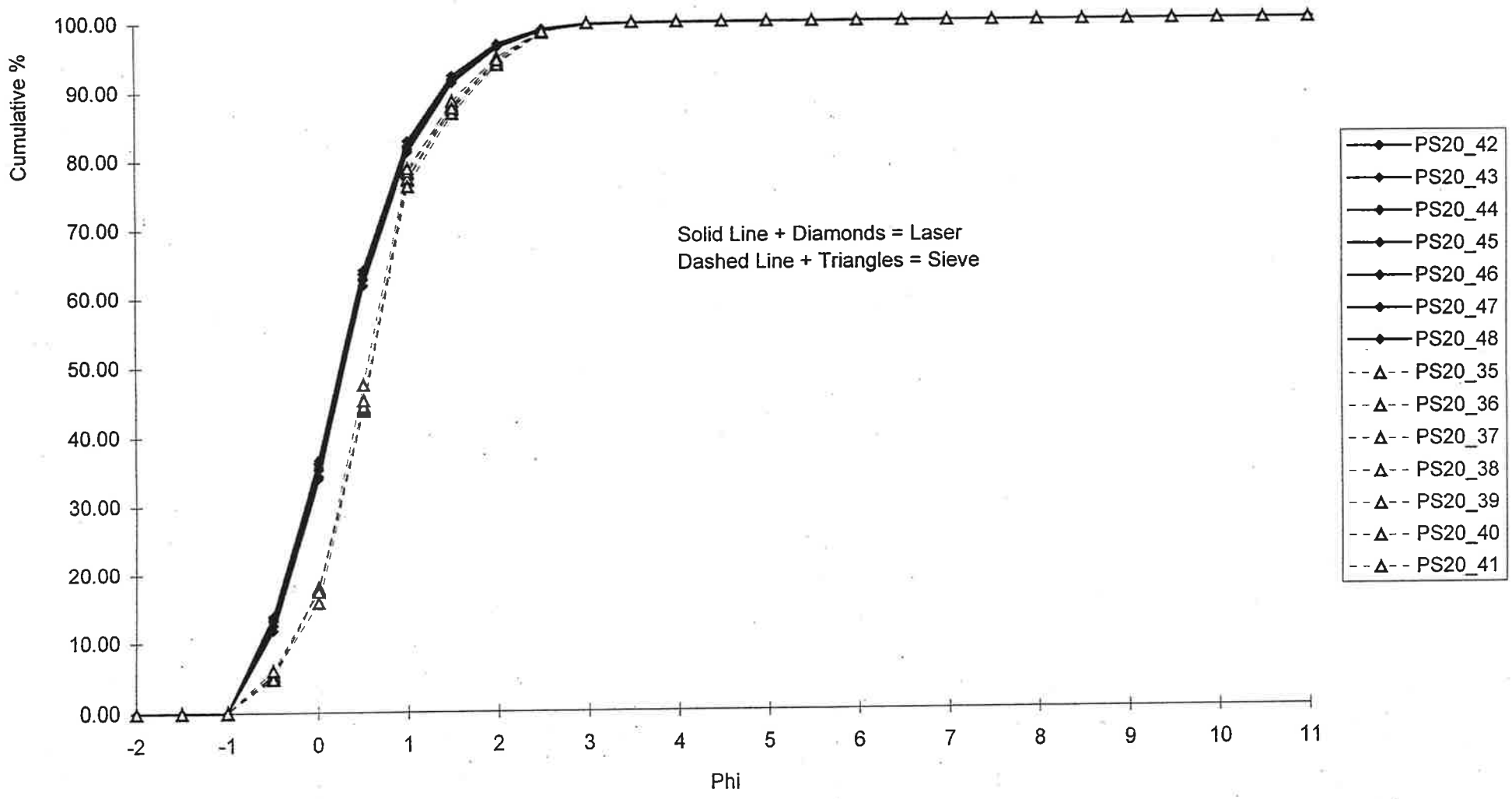


Figure 2. Particle size distribution curves resulting from analysis of fourteen replicate samples of sediment distributed as PS21. Seven samples analysed by sieve and seven samples analysed by Laser.

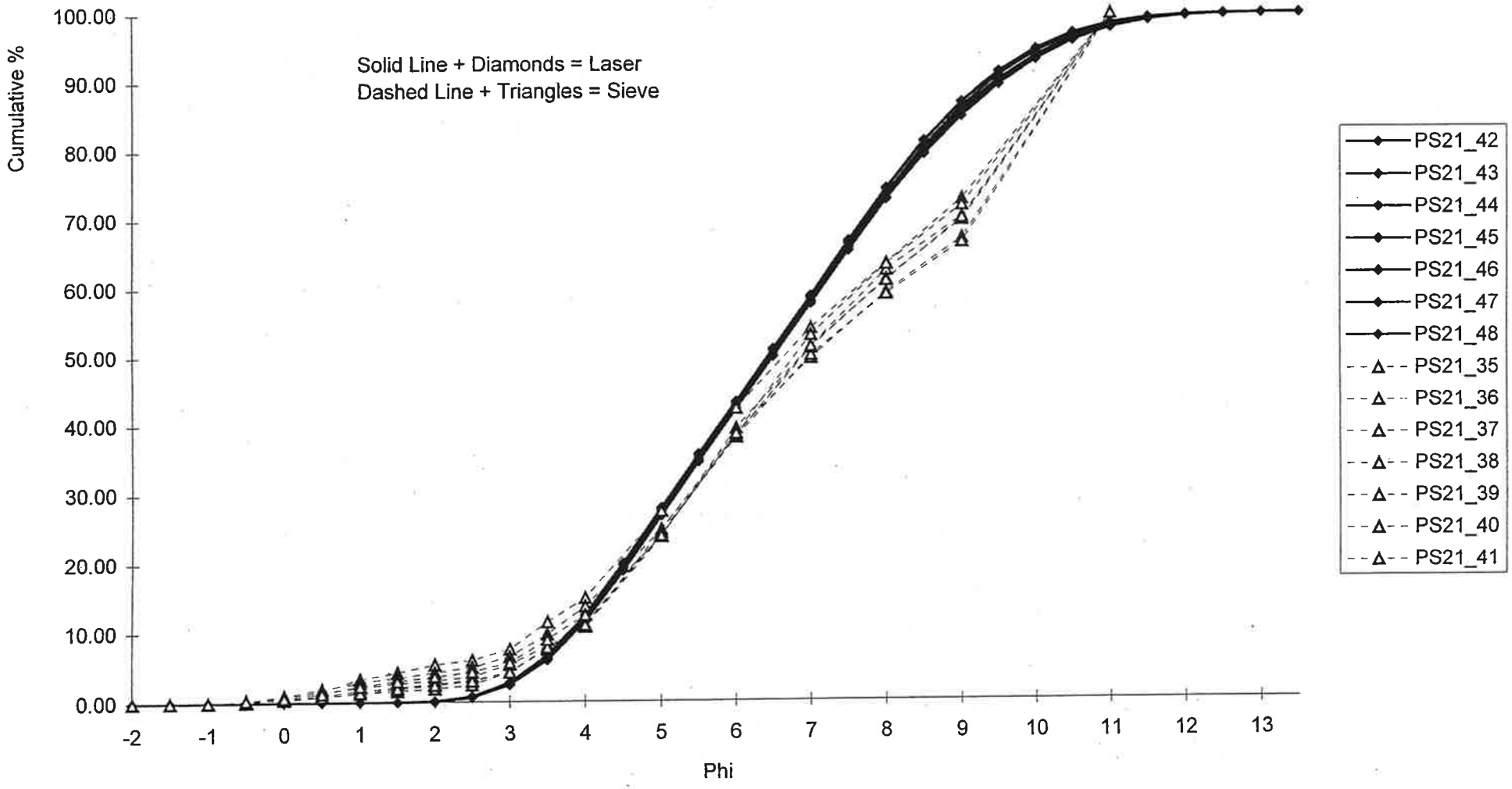


Figure 3. Particle size distribution curves from participating laboratories for sediment samples from PS20.

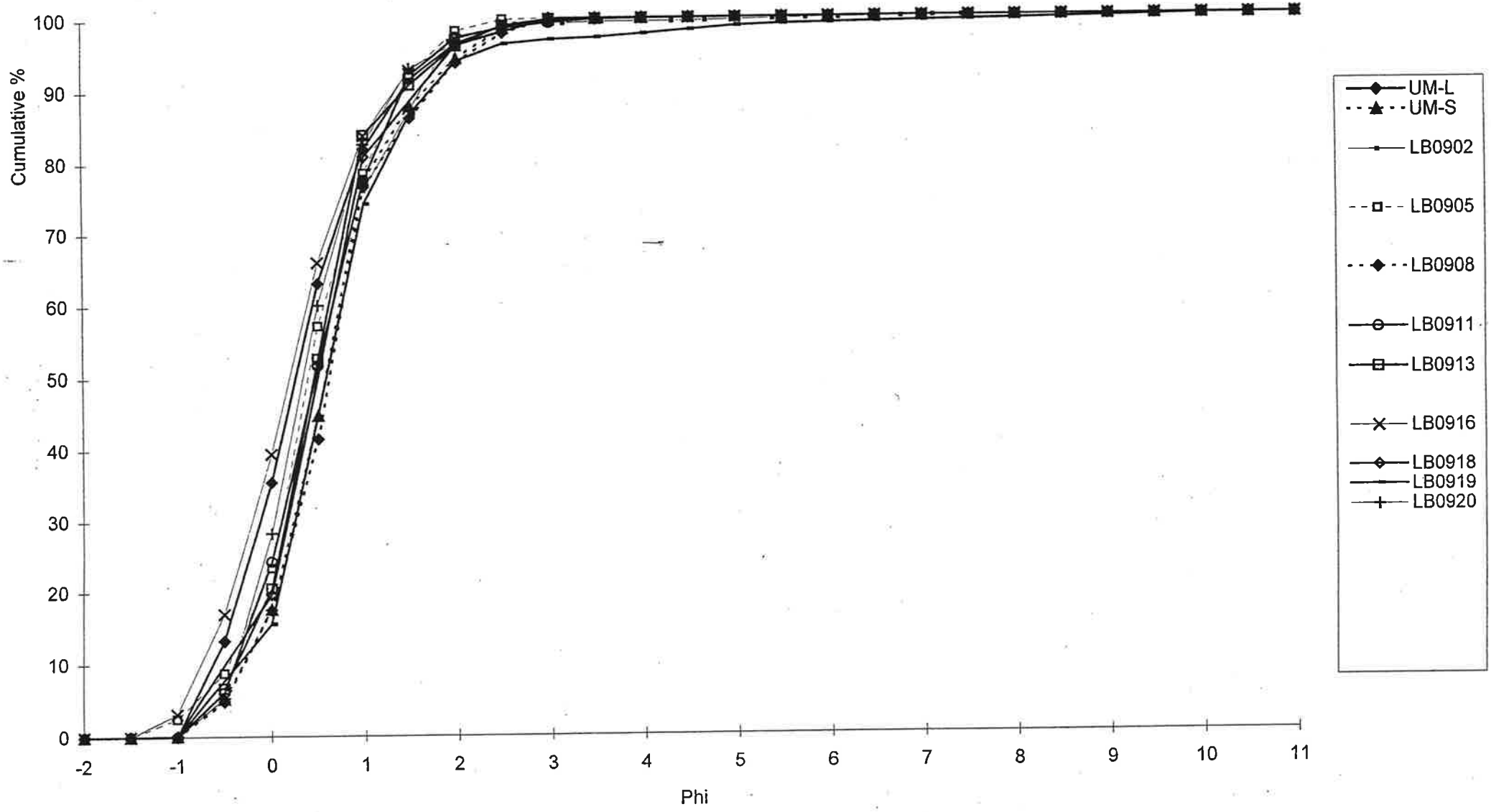


Figure 4. Particle size distribution curves from participating laboratories for sediment samples from PS21.

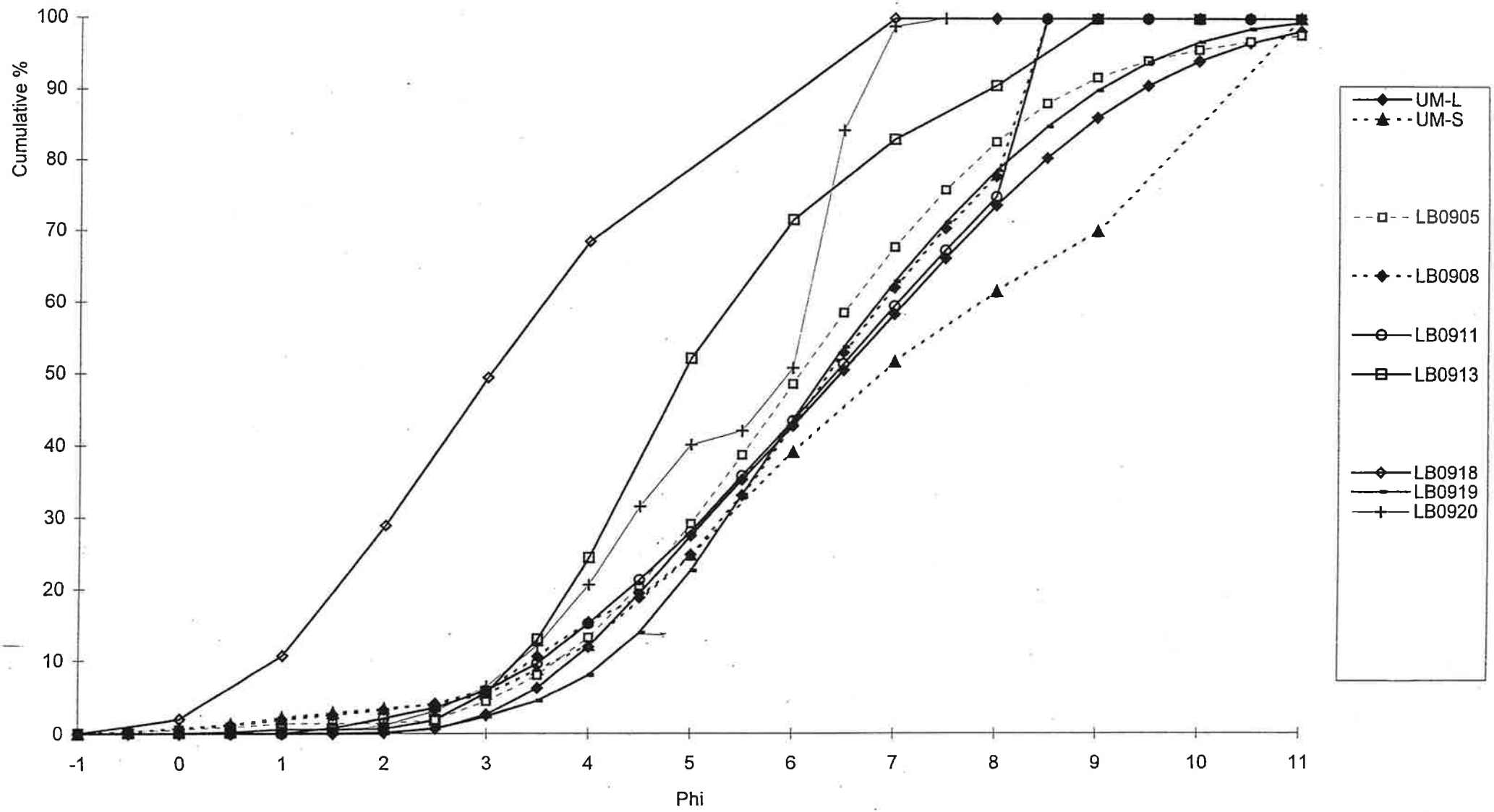


Figure 5. Z-scores for PS20 derived statistics (replicated data not displayed).

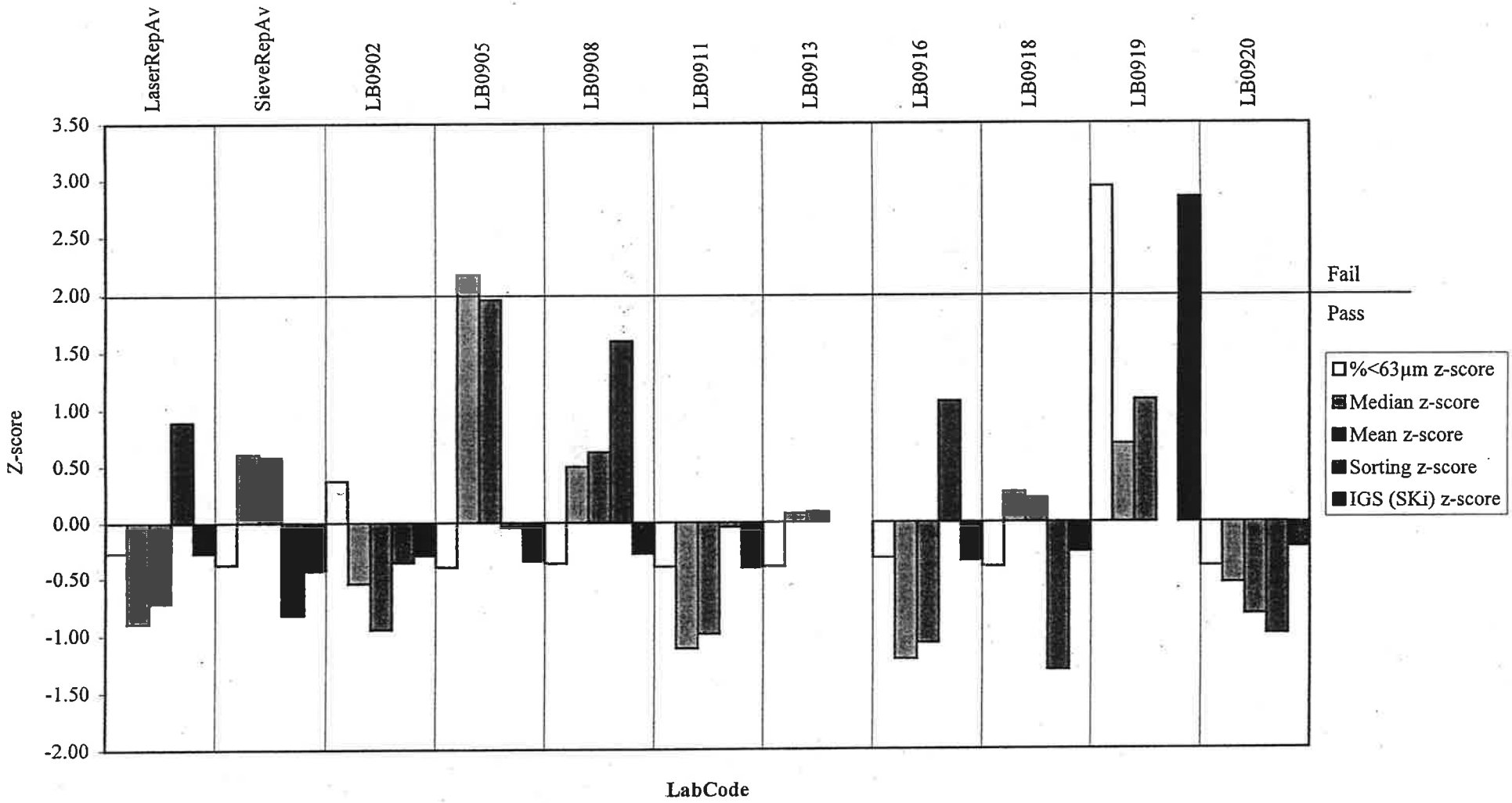


Figure 6. Z-scores for PS21 derived statistics (replicated data not displayed).

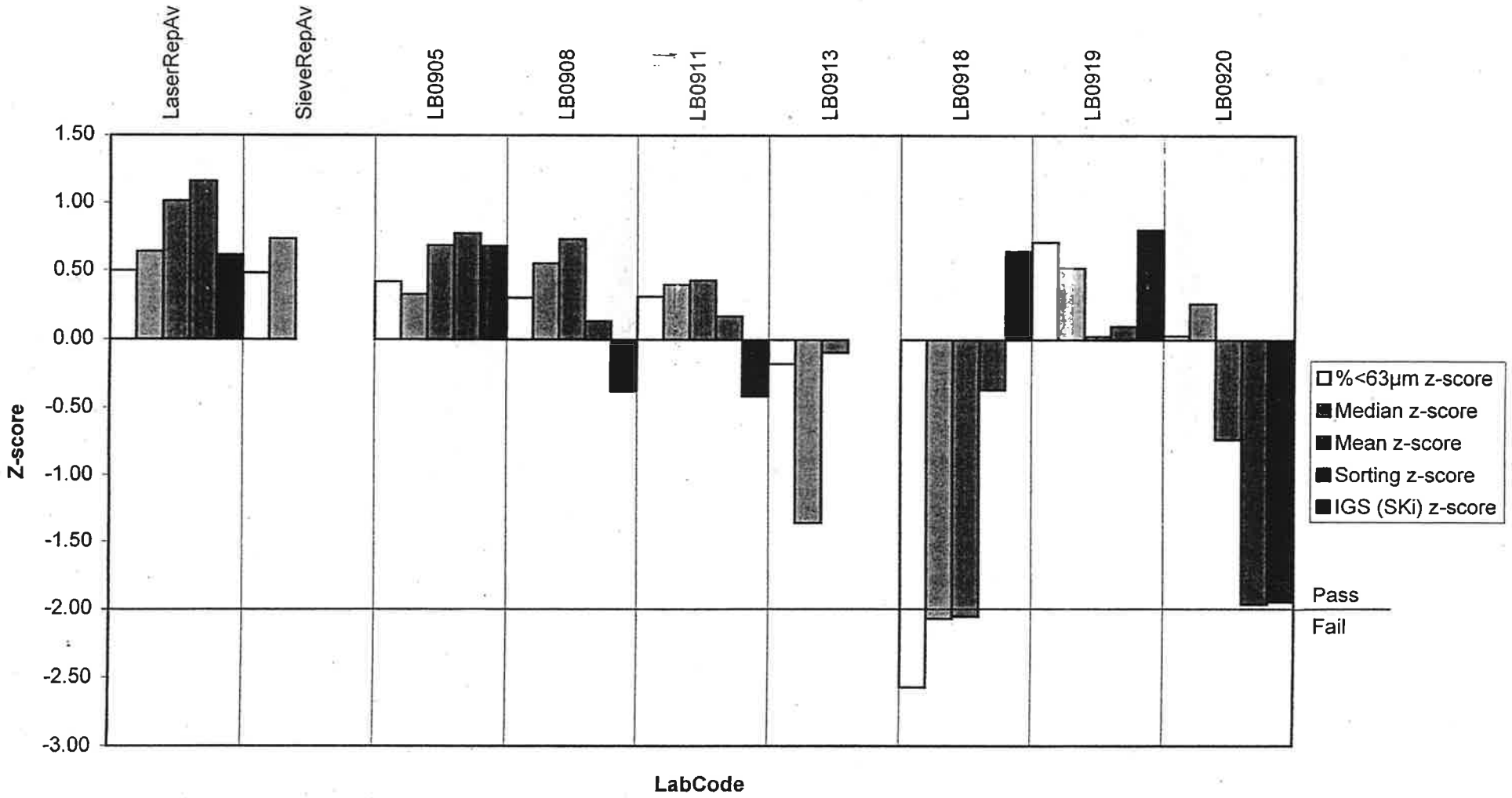


Figure 7. The number of differences from the AQC identification of specimens distributed in RT20 for each of the participating laboratories. Arranged in order of increasing number of differences.

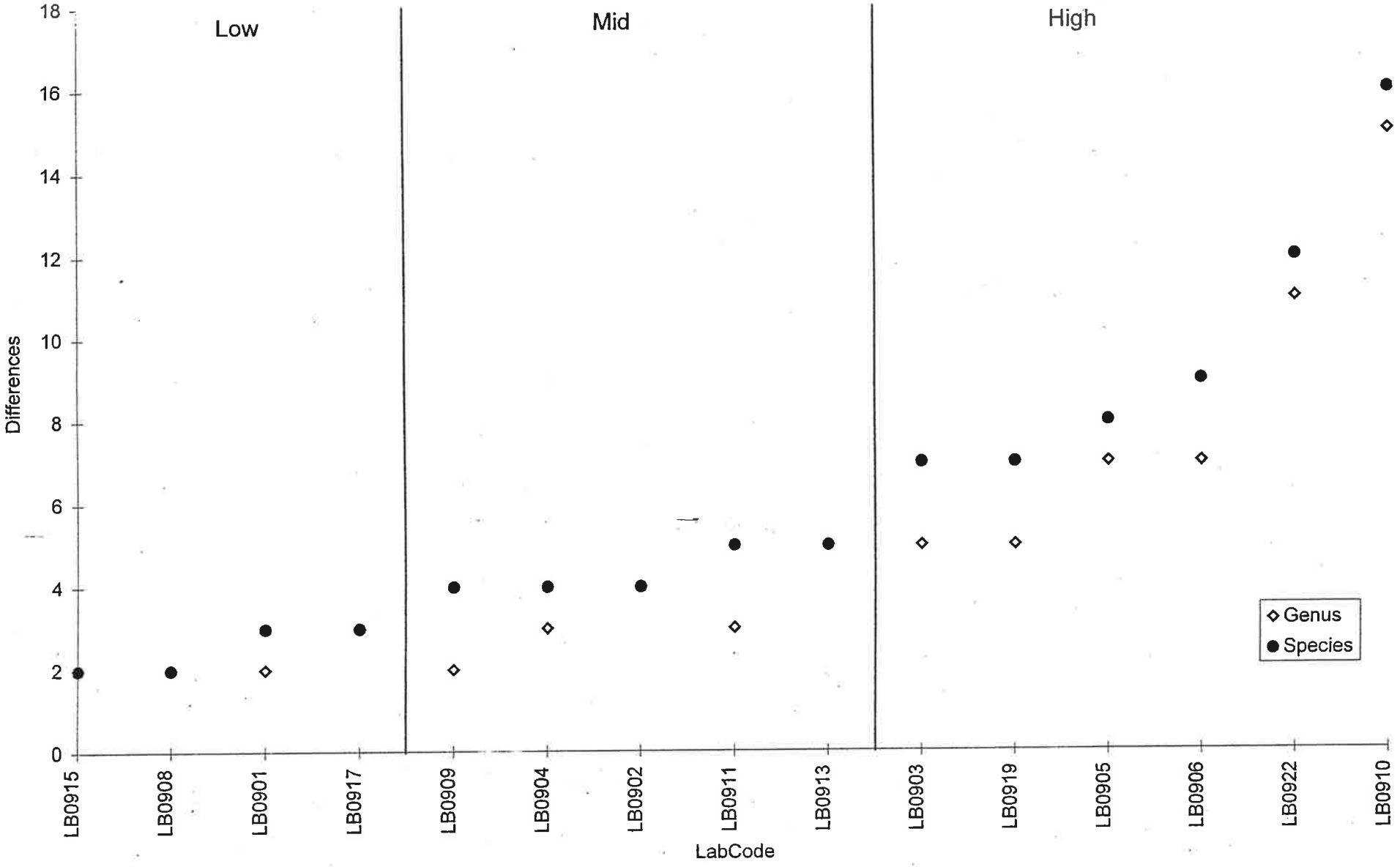
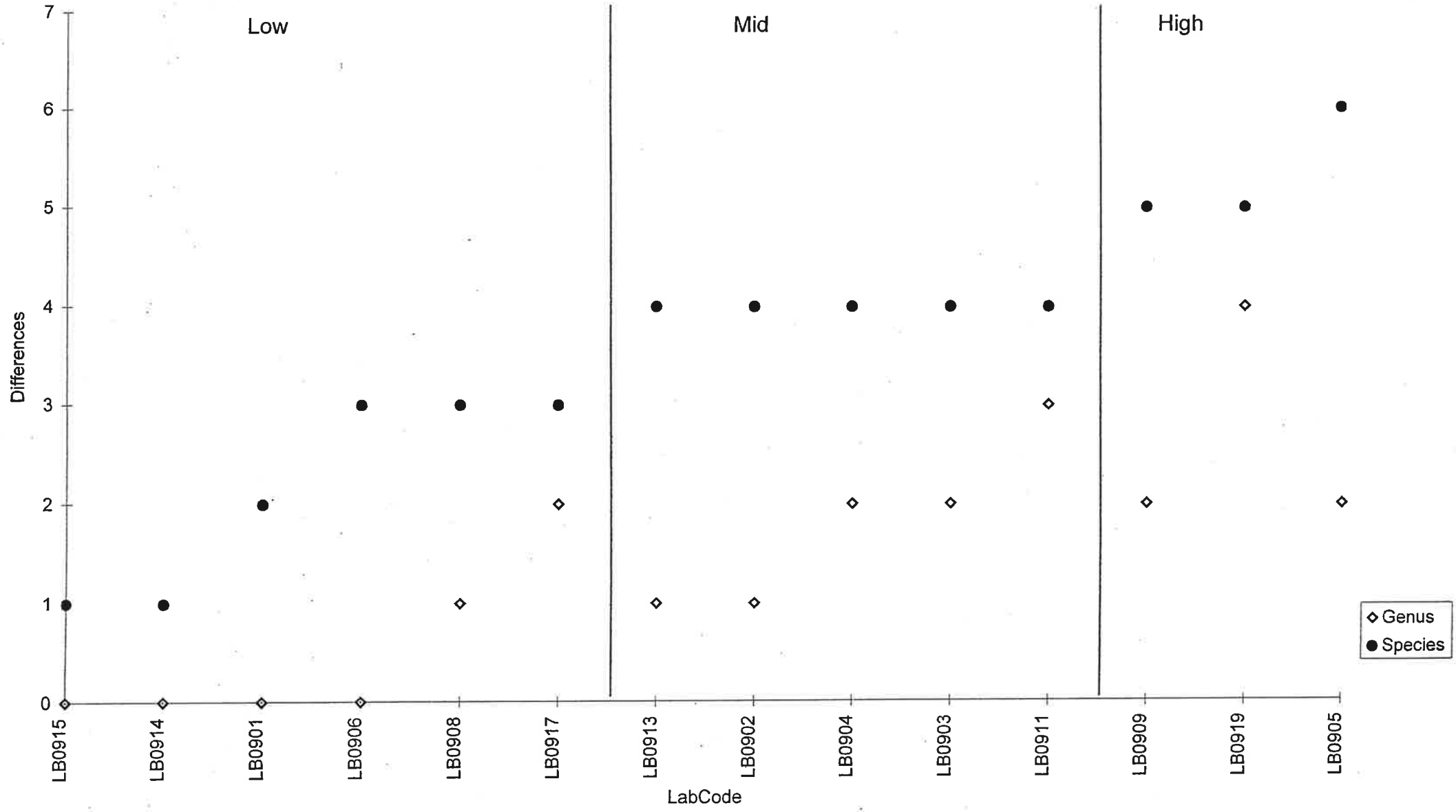


Figure 8. The number of differences from the AQC identification of specimens distributed in RT21 for each of the participating laboratories. Arranged in order of increasing number of differences.



Section 6 Contd.

Contractor Report - Appendices:

Appendix I.

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. Participating laboratories are given **free choice** of taxa they wish to submit for this exercise. 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. Unicomarine reserve the right to return specimens 'unidentified' if unacceptable mixtures of species are contained within a single taxon vial.

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 or inclusion in a future NMBAQCS Ring Test.

Timescale:

Please send specimens to Unicomarine Ltd. by 1st November 2002. 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	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
2	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
3	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
4	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
5	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
6	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
7	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
8	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
9	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
10	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
11	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
12	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
13	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
14	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
15	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
16	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
17	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
18	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
19	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
20	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
21	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
22	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
23	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
24	Participating Laboratory to select	Participating Laboratory to select	NMMP source (if applicable)
25	Participating Laboratory to select	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 Derived Statistics targets

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.

Main Report: Appendices 1 - 8

(NB pagination resumes from Section 5)

APPENDIX 1

NATIONAL MARINE BIOLOGICAL AQC COMMITTEE

Membership - Scheme Year 9 (2002/03)

Dr. M. Service (Chair)	DARDNI (Department of Agriculture and Rural Development for Northern Ireland)
Mrs. E . Hamilton (Contract Manager)	SEPA South East (Scottish Environment Protection Agency)
Mr. T. Mackie (Secretary)	EHS, DOENI (Environment & Heritage Service, Department of Environment, Northern Ireland)
Mr. N. Proctor*	IECS (Institute of Estuarine & Coastal Studies. University of Hull)
Mr. M. Robertson	FRS (Fisheries Research Services, Aberdeen)
Dr. H. Rees	CEFAS (Centre for Environment, Fisheries and Aquaculture Science)
Mr K. Cooper*	CEFAS
Mr. R. Proudfoot	Environment Agency
Ms S. Peaty	Environment Agency, North-east
Ms. L. Richardson	Environment Agency, Wales
Dr. J. Davies	JNCC (Joint Nature Conservancy Council, Peterborough)
Mr. M. O'Reilly	SEPA South West

(* as of February 2002)

APPENDIX 2

ROLE OF THE NATIONAL MARINE BIOLOGICAL AQC 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

Scheme Year 9 - 2002/2003

AstraZeneca Ltd
(CEFAS): Centre for Environment, Fisheries and Aquaculture Science
(DARDNI): Department of Agriculture and Rural Development for Northern Ireland
Environment Agency: North East, Anglian, Thames, Southern, South West, Wales - Llanelli, Wales - Cardiff
Environment & Heritage Service , Water Management Unit (Northern Ireland):
EMU Environmental Ltd
ERT (Scotland) Lt:
Hebog Environmental
Institute of Estuarine and Coastal Sciences (IECS)
Institute of Aquaculture, University of Stirling:
Marine Ecological Services Ltd
SEAS Ltd:
Scottish Environment Protection Agency(SEPA): Highlands, Islands & Grampian Area
South East Area
South West Area

Svitzer Ltd.

APPENDIX 5
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**
Taxonomic 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)	**Individuals missed in residue**	**Taxa missed in residue**	**Taxonomic errors in extracted fauna**	**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 (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 5 (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)
	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
	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 6

BENTHIC INVERTEBRATE TAXONOMIC WORKSHOP PROGRAMME

NMBAQC Scheme Taxonomic Workshop 24th-28th November 2003 (Dove Marine Laboratory, Cullercoats, Tynemouth)

Day	Session	Programme	Aims	Leader
24th Nov 2003	am	Arrival. Registration. Laboratory set-up.	Register participants. To prepare laboratory equipment for practical sessions the following day.	-
	2:00pm	Introduction. General information.	Welcome participants. Q&A session regarding workshop. Outline timetable.	Tim Mackie (NMBAQCC) David Hall (Unicomarine Ltd.)
	2:30pm	Talk – The Dove Marine Laboratory. History. Research. Local attractions. Lab. rules (H&S issues).	To give history of Dove Marine Lab. and facilities. Tour/Maps – areas of local interest (biological and otherwise). Pub & food guide.	Jane Delany (Dove Mar. Lab.)
	3:45pm	Talk – Impacts of trawling on benthic biogeochemistry – PhD thesis.	Outline one of the research projects at the Dove.	Phil Percival (Dove Mar. Lab.)
	4:30pm	Talk – Ecological functioning of the marine benthos and the impacts of human activities – PhD thesis.	Outline one of the research projects at the Dove.	Julie Bremner (Dove Mar. Lab.)
25th Nov 2003	9:00am	Discussion / Demonstration – Oligochaeta. Literature. Problem areas. Identification techniques.	To introduce literature containing details of gross morphological features for species identification.	Tim Worsfold (Unicomarine Ltd.)
		Practical - Examination & identification of range of Oligochaeta taxa from reference material.	To use new literature to view own and supplied specimens. View / verify reference material.	Tim Worsfold (Unicomarine Ltd.)
	4:30pm	Talk – European Fisheries Ecosystem Plan – EU funded project (www.efep.org).	Outline one of the research projects at the Dove.	Odette Paramor (Dove Mar. Lab.)
26th Nov 2003	9:00am	Discussion / Demonstration - Introduction to Echinodermata. The five classes. Literature. Problem areas. Demonstration of the classes. Important morphological features of Echinoidea, Holothurioidea, Ophiuroidea. Identification techniques.	To introduce the major features / terminology used for echinoderm identification.	Bernard Picton (Ulster Museum)

		Practical - Examination & identification of range of Echinoderm taxa from reference material.	To obtain identification experience. View / verify reference material.	Bernard Picton (Ulster Museum)
	4:30pm	Sea Life Aquarium group trip.	Visit local aquarium and view live examples of local fauna.	-
27th Nov 2003	9:00am	Discussion / Demonstration - Introduction to Lumbrineridae / Dorvilleidae. Literature. Problem areas. Identification techniques.	To obtain familiarity with the major features of lumbrinerids and dorvilleids.	Eivind Oug (NIVA)
		Practical - Examination & identification of range of Lumbrineridae and Dorvilleidae taxa from reference material.	To obtain familiarity with the major identification features. Gain greater experience of identifying lumbrinerids and dorvilleids. View / verify reference material.	Eivind Oug (NIVA)
	7:30pm	Workshop Dinner – Newcastle City Centre, Spanish restaurant, menu and prices TBA	-	-
28th Nov 2003	9:00am	Discussion - Summary of week. Q&A session.	Distribute/collect workshop feedback forms.	Tim Mackie (NMBAQCC) David Hall (Unicomarine Ltd.)
	am	Departure.	-	-

APPENDIX 7

ACOUSTIC GROUND DISCRIMINATION WORKSHOP PROGRAMME

Mapping seabed habitats in UK waters

Practical Acoustic Ground Discrimination Workshop
6-11 September 2003

Executive summary of workshop programme:

In recent years the need to map the distribution of habitats and biota on the seabed has arisen with an increase in the demand for information on the status of the natural environment and the impact of man-made activities. The rapid pace of developments in this field of work, driven by continuous improvements in acoustic techniques (side-scan sonar, multibeam sonar, acoustic ground discrimination systems), has revolutionised the way we are able to image, map and understand the seabed environment. Methodologies for wide-scale mapping of sublittoral habitats, in both a conservation management and resource exploration context, have been developed under a number of research and development projects (e.g. Brown et al 2001, 2002; Foster-Smith et al 1999, 2000; Kostylev et al 2001; Service 1998), and in recent years a number of nations have moved towards National Seabed Mapping programmes utilizing these techniques (Ireland, Norway, Canada, Belgium).

In the UK an increasing number of research/contract groups are undertaking broad-scale seabed mapping activities at various sites around the UK coastline, often with little knowledge of experience that exists amongst other groups. In a recent Status Report compiled for the ICES Working Group on Marine Habitat Mapping, a total of 139 mapping initiatives were identified from around the UK coastline linked to conservation management, many of which were conducted without adopting any standardised methodology (ICES WGMHM report, Sandy Hook, New Jersey, 2003). A large percentage of these surveys used the application of acoustic mapping techniques (in particular the use of acoustic ground discrimination systems – AGDS), in conjunction with ground-truth sampling, to monitor and map seabed habitats at a number of Special Areas of Conservation (SACs) around the UK coastline. Whilst this approach offers advantages over more traditional style benthic grab surveys, the accuracy of the spatial distribution maps produced from such surveys has at time been questioned. It is therefore timely that the main questions relating to the use of this acoustic system for such applications are addressed, and that we look towards a more integrated approach to mapping seabed habitats in UK coastal waters for the future.

A **Practical Workshop** focussing on the use of one particular, widely used AGDS system (RoxAnn) is therefore proposed for the period **6-11 September 2003**. A small number of key research teams will be invited to partake in the workshop. Two days will be spent at sea addressing data collection issues followed by two and a half days of data processing back in the laboratory. The final session of the workshop (**10/11 September**) will then be opened up to all interested parties within the UK; the focus will be to present the findings of the AGDS workshop to non-specialist environmental managers/advisors involved in the implementation and end use of biotope maps. Issues relating to accuracy, predictive capability and system limitations will be discussed to provide a better understanding of this mapping approach to non-specialists who use the out-puts from such surveys.

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Practical Acoustic Ground Discrimination Workshop

The Purpose:

An increasing number of research/contract groups are undertaking broad-scale seabed mapping activities at various sites around the UK coastline, often with little knowledge of experience that exists amongst other groups. This proposal is for funding to hold a practical workshop that would bring together UK research/contract groups who use the acoustic ground discrimination system (AGDS), RoxAnn, for the production of biotope maps. The workshop would compare and contrast mapping methodology and ultimately biotope maps produced by each group over the same area of seabed using the same research vessel. This would fully evaluate the utility of the acoustic system in question for the production of such maps, improve communication between UK groups working in this field, and lead to the production of guidelines/recommendations on best practice for the production of full-coverage seabed biotope maps using AGDS. The final afternoon of the workshop would be opened up to all interested parties within the UK, in particular non-technical managers/advisors involved in the implementation and end use of such biotope maps, to present the findings from the workshop and outline benefits, problems and limitations associated with biotope maps produced using this approach.

Background:

Marine benthic habitats are under threat from a wide range of anthropogenic activities (e.g. fishing impacts, construction activities, oil and gas exploitation, dredged material disposal, aggregate extraction). Recent developments in seabed mapping techniques, driven by continuous improvements in acoustic systems (e.g. side-scan sonar, multibeam sonar, acoustic ground discrimination systems), offer the potential to radically alter approaches to monitoring and mapping this component of the marine ecosystem. Such an approach provides a means to conduct cost-effective, wide-scale reconnaissance surveys, which may serve a number of important purposes. For example, they may be employed in identifying seabed (or sub-seabed) features of conservation or resource interest, as an exploratory tool to facilitate the generation of effective site-specific sampling designs, or in the determination of representative reference sites against which changes at impacted locations may be compared in long-term monitoring programmes. In recent years the application of acoustic mapping methodology (in particular the use of acoustic ground discrimination systems – AGDS), used in conjunction with ground-truth sampling, has become common practice in monitoring and mapping seabed habitats at a number of Special Areas of Conservation (SACs) around the UK coastline (e.g. Davies 1999; Foster-Smith and Sotheran, 1999; Foster-Smith et al 1999, 2000; Service 1998; Service and Magorrian 1997). Whilst this approach offers advantages over more traditional style benthic grab surveys, the accuracy of the spatial distribution maps produced from such surveys has at time been questioned.

The workshop:

The proposed workshop will aim to critically evaluate the use of the Acoustic Ground Discrimination System, RoxAnn, for use in mapping seabed biotopes. In recent years this acoustic system has been heavily used in the production of spatial distribution maps of seabed habitats and benthic communities in coastal SACs and other regions of scientific or conservation interest (Brown et al 2001, 2002; Davies 1999; Foster-Smith et al 1999, 2000, 2001; Pinn et al 1998; Robertson and Pinn 1999; Service 1998; Service and Magorrian 1997). However, issues such as data quality,

repeatability of survey, and predictive capability of the system have come into question.

A small test site on the west coast of Scotland within close proximity to DML encompassing a wide range of benthic habitats will be chosen as the study site (probably within the Firth of Lorn SAC). The workshop will invite a number of research/survey teams working with the AGDS RoxAnn to apply their own mapping methodology over this study area.

Each team will be encourage to use their own RoxAnn systems during a 2 day data collection workshop at sea. Issues such as survey design, system set up and data quality assessment will be addressed. A common ground-truthing data set (underwater video data) will also be collected from within the test site during this time, and issues relating to the selection of ground-truthing station will be discussed.

The common ground-truthing data set will then be used by each team to process the RoxAnn data sets back at the laboratory during a 2-day data-processing workshop. Workshop sessions will be run covering various aspects of data handling, quality assessment and data processing to establish methods of best practice. Spatial coverage maps will be produced from each of the RoxAnn data sets and the accuracy and predictive capability of each map will then be tested against an external ground-truthing data set collected prior to the workshop by SAMS/DARD. A minimum of 3 different RoxAnn data sets will be collected and processed during the workshop (weather permitting) to assess aspects such as between-system variability, survey design and data quality. A workshop report will be produced stating recommended best practices for mapping marine benthic habitats using the AGDS RoxAnn based on the out-put of the various RoxAnn surveys.

The final session of the workshop will be opened up to all interested parties within the UK; the focus will be to present the findings of the workshop to non-specialist environmental managers/advisors involved in the implementation and end use of biotope maps. Issues relating to accuracy, predictive capability and system limitations will be discussed to provide a better understanding of this mapping approach to non-specialists using the out-puts from such surveys.

Research Objectives:

- To compare the reliability of the AGDS RoxAnn, for the production of full spatial coverage maps of seabed habitats and biotopes. This will be achieved by comparing the out-put from a number of different RoxAnn systems over the same area of seabed.

- To compare and evaluate different approaches to seabed mapping between different research teams within the UK, with the aim of identifying and standardising best practice.

- To assess the predictive capability of biotope maps produced using RoxAnn through the collection and application of an external ground-truthing data set.

- To report on the significance of the findings for the management and monitoring of SACs.

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- To provide a better understanding to non-specialist environmental managers/advisors of the techniques and data processing methodology involved in the production of full-spatial coverage biotope maps produced using the AGDS RoxAnn, and to high-light potential benefits/limitations of biotope maps produced in this way.

Suggested Groups:

Workshop organisers:
Dr. Craig Brown. The Scottish Association for Marine Science, Dunstaffnage Marine Laboratory, Dunbeg, Oban, Argyll, PA37 1QA, Scotland

Dr. Matthew Service. Department of Agriculture and Rural Development (DARD), Agriculture and Environmental Science Division, Newforge Lane, Belfast, BT9 5PX

Dr. Robert Foster-Smith. Envision Mapping Research Group, School of Marine Science & Technology, Newcastle University, Newcsatle upon Tyne, NE1 7RU

SAMS/DARD would be responsible for the collection of the external ground-truth data (underwater video) and sidescan data prior to the workshop, and would lead on the sea-going workshop.

Envision Mapping Research Group would lead on the laboratory based data-processing workshop.

A small number of UK research teams with experience in RoxAnn data collection and processing will be invited to partake in the workshop.

Benefits:

It is expected that for a modest level of funding the utility of RoxAnn as a tool to map seabed habitats would to be fully evaluated. Standardising methodology for the analysis of AGDS data through inter-group discussion/collaboration would be of benefit to the wider scientific community involved in habitat mapping studies by establishing protocols for interpretation of AGDS data. Dissemination of information regarding the benefits and limitations of biotope maps produced in this way to environmental managers who use the out-puts from such surveys, but who may not have a clear understanding of how the maps are produced, and the limitations associated with the techniques employed.

Timetable (6 – 11 September 2003):

Day	Target	Work involved
Pre–workshop (2 days August 2003)	Collection of contingency Roxann data set (in case of bad weather), sidescan sonar data and external ground-truth data	1-2 days of survey on RV Seol Mara. Surveys with RoxAnn (contingency data set), sidescan sonar and collection of external validation underwater video footage (DARD/SAMS)
Saturday 6th/ Sunday 7th	Mobilisation of RV Calanus with survey gear. Introduction to workshop. Discussion of structure of workshop. Sea-going workshop - data collection.	RoxAnn surveys over the study site using at least 3 different RoxAnn systems and various survey strategies. Collection of a common ground-truthing data set using underwater video (and grab).

Monday 8th / Tuesday 9th / Wednesday 10th (am)	Data processing and report preparation	Each group works up data sets and produces a habitat/biotope map. Validation of maps using external ground-truth data. Collective sessions on data quality assessment, post-processing and map validation to be run (Envision Mapping). Production of project report and recommendations/conclusions.
Wednesday 10th (pm)	Open session to non-technical environmental managers	Findings from the workshop presented to generic practitioners and environmental managers. General discussion relating to Seabed mapping in SACs
Wednesday 10th evening		Workshop Dinner
Thursday 11th (am)	Open session to non-technical environmental managers	Further discussion and wash-up session

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APPENDIX 8

OVERVIEW OF BENTHIC INVERTEBRATE CLASSIFICATION PROJECT

CLASSIFICATION TOOLS: ASSESSING BENTHIC INVERTEBRATE COMMUNITIES

AIMS:
The R & D project (E1-116) assesses the use of existing classification tools in determining the ecological assessment of the benthic invertebrate communities for the purposes of the Water Framework Directive (WFD).

The WFD states that the classification of benthic invertebrate fauna in transitional and coastal waters must be based on (i) composition and (ii) abundance.
Disturbance sensitive taxa and taxa indicative of pollution are also mentioned.

In order to be effective, the classification tools need to meet the following criteria:
(i) to be sensitive to stress at low levels
(ii) to demonstrate predictable change with increasing degrees of stress
(iii) to be specific to anthropogenic disturbance
(iv) to be applicable to a wide range of estuaries and coastal waters
(v) to be easily understood by non-specialists

STATISTICAL APPROACHES:
The following tools are being considered for use in assessing the ecological status of a water body using the benthic invertebrate community. It is believed that no single metric will be used in isolation, rather that a multimetric approach will be required to distinguish biological community change.

Metrics currently being calculated:

Univariate tools

Primary
Number of taxa (S)
Abundance (A)

Secondary statistics -Diversity Indices
Shannon-Wiener (H')
Pielou - Eveness (J')
Margalef – Richness (d)
Simpson (D)
Fisher
Brillouin

Taxonomic Distinctness Index[1] (Δ, Δ^*, Δ^+).

Functional Indices

Infaunal Trophic Index (ITI)
Biotic Index (AMBI)[2]

Currently, the project team is calculating the above metrics for sites from a wide range of transitional and coastal waters using historical EA data. The combination of metrics required to provide an ecological assessment for the different 'types' of transitional and coastal waters will be progressed once the typology project has reported.

Multivariate statistics such as multi-dimensional scaling ordination (MDS), principal components analysis (PCA) and cluster analysis are being used to investigate the benthic datasets and to assess the suitability of the metrics proposed for use for status classification. Statistical testing is being carried out using the PRIMER (Plymouth Routines in Multivariate Ecological Research) statistical software. SIMPER (similarity percentages), ANOSIM (analysis of similarities), and BIO-ENV (matching biotic to environmental patterns) analyses are also being used to assess the ecological status of a water body based on the biological composition.

Notes:

[1] The taxonomic distinctness index is being further investigated following work for DEFRA with respect to NMMP indicators. Please refer to the report (Somerfield, Clarke & Warwick 2003) for the technical overview of the method and approaches for defining ecological groups. Further investigation of this index will be carried out to determine the robustness of the index for use in ecological appraisal for the WFD.

[2]Borja *et al.* (2000) developed the AZTI Marine Biotic Index (AMBI) for soft bottom benthos based initially on studies at the basque Fisheries and Food Technological Institute (Aviautzatouaiellills Zleutei eta Tellnoloii Illeituta) and then extended to other European estuarine and coastal environments.The index is derived from theproportions of individual abundance in five ecological which are related to the degree of sensitivity/tolerance to an environmental stress (organic) gradient.

(see. Borja, A.; J. Franco & V. Perez, 2000. A marine biotic index to establish the ecological quality of soft bottom benthos within European estuarine and coastal environments *Marine Pollution Bulletin* 40(12): 1100-1114).