NATIONAL MARINE BIOLOGICAL ANALYTICAL QUALITY CONTROL SCHEME

National Marine Biological AQC

1998/99

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National Marine Biological AQC Coordinating Committee

Unicomarine Ltd

NATIONAL MARINE BIOLOGICAL ANALYTICAL QUALITY CONTROL SCHEME

Annual Report 1998/1999

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1. OVERALL SUMMARY

- The National Marine Biological AQC Scheme (NMBAQC Scheme) has completed its fifth year in 1998/99. The background to the scheme is described in previous annual reports.

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

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

- Participation in the scheme remained high with up to twenty eight laboratories participating. Fifteen of these laboratories submitted data for NMMP, nine were consultants or private contractors and the remainder non NMMP government labs. Interest had been expressed by some non NMMP labs in 'selective' participation where particular components of the scheme could be excluded/included for them. NMMP labs were required to participate in all relevant components. Overall the scheme was well supported.

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

- There was considerable variation in the way different participating laboratories approached the scheme components. There were long time delays and some non returns of essential data, presenting reporting and 'flagging' difficulties.

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

- Problems with biomass analysis were again evident with a great deal of variation amongst labs. Consideration to be given to the preparation of a standardised protocol and reporting format.

- Serious problems still exist in sorting accuracy, although there is a slight improvement on previous years. Laboratories should target taxa commonly being overlooked.

- There was improved extraction efficiency and taxonomic identification of the MB sample compared to last year.

- Overall fall in the results for the OS component compared to the 1997/98 circulation.

- Particle size exercises again highlighted the variation in results depending on the technique employed. These differences are further emphasised by certain sediment characteristics.

- Efforts to achieve better data feedback to participants were hindered by late returns and non returns of data. Laboratories who miss data or sample return deadlines will be deemed to have failed. The use of e-mail to facilitate rapid data transfer is strongly recommended where practicable.

- Ring Test Bulletins (RTB) have been introduced to improve feedback and emphasise the learning aspect of this component.

- NMMP Laboratories achieved a 64% overall pass rate in the Own Sample exercise. This is an improvement on previous years (56%) but the low value is again due to non returns of OS data.

- Failure of some NMMP laboratories to achieve the necessary overall standards may affect the inclusion of their data submissions to the NMMP database.
- A Scheme Statement of Performance has been developed for issue to participants.
- NMMP II, for temporal trends analysis, began in January 1999.
- The Co-ordinating Committee have commissioned an independent review of standards with expected completion in Autumn 1999.
- A sub-group of the Co-ordinating Committee has been formed to consider AQC measures for epibenthic(flora) surveys and biotope mapping.
- The Co-ordinating Committee has instigated steps to commission an independent audit of the scheme with expected completion spring 2000.
- A workshop on Sampling Strategies and Survey Design planned in 1998-99 was completed in May 1999.
- Unicomarine Ltd. continue to operate the scheme successfully.
- Overall co-ordination of the scheme was undertaken by the National Co-ordinating Committee (Appendix 1) reporting to NMMP Working Group at UK level.

2. SCOPE OF THE SCHEME

The fifth year of the scheme was designed to build on the data from previous years and highlighting the standards achieved, while continuing the emphasis on participant supplied samples. In total ten participant supplied samples (OS) have now been judged against the standards derived in 1996/97. To this end the format of the scheme in 1998/99 followed last year's formula.

Scheduled circulations:

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

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

c). Two contractor supplied natural marine sediment samples for particle size analysis (PS).

d). One contractor supplied macrobenthic sample (MB).

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

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

3. ISSUES ARISING

3.1 The composition and aims of the scheme

The statements made in last year's report hold true for 1998/99

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

- The **Laboratory Reference** was perceived as a parallel to OS returns *ie.* this component test would apply quality control to 'own specimens'. It has transpired however that while some laboratories are only beginning to set up a marine voucher collection, others have used the LR exercise to acquire a second opinion on their 'difficult specimens' from a consultant, rather than as a check on a range of their 'standard' fauna. Should this component acquire a pass / fail standard, labs may well choose to send specimens they are confident in to achieve a high score! In the mean time labs are urged to consider this component in a more 'random' fashion selecting a range of beasts from across a spectrum of taxa, substrates and salinities if possible.

- The **MB sample**, though sourced from a geographical location unfamiliar to many participants, was designed to examine sample processing skills in addition to taxonomic skills. It became apparent that a few labs had some serious problems overlooking a number of taxa in addition to many others overlooking some specimens. While overlooking a few individuals might be deemed to be insignificant, should these individuals comprise several taxa in a sparse community, interpretation could be compromised. The MB component is considered by many labs to be irrelevant or too time consuming and returns are not forthcoming.

- Determining **biomass** is a new skill for many laboratories that do not complete this analysis routinely. The derivation of a standardised effective protocol requires addressing by the committee. Biomass determination is a requirement of NMMP labs but no standard has been assigned by the AQC Committee, until skills and protocols have been agreed and tackled.

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

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

3.2 Participation

The initial twenty eight participants in 1998/99 comprised private contractors, university labs and Government labs in Scotland, Northern Ireland, England and Wales. Fifteen laboratories provide data or analytical services for NMMP components and submit data to the NMMP data base. A number of the participants subcontract to a second or third party. While it is in the interest of all laboratories to participate in all components of the scheme, in order to gauge their performance, some laboratories may favour completing certain components over others which will be compatible with their commercial interests, budgets or time constraints. This is their choice provided no contractual agreement is broken. **However, all laboratories submitting data to the NMMP should complete the whole programme whether pass / fail standards have been devised or not for individual components.**

3.3 Submission of data

Despite long time periods for data returns there are still problems with late or non returns and use of incorrect formats. **Only four NMMP laboratories supplied all the data from all the relevant components.** Two supplied no data at all while the rest failed to supply at least one component.

Recognising the value of flags, laboratories tended to favour the supply of OS and PS data at the expense of the rest of the scheme.

3.4 Data feedback

As in previous years considerable problems were encountered feeding back data due to late or non returns and incorrect data formats.

Laboratories who miss data or sample return deadlines will be deemed to have failed.

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

3.5 Targets and Standards

As in 1997/98, it was agreed that the separate components of the Own Samples and PS only would be scored against the targets. Each of the three Own Samples (OS08-10) generated three pass/fail flags based upon taxa and individuals recorded and the Bray-Curtis Similarity index. Thus for those labs returning data, 9 separate criteria can be assigned as pass or fail. The committee agreed it would be reasonable that in order to achieve an overall Own Sample component pass, the standards should be achieved or exceeded on >=6/9 flags.

While individually very few laboratories had consistent problems, applying the agreed level of pass, eight out of the nineteen participating labs failed the OS exercise overall.

Of the eight labs which failed, five supplied insufficient or no OS data (these are deemed to have failed).

Achievement of the biological standards appear to be posing a challenge for a number of laboratories. An independent review of standards has been commissioned for completion in autumn 1999.

Particle size analysis poses less of a challenge to laboratories. For PS12 all laboratories returning data passed, the remaining nine laboratories which did not return their data are deemed to have failed. PS13 showed far greater scatter of data received. Seven laboratories failed (this number is unusually high due to four laboratories using combined data from a failing laboratory) and a further eight laboratories failed to return data and thus are also deemed to have failed.

4. SCHEME PROPOSAL FOR 1999/2000

The core programme for the scheme in the coming year 1999/2000 will contain the following components.

1. Own samples
2. Ring Tests including a targeted ring test and laboratory generated reference collection
3. Macrobenthic 'Bucket' sample
4. PSA samples

The Co-ordinating Committee has commissioned an independent review of standards with expected completion autumn 1999. The committee has also instigated steps to commission an independent audit of the scheme with expected completion spring 2000.

A workshop on Sampling Strategies and Survey Design was completed in May 1999. (Another workshop on Beginners Invertebrate Taxonomy will be held in October 1999 and a potential future workshop will deal with a specific taxonomic group, possibly in spring 2000).

5. CO-ORDINATING COMMITTEE ACTIVITIES AND PROJECTS

From its conception in 1993 the primary function of the NMABAQC scheme was to meet the benthic quality control needs of the UK National (Marine) Monitoring Plan. With this in mind the membership of the co-ordinating committee was drawn principally from those Government bodies and statutory agencies providing data to the NMP. However, from the onset it was clear the scheme would draw participants from wider benthic biology community including many commercial bodies with this in mind one committee member (DR M Elliot) represents these wider interests.

During the period covered by this report the co-ordinating committee met four times with the principal purpose of discussing management aspects of the scheme and ensuring that any problems reported to the schemes contractors or the scheme manager were dealt with. However, during the year the committee devoted time to a number of special activities.

5.1 NMMP Developments

As the NMMP moved from reporting its initial spatial survey into temporal trends strategy the original NMMP Plan or "Blue Book" was rewritten to become the "Green Book" containing details of samples sites and procedures. The Co-ordinating Committee reviewed and contributed to those aspects relevant to benthic biology including the co-ordination of biological and chemical sampling. As part of their departmental role two committee members also sit on the NMMP WG. The Co-ordinating Committee administers the application of pass/fail standards to the quality on benthic data sets submitted to UK database as part of its role in supporting the NMMP. In recognition of the fact that standards were originally set in the absence of supporting data the committee commissioned a review of standard setting from an independent UK benthic biologist and the results of this are expected in the autumn of 1999.

5.2 Workshops

In past years the NMBAQC Committee has organised and supported workshops in conjunction with ECSA. The outcomes of the benthic sampling workshop on the Humber were finalised during the year.

5.3 Epibenthos

As the EC Habitats Directive has begun to be implemented and the monitoring of Marine SAC's begin the UK lead organisation in this area (JNCC) has recognised the need for appropriate AQC measures and accordingly has joined the NMBAQC scheme and is now represented on the Co-ordinating Committee. A sub-group has now been tasked to consider AQC measures for epibenthic(flora) surveys and biotope mapping. It is likely that the forthcoming EC Framework Directive will also lead to further scope for development in this area.

5.4 Scheme Audit

Although most aspects of the scheme have been generally well received and any problems arising dealt with by the committee, several participants have raised questions regarding the scope and management of the scheme. Particularly where contracting bodies have stipulated that membership of the scheme is a necessary qualification for obtaining contracts. Mindful of this the Co-ordinating Committee has begun steps to commission an independent audit of the scheme. It is likely that this will be conducted by a European laboratory and to be completed by the Spring of 2000.

Scheme members have made contact with colleague in Europe and the United States and although as yet no formal links have developed a number European countries have expressed interest in the structures adopted by the UK Scheme.

6. Financial summary 1998/1999

The fifth year of the scheme has been completed..

Fees in 1998/99 remained the same as 1997/978. Non NMMP laboratories were eligible to take advantage of the 'split fee' according to the components required although many elected to participate

fully. NMMP Laboratories participating in workshops held during the year were subsidised through the scheme to encourage and develop taxonomic and sampling skills.

The scheme handled funds for publication of the NMMP Holistic report.

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

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

Financial Summary 1998/1999

	INCOME	***EXPENDITURE***
Participant Fees	*43,071.25*	
Interest	*3,056.39*	
Core project fees *Additional projects(NMP report)*	 *7,050.00*	*45,699.27* *6,995.00*
Management fee		*0.00*
Hospitality Travel & Subsistence		*576.50*
Funds carried forward from 94/95-97/98	*54,040.54*	
Available funds at year end	***£ 53,947.41***	

Report from Contractor

7. REPORT FROM THE CONTRACTOR

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Appendix 1. The list of groups distributed to laboratories for selection of species for the Laboratory Reference exercise (LR03).

Appendix 2. Description of the Scheme standards for each component.

Summary of performance

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

The Scheme consisted of five components:

- Analysis of a single estuarine macrobenthic sample.
- Analysis of two sediment samples for physical description.
- Identification of two sets of twenty-five animal specimens.
- Re-analysis by Unicomarine Ltd. of 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 fourth year of the Scheme. The results for each of the Scheme components are presented and discussed. Comments are provided on the performance for each of the participating laboratories in each of the components.

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

Comparison of the results from the laboratories with those from analysis by Unicomarine Ltd. was made using the Bray-Curtis similarity index. The value of the index varied between approximately 78% and 99% and was better than 80% in 90% of comparisons and better than 90% in 60% of comparisons.

The results for the **Own samples (OS)** were broadly similar to those from the Macrobenthic sample. Agreement between the laboratories and Unicomarine Ltd. was generally good. In 52% of the comparisons the value of the Bray-Curtis similarity index was greater than 95% and in most cases (71%) the value of the index was greater than 90%.

The influence of analytical technique on the results returned for the **Particle Size exercises (PS)** was marked, as had been found in previous circulations. In most cases there was good agreement between laboratories using the same technique.

Two **Ring Tests (RT)** of twenty-five animal specimens were distributed. One set contained general fauna and the other set consisted of twenty-five specimens of Amphipoda. For the general set of fauna (RT12) there was fairly good agreement between the identifications made by the participating laboratories and those made by Unicomarine Ltd. The 'targeted' set (RT13) posed even fewer problems with 80% less differences at the generic level and 33% less at species level.

The identification of a set of twenty-five species selected by the participating laboratories from a list distributed by Unicomarine Ltd. were generally accurate. No clear problem areas were identified. However there were differences in the approach to this **Laboratory Reference (LR)** exercise by the individual laboratories.

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

1. Introduction

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

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

The fifth year of the Scheme (1998/99) followed the format of the fourth year. A series of exercises involved the distribution of test materials to participating laboratories and the centralised examination of returned data and samples. During the course of the year up to twenty-eight laboratories participated in the Scheme.

As in previous years, some laboratories elected to be involved in limited aspects of the Scheme. In addition some joined after the samples for a particular exercise had been distributed; others chose not to submit samples for the Own Sample component. NMMP laboratories were required to participate in all components and standards applied to agreed components.

In this report attainment targets have been applied for the OS and PS components only (as described in the Annual Report for 1996/97). These targets have been applied to the results from laboratories (Section 5) 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 "Deemed Fail" flag has been assigned. The three different flags (Pass, Fail and Deemed Fail) are indicated in the Tables presenting the comparison of laboratory results with the standards.

2. Description of the Scheme Components

The three core components; Macrobenthic sample analysis (MB), Ring Test identification (RT), and Particle Size analysis (PS) and the two more recently introduced components; Laboratory Reference (LR) and Own Sample (OS) were continued into the fifth year.

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 report for 1994/95 and 1995/96. For some laboratories email has become the preferred mechanism of communication. It is considered to be a very useful mechanism but must remain an option until email facilities are available to all participating laboratories.

2.1.2 Data returns

Return of data to Unicomarine Ltd. followed the same process as in previous years. Pre-formatted discs with spreadsheet based forms (tailored to the receiving laboratory) were distributed with each circulation in addition to hard copies. A range of file formats were required to cover all applications in use by participating laboratories. All returned data have been converted to Excel 97 format for storage and analysis. Slow or missing returns for exercises lead to delays in processing the data and resulted in difficulties with reporting and rapid feedback of results to laboratories.

2.1.3 *Confidentiality*

To preserve the confidentiality of participating laboratories the practice of identifying laboratories with a two-digit Laboratory Code was continued. The code was changed in April 1998 and new codes assigned. **In the present report all references to Laboratory Codes are the new (post-April 1998) codes.**

In April 1999 a further laboratory code change was implemented. These are in use for 1999/2000 but do not appear in this current report. These new codes will be 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 six will be recorded as LB0604.

2.2 Macrobenthic Samples (MB)

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

2.2.1 *Preparation of the Samples*

Sample MB06 was collected at the confluence of the Rivers Stour and Orwell, Harwich, Essex; in an area of muddy shell sediment. A set of forty samples was collected using a 0.1m² Day Grab. Sampling was carried out while at anchor and samples for distribution were collected within a five hour period. All grabs taken were full. Sieving was carried out on-board using a mesh of 0.5mm, followed by fixing in buffered formaldehyde solution. Samples were washed after a week in the fixative, prior to transfer to 70% IMS, in which condition they were distributed.

2.2.2 *Analysis required - MB*

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

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

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

2.2.3 *Post-return analysis*

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

2.3 Own Sample (OS)

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

2.3.1 *Analysis required*

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

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

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

Upon receipt at Unicomarine Ltd. all OS samples were re-analysed by the same operator. The sorted residue was re-examined and any countable material extracted. Identified fauna was checked for the accuracy of enumeration and identification and all specimens were re-weighed using the same procedure as for the MB exercise.

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 1998/99. Both samples were derived from natural sediments and prepared as described below. In each case replicates of the distributed samples were analysed using both laser diffraction and sieve analysis techniques.

2.4.1 *Preparation of the Samples*

2.4.1.1 *Natural samples*

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

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

2.4.2 *Analysis required*

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

2.5 Ring Test Specimens (RT)

This component of the Scheme examined inter-laboratory variation in the ability to identify fauna and attempted to determine whether any errors were the result of inadequate keys, or the incorrect use of satisfactory keys.

Two sets of twenty-five specimens were distributed in 1998/99. The first of the year's RT circulations (RT12) was of the same form as for the earlier years - the specimens included representatives of the major phyla and approximately 50% of the taxa were polychaete worms. The second circulation (RT 13) 'targeted' specimens of Amphipoda. This faunal group had been identified from earlier RT circulations and MB exercises as causing laboratories significant problems with identification.

2.5.1 *Preparation of the Samples*

The specimens distributed were obtained from a range of surveys from around the UK. Every attempt was made to provide animals in good condition and of similar size for each laboratory. Each specimen sent was uniquely identifiable by means of a coded label and all material has been retained for subsequent checking. In a number of instances, particularly with small species, two specimens were distributed. Where relevant every effort was made to ensure all specimens of a given species were of the same sex.

For the standard RT (RT12) and the 'targeted' RT (RT13) circulations, all specimens were taken from replicate grabs within a single survey and in most cases they were replicates from a single sampling station.

2.5.2 *Analysis required*

The participating laboratories were required to identify each of the RT specimens to the level of species. Also requested was the Marine Conservation Society code for the specimen (where available) and brief information on the keys or other literature used to determine the identification. All specimens were to be returned to Unicomarine Ltd. for verification and resolution of any disputed identifications. This was the same procedure as for earlier circulations.

2.6 Laboratory Reference (LR)

A repeat of the laboratory reference exercise completed last year was included in 1998/99 (LR03). 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, following certain guidelines, of twenty-five specimens for re-examination by Unicomarine.

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 families was distributed to participating laboratories with a request that an example of a named species selected from each of the listed taxonomic groups be sent to Unicomarine Ltd. Thus, for example, although all laboratories were requested to send an identified specimen of a polychaete from the genus *Nephtys,* different species were sent by the laboratories. The groups listed included the major families typically encountered in marine benthic surveys. The list of groups as distributed is given in Appendix 1.

2.6.2 *Analysis*

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

3. Results

Most of the exercises in 1998/99 were undertaken by approximately twenty-eight laboratories. Changes in the number of participants during the year and differences in the number of exercises in which laboratories participated meant that some exercises had more data returned than others. There were again large differences between laboratories in their ability to meet the target deadlines, even though these had been extended for some exercises this year due to variations in seasonal workload between

laboratories. Sub-contracting by participating laboratories of certain sample analyses may also have contributed to delays.

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

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

3.1 Macrobenthic Samples (MB)

3.1.1 General comments

The distributed sediment (MB06) was from a muddy shell substratum taken from a depth of approximately 6m. The samples were very diverse with an average of forty-seven species and seven hundred and sixteen individuals, covering a variety of phyla. The composite list from all samples was approximately one hundred and eighteen species. A number of samples returned had been stained with Rose Bengal. Overall, of the twenty-two laboratories participating in this exercise, ten laboratories returned samples and data; twelve did not.

3.1.2 Efficiency of sample sorting

Table 1 presents for sample MB06, 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.

3.1.2.1 Number of Taxa

It may be seen from Table 1 (column 5) that there was considerable variation between laboratories in the percentage of taxa identified in the samples. Up to seven taxa (17% of the total taxa in the sample) were either not extracted or not recognised within the picked material. On average Unicomarine Ltd. recorded two more taxa than the participating laboratories.

Re-sorting of the sample residue following analysis by the participating laboratories retrieved small numbers of individuals from all samples. These data are presented in columns 10 to 12 of Table 1. Up to 53 individuals were not extracted from the samples (8% of the total in the sample). The average number of unpicked individuals was nineteen.

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. Of those laboratories that provided their residue for re-analysis, only one laboratory extracted representatives of all the species present in their samples and in the worst instance four completely new taxa were missed during the picking stage of this exercise.

3.1.2.2 Number of Individuals

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 represented in most cases less than 5% of the true total number in the sample (9 out of 10 laboratories), though 5.1% were missed in the worst instance. A breakdown of the missed individuals by taxonomic group is presented in Table 2.

3.1.2.3 *Uniformity of identification*

Most of the species in the distributed sample were identified correctly by the participating laboratories. In the worst instance eleven taxonomic differences were recorded (Table 1, column 15). On average four 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 considerable variation among laboratories in the values calculated for the index, from 78% to 99%, with an average value of 91%. The index for the majority of laboratories (9 of 10) was in excess of 80%. The variation and relatively low average Bray-Curtis similarity indices can be attributed to several factors. In some cases, new taxa (*i.e.* taxa not already recorded by the participating laboratory) were found in the residue by Unicomarine Ltd. Additional individuals of taxa already recorded by participating laboratories were also often found in the residue. There were also identification differences involving large numbers of individuals. An indication of the particular reason for the relatively poor agreement between the analysis of the sample by Unicomarine Ltd. and the participating laboratories is given where relevant in Section 6.

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 MB06 circulation is presented in Table 3. Two laboratories did not supply biomass data. The average difference between the two values was +26%, with the measurement made by Unicomarine Ltd. typically being less (*i.e.* lighter) than that made by the participating laboratory. The range was -28% (measurements by laboratory were lighter than those made by Unicomarine Ltd.) to +44% (measurements by laboratory were greater than those made by Unicomarine Ltd.).

3.2 Own Sample (OS)

3.2.1 *General comments*

Following the request to participating laboratories to submit a list of samples for re-analysis, forty-two samples were received from fourteen laboratories, together with descriptions of their origin and the collection and analysis procedures employed. Samples were identified as OS08, OS09 and OS10 on receipt. Eight laboratories did not participate in this component although notification of non-participation was only received from three. The nature of the samples varied markedly. Samples were received from estuarine and marine locations, both intertidal and subtidal. The sediment varied from mud to gravel and from 10ml to 5l of residue. The associated fauna of the samples was also very varied; the number of taxa recorded ranged from 2 to 89, and the number of individuals from 4 to 1254. All NMMP labs were required to participate in this exercise. Overall, of the twenty-two laboratories participating in this exercise, fourteen laboratories returned all three Own Samples. Five laboratories failed to supply Unicomarine Ltd. with a list of samples from which to select their samples.

3.2.2 *Efficiency of sample sorting*

Table 4 displays a summary of the data obtained from the analysis of the Own Sample exercise. All taxa identified by the participating laboratory were included in the analysis. In nineteen cases (45% of the comparisons) the number of taxa recorded by the participating laboratories was identical to that obtained by Unicomarine Ltd. (Table 4, column 4). In the twenty-three exceptions, the difference was at most fifteen taxa and the average difference was one taxon.

The data for the numbers of individuals recorded (Table 4, columns 6 & 7) shows a range of differences from the value obtained from re-analysis of between 0% and 67%. The average difference is 9% (only ten samples exceeded this average). Two samples were received without their sorted residue for re-examination. Eleven of the samples received showed 100% extraction of fauna from residue (Table 4,

column 12), and in eleven samples various numbers of individuals (but no new taxa) were missed during sorting (Table 4, column 11). The remaining eighteen samples contained taxa in the residue which were not previously extracted, the worst example being sixteen new taxa found in the residue (Table 4, column 10). In the worst instance residue was found to contain one hundred and ninety-six individuals, including nine previously unrecorded taxa.

3.2.3 *Uniformity of identification*

Taxonomic differences between participating laboratory and Unicomarine Ltd. results were found in twenty-five of the samples received. An average of less than two taxonomic differences per laboratory were recorded; in the worst instance seven 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 4, column 14) ranged from 36% to 100%, with an average of 89%. This indicates that, with the exception of six samples, there was a fairly high degree of similarity between the data-sets produced separately from the same sample by the participating laboratories and Unicomarine Ltd. Four samples gave similarity figures of 100%. The best overall results were achieved by LB04, whose results consisted of 100%, 99.7% and 99.8% similarity scores. It is worth noting that a small number of differences between samples can result in a large difference in the Bray-Curtis index. This difference does not necessarily reflect the laboratory's interpretative ability.

3.2.5 *Biomass determinations*

It was not possible to make a comparison of the biomass determination in all cases; in some no data were provided, in others it was in a different format from that requested. Table 5 shows the comparison of the participating laboratory and Unicomarine Ltd. biomass figures by major taxonomic groups. Thirty-nine of the forty-two samples received could be used in this comparative exercise. The total biomass values obtained by the participating laboratories were all higher than those obtained by Unicomarine Ltd. The average was a +34% difference between the two sets of results, the range was from +2% to +69%. 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 46% for polychaetes, 46% for crustaceans and 20% for molluscs. These figures are markedly different to those produced by this same exercise in the last two 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.

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 PS12, fourteen out of the twenty-three participating laboratories returned data (including labs with grouped results); nine did not. For PS13, fourteen out of the twenty-two participating laboratories returned data and eight did not.

3.3.2 *Analysis of sample replicates*

Replicate samples of the sediment used for the two PS distributions were analysed using both sieve and laser techniques. This was adopted after the earlier results indicated a clear difference according to the analytical technique used to obtain them. Half of the replicates were analysed using the Malvern laser and half by the sieve and pipette technique.

There was good agreement between the replicate samples from PS12; the shape of the distribution curves was similar for the two analytical techniques and they were closely grouped. This sample had a very low fine fraction (average of <0.8% <63µm. Results for the individual replicates are provided in Table 6 and are displayed in Figure 1.

Sample PS13 was much finer and there was a more obvious difference between the two techniques. The spread of results for laser analysis was rather broader than for the sieve. Results for the individual replicates are provided in Table 7 and are displayed in Figure 2.

3.3.3 *Results from participating laboratories*

Summary statistics for the two PS circulations are presented in Tables 8 and 9. After resolution of the differences in format, the size distribution curves for each of the sediment samples were plotted and are presented in Figures 3 and 4. Included on each of these Figures for comparison is the mean distribution curve for the replicate samples as obtained by Unicomarine Ltd.

It should be noted that three laboratories which normally sub-contract particle size analysis to the same independent laboratory (also participating), elected to utilise the results from this laboratory. Accordingly the results from this laboratory have been used in the Figures and Tables as appropriate though a few points should be noted. In Figures 3 and 4, which present the size distribution curves for PS12 and PS13 respectively, only a single line is shown though it applies to six laboratories (the sub-contractor and the five laboratories utilising their results. In Tables 8 and 9, which present the summary statistics for PS12 and PS13 respectively, although the results are displayed for all six laboratories, the value supplied (by the sub-contractor) has been included only once in the calculation of mean values for the exercise. Performance flags (as discussed in Section 5) have been assigned in the same manner as for other laboratories.

3.3.3.1 *PS12*

There was good agreement for PS12 between the results from the analysis of replicates and those from the participating laboratories. The difference between the analytical techniques was clear (see Figure 3), as had been found in the analysis of the replicate samples.

3.3.3.2 *PS13*

There was more spread in the results for this sample (which had a much higher proportion of sediment in the silt-clay fraction) and the difference between the techniques was less marked (see Figure 4). The results from one laboratory were clearly different to those from the majority of laboratories, being displaced markedly towards the coarser fractions. Results for two other laboratories were also rather separated from the majority towards the finer fraction. In this case the difference was less marked.

3.4 Ring Test Circulations (RT)

3.4.1 *General comments*

The implementation of this part of the Scheme was the same as for the first four years. A number of labs use this part of the scheme as a training exercise and have selected it preferentially over other components. NMMP labs are required to participate in this component though it is not used when assigning pass or fail flags. Two circulations of twenty-five specimens were made. For RT12 the species were from a variety of Phyla (as for previous years) while for RT13 twenty-five Amphipoda specimens were 'targeted' for circulation. Other aspects of the two circulations, in particular the method of scoring results, were the same as for previous circulations. Overall twenty-four laboratories were distributed with RT12 and twenty-three distributed with RT13 specimens. For RT12, eighteen laboratories returned samples and data; six did not. For RT13, fifteen laboratories returned samples and data; eight did not.

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:

- Variation in the 'accepted' spellings, e.g. *Atylus swammerdamei, A. swammerdami.*
- Use of a different synonym for a species, e.g. *Skenea nitens* for *Dikoleps pusilla.*
- Simple mis-spelling of a name, e.g. *Diskoleps* for *Dikoleps.*

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 10 and 11, respectively, present the identifications made by each of the participating laboratories for each of the twenty-five specimens in RT circulations RT12 and RT13. For clarity the name is given only in those instances where the generic or specific name given by the laboratory differed from the AQC identification. Where it was considered that the name referred to the same species as the AQC identification but differed for one of the reasons indicated above, then the name is presented in brackets "[name]". Errors of spelling or the use of a different synonym are not bracketed in this way if the species to which the laboratory was referring was not the same as the AQC identification. A dash "-" in the Tables indicates that the name of the genus (and / or species) given by the laboratory was considered to be the same as the AQC identification.

3.4.2.1 *Scoring of RT results*

The method of scoring was to increase a laboratory's score by one for each difference between their identification and the AQC identification *i.*e. for each instance where text other than a dash or a bracketed name appears in the appropriate column in Tables 10 and 11. 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 1997/98 as there was only a single 'standard' exercise (RT12). RT13 was targeted on Amphipoda. The circulation was designed as more of a learning exercise to discover where particular difficulties lie within these individuals. Results were forwarded to the participating laboratories as soon as practicable. Each participant also received a ring test bulletin (RTB12 and RTB13), these outlined the reasons for individual laboratories identification discrepancies.

3.4.3.1 *Twelfth distribution – RT12*

Table 10 presents the results for the RT12. For the majority of the distributed taxa there was good agreement between participating laboratories and the identification made by Unicomarine Ltd. A small number of taxa were again responsible for the majority of differences and these are described briefly below.

Four species (*Modiolarca tumida., Tharyx 'A', Dikoleps pusilla* and *Ophelina modesta*) accounted for 50% of the differences at the level of genus. Five species (*Mya arenaria, Modiolarca tumida., Tharyx 'A', Dikoleps pusilla* and *Ophelina modesta*) accounted for 50% of the differences at the level of species. Five of the twenty-five circulated specimens were correctly identified by all participating

laboratories. Further details and analysis of results can be found in the relevant Ring Test Bulletin (RTB12) which was circulated to each laboratory from which results were received.

3.4.3.2 *Thirteenth distribution – RT13*

RT13 contained twenty-five Amphipoda specimens. The results from the circulation are presented in Table 11 in the same manner as for the other circulations. For the majority of the distributed taxa there was a very good agreement between participating laboratories and the identification made by Unicomarine Ltd. A small number of taxa were again responsible for the majority of differences and these are described briefly below.

The agreement at the generic level was very high, only nine errors were recorded. One specimen (*Orchomene humilis*) accounted for 56% of the differences recorded at the generic level. At the species level four specimens accounted for 59% of the differences recorded (*Bathyporeia pelagica, Ampelisca tenuicornis, Orchomene humilis* and *Siphonoecetes kroyeranus*). Twelve of the twenty-five circulated specimens were correctly identified by all participating laboratories. Further details and analysis of results can be found in the relevant Ring Test Bulletin (RTB13) which was circulated to each laboratory from which results were received.

3.4.4 *Differences between participating laboratories*

Figures 5 and 6 present the number of differences recorded at the level of genus and species for each of the participating laboratories, for RT circulations RT12 and RT13 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.

3.4.5 *Differences by taxonomic group*

Most of the differences of identification in RT12 were of polychaetes, with approximately 59% of the total number of generic differences and 52% of specific differences being attributable to Polychaeta. Mollusca were responsible for 34% of the total number of generic differences and 35% of specific differences.

3.5 Laboratory Reference (LR)

3.5.1 *General comments*

The value of reference material in assisting the process of identification cannot be over-emphasised. Accordingly the 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 twenty-two laboratories participating in this exercise, thirteen laboratories returned samples and data; nine did not.

3.5.2 *Returns from participating laboratories*

The identification of the specimens received from the participating laboratories was checked and the number of differences at the level of genus and species calculated, in the same manner as for the RT exercises. The results for this component are presented in Table 12. There was generally very good agreement between the identifications made by the participating laboratories and those made by Unicomarine Ltd.

4. Discussion of Results

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

4.1 Macrobenthic Analyses

The sample distributed as MB06 posed different problems for participating laboratories compared to some of the samples of previous circulations. The extraction of fauna from the sediment was time consuming due its gritty consistency and also empty *Crepidula fornicata* shells forming both hard surfaces for sessile epifauna and soft mud filled cavities utilised by small polychaetes. All participating laboratories failed to extract all the countable material. Identification also caused isolated problems, especially in the following groups; Cirratulidae, *Polydora* and *Lumbrineris.* As a consequence, four out of the ten returning laboratories attained a Bray-Curtis similarity index less than 90%. The average Bray-Curtis figure of 91% is higher than that recorded for MB05 (1997/98) and MB04 (1996/97).

There was considerable variation between the estimates of total biomass made by the participating laboratories and Unicomarine Ltd. In most cases measurements made by the participating laboratories were greater than those made by Unicomarine Ltd., up to a maximum of 44% heavier (Laboratories 1 and 19). In one instance (Laboratory 8) the measurement was lighter (-28%). Overall the average difference between the values determined by the participating laboratories Unicomarine Ltd. was +26% (i.e. laboratory measurements were heavier than those made by Unicomarine Ltd.).

It seems likely that the main reason for the observed differences between the measurements is more thorough drying by Unicomarine Ltd. 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 MB06 was +26%, while for 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 MB06 exercise. The average value of the index was 89% for the OS, compared with 91% for MB06. The average values of the other individual measures of processing performance (% of taxa extracted and identified, % individuals extracted) were better for the MB06 exercise. The differences between these exercises were enhanced further by the generally better identification of the fauna in the OS samples, the average number of taxonomic differences for the MB06 exercise was more than four compared with the figure of just over one for the OS returns. This was to be expected considering that in most cases participating laboratories would be much more familiar with the fauna of their OS samples. Bray-Curtis index is influenced more by differences in the identification of a number of taxa than by relatively small differences in the estimated abundance of any given taxon. In summary although the average Bray-Curtis figures between these two exercises are similar, the OS returns had fewer taxonomic differences and contained more missed individuals and taxa in their residues compared with the MB06 returns.

There was a slight increase in the number of samples returned for this component compared with the previous year. However, there was fall in the overall results achieved. In the 1997/98 year (OS 05, 06 and 07) the average Bray-Curtis figure was 93.6% and seven samples fell below the 90% Bray-Curtis pass mark. In the present year (1998/99, OS 08, 09 and 10) the average Bray-Curtis figure was 89.3% and twelve samples achieved less than 90%. However, it would be unfair to say that the overall standards have dropped this year as it takes a few very low scoring samples to bring the averages down. For example one of this years' samples achieved a Bray-Curtis similarity score of only 36%. If this

sample were not included in the statistical analysis then the average similarity score would be 90.6% which would be flagged (using the Scheme standards) as a pass rather than a borderline fail (89.3%).

Since the beginning of the OS component one hundred and thirty-three samples have been received (OS01 – 10). The average Bray-Curtis similarity figure is 92%. Thirty samples have fallen below the 90% pass mark (23%). Twenty-one samples have achieved a similarity figure of 100% (16% of all returns). Whether laboratories are giving special attention to the samples that they submit for the OS component remains to be seen. However it must be noted that the extraction of fauna is an area in which several participating laboratories could review their efficiency. All countable fauna must be extracted to record a truly representative sample, although this is rarely the case due to time restraints or inefficient methods used. A sample that has been poorly picked stands high possibility of being unrepresentative regardless of the quality of subsequent faunal identifications, and should the sorted residue be disposed of this cannot be rectified. Laboratories should study their detailed OS and MB reports and target the particular taxon or groups of taxa that are being commonly overlooked during the picking stages of sample analysis. It must be resolved whether the individuals are either not recognised as countable or not scanned using the extraction methods employed. If it is the former, then training is appropriate. If the latter is the case then a review of current extraction methods should be conducted. An assortment of approaches would be appropriate in accordance to sediment type and faunal composition.

4.3 Particle Size Analyses

As has been observed on previous circulations there was a clear difference between the two main techniques employed for analysis of the samples (laser and sieve). The sample distributed as PS12 appeared from an analysis of replicates (Figure 1) to be very uniform and the results from participating laboratories (Figure 3) were quite closely grouped.

The agreement between the PS13 replicates analysed by sieve was also good though there was more scatter in the results from the laser for replicates from the same sample. There was more scatter in the results from participating laboratories.

As has been stated in the previous annual report the clear difference between the analytical techniques means that there can be no single 'correct' determination of the particle size distribution of a sediment sample. It is essential that the analytical method is stated when attempting to compare results. The situation is complicated further by the fact that the difference between the techniques also varies with the nature of the sediment sample. In Figures 3 and 4 the technique employed is indicated (as far as could be determined from the returns made by the laboratory). In most cases either sieve or laser analysis was used though in a few cases a mixed technique was employed; this is indicated by a different line type in the Figures.

4.4 Ring Test distributions

The results were in general comparable with those from the first four 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 introduction of ring test bulletins (RTB) have further emphasised the learning aspect of this component.

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 however. For the laboratories returning a collection, the average number of differences at the level of genus was 0.8, and in most cases (11 of 13) laboratories had no differences or only a single difference. The situation was similar for identification at the level of species where the majority of laboratories achieved at most a single difference in identification (9 of 13 laboratories). The average number of specific differences was 1.3. 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 12 are arranged by LabCode; it is not considered appropriate to assign any rank to the laboratories. Each participant should deliberate therefore on the aim of this component in terms of data quality assessment.

5. Application of NMBAQC Scheme standards

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

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

As mentioned in the Introduction, non-return of samples or results for the PS and OS components resulted in the assignment of a "Deemed Fail" flag to the laboratory (see also Section 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 13 (OS) and Table 14 (PS). The assigned flags for each laboratory for each component are also given. An assessment is performed separately for each of the three OS samples. Pooling the results for the samples and applying a single flag was inappropriate because of the wide variation in the nature of the samples received from an individual laboratory. The tables should be should be read in conjunction with the comments on individual laboratories' results made in Section 6.

In some cases, although returns for the PS exercises were made by laboratories, only data for the production of the particle size distribution curves was provided. No flag has been assigned if the required summary statistics were not also provided by the laboratory. Where no returns were made for the exercise this is indicated with a "-".

It can be seen from Table 13 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 88% of the comparisons were considered to have passed the enumeration of taxa standard; 81% exceeded the enumeration of individuals standard and 71% passed the Bray-Curtis comparison standard. Of the nineteen laboratories participating in this component only fourteen supplied samples for reanalysis; eleven achieved an overall pass flag; three failed; five laboratories which failed to supply samples or indicate their intentions have been flagged as 'Deemed fail'.

Performance with respect to the biomass standard was much less good however with less than a quarter of the participating laboratories (21%) meeting the required standard. It should be noted that there was a smaller number of laboratories for which the results from the biomass exercise were considered suitable for comparison with the standard.

Application of the standards to the results for the PS component is shown in Table 14. It may be seen that nine laboratories failed to meet the standard in PS12 (all Deemed Fails) and fifteen laboratories failed to meet the standard in PS13 (seven Fails and eight Deemed Fails).

5.2 Comparison with results from previous year

A comparison of the 1996/97, 1997/98 and 1998/99 results overall is presented in Table 15. The Table shows the number of laboratories assigned "Deemed Fail", "Fail" and "Pass" flags for the OS and PS exercises over the three years. For the OS component, there has been an increase in the percentage of laboratories achieving a Pass flag (48% to 57% to 58%, considering all participants). This apparent increase is the result of fewer laboratories participating this year and therefore not being awarded 'deemed fail' flags. The situation is reversed for the PS component where a small fall in overall performance is apparent (96% to 89%). Table 16 shows the trend of OS flags for participating laboratories over the past three years. There appears to be a fairly high level of consistency within each laboratory. Monitoring the situation over a longer period is required before a firm statement about changes in laboratory standards could be made.

6. Comments on individual laboratories

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

- Incomplete sorting and extraction of individuals from whole samples.
- Particular taxonomic problems in RT's and whole samples
- Accuracy in biomass measurement

Where possible these are noted for each laboratory listed below.

Also in the comments below, the results for RT12 and RT13 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** (good agreement with Unicomarine identifications), **Mid** and **High** (poor agreement relative to all laboratory results). Each laboratory has been placed into a group for information only, on this basis.

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

Laboratory - LB01

Macrobenthos

Four taxonomic differences. Four vials contained mixtures of species. Twenty-three individuals not picked from residue, including one previously unpicked taxon. Count variance of three individuals. Bray-Curtis similarity index of 97.3%. Biomass on average 44% heavier than Unicomarine Ltd.

Own Sample

OS08 – Two taxonomic differences. One vial contained a mixture of species. Eighteen individuals not picked from residue, including one previously unpicked taxon. Count variance of three individuals. Bray-Curtis similarity index of 91.3%. Biomass on average 61% heavier than Unicomarine Ltd.

OS09 – Three vials contained mixtures of species. Twenty-six individuals not picked from residue. Count variance of nine individuals. Bray-Curtis similarity index of 98.8%. Biomass on average 48% heavier than Unicomarine Ltd.

OS10 – Only the ¼ sub-sample analysed. Seven vials contained mixtures of species. One taxonomic difference (*Pholoe inornata / synophthalmica* mixture). Thirty-six individuals not picked from residue. Count variance of seventeen individuals. Bray-Curtis similarity index of 98.4%. Biomass on average 69% heavier than Unicomarine Ltd.

Particle size

PS12 – No data received.
PS13 – No data received.

Ring Test

RT12 – Two generic and two specific differences. Number of AQC identifications in Mid group.
RT13 – One generic and two specific differences. Number of AQC identifications in Mid group.

Laboratory Reference

No specimens received.

Laboratory - LB02

Macrobenthos

Not participating in this exercise.

Own Sample

OS08 – Not participating in this exercise.
OS09 – Not participating in this exercise.
OS10 – Not participating in this exercise.

Particle size

PS12 – No major differences in size distribution curve.
PS13 – No major differences in size distribution curve.

Ring Test

RT12 – Five generic and six specific differences. Number of AQC identifications in High group.
RT13 – Not participating in this exercise.

Laboratory Reference

One generic and three specific difference. One name change.

Laboratory - LB03

Macrobenthos

Nematoda not picked from the residue. Two taxonomic differences (*Mytilus edulis juv.* and *Cirriformia tentaculata juv.*). Twenty-three individuals not picked from residue, including two previously unpicked taxa. Count variance of four individuals. Bray-Curtis similarity index of 94.3%. Biomass data not supplied.

Own Sample

OS08 – Not participating in this exercise this year; no suitable samples.
OS09 – Not participating in this exercise this year; no suitable samples.
OS10 – Not participating in this exercise this year; no suitable samples.

Particle size

PS12 – No major differences in size distribution curve.
PS13 – No major differences in size distribution curve.

Ring Test

RT12 – All specimens identified correctly. Number of AQC identifications in Low group.
RT13 – Four specific differences. Number of AQC identifications in High group.

Laboratory Reference

No specimens received.

Laboratory - LB04

Macrobenthos

Eleven taxonomic differences. Six vials contained mixtures of species. Six individuals not picked from residue including one previously unpicked taxon. Count variance of sixteen individuals. Bray-Curtis similarity index of 84.4%. Biomass on average 19% heavier than Unicomarine Ltd.

Own Sample

OS08 – Bray-Curtis similarity index of 100%. Biomass on average 3% heavier than Unicomarine Ltd.
OS09 – Two vials contained mixtures of species. Count variance of one individual. Bray-Curtis similarity index of 99.7%. Biomass on average 39% heavier than Unicomarine Ltd.
OS10 – One individual not picked from residue. Bray-Curtis similarity index of 99.8%. Biomass on average 2% heavier than Unicomarine Ltd.

Particle size

PS12 – No data received.
PS13 – No major differences in size distribution curve.

Ring Test

RT12 – No data received.
RT13 – Four specific differences. Number of AQC identifications in High group.

Laboratory Reference

One generic and one specific difference. One spelling error.

Laboratory - LB05

Macrobenthos

No sample returned.

Own Sample

OS08 – No response to initial sample selection form.
OS09 – No response to initial sample selection form.
OS10 – No response to initial sample selection form.

Particle size

PS12 – No data received.
PS13 – No data received.

Ring Test

RT12 – Two generic and three specific differences. Number of AQC identifications in Mid group.
RT13 – No results received.

Laboratory Reference

No specimens received.

Laboratory - LB06

Macrobenthos

No sample returned.

Own Sample

OS08 – One taxonomic difference. One vial contained a mixture of species. Count variance of one individual. One individual not picked from residue, this being a previously unpicked taxon (*Nucula nitidosa*). Bray-Curtis similarity index of 96.4%. Biomass on average 18% heavier than Unicomarine Ltd.
OS09 – Two taxonomic differences. One vial contained a mixture of species. Bray-Curtis similarity index of 89.1%. Biomass on average 22% heavier than Unicomarine Ltd.
OS10 – Bray-Curtis similarity index of 100%. Biomass on average 35% heavier than Unicomarine Ltd.

Particle size

PS12 – Data from centralised analysis; No major differences in size distribution curve.
PS13 – Data from centralised analysis; Size distribution curve slightly elevated.

Ring Test

RT12 – All specimens identified correctly. Number of AQC identifications in Low group.
RT13 – One specific difference. Number of AQC identifications in Low group.

Laboratory Reference

All specimens identified correctly. Three name changes.

Laboratory - LB07

Macrobenthos

No sample returned.

Own Sample

OS08 – Not participating in this exercise this year; no suitable samples.
OS09 – Not participating in this exercise this year; no suitable samples.
OS10 – Not participating in this exercise this year; no suitable samples.

Particle size

PS12 – Not participating in this exercise.
PS13 – Not participating in this exercise.

Ring Test

RT12 – Six generic and seven specific differences. Number of AQC identifications in High group.
RT13 – One generic and two specific differences. Number of AQC identifications in Mid group.

Laboratory Reference

No specimens received.

Laboratory - LB08

Macrobenthos

Three taxonomic differences. Count variance of three individual. Four vials contained mixtures of species. Ten individuals not picked from residue including four previously un-picked taxa (*Molgula manhattensis*, *Acariformes*, *Mysella bidentata* and *Abra alba*). Bray-Curtis similarity index of 89.1%. Biomass on average 28% lighter than Unicomarine Ltd.

Own Sample

OS08 – Three taxonomic differences. Count variance of two individuals. Bray-Curtis similarity index of 83%. Biomass on average 4% heavier than Unicomarine Ltd.
OS09 – Count variance of fifteen individuals. Bray-Curtis similarity index of 99.1%. Biomass on average 38% heavier than Unicomarine Ltd.
OS10 – Count variance of four individuals. One individual not picked from the residue (*Corophium arenarium*). Bray-Curtis similarity index of 98.6%. Biomass on average 9% heavier than Unicomarine Ltd.

Particle size

PS12 – No major differences in size distribution curve.
PS13 – Distribution curve offset to coarser scale relative to majority of curves.

Ring Test

RT12 – One generic and one specific difference. Number of AQC identifications in Low group.
RT13 – Three specific differences. Number of AQC identifications in High group.

Laboratory Reference

All specimens identified correctly.

Laboratory - LB09

Macrobenthos

One taxonomic difference. Count variance of three individual. Eight individuals not picked from residue including three previously un-picked taxa (*Molgula manhattensis, Sabellaria spinulosa* and *Syllidia armata*). Bray-Curtis similarity index of 95%. Biomass data not supplied.

Own Sample

OS08 – Two taxonomic differences. One spelling error. Bray-Curtis similarity index of 87.5%. Biomass data not supplied.
OS09 – Three taxonomic differences. Count variance of one individual. Four individuals not picked from residue including one previously un-picked taxa (*Escharella ventricosa*). Bray-Curtis similarity index of 93.5%. Biomass data not supplied.
OS10 – Two taxonomic differences. One individual not picked from residue this being a previously un-picked taxon (*Modiolus sp. juv.*). Bray-Curtis similarity index of 94.1%. Biomass data not supplied.

Particle size

PS12 – No data received.
PS13 – No major differences in size distribution curve.

Ring Test

RT12 – Two generic and two specific differences. Number of AQC identifications in Mid group.
RT13 – All specimens identified correctly. Number of AQC identifications in Low group.

Laboratory Reference

No specimens received.

Laboratory - LB10

Macrobenthos

Seven taxonomic differences. Count variance of seven individuals. Four vials contained a mixture of species. Twenty-two not picked from residue including one previously un-picked taxon (*Mytilus edulis juv.*). Bray-Curtis similarity index of 77.9%. Biomass on average 27% heavier than Unicomarine Ltd.

Own Sample

OS08 – Two taxonomic differences. Count variance of one individual. One vial contained a mixture of species. Nineteen individuals not picked from residue. Bray-Curtis similarity index of 95.3%. Biomass on average 22% heavier than Unicomarine Ltd.
OS09 – Two taxonomic differences. Count variance of three individuals. Seven vials contained mixtures of species. One hundred and ninety-six individuals not picked from residue including nine previously un-picked taxa. Bray-Curtis similarity index of 89.3%. Biomass on average 16% heavier than Unicomarine Ltd.
OS10 – Seven taxonomic differences. One vial contained a mixture of species. One hundred individuals not picked from residue including sixteen previously un-picked taxa. Bray-Curtis similarity index of 80.7%. Biomass on average 42% heavier than Unicomarine Ltd.

Particle size

PS12 – No major differences in size distribution curve.
PS13 – No major differences in size distribution curve.

Ring Test

RT12 – All specimens identified correctly. Number of AQC identifications in Low group.
RT13 – One specific difference. Number of AQC identifications in Low group.

Laboratory Reference

One specific difference.

Laboratory - LB11

Macrobenthos

Not participating in this component.

Own Sample

OS08 – Not participating in this component.
OS09 – Not participating in this component.
OS10 – Not participating in this component.

Particle size

PS12 – Not participating in this component.
PS13 – Not participating in this component.

Ring Test

RT12 – Two specific differences. Number of AQC identifications in Mid group.
RT13 – One generic and three specific differences. Number of AQC identifications in High group.

Laboratory Reference

Not participating in this component.

Laboratory - LB12

Macrobenthos

No sample returned.

Own Sample

OS08 – No response to initial sample selection form.
OS09 – No response to initial sample selection form.
OS10 – No response to initial sample selection form.

Particle size

PS12 – No data received.
PS13 – No data received.

Ring Test

RT12 – No results received.
RT13 – Four generic and eleven specific differences. Number of AQC identifications in High group.

Laboratory Reference

No specimens received.

Laboratory - LB13

Macrobenthos

No sample returned.

Own Sample

OS08 – One taxonomic difference. Count variance of one individual (*Mysidacea* specimen was headless). Two individuals not picked from the residue. Bray-Curtis similarity index of 91.7%. Biomass on average 60% heavier than Unicomarine Ltd.
OS09 – One taxonomic difference (individuals of *Tharyx 'A'* further split by participating laboratory). Count variance of twenty-four individuals. One vial contained a mixture of species. Six individuals not picked from the residue including two previously unpicked taxa (*Mytilus edulis juv* and *Hydrobia ulvae*). Bray-Curtis similarity index of 43.9%. Biomass on average 47% heavier than Unicomarine Ltd.
OS10 – Two taxonomic differences. Fourteen individuals not picked from the residue including three previously unpicked taxa (*Diastylis sp. juv., Perioculodes longimanus* and *Bathyporeia elegans*). Bray-Curtis similarity index of 35.7%. Biomass on average 54% lighter than Unicomarine Ltd.

Particle size

PS12 – Data from centralised analysis; No major differences in size distribution curve.
PS13 – Data from centralised analysis; Size distribution curve slightly elevated.

Ring Test

RT12 – No results received.
RT13 – No results received.

Laboratory Reference

No specimens received.

Laboratory - LB14

Macrobenthos

Five taxonomic differences. Count variance of five individuals. Seven vials contained mixtures of species. Two individuals not picked from residue. Bray-Curtis similarity index of 89.3%. Biomass on average 35% heavier than Unicomarine Ltd.

Own Sample

OS08 – Count variance of three individuals. Two individuals not picked from residue these being a previously unpicked taxon (*Hydrobia ulvae*). Bray-Curtis similarity index of 97.5%.Biomass on average 58% heavier than Unicomarine Ltd.
OS09 – Bray-Curtis similarity index of 100%. Biomass on average 64% heavier than Unicomarine Ltd.
OS10 – Two individuals not picked from the residue these being a previously unpicked taxon (*Hydrobia ulvae*). Bray-Curtis similarity index of 83.3%. Biomass on average 59% heavier than Unicomarine Ltd.

Particle size

PS12 – No major differences in size distribution curve.
PS13 – No major differences in size distribution curve.

Ring Test

RT12 – Two generic and two specific differences. Number of AQC identifications in Mid group.
RT13 – All specimens identified correctly. Number of AQC identifications in Low group.

Laboratory Reference

One generic and one specific difference.

Laboratory - LB15

Macrobenthos

Five taxonomic differences. Count variance of thirty-five individuals. Two vials contained a mixture of species. Fifty-three individuals not picked from residue including four previously un-picked taxa (*Crepidula fornicata juv., Saccoglossus sp., Abra alba.* and *Parvicardium exiguum*). Bray-Curtis similarity index of 91.9%. Biomass on average 29% heavier than Unicomarine Ltd.

Own Sample

OS08 – Four taxonomic differences. Count variance of one individual. One vial contained a mixture of species. Eight individuals not picked from residue (mostly Mollusca) including five previously un-picked taxa. Bray-Curtis similarity index of 71%. Biomass on average 5% heavier than Unicomarine Ltd.
OS09 – Count variance of ten individuals. Bray-Curtis similarity index of 96.5%. Biomass on average 38% heavier than Unicomarine Ltd.
OS10 – Count variance of four individuals. Bray-Curtis similarity index of 99.2%. Biomass on average 22% heavier than Unicomarine Ltd.

Particle size

PS12 – No major differences in size distribution curve.
PS13 – Curve somewhat offset to finer fractions relative to majority of results.

Ring Test

RT12 – Six generic and six specific differences. Number of AQC identifications in High group.
RT13 – One specific difference. Number of AQC identifications in Low group.

Laboratory Reference

One generic and three specific differences. Three name changes. Two spelling errors.

Laboratory - LB16

Macrobenthos

Not participating in the scheme this year.

Own Sample

OS08 – Not participating in the scheme this year.
OS09 – Not participating in the scheme this year.
OS10 – Not participating in the scheme this year.

Particle size

PS12 – Not participating in the scheme this year.
PS13 – Not participating in the scheme this year.

Ring Test

RT12 – Not participating in the scheme this year.
RT13 – Not participating in the scheme this year.

Laboratory Reference

Not participating in the scheme this year.

Laboratory - LB17

Macrobenthos

Not participating in this component.

Own Sample

OS08 – Not participating in this component.
OS09 – Not participating in this component.
OS10 – Not participating in this component.

Particle size

PS12 – Not participating in this component.
PS13 – Not participating in this component.

Ring Test

RT12 – No results received.
RT13 – No results received.

Laboratory Reference

Not participating in this component.

Laboratory - LB18

Macrobenthos

Not participating in the scheme this year.

Own Sample

OS08 – Not participating in the scheme this year.

OS09 – Not participating in the scheme this year.
OS10 – Not participating in the scheme this year.

Particle size

PS12 – Not participating in the scheme this year.
PS13 – Not participating in the scheme this year.

Ring Test

RT12 – Not participating in the scheme this year.
RT13 – Not participating in the scheme this year.

Laboratory Reference

Not participating in the scheme this year.

Laboratory - LB19

Macrobenthos

Four taxonomic differences. Count variance of forty-eight individuals. Six vials contained a mixture of species. Twenty-eight individuals not picked from residue including one previously un-picked taxon (*Acariformes*). Bray-Curtis similarity index of 96.7%. Biomass on average 44% heavier than Unicomarine Ltd.

Own Sample

OS08 – Two taxonomic differences. Count variance of twenty individuals (numerous dead *Mytilus edulis juv.* counted by participating laboratory). One hundred and ninety-four individuals not picked from residue including one previously un-picked taxon (*Carcinus maenas juv.*). Bray-Curtis similarity index of 73.3%. Biomass on average 45% heavier than Unicomarine Ltd.
OS09 – One taxonomic differences. Count variance of five individuals. One vial contained a mixture of species. Seven individuals not picked from residue including three previously un-picked taxa. Bray-Curtis similarity index of 97.3%. Biomass on average 24% heavier than Unicomarine Ltd.
OS10 – Four taxonomic differences. Count variance of four individuals. Two vials contained a mixture of species. Sixteen individuals not picked from residue including six previously un-picked taxa. Bray-Curtis similarity index of 93%. Biomass on average 34% heavier than Unicomarine Ltd.

Particle size

PS12 – No major differences in size distribution curve.
PS13 – Not participating in this exercise.

Ring Test

RT12 – One generic and two specific differences. Number of AQC identifications in Mid group.
RT13 – One specific difference. Number of AQC identifications in Low group.

Laboratory Reference

All specimens correctly identified.

Laboratory - LB20

Macrobenthos

No sample returned.

Own Sample

OS08 – One taxonomic difference. Count variance of one individual. Eight individuals not picked from residue. Bray-Curtis similarity index of 93.3%. Biomass on average 33% heavier than Unicomarine Ltd.
OS09 – Three taxonomic differences. Count variance of thirty-eight individuals. Two vials contained mixtures of species. One hundred and thirty-seven individuals not picked from the residue including two previously unpicked taxa (*Polycirrus sp.* and *Cheirocratus sp.*). Bray-Curtis similarity index of 90.5%. Biomass on average 13% heavier than Unicomarine Ltd.
OS10 – One taxonomic difference. Six individuals not picked from the residue. Bray-Curtis similarity index of 93.1%. Biomass on average 47% heavier than Unicomarine Ltd.

Particle size

PS12 – Data from centralised analysis; No major differences in size distribution curve.
PS13 – Data from centralised analysis; Size distribution curve slightly elevated.

Ring Test

RT12 – One generic and four specific differences. Number of AQC identifications in High group.
RT13 – One generic and four specific differences. Number of AQC identifications in High group.

Laboratory Reference

One specific difference. Three name changes. Two spelling errors.

Laboratory - LB21

Macrobenthos

No sample returned.

Own Sample

OS08 – Six individuals not picked from residue including two previously un-picked taxa (*Hydrobia ulvae* and *Mytilus edulis juv.*). Bray-Curtis similarity index of 95.1%. Biomass on average 54% heavier than Unicomarine Ltd.
OS09 – Three taxonomic differences. Seven individuals not picked from residue including two previously un-picked taxa (*Rissoa interrupta* and *Retusa obtusa*). Bray-Curtis similarity index of 53.7%. Biomass on average 45% heavier than Unicomarine Ltd.
OS10 – Four taxonomic differences. Count variance of one individual. One vial contained a mixture of species. Seventeen individuals not picked from residue including two previously un-picked taxa (*Rissoa interrupta* and *Polydora caulleryi*). Bray-Curtis similarity index of 60.4%. Biomass on average 46% heavier than Unicomarine Ltd.

Particle size

PS12 – No data received.
PS13 – No data received.

Ring Test

RT12 – Six generic and seven specific differences. Number of AQC identifications in High group.
RT13 – No results received.

Laboratory Reference

Two generic and two specific differences. One vial not received. One specimen missing from vial.

Laboratory - LB22

Macrobenthos

No sample returned.

Own Sample

OS08 – Count variance of fifteen individuals. One vial contained a mixture of species. Four individuals not picked from residue. Bray-Curtis similarity index of 98.6%. Biomass on average 18% heavier than Unicomarine Ltd.
OS09 – Count variance of sixteen individuals. One vial contained a mixture of species. Three individuals not picked from residue. Bray-Curtis similarity index of 98.6%. Biomass on average 11% heavier than Unicomarine Ltd.
OS10 – Bray-Curtis similarity index of 100%. Biomass on average 29% heavier than Unicomarine Ltd.

Particle size

PS12 – Data from centralised analysis; No major differences in size distribution curve.
PS13 – Data from centralised analysis; Size distribution curve slightly elevated.

Ring Test

RT12 – Four generic and six specific differences. Number of AQC identifications in High group.
RT13 – No results received.

Laboratory Reference

One generic and one specific difference.

Laboratory - LB23

Macrobenthos

No sample returned.

Own Sample

OS08 – No response to initial sample selection form.
OS09 – No response to initial sample selection form.
OS10 – No response to initial sample selection form.

Particle size

PS12 – No data received.
PS13 – No data received.

Ring Test

RT12 – No results received.
RT13 – No results received.

Laboratory Reference

No specimens received.

Laboratory - LB24

Macrobenthos

Count variance of two individuals. One vial contained a mixture of species. Twelve individuals not picked from the residue including one previously unpicked taxon. Bray-Curtis similarity index of 98.8%. Biomass on average 40% heavier than Unicomarine Ltd.

Own Sample

OS08 – Not participating in this component this year.
OS09 – Not participating in this component this year.
OS10 – Not participating in this component this year.

Particle size

PS12 – No major differences in size distribution curve.
PS13 – Curve somewhat offset to finer fractions relative to majority of results.

Ring Test

RT12 – Three generic and four specific differences. Number of AQC identifications in High group.
RT13 – One generic and two specific differences. Number of AQC identifications in Mid group.

Laboratory Reference

One generic and one specific difference. One name change.

Laboratory - LB25

Macrobenthos

No sample returned.

Own Sample

OS08 – No response to initial sample selection form.
OS09 – No response to initial sample selection form.
OS10 – No response to initial sample selection form.

Particle size

PS12 – No data received.
PS13 – No data received.

Ring Test

RT12 – Three generic and four specific differences. Number of AQC identifications in High group.
RT13 – No results received.

Laboratory Reference

Two generic and four specific differences. Only twenty-three specimens received.

Laboratory - LB26

Macrobenthos

No sample returned.

Own Sample

OS08 – No response to initial sample selection form.
OS09 – No response to initial sample selection form.
OS10 – No response to initial sample selection form.

Particle size

PS12 – No data received.
PS13 – No data received.

Ring Test

RT12 – No results received.
RT13 – No results received.

Laboratory Reference

No specimens received.

Laboratory - LB27

Macrobenthos

Not participating in this exercise.

Own Sample

OS08 – One taxonomic difference. Count variance of one individual. One vial contained mixture of species. Ten individuals not picked from the residue (*Hydrobia ulvae*). Bray-Curtis similarity index of 98.7%. Biomass on average 30% heavier than Unicomarine Ltd.
OS09 – One taxonomic differences. Two vials contained mixtures of species. No residue supplied for reanalysis. Bray-Curtis similarity index of 95.4%. Biomass on average 33% heavier than Unicomarine Ltd.
OS10 – One recording error (*Eteone longa agg.* recorded as *Pygospio elegans*). Two vials contained mixtures of species. No residue supplied for reanalysis. Bray-Curtis similarity index of 96.3%. Biomass on average 29% heavier than Unicomarine Ltd.

Particle size

PS12 – No major differences in size distribution curve.
PS13 – No data received.

Ring Test

RT12 – Not participating in this exercise.
RT13 – Not participating in this exercise.

Laboratory Reference

Not participating in this exercise.

Laboratory - LB28

Macrobenthos

Not participating in this exercise.

Own Sample

OS08 – Not participating in this exercise.
OS09 – Not participating in this exercise.
OS10 – Not participating in this exercise.

Particle size

PS12 – No major differences in size distribution curve.
PS13 – Size distribution curve slightly elevated.

Ring Test

RT12 – Not participating in this exercise.
RT13 – Not participating in this exercise.

Laboratory Reference

Not participating in this exercise.

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 and this adversely influenced the ability to report on the results. Laboratories should endeavour to report within the requested time; this would greatly facilitate the analysis of results and effective feedback. E-mail as an option for correspondence facilitates data transfer and its use is strongly recommended where practicable.
2. 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 "flags". Non-return of data will result in assignment of a "Deemed Fail" flag. A "Deemed Fail" is to be perceived as far worse then a "Fail" flag.
3. There were problems associated with the measurement of biomass for individual species. Additional 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. Biomass procedures should not render the specimens indistinguishable.
4. Clear differences in the results obtained by different analytical methods 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.
5. Laboratories are strongly recommended to implement an in-house reference collection of fauna. The maintenance of a comprehensive collection has numerous benefits for improving identification ability, maintaining consistency of identification between surveys and access to growth series material.
6. Some of the problems with identification, which arose throughout the various components of the scheme, included certain Mollusca, these are to be the subject of a targeted RT. This will be circulated in the later part of scheme year six.
7. There are still some serious problems of individuals and taxa missed at the sorting stage. However, the figures for these sorting errors are slightly lower than in previous years exercises. In the MB exercise up to 4 taxa (11% of the actual total taxa in the sample) were not extracted. As was the case last year, all laboratories missed individuals in the residue. In the worst instance 53 individuals (8% of total individuals in the sample) were not extracted from the residue. The situation was worse for some of the OS samples where a maximum of 16 taxa and up to 50% of the taxa were not extracted. In the worst instance 196 individuals were not picked from the residue and up to 67% of the total individuals remained in the residue. On average for the OS exercise, 1.48 taxa were not extracted compared with 0.45 and 1.39 taxa from last two years data, respectively. Enumeration of sorted individuals is generally good. However, where taxa and individuals are missed during the extraction of fauna from the sediment, laboratories should determine why certain taxa are not extracted. This could be due to the taxon not being recognised as countable or to a 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.
8. The limitations of the Bray-Curtis similarity index should be recognised when interpreting the results from the OS and MB exercises. Of particular importance is the potential for a relatively large effect on the index of few differences in identification and the associated danger of misinterpreting a low index in terms of quality of service.

9. Protocols should 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.

10. Implementation of an improved learning structure to the scheme through detailed individual exercise reports has been successfully implemented this year. For the LR, OS and MB exercises, detailed results to be forwarded to each laboratory as soon as practicable, such as is done for RT and PS exercises. After each RT exercise a bulletin is produced, reviewing the literature used and illustrating the correct identification of the more troublesome taxa (this could also be set-up as a web page).

11. The current OS 'Flagging' criteria should be reviewed. The use of taxa, individual and Bray-Curtis scores combined with a 'six from nine' pass threshold (see Section 5) could theoretically pass a laboratory which picks and counts all the individuals exactly but identifies all the species incorrectly. The flagging could be divided into two sections to reflect the importance of achieving potentially truly representative data (i.e. completely picked residues) and also accurately identified taxa. A balance must be struck; there is little point having an excellently identified sample which was poorly picked and is consequently unrepresentative of the true sample.

8. References

Howson, C.M. (ed), 1987. Directory of the British marine fauna and flora. A coded checklist of the marine fauna and flora of the British Isles and its surrounding seas. Marine Conservation Society.

Tables

Table 1. Results from the analysis of Macrobenthic sample MB06 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
LB01	54	56	-2	3.6	1042	1062	-20	1.9	1	23	2.2	3	97.35	4
LB02	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB03	41	44	-3	6.8	636	655	-19	2.9	2	23	3.5	4	94.35	2
LB04	52	56	-4	7.1	981	971	10	1.0	1	6	0.6	16	84.36	11
LB05	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB06	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB07	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB08	30	35	-5	14.3	388	395	-7	1.8	4	10	2.5	3	89.14	3
LB09	22	25	-3	12.0	264	269	-5	1.9	3	8	3.0	3	94.95	1
LB10	55	58	-3	5.2	639	668	-29	4.3	1	22	3.3	-7	77.90	7
LB11	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB12	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB13	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB14	35	37	-2	5.4	352	349	3	0.9	0	2	0.6	5	89.30	5
LB15	34	41	-7	17.1	629	647	-18	2.8	4	53	8.2	35	91.85	5
LB16	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB17	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB18	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB19	66	70	-4	5.7	1423	1499	-76	5.1	1	28	1.9	-48	96.65	4
LB20	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB21	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB22	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB23	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB24	49	50	-1	2.0	634	648	-14	2.2	1	12	1.9	-2	98.75	0
LB25	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB26	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB27	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB28	-	-	-	-	-	-	-	-	-	-	-	-	-	-

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

Table 2. Comparison of the efficiency of extraction of fauna by the participating laboratories for the major taxonomic groups present in sample MB06.

LabCode		Nemertea	Polychaeta	Oligochaeta	Pycnogonida	Crustacea	Echinodermata	Mollusca	Other	Overall
LB01	UM count	3	863	11	29	25	2	6	123	1062
	PL missed	1	12	1	3	2	0	1	3	23
	%missed	33.3	1.4	9.1	10.3	8.0	0.0	16.7	2.4	2.2
LB02	UM count	-	-	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB03	UM count	-	546	27	2	15	-	44	21	655
	PL missed	-	9	0	1	1	-	8	4	23
	%missed	-	1.6	0.0	50.0	6.7	-	18.2	19.0	3.5
LB04	UM count	11	770	12	5	7	1	22	143	971
	PL missed	0	2	0	0	1	0	3	0	6
	%missed	0.0	0.3	0.0	0.0	14.3	0.0	13.6	0.0	0.6
LB05	UM count	-	-	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB06	UM count	-	-	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB07	UM count	-	-	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB08	UM count	-	371	6	-	3	-	9	6	395
	PL missed	-	2	0	-	1	-	5	2	10
	%missed	-	0.5	0.0	-	33.3	-	55.6	33.3	2.5
LB09	UM count	-	230	1	-	1	-	10	27	269
	PL missed	-	2	0	-	0	-	2	4	8
	%missed	-	0.9	0.0	-	0.0	-	20.0	14.8	3.0
LB10	UM count	2	472	23	11	17	2	13	128	668
	PL missed	0	10	0	0	3	0	8	1	22
	%missed	0.0	2.1	0.0	0.0	17.6	0.0	61.5	0.8	3.3
LB11	UM count	-	-	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB12	UM count	-	-	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB13	UM count	-	-	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB14	UM count	-	257	7	5	1	1	5	73	349
	PL missed	-	1	0	0	0	0	1	0	2
	%missed	-	0.4	0.0	0.0	0.0	0.0	20.0	0.0	0.6
LB15	UM count	-	511	10	16	16	3	13	78	647
	PL missed	-	24	1	1	1	0	9	17	53
	%missed	-	4.7	10.0	6.3	6.3	0.0	69.2	21.8	8.2
LB16	UM count	-	-	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-

Table 2. Comparison of the efficiency of extraction of fauna by the participating laboratories for the major taxonomic groups present in sample MB06.

LabCode		Nemertea	Polychaeta	Oligochaeta	Pycnogonida	Crustacea	Echinodermata	Mollusca	Other	Overall
LB17	UM count	-	-	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB18	UM count	-	-	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB19	UM count	5	1286	26	12	33	1	33	103	1499
	PL missed	0	11	1	1	1	0	3	11	28
	%missed	0.0	0.9	3.8	8.3	3.0	0.0	9.1	10.7	1.9
LB20	UM count	-	-	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB21	UM count	-	-	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB22	UM count	-	-	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB23	UM count	-	-	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB24	UM count	-	460	3	37	14	-	9	125	648
	PL missed	-	2	0	0	0	-	8	2	12
	%missed	-	0.4	0.0	0.0	0.0	-	88.9	1.6	1.9
LB25	UM count	-	-	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB26	UM count	-	-	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-
LB27	UM count	-	-	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-	-	-

Key:

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

Table 3. Comparison of the estimates of biomass made by the participating laboratories with those made by Unicomarine Ltd. for the major taxonomic groups present in sample MB06. Values are in grams (g).

LabCode		Nemertea	Polychaeta	Oligochaeta	Pycnogonida	Crustacea	Echinodermata	Mollusca	Other	Overall
LB01	PL	0.004	1.291	0.004	0.046	0.063	0.002	0.201	0.035	1.646
	UM	0.0001	0.7047	0.0007	0.0102	0.0292	0.0007	0.143	0.0358	0.9244
	%diff.	97.5	45.4	82.5	77.8	53.7	65.0	28.9	-2.3	43.8
LB02	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB03	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB04	PL	0.0018	0.4614	-	0.0016	-	-	-	0.3178	0.7826
	UM	0.0016	0.3935	-	0.0016	-	-	-	0.2363	0.633
	%diff.	11.1	14.7	-	0.0	-	-	-	25.6	19.1
LB05	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB06	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB07	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB08	PL	-	0.1726	0.0008	-	1.6736	-	5.8619	0.0001	7.709
	UM	-	0.2289	0.0005	-	3.3876	-	6.2302	0.0001	9.8473
	%diff.	-	-32.6	37.5	-	-102.4	-	-6.3	0.0	-27.7
LB09	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB10	PL	0.0004	0.7115	0.001	0.1599	0.7437	0.0019	0.0022	3.9567	5.5773
	UM	0.0002	0.3997	0.0003	0.1496	0.4111	0.0018	0.0014	3.0948	4.0589
	%diff.	50.0	43.8	70.0	6.4	44.7	5.3	36.4	21.8	27.2
LB11	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB12	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB13	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB14	PL	-	0.35922	0.00017	0.13230	0.00067	0.00017	0.00079	1.36180	1.85512
	UM	-	0.2049	0.0003	0.1213	0.0005	0.0001	0.0008	0.8867	1.2146
	%diff.	-	43.0	-76.5	8.3	25.4	41.2	-1.3	34.9	34.5

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 MB06. Values are in grams (g).

LabCode		Nemertea	Polychaeta	Oligochaeta	Pycnogonida	Crustacea	Echinodermata	Mollusca	Other	Overall
LB15	PL	-	0.7083	0.0014	0.2241	0.0253	0.0017	0.0061	4.8201	5.787
	UM	-	0.3745	0.0003	0.2034	0.0063	0.0013	0.0012	3.5501	4.1371
	%diff.	-	47.1	78.6	9.2	75.1	23.5	80.3	26.3	28.5
LB16	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB17	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB18	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB19	PL	0.0063	2.0342	0.0021	0.0083	0.0785	0.4429	0.0179	4.8905	7.4807
	UM	0.0043	0.8586	0.0004	0.0038	0.0325	0.3667	0.0115	2.9145	4.1923
	%diff.	31.7	57.8	81.0	54.2	58.6	17.2	35.8	40.4	44.0
LB20	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB21	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB22	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB23	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB24	PL	-	0.5888	0.0005	0.0174	0.3981	-	0.0002	1.7826	2.7876
	UM	-	0.331	0.0002	0.0091	0.2285	-	0.0008	1.1034	1.673
	%diff.	-	43.8	60.0	47.7	42.6	-	-300.0	38.1	40.0
LB25	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB26	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-
LB27	PL	-	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-	-

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

Table 4. Results from the analysis of Own Samples (OS08 to OS10) 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
LB01 OS08	8	9	-1	11.1	171	186	-15	8.1	1	18	9.7	3	91.32	2	Biomass 3 decimal places
LB01 OS09	10	10	0	0.0	948	965	-17	1.8	0	26	2.7	9	98.80	0	Biomass 3 decimal places
LB01 OS10	27	29	-2	6.9	1235	1254	-19	1.5	0	36	2.9	17	98.35	1	Biomass 3 dec. place, sub-sampled
LB02															Not participating in this component
LB03															Not participating in this component
LB04 OS08	18	18	0	0.0	183	183	0	0.0	0	0	0.0	0	100.00	0	
LB04 OS09	29	29	0	0.0	149	148	1	0.7	0	0	0.0	1	99.66	0	
LB04 OS10	7	7	0	0.0	234	235	-1	0.4	0	1	0.4	0	99.79	0	
LB05 OS08	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB05 OS09	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB05 OS10	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB06 OS08	19	21	-2	9.5	83	83	0	0.0	1	1	1.2	1	96.39	1	
LB06 OS09	18	19	-1	5.3	46	46	0	0.0	0	0	0.0	0	89.13	2	
LB06 OS10	5	5	0	0.0	7	7	0	0.0	0	0	0.0	0	100.00	0	
LB07															Not participating in this component
LB08 OS08	8	6	2	25.0	52	54	-2	3.7	0	0	0.0	-2	83.02	3	
LB08 OS09	6	5	1	16.7	1138	1123	15	1.3	0	0	0.0	15	99.07	0	
LB08 OS10	12	11	1	8.3	176	181	-5	2.8	0	1	0.6	-4	98.60	0	
LB09 OS08	14	14	0	0.0	40	40	0	0.0	0	0	0.0	0	87.50	2	No Biomass
LB09 OS09	44	45	-1	2.2	118	121	-3	2.5	1	4	3.3	1	93.50	3	No Biomass
LB09 OS10	25	26	-1	3.8	41	42	-1	2.4	1	1	2.4	0	94.12	2	No Biomass
LB10 OS08	34	34	0	0.0	310	330	-20	6.1	0	19	5.8	-1	95.31	2	
LB10 OS09	66	75	-9	12.0	965	1164	-199	17.1	9	196	16.8	-3	89.35	2	
LB10 OS10	74	89	-15	16.9	251	351	-100	28.5	16	100	28.5	0	80.66	7	
LB11															Not participating in this component
LB12 OS08	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB12 OS09	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB12 OS10	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB13 OS08	9	8	1	11.1	66	67	-1	1.5	0	2	3.0	1	91.73	1	
LB13 OS09	7	9	-2	22.2	562	592	-30	5.1	2	6	1.0	-24	43.85	1	sub-sample
LB13 OS10	4	7	-3	42.9	7	21	-14	66.7	3	14	66.7	0	35.71	2	
LB14 OS08	8	9	-1	11.1	99	98	1	1.0	1	2	2.0	3	97.46	0	
LB14 OS09	2	2	0	0.0	4	4	0	0.0	0	0	0.0	0	100.00	0	
LB14 OS10	1	2	-1	50.0	5	7	-2	28.6	1	2	28.6	0	83.33	0	
LB15 OS08	17	23	-6	26.1	48	57	-9	15.8	5	8	14.0	-1	71.03	4	
LB15 OS09	5	5	0	0.0	147	137	10	6.8	0	0	0.0	10	96.48	0	
LB15 OS10	5	5	0	0.0	242	238	4	1.7	0	0	0.0	4	99.17	0	

Table 4. Results from the analysis of Own Samples (OS08 to OS10) 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
LB16															Not participating in this component
LB17															Not participating in this component
LB18															Not participating in this component
LB19 OS08	22	22	0	0.0	310	484	-174	36.0	1	194	40.1	20	73.30	2	
LB19 OS09	40	41	-1	2.4	224	226	-2	0.9	3	7	3.1	5	97.33	1	
LB19 OS10	59	67	-8	11.9	276	296	-20	6.8	6	16	5.4	-4	93.01	4	
LB20 OS08	19	19	0	0.0	123	132	-9	6.8	0	8	6.1	-1	93.33	1	
LB20 OS09	40	40	0	0.0	934	1109	-175	15.8	2	137	12.4	-38	90.46	3	
LB20 OS10	28	28	0	0.0	84	90	-6	6.7	0	6	6.7	0	93.10	1	
LB21 OS08	9	11	-2	18.2	58	64	-6	9.4	2	6	9.4	0	95.08	0	
LB21 OS09	8	10	-2	20.0	17	24	-7	29.2	2	7	29.2	0	53.66	3	
LB21 OS10	23	25	-2	8.0	39	57	-18	31.6	2	17	29.8	-1	60.42	4	
LB22 OS08	16	16	0	0.0	820	809	11	1.3	0	4	0.5	15	98.59	0	
LB22 OS09	10	10	0	0.0	611	598	13	2.1	0	3	0.5	16	98.59	0	
LB22 OS10	4	4	0	0.0	146	146	0	0.0	0	0	0.0	0	100.00	0	
LB23 OS08	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB23 OS09	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB23 OS10	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB24															Not participating in this component
LB25 OS08	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB25 OS09	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB25 OS10	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB26 OS08	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB26 OS09	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB26 OS10	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB27 OS08	6	6	0	0.0	409	418	-9	2.2	0	10	2.4	1	98.67	1	Cautious id
LB27 OS09	7	8	-1	12.5	65	65	0	0.0	-	-	-	-	95.39	1	No Residue - Cautious id
LB27 OS10	9	9	0	0.0	80	84	-4	4.8	-	-	-	-	96.34	0	No Residue - Cautious id
LB28															Not participating in this component

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

Table 5. 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 OS08-OS10.

Sample OS08

LabCode		Nemertea	Polychaeta	Oligochaeta	Pycnogonida	Crustacea	Echinodermata	Mollusca	Other	Overall
LB01	PL	-	0.2350	0.0170	-	-	-	0.2920	0.0010	0.5450
	UM	-	0.0887	0.0027	-	-	-	0.1187	0.0001	0.2102
	%diff.	-	62.3	84.1	-	-	-	59.3	90.0	61.4
LB02	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB03	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB04	PL	-	0.6806	-	-	-	0.0230	0.6453	-	1.3489
	UM	-	0.6599	-	-	-	0.0247	0.6183	-	1.3029
	%diff.	-	3.0	-	-	-	-7.4	4.2	-	3.4
LB05	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB06	PL	0.0094	1.1389	-	-	6.1023	0.3162	5.0355	0.0587	12.6610
	UM	0.0055	0.7400	-	-	4.9524	0.2508	4.4184	0.0437	10.4108
	%diff.	41.5	35.0	-	-	18.8	20.7	12.3	25.6	17.8
LB07	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB08	PL	-	0.0110	-	-	0.0034	-	0.5540	-	0.5684
	UM	-	0.0118	-	-	0.0030	-	0.5315	-	0.5463
	%diff.	-	-7.3	-	-	11.8	-	4.1	-	3.9
LB09	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB10	PL	0.4039	1.6175	-	-	-	-	16.6370	1.4813	20.1397
	UM	0.2373	0.8606	-	-	-	-	14.0339	0.6342	15.7660
	%diff.	41.2	46.8	-	-	-	-	15.6	57.2	21.7
LB11	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB12	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB13	PL	-	0.0590	0.0080	-	0.0110	-	-	0.0020	0.0800
	UM	-	0.0227	0.0037	-	0.0056	-	-	0.0004	0.0324
	%diff.	-	61.5	53.8	-	49.1	-	-	80.0	59.5
LB14	PL	-	0.0434	0.0586	-	0.0003	-	0.0000	-	0.1023
	UM	-	0.0204	0.0222	-	0.0001	-	0.0000	-	0.0427
	%diff.	-	53.0	62.1	-	66.7	-	-	-	58.3
LB15	PL	-	0.0203	0.0001	-	0.0006	0.0004	0.0028	7.0816	7.1058
	UM	-	0.0124	0.0001	-	0.0001	0.0002	0.0022	6.7627	6.7777
	%diff.	-	38.9	0.0	-	83.3	50.0	21.4	4.5	4.6

Table 5. 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 OS08-OS10.

Sample OS08

LabCode		Nemertea	Polychaeta	Oligochaeta	Pycnogonida	Crustacea	Echinodermata	Mollusca	Other	Overall
LB16	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB17	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB18	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB19	PL	0.0061	0.0325	0.0121	-	0.0300	-	0.1186	0.0010	0.2003
	UM	0.0033	0.0155	0.0073	-	0.0109	-	0.0733	0.0004	0.1107
	%diff.	45.9	52.3	39.7	-	63.7	-	38.2	60.0	44.7
LB20	PL	-	0.3471	0.0002	-	0.0163	-	0.1699	0.0001	0.5336
	UM	-	0.1966	0.0001	-	0.0034	-	0.1548	0.0001	0.3550
	%diff.	-	43.4	50.0	-	79.1	-	8.9	0.0	33.5
LB21	PL	0.0016	0.3778	-	-	0.0127	-	0.0325	-	0.4246
	UM	0.0006	0.1718	-	-	0.0040	-	0.0197	-	0.1961
	%diff.	62.5	54.5	-	-	68.5	-	39.4	-	53.8
LB22	PL	0.0018	1.1215	0.0093	-	0.0355	-	2.8244	-	3.9925
	UM	0.0010	0.6418	0.0065	-	0.0219	-	2.5845	-	3.2557
	%diff.	44.4	42.8	30.1	-	38.3	-	8.5	-	18.5
LB23	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB24	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB25	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB26	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB27	PL	-	0.4450	-	-	0.0010	-	1.6630	-	2.1090
	UM	-	0.1658	-	-	0.0002	-	1.3199	-	1.4859
	%diff.	-	62.7	-	-	80.0	-	20.6	-	29.5

Key:

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

Table 5. 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 OS08-OS10.

Sample OS09

LabCode		Nemertea	Polychaeta	Oligochaeta	Pycnogonida	Crustacea	Echinodermata	Mollusca	Other	Overall
LB01	PL	-	3.0280	0.0910	-	0.0020	-	0.4540	-	3.5750
	UM	-	1.4254	0.0408	-	0.0002	-	0.3999	-	1.8663
	%diff.	-	52.9	55.2	-	90.0	-	11.9	-	47.8
LB02	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB03	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB04	PL	-	0.0705	-	-	0.0697	0.7250	0.0702	0.0130	0.9484
	UM	-	0.0697	-	-	0.0685	0.3763	0.0548	0.0136	0.5829
	%diff.	-	1.1	-	-	1.7	48.1	21.9	-4.6	38.5
LB05	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB06	PL	0.2299	0.6094	-	-	1.9627	0.2991	1.0411	0.0009	4.1431
	UM	0.1511	0.3979	-	-	1.4314	0.2343	1.0246	0.0009	3.2402
	%diff.	34.3	34.7	-	-	27.1	21.7	1.6	0.0	21.8
LB07	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB08	PL	-	0.0004	0.0001	-	1.1949	-	-	0.0015	1.1969
	UM	-	0.0003	0.0001	-	0.7416	-	-	0.0014	0.7434
	%diff.	-	25.0	0.0	-	37.9	-	-	6.7	37.9
LB09	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB10	PL	0.0150	3.4280	-	-	0.0002	1.5972	31.0094	1.3145	37.3643
	UM	0.0059	1.7108	-	-	0.0001	1.1815	27.9161	0.7376	31.5520
	%diff.	60.7	50.1	-	-	50.0	26.0	10.0	43.9	15.6
LB11	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB12	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB13	PL	-	0.2360	-	-	-	-	0.1290	-	0.3650
	UM	-	0.0993	-	-	-	-	0.0932	-	0.1925
	%diff.	-	57.9	-	-	-	-	27.8	-	47.3
LB14	PL	-	0.0007	0.0002	-	-	-	-	-	0.0008
	UM	-	0.0002	0.0001	-	-	-	-	-	0.0003
	%diff.	-	71.0	33.3	-	-	-	-	-	64.3
LB15	PL	-	0.0096	0.0301	-	0.0809	-	-	0.0005	0.1211
	UM	-	0.0060	0.0199	-	0.0489	-	-	0.0001	0.0749
	%diff.	-	37.5	33.9	-	39.6	-	-	80.0	38.2

Table 5. 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 OS08-OS10.

Sample OS09

LabCode		Nemertea	Polychaeta	Oligochaeta	Pycnogonida	Crustacea	Echinodermata	Mollusca	Other	Overall
LB16	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB17	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB18	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB19	PL	0.0159	1.4743	-	-	0.9768	0.2392	8.3328	0.1813	11.2203
	UM	0.0098	0.7206	-	-	0.4344	0.1854	7.1538	0.0616	8.5656
	%diff.	38.4	51.1	-	-	55.5	22.5	14.1	66.0	23.7
LB20	PL	-	0.8318	0.0001	-	0.0053	-	20.8597	0.0002	21.6971
	UM	-	0.4617	0.0001	-	0.0017	-	18.4150	0.0001	18.8786
	%diff.	-	44.5	0.0	-	67.9	-	11.7	50.0	13.0
LB21	PL	0.0001	0.0037	-	-	0.0001	-	0.0036	0.0001	0.0076
	UM	0.0001	0.0014	-	-	0.0001	-	0.0025	0.0001	0.0042
	%diff.	0.0	62.2	-	-	0.0	-	30.6	0.0	44.7
LB22	PL	-	0.9070	0.0001	-	0.0434	-	3.5330	-	4.4835
	UM	-	0.6067	0.0001	-	0.0241	-	3.3627	-	3.9936
	%diff.	-	33.1	0.0	-	44.5	-	4.8	-	10.9
LB23	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB24	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB25	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB26	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB27	PL	-	0.1750	-	-	-	-	0.3680	-	0.5430
	UM	-	0.0645	-	-	-	-	0.2967	-	0.3612
	%diff.	-	63.1	-	-	-	-	19.4	-	33.5

Key:

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

Table 5. 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 OS08-OS10.

		Sample OS10								
LabCode		Nemertea	Polychaeta	Oligochaeta	Pycnogonida	Crustacea	Echinodermata	Mollusca	Other	Overall
LB01	PL	0.0020	2.3090	0.2330	-	0.0020	-	0.9960	-	3.5420
	UM	0.0002	0.7201	0.0815	-	0.0003	-	0.2998	-	1.1019
	%diff.	90.0	68.8	65.0	-	85.0	-	69.9	-	68.9
LB02	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB03	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB04	PL	-	-	-	-	0.0208	-	0.5501	0.0208	0.5917
	UM	-	-	-	-	0.0148	-	0.5447	0.0199	0.5794
	%diff.	-	-	-	-	28.8	-	1.0	4.3	2.1
LB05	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB06	PL	-	0.0181	-	-	0.0261	-	-	-	0.0442
	UM	-	0.0120	-	-	0.0166	-	-	-	0.0286
	%diff.	-	33.7	-	-	36.4	-	-	-	35.3
LB07	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB08	PL	-	0.1198	-	-	0.0285	-	28.4737	-	28.6220
	UM	-	0.0745	-	-	0.0185	-	25.9875	-	26.0805
	%diff.	-	37.8	-	-	35.1	-	8.7	-	8.9
LB09	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB10	PL	0.0008	0.4969	-	-	0.0048	0.0030	0.3174	0.0730	0.8959
	UM	0.0003	0.1842	-	-	0.0020	0.0022	0.2746	0.0550	0.5183
	%diff.	62.5	62.9	-	-	58.3	26.7	13.5	24.7	42.1
LB11	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB12	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB13	PL	-	0.0541	-	-	0.0001	-	-	-	0.0542
	UM	-	0.0251	-	-	0.0001	-	-	-	0.0252
	%diff.	-	53.6	-	-	0.0	-	-	-	53.5
LB14	PL	-	-	0.0024	-	-	-	-	-	0.0024
	UM	-	-	0.0010	-	-	-	-	-	0.0010
	%diff.	-	-	58.8	-	-	-	-	-	58.8
LB15	PL	-	0.1660	0.1377	-	0.0281	-	0.5135	0.2144	1.0597
	UM	-	0.0729	0.0656	-	0.0228	-	0.4625	0.2022	0.8260
	%diff.	-	56.1	52.4	-	18.9	-	9.9	5.7	22.1

Table 5. 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 OS08-OS10.

		Sample OS10								
LabCode		Nemertea	Polychaeta	Oligochaeta	Pycnogonida	Crustacea	Echinodermata	Mollusca	Other	Overall
LB16	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB17	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB18	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB19	PL	0.0793	2.0768	-	-	0.0313	10.0648	1.3931	0.0022	13.6475
	UM	0.0514	1.0769	-	-	0.0132	6.6347	1.2175	0.0015	8.9952
	%diff.	35.2	48.1	-	-	57.8	34.1	12.6	31.8	34.1
LB20	PL	-	0.5204	0.0002	-	0.1583	-	0.0110	0.0008	0.6907
	UM	-	0.2965	0.0001	-	0.0629	-	0.0064	0.0003	0.3662
	%diff.	-	43.0	50.0	-	60.3	-	41.8	62.5	47.0
LB21	PL	-	0.4631	-	0.0002	0.0846	-	0.3272	0.0001	0.8752
	UM	-	0.2231	-	0.0001	0.0378	-	0.2102	0.0001	0.4713
	%diff.	-	51.8	-	50.0	55.3	-	35.8	0.0	46.1
LB22	PL	-	-	-	-	0.1073	-	0.1174	-	0.2247
	UM	-	-	-	-	0.0590	-	0.0997	-	0.1587
	%diff.	-	-	-	-	45.0	-	15.1	-	29.4
LB23	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB24	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB25	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB26	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB27	PL	-	0.0470	0.0010	-	0.0040	-	0.1970	-	0.2490
	UM	-	0.0113	0.0002	-	0.0029	-	0.1616	-	0.1760
	%diff.	-	76.0	80.0	-	27.5	-	18.0	-	29.3

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

Table 6. Summary of the results of particle size analysis of the replicate samples from sediment circulation PS12.

PS12	% Clay & Silt	Median (phi)	Mean (phi)	Sorting	Skew
PS12 - 01 - laser	0.91	1.22	1.18	0.39	0.034
PS12 - 02 - laser	0.99	1.20	1.16	0.41	0.033
PS12 - 03 - laser	0.00	1.22	1.19	0.35	0.046
PS12 - 04 - laser	4.40	1.32	1.27	0.69	0.305
PS12 - 05 - laser	1.25	1.25	1.23	0.36	0.068
PS12 - 06 - laser	1.18	1.25	1.22	0.35	0.051
PS12 - 07 - laser	1.35	1.25	1.22	0.39	0.072
PS12 - 08 - sieve	0.17	1.53	1.55	0.35	0.06
PS12 - 09 - sieve	0.15	1.60	1.58	0.34	-0.09
PS12 - 10 - sieve	0.15	1.49	1.49	0.35	0.03
PS12 - 11 - sieve	0.16	1.60	1.58	0.34	-0.09
PS12 - 12 - sieve	0.14	1.49	1.51	0.35	0.08
PS12 - 13 - sieve	0.14	1.61	1.58	0.34	-0.13
PS12 - 14 - sieve	0.07	1.51	1.52	0.36	0.03

Table 7. Summary of the results of particle size analysis of the replicate samples from sediment circulation PS13.

PS13	% Clay & Silt	Median (phi)	Mean (phi)	Sorting	Skew
PS13 - 31A - laser	75.62	5.47	3.82	2.42	0.127
PS13 - 32A - laser	71.55	5.44	3.60	2.73	0.030
PS13 - 33A - laser	81.82	5.77	3.83	2.19	0.198
PS13 - 34A - laser	73.11	5.64	3.65	2.70	0.038
PS13 - 35A - laser	81.26	5.83	4.84	2.19	0.163
PS13 - 36A - laser	77.66	5.91	3.80	2.56	-0.010
PS13 - 37A - laser	80.07	5.81	4.61	2.32	0.150
PS13 - 38A - sieve	87.09	5.96	*	*	*
PS13 - 39A - sieve	86.84	5.92	*	*	*
PS13 - 40A - sieve	56.71	5.97	*	*	*
PS13 - 41A - sieve	87.75	6.13	*	*	*
PS13 - 42A - sieve	87.39	5.97	*	*	*
PS13 - 43A - sieve	86.60	5.97	*	*	*
PS13 - 44A - sieve	87.43	5.93	*	*	*

* statistic could not be calculated

Table 8. Summary of the particle size information received from participating laboratories for the twelfth particle size distribution - PS12.

Lab	Method	%<63µm	Median	Mean	Sort	IGS (SKi)
LB01	-	-	-	-	-	-
LB02	S/P	0.50	1.04	1.04	0.44	0.36
LB03	S	0.53	1.40	1.57	0.45	1.49
LB04	-	-	-	-	-	-
LB05	-	-	-	-	-	-
LB06*	L	2.55	1.23	1.2	0.43	0.121
LB07	not participating in this component					
LB08	S	0.41	1.51	1.53	0.45	1.29
LB09	-	-	-	-	-	-
LB10	S/CC	1.07	1.61	1.62	0.59	-0.120
LB11	not participating in this component					
LB12	-	-	-	-	-	-
LB13*	L	2.55	1.23	1.2	0.43	0.121
LB14	DS/L	1.22	1.82	1.78	0.39	0.020
LB15	FD/DS	0.00	1.60	1.57	0.36	-0.070
LB16	not participating in this component					
LB17	not participating in this component					
LB18	not participating in this component					
LB19	L	3.92	1.30	1.34	0.44	0.23
LB20*	L	2.55	1.23	1.2	0.43	0.121
LB21	-	-	-	-	-	-
LB22*	L	2.55	1.23	1.2	0.43	0.121
LB23	-	-	-	-	-	-
LB24	DS	0.13	-	-	-	-
LB25	-	-	-	-	-	-
LB26	-	-	-	-	-	-
LB27	FSC	0.00	1.60	1.65	0.30	0.18
LB28	L	2.55	1.23	1.20	0.43	0.121

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

Summary	%<63µm	Median	Mean	Sort	IGS (SKi)
Number of values	10	9	9	9	9
Mean of laboratories	1.03	1.46	1.48	0.43	0.39
Mean of 7 replicates (laser)	1.44	1.24	1.21	0.42	0.09
Mean of 7 replicates (sieve)	0.14	1.55	1.54	0.35	-0.02
Laboratory minimum	0.00	1.04	1.04	0.30	-0.12
Laboratory maximum	3.92	1.82	1.78	0.59	1.49

#N/A statistic not calculable

Table 9. Summary of the particle size information received from participating laboratories for the thirteenth particle size distribution - PS13.

Lab	Method	%<63µm	Median	Mean	Sort	IGS (SKi)
LB01	-	-	-	-	-	-
LB02	S/P	86.90	5.35	5.34	1.78	-3.95
LB03	S/P/CC	88.03	5.20	5.84	2.20	-0.25
LB04	L	87.38	5.98	5.16	2.03	0.18
LB05	-	-	-	-	-	-
LB06*	L	70.95	5.00	3.46	1.75	-0.241
LB07	not participating in this component					
LB08	S	63.92	4.22	3.46	1.59	-1.27
LB09	L	84.12	5.84	6.15	2.25	0.19
LB10	WS/DS/CC	86.28	5.70	5.56	1.65	-0.043
LB11	not participating in this component					
LB12	-	-	-	-	-	-
LB13*	L	70.95	5.00	3.46	1.75	-0.241
LB14	WS/DS/L	85.58	5.92	6.01	1.78	-0.080
LB15	FD/L	93.80	6.60	6.40	1.47	-0.210
LB16	not participating in this component					
LB17	not participating in this component					
LB18	not participating in this component					
LB19	not participating in this component					
LB20*	L	70.95	5.00	3.46	1.75	-0.241
LB21	-	-	-	-	-	-
LB22*	L	70.95	5.00	3.46	1.75	-0.241
LB23	-	-	-	-	-	-
LB24	DS/L	87.91	-	-	-	-
LB25	-	-	-	-	-	-
LB26	-	-	-	-	-	-
LB27	-	-	-	-	-	-
LB28	L	70.95	5.00	3.46	1.75	-0.241

Key to methods:

L - Laser analysis	DS - Dry sieve	CC - Coulter counter
S - Sieve	WS - Wet sieve	FD - Freeze dried
P - Pipette		n/c - not calculated

L* - data for this laboratory not included in calculations below (see text)

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

Summary	%<63µm	Median	Mean	Sort	IGS (SKi)
Number of values	10	9	9	9	9
Mean of laboratories	83.49	5.53	5.26	1.83	-0.63
Mean of 7 replicates (laser)	77.30	5.70	4.02	2.44	0.10
Mean of 7 replicates (sieve)	82.83	5.98	#N/A	#N/A	#N/A
Laboratory minimum	63.92	4.22	3.46	1.47	-3.95
Laboratory maximum	93.80	6.60	6.40	2.25	0.19

Table 10. The identifications of the fauna made by participating laboratories for RT12. Names are given only where different from the AQC identification.

RT12	Taxon	LB01	LB03	LB05	LB07	LB09	LB11	LB13	LB15	LB17
RT1201	Lepidonotus squamatus	--	--	--	--	--	--	0 0	--	0 0
RT1202	Acanthodoris pilosa	--	--	--	--	--	--	0 0	--	0 0
RT1203	Pisione remota	--	--	--	--	--	--	0 0	--	0 0
RT1204	Mya arenaria	Scrobicularia plana	--	--	--	--	- truncata	0 0	--	0 0
RT1205	Endeis spinosa	--	--	--	--	--	--	0 0	- [laevis]	0 0
RT1206	Caecum glabrum	--	--	--	Akera bullata	--	--	0 0	--	0 0
RT1207	Philine aperta	--	--	- [cf. aperta]	--	--	--	0 0	--	0 0
RT1208	Fabricia sabella	--	--	--	--	- [stellaris]	--	0 0	Fabriciola baltica	0 0
RT1209	Paraonis fulgens	--	--	--	--	--	--	0 0	Levinsenia gracilis	0 0
RT1210	Modiolarca tumida	Musculus discors	--	--	Musculus costulatus	Musculus discors	--	0 0	Musculus discors	0 0
RT1211	Protodorvillea kefersteini	--	--	--	--	--	--	0 0	--	0 0
RT1212	Tharyx A	- [sp. A]	- [sp. A]	- [species A]	- Killariensis	Aphelochaeta sp.A	--	0 0	Aphelochaeta sp. A	0 0
RT1213	Polydora quadrilobata	--	--	- caulleryi	Pseudopolydora antennata	--	--	0 0	--	0 0
RT1214	Pandalina brevirostris	--	--	--	--	--	--	0 0	--	0 0
RT1215	Galathowenia oculata	--	[Myriochele] -	Myriochele heeri	[Myriochele] -	[Myriochele] -	--	0 0	[Myriochele] -	0 0
RT1216	Crangon allmanni	--	--	--	--	--	- [allmani]	0 0	--	0 0
RT1217	Dikoleps pusilla	[Diskoleps] -	- [nitens]	--	--	[Skenea] [nitens]	--	0 0	Skenea serpuloides	0 0
RT1218	Paradoneis lyra	--	--	--	--	--	--	0 0	--	0 0
RT1219	Prionospio fallax	--	- [malmgreni]	- [cf. fallax]	--	--	--	0 0	--	0 0
RT1220	Ophelina modesta	--	--	Ophelia rathkei	Armandia cirrhosa	--	- juv.	0 0	--	0 0
RT1221	Kefersteinia cirrata	--	--	--	Hesiospina similis	[Kefersteini] -	--	0 0	--	0 0
RT1222	Pomatoceros lamarcki	--	--	--	--	--	--	0 0	--	0 0
RT1223	Onoba semicostata	--	--	--	--	--	--	0 0	--	0 0
RT1224	Crangon crangon	--	--	--	--	--	--	0 0	--	0 0
RT1225	Psammechinus miliaris	--	--	--	Strongylocentrotus droebachiensis	--	--	0 0	Paracentrotus lividus	0 0

RT12	Taxon	LB02	LB04	LB06	LB08	LB10	LB12	LB14	LB16	LB18
RT1201	Lepidonotus squamatus	--	0 0	--	--	--	0 0	--	0 0	0 0
RT1202	Acanthodoris pilosa	Adalaria proxima	0 0	--	--	--	0 0	--	0 0	0 0
RT1203	Pisione remota	--	0 0	--	--	--	0 0	--	0 0	0 0
RT1204	Mya arenaria	--	0 0	--	--	--	0 0	--	0 0	0 0
RT1205	Endeis spinosa	- charybdaea	0 0	- [laevis]	--	--	0 0	--	0 0	0 0
RT1206	Caecum glabrum	--	0 0	--	--	--	0 0	--	0 0	0 0
RT1207	Philine aperta	--	0 0	--	--	--	0 0	--	0 0	0 0
RT1208	Fabricia sabella	--	0 0	--	--	--	0 0	Fabriciola baltica	0 0	0 0
RT1209	Paraonis fulgens	Levinsenia gracilis	0 0	--	--	--	0 0	--	0 0	0 0
RT1210	Modiolarca tumida	--	0 0	--	[Musculus] [marmoratus]	--	0 0	--	0 0	0 0
RT1211	Protodorvillea kefersteini	--	0 0	--	- [keferstenii]	--	0 0	--	0 0	0 0
RT1212	Tharyx A	Aphelochaeta "A"	0 0	--	- [A']	- [sp. "A"]	0 0	Aphelochaeta sp. A	0 0	0 0
RT1213	Polydora quadrilobata	Pseudopolydora antennata	0 0	--	--	--	0 0	--	0 0	0 0
RT1214	Pandalina brevirostris	--	0 0	--	--	--	0 0	--	0 0	0 0
RT1215	Galathowenia oculata	[Myriochele] -	0 0	[Myriochele] -	Myriochele heeri	--	0 0	--	0 0	0 0
RT1216	Crangon allmanni	--	0 0	- [allmani]	--	--	0 0	--	0 0	0 0
RT1217	Dikoleps pusilla	- [nitens]	0 0	[Skenea] [nitens]	[Skenea] [nitens]	--	0 0	--	0 0	0 0
RT1218	Paradoneis lyra	--	0 0	--	--	--	0 0	--	0 0	0 0
RT1219	Prionospio fallax	--	0 0	--	--	--	0 0	--	0 0	0 0
RT1220	Ophelina modesta	--	0 0	[Ophilina] -	--	--	0 0	--	0 0	0 0
RT1221	Kefersteinia cirrata	Periboea longocirrata	0 0	--	--	--	0 0	--	0 0	0 0
RT1222	Pomatoceros lamarcki	--	0 0	--	--	--	0 0	--	0 0	0 0
RT1223	Onoba semicostata	--	0 0	--	--	--	0 0	--	0 0	0 0
RT1224	Crangon crangon	--	0 0	--	--	--	0 0	--	0 0	0 0
RT1225	Psammechinus miliaris	--	0 0	--	--	--	0 0	--	0 0	0 0

Table 10. The identifications of the fauna made by participating laboratories for RT12. Names are given only where different from the AQC identification.

RT12	Taxon	LB19	LB21	LB23	LB25	LB27
RT1201	Lepidonotus squamatus	--	--	0 0	--	0 0
RT1202	Acanthodoris pilosa	--	--	0 0	--	0 0
RT1203	Pisione remota	--	--	0 0	--	0 0
RT1204	Mya arenaria	- truncata	- truncata	0 0	- [arenia]	0 0
RT1205	Endeis spinosa	--	--	0 0	--	0 0
RT1206	Caecum glabrum	--	--	0 0	--	0 0
RT1207	Philine aperta	--	--	0 0	--	0 0
RT1208	Fabricia sabella	--	--	0 0	--	0 0
RT1209	Paraonis fulgens	--	--	0 0	--	0 0
RT1210	Modiolarca tumida	Musculus costulatus	Musculus discors	0 0	--	0 0
RT1211	Protodorvillea kefersteini	--	--	0 0	--	0 0
RT1212	Tharyx A	- [sp.A]	Aphelochaeta vivipara	0 0	- killariensis	0 0
RT1213	Polydora quadrilobata	--	Pseudopolydora pulchra	0 0	--	0 0
RT1214	Pandalina brevirostris	--	--	0 0	Palaemon elegans	0 0
RT1215	Galathowenia oculata	--	--	0 0	[Galathowenia (Myriochele)] -	0 0
RT1216	Crangon allmanni	--	- [allmani]	0 0	--	0 0
RT1217	Dikoleps pusilla	--	Skenea serpuloides	0 0	Skeenia serpuloides	0 0
RT1218	Paradoneis lyra	--	Levinsenia sp.	0 0	--	0 0
RT1219	Prionospio fallax	--	--	0 0	--	0 0
RT1220	Ophelina modesta	--	Ophelia borealis?	0 0	--	0 0
RT1221	Kefersteinia cirrata	--	- [cirrata var hibernica]	0 0	--	0 0
RT1222	Pomatoceros lamarcki	--	--	0 0	--	0 0
RT1223	Onoba semicostata	--	--	0 0	Partulida pellucida	0 0
RT1224	Crangon crangon	--	--	0 0	--	0 0
RT1225	Psammechinus miliaris	--	--	0 0	--	0 0

RT12	Taxon	LB20	LB22	LB24	LB26	LB28
RT1201	Lepidonotus squamatus	--	--	--	0 0	0 0
RT1202	Acanthodoris pilosa	--	--	--	0 0	0 0
RT1203	Pisione remota	--	--	--	0 0	0 0
RT1204	Mya arenaria	- truncata	--	--	0 0	0 0
RT1205	Endeis spinosa	- charybdaea	- [laevis]	- charybdaea	0 0	0 0
RT1206	Caecum glabrum	--	--	--	0 0	0 0
RT1207	Philine aperta	--	- quadrata?	--	0 0	0 0
RT1208	Fabricia sabella	- [stellaris]	- [stellaris]	--	0 0	0 0
RT1209	Paraonis fulgens	[Paraneis] -	[Paranois] [fulgens?]	--	0 0	0 0
RT1210	Modiolarca tumida	--	--	--	0 0	0 0
RT1211	Protodorvillea kefersteini	--	--	--	0 0	0 0
RT1212	Tharyx A	- [a']	Aphelochaeta A'	Caulleriella zetlandica	0 0	0 0
RT1213	Polydora quadrilobata	--	--	--	0 0	0 0
RT1214	Pandalina brevirostris	--	--	--	0 0	0 0
RT1215	Galathowenia oculata	[Myriochele] -	Myriochele sp.	--	0 0	0 0
RT1216	Crangon allmanni	--	- [allmani]	--	0 0	0 0
RT1217	Dikoleps pusilla	[Skenea] [nitens]	Skenea basistriata	Skenea serpuloides	0 0	0 0
RT1218	Paradoneis lyra	--	--	--	0 0	0 0
RT1219	Prionospio fallax	--	Prionospio (Minuspio) cirrifera	Minuspio cirrifera	0 0	0 0
RT1220	Ophelina modesta	Polyophthalmus pictus	--	--	0 0	0 0
RT1221	Kefersteinia cirrata	- [cirrhata]	--	--	0 0	0 0
RT1222	Pomatoceros lamarcki	--	- [lamarki]	--	0 0	0 0
RT1223	Onoba semicostata	- aculeus	--	--	0 0	0 0
RT1224	Crangon crangon	--	--	--	0 0	0 0
RT1225	Psammechinus miliaris	--	--	--	0 0	0 0

Key: "-" - Correct record given.
00 - No data. See Report, Section 6, for details.
[__] - Old name or spelling error.

Table 11. The identification of the fauna made by participating laboratories for RT13. Names are given only where different from AQC identification.

RT13	Taxon	LB01	LB03	LB05	LB07	LB09	LB11	LB13
RT1301	Calliopius laeviusculus	--	--	0 0	--	[Calliopus] -	--	0 0
RT1302	Guernea coalita	--	--	0 0	--	--	--	0 0
RT1303	Leptocheirus pectinatus	--	- hirsutimanus	0 0	--	--	--	0 0
RT1304	Leptocheirus hirsutimanus	--	--	0 0	--	--	--	0 0
RT1305	Bathyporeia elegans	--	- pelagica	0 0	--	--	--	0 0
RT1306	Bathyporeia pelagica	--	- tenuipes	0 0	--	--	--	0 0
RT1307	Atylus swammerdamei	--	- [swammerdami]	0 0	--	- [swammerdami]	- [swammerdami]	0 0
RT1308	Atylus vedlomensis	--	--	0 0	--	--	--	0 0
RT1309	Atylus guttatus	--	--	0 0	--	--	--	0 0
RT1310	Ampelisca tenuicornis	--	--	0 0	--	--	--	0 0
RT1311	Photis longicaudata	--	--	0 0	--	--	--	0 0
RT1312	Pontocrates arenarius	--	--	0 0	--	--	--	0 0
RT1313	Bathyporeia pilosa	--	--	0 0	--	--	--	0 0
RT1314	Bathyporeia nana	--	--	0 0	--	--	- pilosa	0 0
RT1315	Bathyporeia sarsi	--	--	0 0	--	--	--	0 0
RT1316	Corophium crassicorne	--	--	0 0	--	--	--	0 0
RT1317	Orchomene humilis	Nannonyx goesi	--	0 0	[Orchomena] -	--	Nannonyx goesii	0 0
RT1318	Corophium crassicorne	--	--	0 0	--	--	--	0 0
RT1319	Lysianassa ceratina	--	--	0 0	[Lysiannssa] -	[Lyssianassa] -	--	0 0
RT1320	Ceradocus semiserratus	--	--	0 0	- [semiscerratus]	--	--	0 0
RT1321	Socarnes erythrophthalmus	--	--	0 0	--	[Sorcarnes] [erythropthalmus]	--	0 0
RT1322	Parametaphoxus fultoni	--	[Metaphoxus] -	0 0	Harpinia pectinata	[Metaphoxus] -	--	0 0
RT1323	Urothoe elegans	--	--	0 0	--	--	--	0 0
RT1324	Harpinia pectinata	--	--	0 0	--	--	--	0 0
RT1325	Siphonoecetes kroyeranus	- striatus	- striatus	0 0	- striatus	[Siphonocetes] -	- striatus	0 0

RT13	Taxon	LB02	LB04	LB06	LB08	LB10	LB12	LB14
RT1301	Calliopius laeviusculus	0 0	[Calliopus] -	--	--	[Calliopus] -	[Calliopus] -	--
RT1302	Guernea coalita	0 0	--	--	--	--	Parametopa kervillei	--
RT1303	Leptocheirus pectinatus	0 0	- hirsutimanus	--	--	- pilosus	- pilosus	--
RT1304	Leptocheirus hirsutimanus	0 0	--	--	--	--	- pectinatus	--
RT1305	Bathyporeia elegans	0 0	- guilliamsoniana	--	- gracilis	--	- sarsi	--
RT1306	Bathyporeia pelagica	0 0	--	- guilliamsoniana	--	--	- tenuipes	--
RT1307	Atylus swammerdamei	0 0	--	- [swammerdami]	- [swammerdamii]	- [swammerdami]	- [swammerdami]	- [swammerdami]
RT1308	Atylus vedlomensis	0 0	--	--	--	--	--	--
RT1309	Atylus guttatus	0 0	--	--	--	--	--	--
RT1310	Ampelisca tenuicornis	0 0	- typica	--	- typica	--	- spinipes	--
RT1311	Photis longicaudata	0 0	--	--	--	--	--	--
RT1312	Pontocrates arenarius	0 0	--	--	--	--	--	--
RT1313	Bathyporeia pilosa	0 0	--	--	--	--	--	--
RT1314	Bathyporeia nana	0 0	--	--	--	- [?nana]	- pilosa	--
RT1315	Bathyporeia sarsi	0 0	--	--	--	--	- nana	--
RT1316	Corophium crassicorne	0 0	--	--	--	--	--	--
RT1317	Orchomene humilis	0 0	- [hummilis]	--	--	--	Socarnes erythrophthalamus	--
RT1318	Corophium crassicorne	0 0	--	--	- [cassicorne]	--	--	--
RT1319	Lysianassa ceratina	0 0	--	--	--	[Lyssianassa] -	Orchomene humilis	--
RT1320	Ceradocus semiserratus	0 0	--	--	--	--	--	--
RT1321	Socarnes erythrophthalmus	0 0	- [erythrophthalamus]	--	[Socarres] [erythrophalmus]	--	Ambasia atlantica	--
RT1322	Parametaphoxus fultoni	0 0	--	[Metaphoxus] -	[Metaphoxus] -	[Metaphoxus] -	--	[Metaphoxus] -
RT1323	Urothoe elegans	0 0	--	--	--	--	--	--
RT1324	Harpinia pectinata	0 0	- [pectinatus]	--	--	--	--	--
RT1325	Siphonoecetes kroyeranus	0 0	- striatus	--	- striatus	--	[Siphonectes] -	[Siphonosetes] -

Table 11. The identification of the fauna made by participating laboratories for RT13. Names are given only where different from AQC identification.

RT13	Taxon	LB15	LB17	LB19	LB21	LB23	LB25	LB27
RT1301	Calliopius laeviusculus	--	0 0	--	0 0	0 0	0 0	0 0
RT1302	Guernea coalita	--	0 0	--	0 0	0 0	0 0	0 0
RT1303	Leptocheirus pectinatus	--	0 0	--	0 0	0 0	0 0	0 0
RT1304	Leptocheirus hirsutimanus	--	0 0	--	0 0	0 0	0 0	0 0
RT1305	Bathyporeia elegans	--	0 0	--	0 0	0 0	0 0	0 0
RT1306	Bathyporeia pelagica	- tenuipes	0 0	- guilliamsoniana	0 0	0 0	0 0	0 0
RT1307	Atylus swammerdamei	- [swammerdami]	0 0	- [swammerdami]	0 0	0 0	0 0	0 0
RT1308	Atylus vedlomensis	--	0 0	--	0 0	0 0	0 0	0 0
RT1309	Atylus guttatus	--	0 0	--	0 0	0 0	0 0	0 0
RT1310	Ampelisca tenuicornis	--	0 0	--	0 0	0 0	0 0	0 0
RT1311	Photis longicaudata	--	0 0	--	0 0	0 0	0 0	0 0
RT1312	Pontocrates arenarius	--	0 0	--	0 0	0 0	0 0	0 0
RT1313	Bathyporeia pilosa	--	0 0	--	0 0	0 0	0 0	0 0
RT1314	Bathyporeia nana	--	0 0	--	0 0	0 0	0 0	0 0
RT1315	Bathyporeia sarsi	--	0 0	--	0 0	0 0	0 0	0 0
RT1316	Corophium crassicorne	--	0 0	--	0 0	0 0	0 0	0 0
RT1317	Orchomene humilis	--	0 0	--	0 0	0 0	0 0	0 0
RT1318	Corophium crassicorne	--	0 0	--	0 0	0 0	0 0	0 0
RT1319	Lysianassa ceratina	--	0 0	--	0 0	0 0	0 0	0 0
RT1320	Ceradocus semiserratus	--	0 0	--	0 0	0 0	0 0	0 0
RT1321	Socarnes erythrophthalmus	--	0 0	--	0 0	0 0	0 0	0 0
RT1322	Parametaphoxus fultoni	[Metaphoxus] -	0 0	--	0 0	0 0	0 0	0 0
RT1323	Urothoe elegans	--	0 0	--	0 0	0 0	0 0	0 0
RT1324	Harpinia pectinata	--	0 0	--	0 0	0 0	0 0	0 0
RT1325	Siphonoecetes kroyeranus	--	0 0	--	0 0	0 0	0 0	0 0

RT13	Taxon	LB16	LB18	LB20	LB22	LB24	LB26	LB28
RT1301	Calliopius laeviusculus	0 0	0 0	--	0 0	--	0 0	0 0
RT1302	Guernea coalita	0 0	0 0	--	0 0	--	0 0	0 0
RT1303	Leptocheirus pectinatus	0 0	0 0	--	0 0	--	0 0	0 0
RT1304	Leptocheirus hirsutimanus	0 0	0 0	--	0 0	--	0 0	0 0
RT1305	Bathyporeia elegans	0 0	0 0	--	0 0	--	0 0	0 0
RT1306	Bathyporeia pelagica	0 0	0 0	- tenuipes	0 0	--	0 0	0 0
RT1307	Atylus swammerdamei	0 0	0 0	- [swammerdami]	0 0	- [swammerdami]	0 0	0 0
RT1308	Atylus vedlomensis	0 0	0 0	--	0 0	--	0 0	0 0
RT1309	Atylus guttatus	0 0	0 0	--	0 0	--	0 0	0 0
RT1310	Ampelisca tenuicornis	0 0	0 0	- typica	0 0	- diadema	0 0	0 0
RT1311	Photis longicaudata	0 0	0 0	--	0 0	--	0 0	0 0
RT1312	Pontocrates arenarius	0 0	0 0	--	0 0	--	0 0	0 0
RT1313	Bathyporeia pilosa	0 0	0 0	--	0 0	--	0 0	0 0
RT1314	Bathyporeia nana	0 0	0 0	--	0 0	--	0 0	0 0
RT1315	Bathyporeia sarsi	0 0	0 0	--	0 0	--	0 0	0 0
RT1316	Corophium crassicorne	0 0	0 0	--	0 0	--	0 0	0 0
RT1317	Orchomene humilis	0 0	0 0	Tryphosella sarsi	0 0	Nannonyx spinimanus	0 0	0 0
RT1318	Corophium crassicorne	0 0	0 0	--	0 0	--	0 0	0 0
RT1319	Lysianassa ceratina	0 0	0 0	--	0 0	--	0 0	0 0
RT1320	Ceradocus semiserratus	0 0	0 0	--	0 0	--	0 0	0 0
RT1321	Socarnes erythrophthalmus	0 0	0 0	--	0 0	--	0 0	0 0
RT1322	Parametaphoxus fultoni	0 0	0 0	[Metaphoxus] -	0 0	--	0 0	0 0
RT1323	Urothoe elegans	0 0	0 0	--	0 0	--	0 0	0 0
RT1324	Harpinia pectinata	0 0	0 0	--	0 0	--	0 0	0 0
RT1325	Siphonoecetes kroyeranus	0 0	0 0	[Siphonecetes] striatus	0 0	--	0 0	0 0

Key: "-" - Correct entry given.
00 - No data. See Report, Section 6, for deta
[__] - Old name or spelling error.

Table 12. Summary of the results from the identification of specimens supplied by participating laboratories for Laboratory Reference exercise LR03.

	Differences	
LabCode	Generic	Specific
01	-	-
02	1	3
03	-	-
04	1	1
05	-	-
06	0	0
07	-	-
08	0	0
09	-	-
10	0	1
11	-	-
12	-	-
13	-	-
14	1	1
15	1	3
16	-	-
17	-	-
18	-	-
19	0	0
20	0	1
21	2	2
22	1	1
23	-	-
24	1	1
25	2	4
26	-	-
27	-	-

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

Table 13. Summary of the performance of participating laboratories in the Own Sample (OS) exercises with respect to the NMBAQC / NMMP standards.

1		2	3	4	5	6	7	8	9	10	11	12	13	14
		Estimation of Taxa			Estimation of Abundance			Estimation of Biomass			Similarity Index			Overall
LabCode		Lab.	Target	Flag	Lab.	Target	Flag	Lab. result	Target	Flag	Target	Lab.	Flag	NMP Flag
LB01	OS08	8	7.0 - 11.0	PASS	171	167.4 - 204.6	PASS	0.5450	0.1682 - 0.2522	*Fail*	90.0	91.32	PASS	PASS
LB01	OS09	10	8.0 - 12.0	PASS	948	868.5 - 1061.5	PASS	3.5750	1.4930 - 2.2396	*Fail*	90.0	98.80	PASS	
LB01	OS10	27	26.1 - 31.9	PASS	1235	1128.6 - 1379.4	PASS	3.5420	0.8815 - 1.3223	*Fail*	90.0	98.35	PASS	
LB02		Not participating in this component					Not participating in this component				Not participating in this component			
LB03		Not participating in this component					Not participating in this component				Not participating in this component			
LB04	OS08	18	16.0 - 20.0	PASS	183	164.7 - 201.3	PASS	1.3489	1.0423 - 1.5635	*PASS*	90.0	100.00	PASS	PASS
LB04	OS09	29	26.1 - 31.9	PASS	149	133.2 - 162.8	PASS	0.9484	0.4663 - 0.6995	*Fail*	90.0	99.66	PASS	
LB04	OS10	7	5.0 - 9.0	PASS	234	211.5 - 258.5	PASS	0.5917	0.4635 - 0.6953	*PASS*	90.0	99.79	PASS	
LB05	OS08	-	-	**Deemed fail**	-	-	**Deemed fail**	-	-	-	90.0	-	**Deemed fail**	**Deemed fail**
LB05	OS09	-	-	**Deemed fail**	-	-	**Deemed fail**	-	-	-	90.0	-	**Deemed fail**	
LB05	OS10	-	-	**Deemed fail**	-	-	**Deemed fail**	-	-	-	90.0	-	**Deemed fail**	
LB06	OS08	19	18.9 - 23.1	PASS	83	74.7 - 91.3	PASS	12.6610	8.3286 - 12.4930	*Fail*	90.0	96.39	PASS	PASS
LB06	OS09	18	17.0 - 21.0	PASS	46	41.4 - 50.6	PASS	4.1431	2.5922 - 3.8882	*Fail*	90.0	89.13	**Fail**	
LB06	OS10	5	3.0 - 7.0	PASS	7	5.0 - 9.0	PASS	0.0442	0.0229 - 0.0343	*Fail*	90.0	100.00	PASS	
LB07		Not participating in this component					Not participating in this component				Not participating in this component			
LB08	OS08	8	4.0 - 8.0	PASS	52	48.6 - 59.4	PASS	0.5684	0.4370 - 0.6556	*PASS*	90.0	83.02	**Fail**	PASS
LB08	OS09	6	3.0 - 7.0	PASS	1138	1010.7 - 1235.3	PASS	1.1969	0.5947 - 0.8921	*Fail*	90.0	99.07	PASS	
LB08	OS10	12	9.0 - 13.0	PASS	176	162.9 - 199.1	PASS	28.6220	20.8644 - 31.2966	*PASS*	90.0	98.60	PASS	
LB09	OS08	14	12.0 - 16.0	PASS	40	36.0 - 44.0	PASS	-	-	-	90.0	87.50	**Fail**	PASS
LB09	OS09	44	40.5 - 49.5	PASS	118	108.9 - 133.1	PASS	-	-	-	90.0	93.50	PASS	
LB09	OS10	25	23.4 - 28.6	PASS	41	37.8 - 46.2	PASS	-	-	-	90.0	94.12	PASS	
LB10	OS08	34	30.6 - 37.4	PASS	310	297.0 - 363.0	PASS	20.1397	12.6128 - 18.9192	*Fail*	90.0	95.31	PASS	**Fail**
LB10	OS09	66	67.5 - 82.5	**Fail**	965	1047.6 - 1280.4	**Fail**	37.3643	25.2416 - 37.8624	*PASS*	90.0	89.35	**Fail**	
LB10	OS10	74	80.1 - 97.9	**Fail**	251	315.9 - 386.1	**Fail**	0.8959	0.4146 - 0.6220	*Fail*	90.0	80.66	**Fail**	
LB11		Not participating in this component					Not participating in this component				Not participating in this component			
LB12	OS08	-	-	**Deemed fail**	-	-	**Deemed fail**	-	-	-	90.0	-	**Deemed fail**	**Deemed fail**
LB12	OS09	-	-	**Deemed fail**	-	-	**Deemed fail**	-	-	-	90.0	-	**Deemed fail**	
LB12	OS10	-	-	**Deemed fail**	-	-	**Deemed fail**	-	-	-	90.0	-	**Deemed fail**	
LB13	OS08	9	6.0 - 10.0	PASS	66	60.3 - 73.7	PASS	0.0800	0.0259 - 0.0389	*Fail*	90.0	91.73	PASS	**Fail**
LB13	OS09	7	7.0 - 11.0	PASS	562	532.8 - 651.2	PASS	0.3650	0.1540 - 0.2310	*Fail*	90.0	43.85	**Fail**	
LB13	OS10	4	5.0 - 9.0	**Fail**	7	18.9 - 23.1	**Fail**	0.0542	0.0202 - 0.0302	*Fail*	90.0	35.71	**Fail**	
LB14	OS08	8	7.0 - 11.0	PASS	99	88.2 - 107.8	PASS	0.1023	0.0342 - 0.0512	*Fail*	90.0	97.46	PASS	PASS
LB14	OS09	2	.0 - 4.0	PASS	4	2.0 - 6.0	PASS	0.0008	0.0002 - 0.0004	*Fail*	90.0	100.00	PASS	
LB14	OS10	1	.0 - 4.0	PASS	5	5.0 - 9.0	PASS	0.0024	0.0008 - 0.0012	*Fail*	90.0	83.33	**Fail**	

Table 13. Summary of the performance of participating laboratories in the Own Sample (OS) exercises with respect to the NMBAQC / NMMP standards.

1		2	3	4	5	6	7	8	9	10	11	12	13	14
		Estimation of Taxa			Estimation of Abundance			Estimation of Biomass			Similarity Index			Overall
LabCode		Lab.	Target	Flag	Lab.	Target	Flag	Lab. result	Target	Flag	Target	Lab.	Flag	NMP Flag
LB15	OS08	17	20.7 - 25.3	**Fail**	48	51.3 - 62.7	**Fail**	7.1058	5.4222 - 8.1332	*PASS*	90.0	71.03	**Fail**	
LB15	OS09	5	3.0 - 7.0	PASS	147	123.3 - 150.7	PASS	0.1211	0.0599 - 0.0899	*Fail*	90.0	96.48	PASS	PASS
LB15	OS10	5	3.0 - 7.0	PASS	242	214.2 - 261.8	PASS	1.0597	0.6608 - 0.9912	*Fail*	90.0	99.17	PASS	
LB16		Not participating in this component					Not participating in this component				Not participating in this component			
LB17		Not participating in this component					Not participating in this component				Not participating in this component			
LB18		Not participating in this component					Not participating in this component				Not participating in this component			
LB19	OS08	22	19.8 - 24.2	PASS	310	435.6 - 532.4	**Fail**	0.2003	0.0886 - 0.1328	*Fail*	90.0	73.30	**Fail**	
LB19	OS09	40	36.9 - 45.1	PASS	224	203.4 - 248.6	PASS	11.2203	6.8525 - 10.2787	*Fail*	90.0	97.33	PASS	PASS
LB19	OS10	59	60.3 - 73.7	**Fail**	276	266.4 - 325.6	PASS	13.6475	7.1962 - 10.7942	*Fail*	90.0	93.01	PASS	
LB20	OS08	19	17.0 - 21.0	PASS	123	118.8 - 145.2	PASS	0.5336	0.2840 - 0.4260	*Fail*	90.0	93.33	PASS	
LB20	OS09	40	36.0 - 44.0	PASS	934	998.1 - 1219.9	**Fail**	21.6971	15.1029 - 22.6543	*PASS*	90.0	90.46	PASS	PASS
LB20	OS10	28	25.2 - 30.8	PASS	84	81.0 - 99.0	PASS	0.6907	0.2930 - 0.4394	*Fail*	90.0	93.10	PASS	
LB21	OS08	9	9.0 - 13.0	PASS	58	57.6 - 70.4	PASS	0.4246	0.1569 - 0.2353	*Fail*	90.0	95.08	PASS	
LB21	OS09	8	8.0 - 12.0	PASS	17	21.6 - 26.4	**Fail**	0.0076	0.0034 - 0.0050	*Fail*	90.0	53.66	**Fail**	**Fail**
LB21	OS10	23	22.5 - 27.5	PASS	39	51.3 - 62.7	**Fail**	0.8752	0.3770 - 0.5656	*Fail*	90.0	60.42	**Fail**	
LB22	OS08	16	14.0 - 18.0	PASS	820	728.1 - 889.9	PASS	3.9925	2.6046 - 3.9068	*Fail*	90.0	98.59	PASS	
LB22	OS09	10	8.0 - 12.0	PASS	611	538.2 - 657.8	PASS	4.4835	3.1949 - 4.7923	*PASS*	90.0	98.59	PASS	PASS
LB22	OS10	4	2.0 - 6.0	PASS	146	131.4 - 160.6	PASS	0.2247	0.1270 - 0.1904	*Fail*	90.0	100.00	PASS	
LB23	OS08	-	-	**Deemed fail**	-	-	**Deemed fail**	-	-	-	90.0	-	**Deemed fail**	
LB23	OS09	-	-	**Deemed fail**	-	-	**Deemed fail**	-	-	-	90.0	-	**Deemed fail**	**Deemed fail**
LB23	OS10	-	-	**Deemed fail**	-	-	**Deemed fail**	-	-	-	90.0	-	**Deemed fail**	
LB24		Not participating in this component					Not participating in this component				Not participating in this component			
LB25	OS08	-	-	**Deemed fail**	-	-	**Deemed fail**	-	-	-	90.0	-	**Deemed fail**	
LB25	OS09	-	-	**Deemed fail**	-	-	**Deemed fail**	-	-	-	90.0	-	**Deemed fail**	**Deemed fail**
LB25	OS10	-	-	**Deemed fail**	-	-	**Deemed fail**	-	-	-	90.0	-	**Deemed fail**	
LB26	OS08	-	-	**Deemed fail**	-	-	**Deemed fail**	-	-	-	90.0	-	**Deemed fail**	
LB26	OS09	-	-	**Deemed fail**	-	-	**Deemed fail**	-	-	-	90.0	-	**Deemed fail**	**Deemed fail**
LB26	OS10	-	-	**Deemed fail**	-	-	**Deemed fail**	-	-	-	90.0	-	**Deemed fail**	
LB27	OS08	6	4.0 - 8.0	PASS	409	376.2 - 459.8	PASS	2.1090	1.1887 - 1.7831	*Fail*	90.0	98.67	PASS	
LB27	OS09	7	6.0 - 10.0	PASS	65	58.5 - 71.5	PASS	0.5430	0.2890 - 0.4334	*Fail*	90.0	95.39	PASS	PASS
LB27	OS10	9	7.0 - 11.0	PASS	80	75.6 - 92.4	PASS	0.2490	0.1408 - 0.2112	*Fail*	90.0	96.34	PASS	
LB28		Not participating in this component					Not participating in this component				Not participating in this component			

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

Table 14. Summary of the performance of participating laboratories in the Particle Size (PS) exercises with respect to the NMBAQC / NMP standards.

PS12 Target range = 0.0 - 11.0

	PS12	
LabCode	Actual	Flag
LB01	-	Deemed Fail
LB02	0.5	PASS
LB03	0.5	PASS
LB04	-	Deemed Fail
LB05	-	Deemed Fail
LB06*	2.6	PASS
LB07	not participating in this component	
LB08	0.4	PASS
LB09	-	Deemed Fail
LB10	1.1	PASS
LB11	not participating in this component	
LB12	-	Deemed Fail
LB13*	2.6	PASS
LB14	1.2	PASS
LB15	0.0	PASS
LB16	not participating in this component	
LB17	not participating in this component	
LB18	not participating in this component	
LB19	3.9	PASS
LB20*	2.6	PASS
LB21	-	Deemed Fail
LB22*	2.6	PASS
LB23	-	Deemed Fail
LB24	0.1	PASS
LB25	-	Deemed Fail
LB26	-	Deemed Fail
LB27	0.0	PASS
LB28	2.6	PASS

PS13 Target range = 73.5 - 93.5

	PS13	
LabCode	Actual	Flag
LB01	-	Deemed Fail
LB02	86.9	PASS
LB03	88.0	PASS
LB04	87.4	PASS
LB05	-	Deemed Fail
LB06*	71.0	**Fail**
LB07	not participating in this component	
LB08	63.9	**Fail**
LB09	84.1	PASS
LB10	86.3	PASS
LB11	not participating in this component	
LB12	-	Deemed Fail
LB13*	71.0	**Fail**
LB14	85.6	PASS
LB15	93.8	**Fail**
LB16	not participating in this component	
LB17	not participating in this component	
LB18	not participating in this component	
LB19	not participating in this component	
LB20*	71.0	**Fail**
LB21	-	Deemed Fail
LB22*	71.0	**Fail**
LB23	-	Deemed Fail
LB24	87.9	PASS
LB25	-	Deemed Fail
LB26	-	Deemed Fail
LB27	-	Deemed Fail
LB28	71.0	**Fail**

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

Table 15. Comparison of the overall performance of laboratories in 1996/97, 1997/98 and 1998/99 with respect to the NMBAQC / NMP standards.

Year	Component	Exercise	Pass	Fail	Deemed Fail	% Pass
1996/97	OS	02, 03, 04	11	3	9	48
1997/98		05, 06, 07	12	1	8	57
1998/99		08, 09, 10	11	3	5	58
1996/97	PS	08, 09	27	1	20	56
1997/98		10, 11	25	3	22	50
1998/99		12, 13	21	7	17	47

Table 16. Comparison of the performance of each laboratory in the Own Sample (OS) exercises for Scheme years 3, 4 and 5.

LabCode (YR5)	Year 3 OS02, 03, & 04	Year 4 OS05, 06, & 07	Year 5 OS08, 09, & 10
01	PASS	PASS	PASS
02	PASS	PASS	N/P
03	Deemed fail	PASS	N/P
04	PASS	PASS	PASS
05	**FAIL**	Deemed fail	Deemed fail
06	PASS	PASS	PASS
07	-	-	N/P
08	PASS	PASS	PASS
09	Deemed fail	PASS	PASS
10	-	-	**FAIL**
11	Deemed fail	N/P	N/P
12	Deemed fail	Deemed fail	Deemed fail
13	Deemed fail	PASS	**FAIL**
14	PASS	PASS	PASS
15	**FAIL***	PASS	PASS
16	PASS	PASS	N/P
17	Deemed fail	N/P	N/P
18	PASS	Deemed fail	N/P
19	PASS	**FAIL**	PASS
20	**FAIL**	Deemed fail	PASS
21	-	Deemed fail	**FAIL**
22	PASS	PASS	PASS
23	Deemed fail	Deemed fail	Deemed fail
24	Deemed fail	N/P	N/P
25	PASS	Deemed fail	Deemed fail
26	Deemed fail	Deemed fail	Deemed fail
27	-	-	PASS
28	-	N/P	N/P
Total returns	14	13	14

Key: N/P - Not participating
"-" - Not in scheme for this circulation
* - Fewer than three samples received

Figures

Figure 1. Particle size distribution curves resulting from analysis of fourteen replicate samples of sediment distributed as PS12. Seven samples analysed by sieve-pipette and seven samples analysed by Laser.

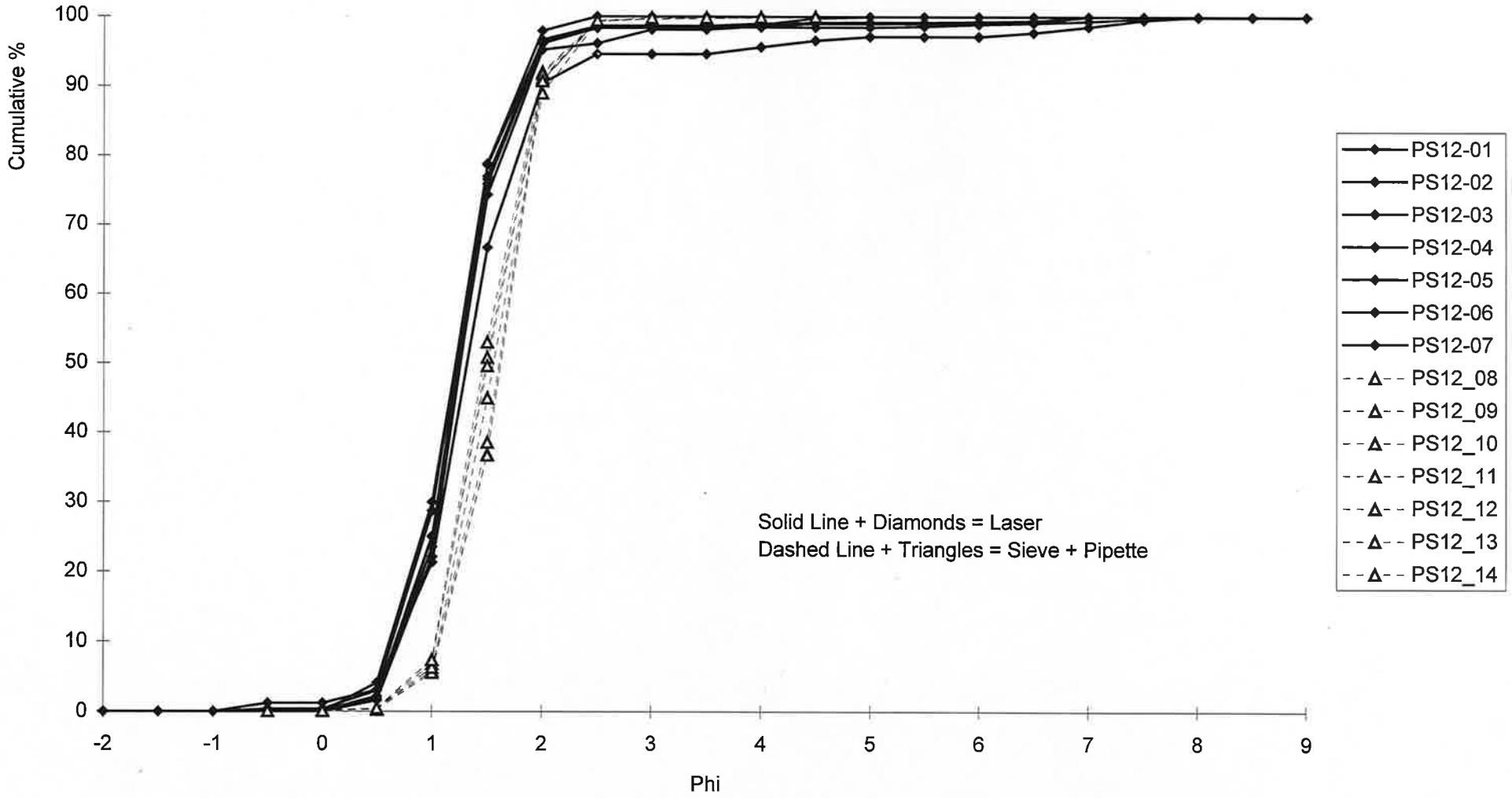


Figure 2. Particle size distribution curves resulting from analysis of fourteen replicate samples of sediment distributed as PS13. Seven samples analysed by sieve-pipette and seven samples analysed by Laser.

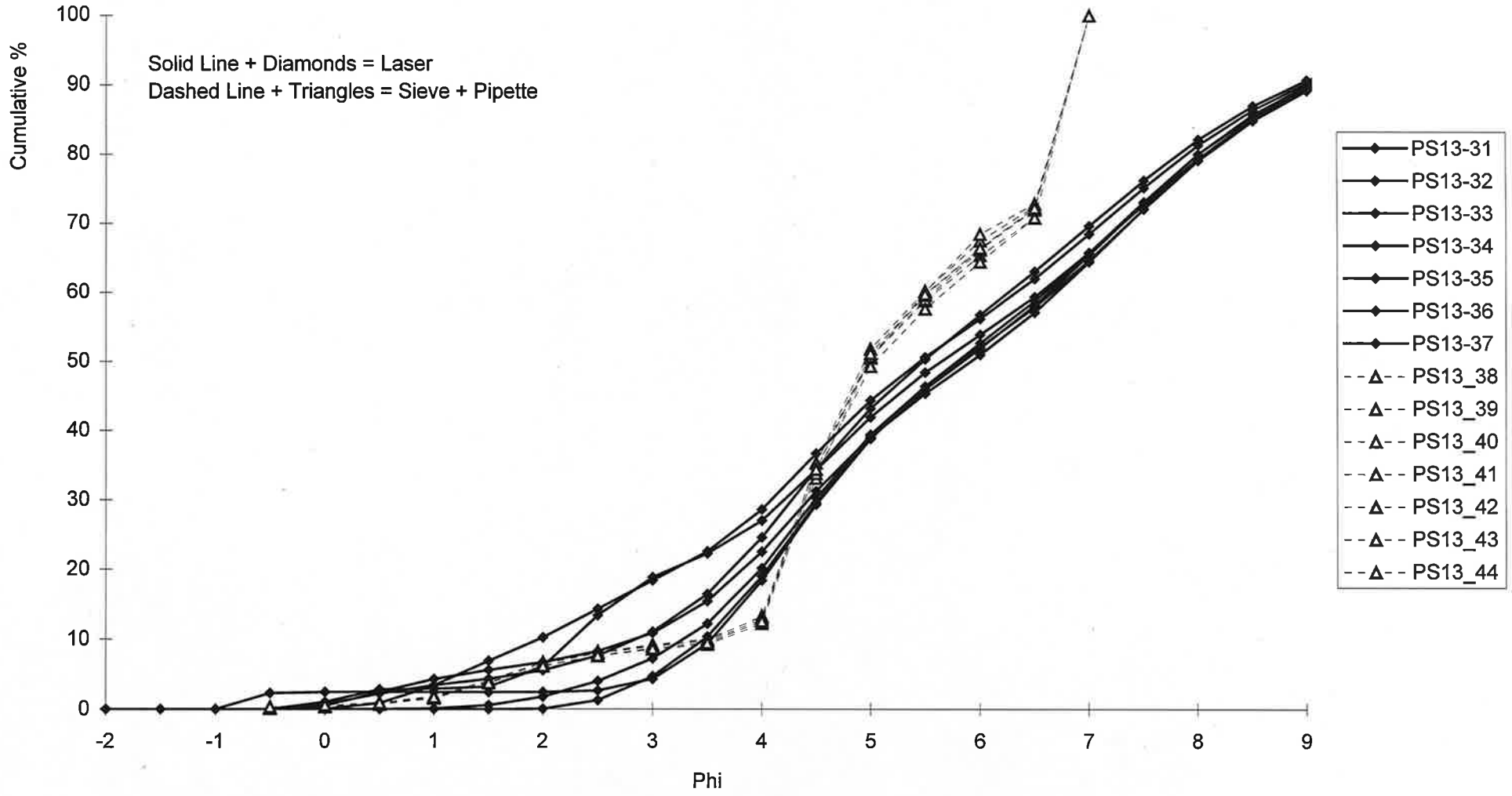


Figure 3. Particle size distribution curves from participating laboratories for sediment samples from PS12. The average values for the AQC analysis of replicates are included.

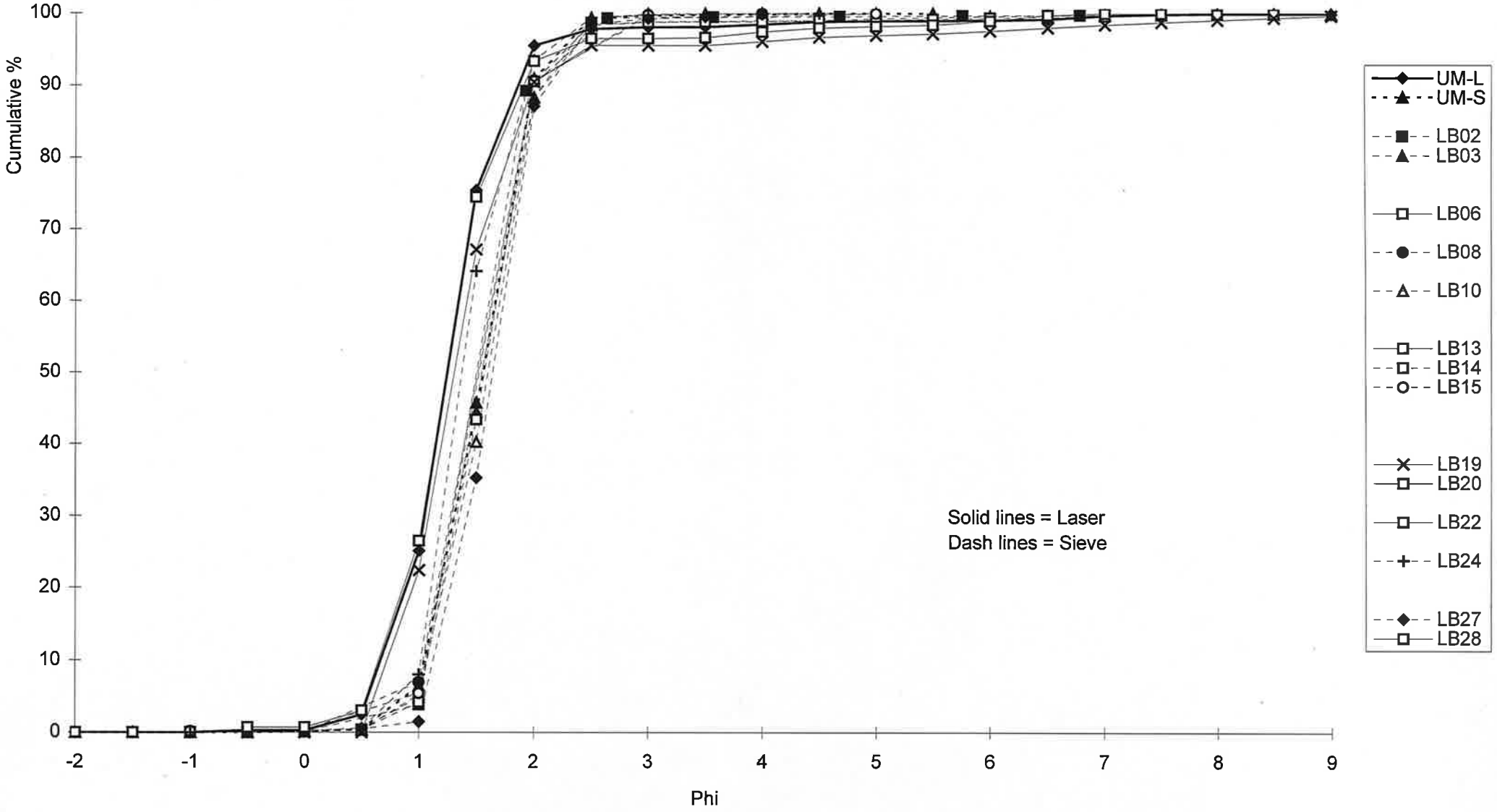


Figure 4. Particle size distribution curves from participating laboratories for sediment samples from PS13. The average values for the AQC analysis of replicates are included.

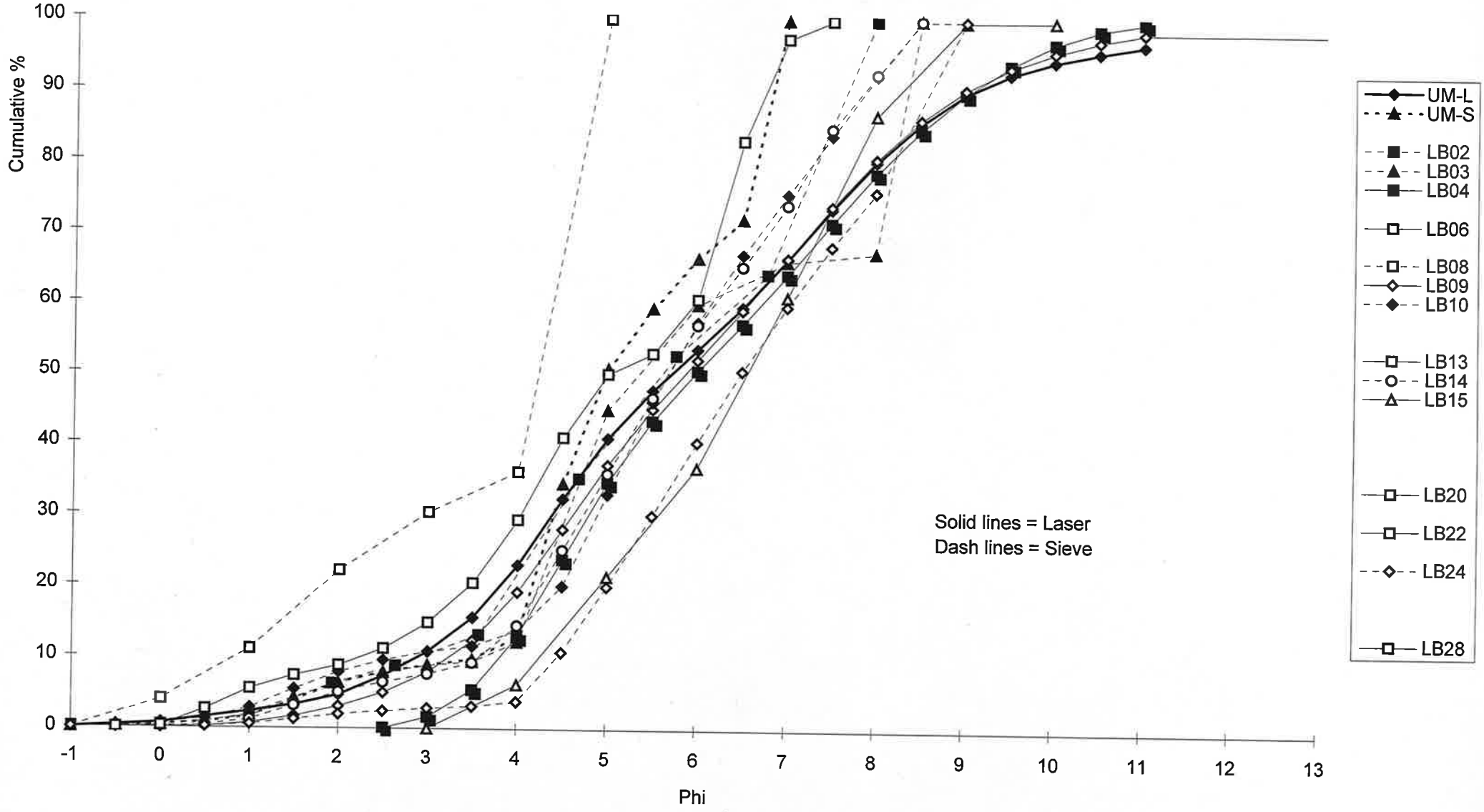


Figure 5. The number of differences from the AQC identification of specimens distributed in RT12 for each of the participating laboratories. Arranged in order of increasing number of differences.

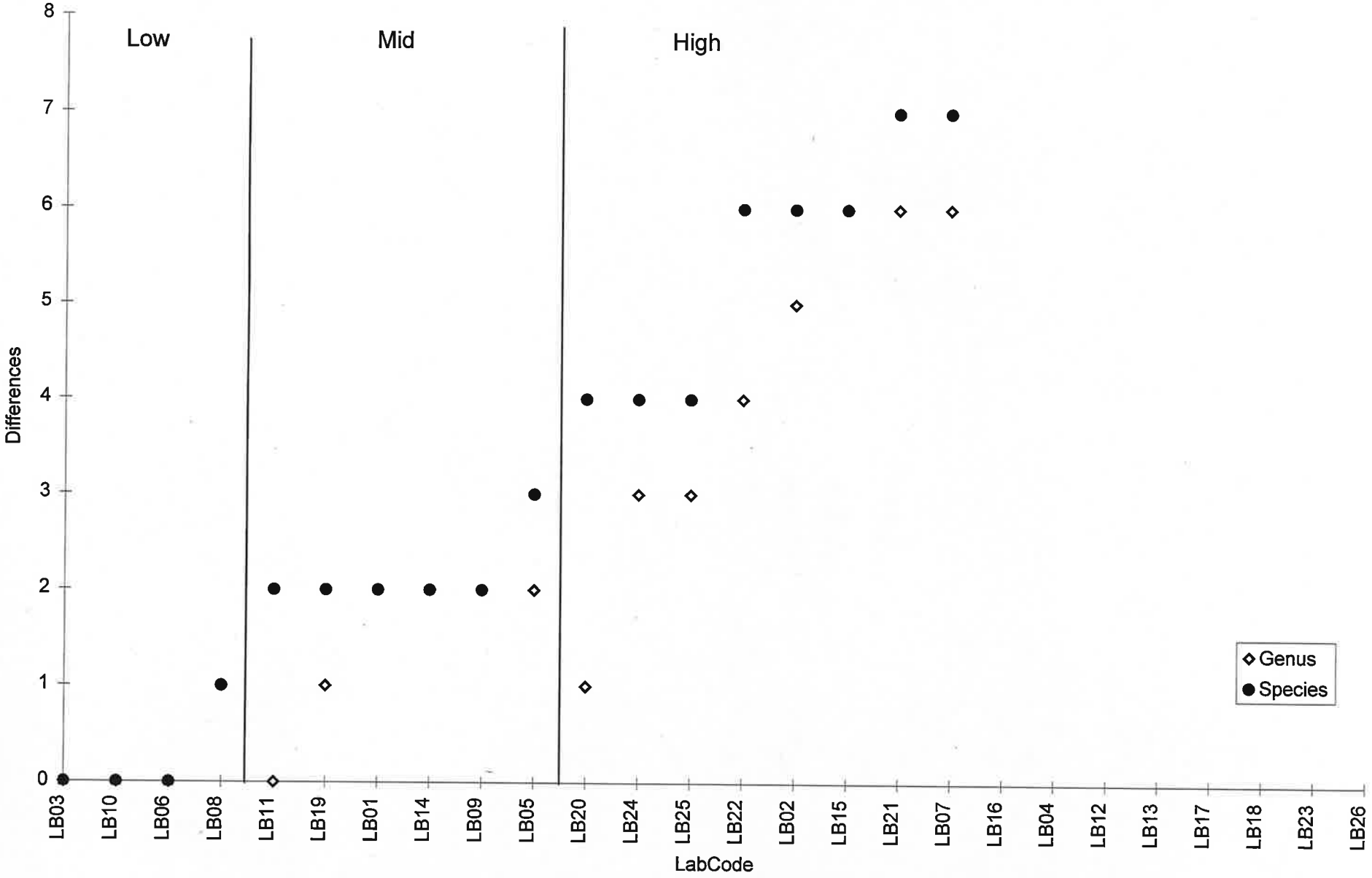
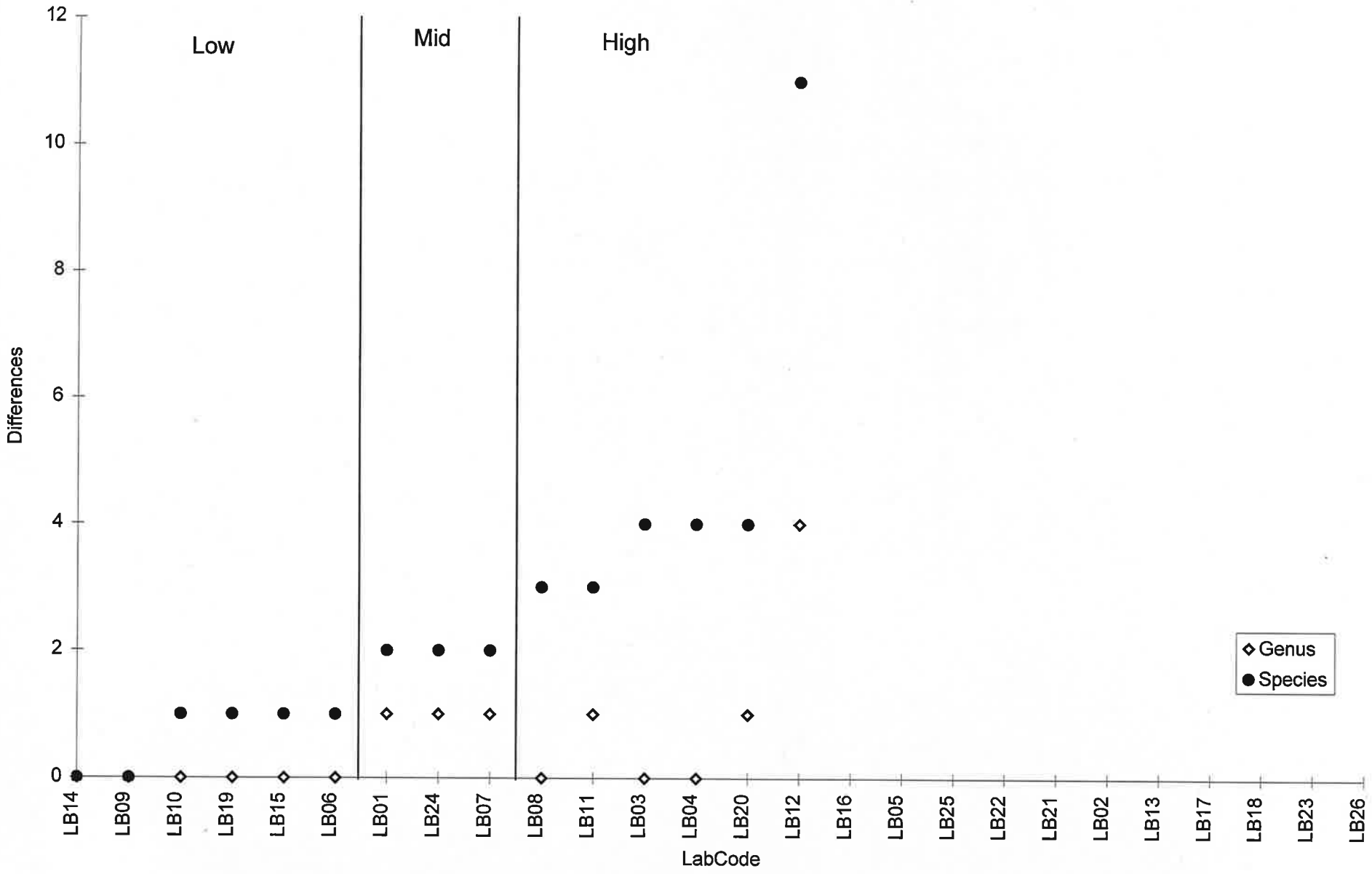


Figure 6. The number of differences from the AQC identification of specimens distributed in RT13 for each of the participating laboratories. Arranged in order of increasing number of differences.



Appendix 1

List of groups from which specimens should be selected for LR03

	Major Group	Group	Note
1	Oligochaeta	Tubificidae	
2	Polychaeta	Ampharetidae or Terebellidae	Choose one
3	Polychaeta	Cirratulidae	
4	Polychaeta	Maldanidae or Sabellidae	Choose one
5	Polychaeta	Hesionidae or Paraonidae	Choose one
6	Polychaeta	Phyllodocidae	
7	Polychaeta	Sigalionidae or Polynoidae	Choose one
8	Polychaeta	Spionidae	
9	Polychaeta	Capitellidae	
10	Polychaeta	Syllidae	
11	Polychaeta	Syllidae	
12	Polychaeta	Glyceridae, Goniadidae, Opheliidae Sphaerodoridae, Eunicida, Magelonidae	Choose one from the list
13	Crustacea	Pontoporeiidae	
14	Crustacea	Lysianassidae	
15	Crustacea	Another gammaridean amphipod family	Choose another family
16	Crustacea	Decapoda	
17	Crustacea	Mysidacea	
18	Crustacea	Tanaidacea	
19	Mollusca	Gastropoda – Opisthobranchia	
20	Mollusca	Gastropoda - non Opisthobranchia	
21	Mollusca	Tellinidae	
22	Mollusca	Mytilidae	
23	Mollusca	Caudofoveata, Scaphopoda, Solenogastres or Polyplacophora	Choose one from the list
24	Echinodermata	Echinoidea, Holothurioidea or Asteroidea	Choose one from the list
25	Other	Sipuncula, Pycnogonida, or Chordata (inverts)	Choose one from the list

Appendix 2

Description of Scheme Standards

In the fifth year of the Scheme (1998/99) required levels of performance were set by the NMBAQC steering committee for the Own Sample and Particle Size Analysis exercises. The flags applied to the various exercises are based on a comparison of the results from sample analysis by Unicomarine Ltd. and those from the laboratory. The OS exercise has several aspects, each with a separate standard. Each of the standards has been calculated independently for each of the three OS exercise. The PS standard is based solely upon the determination of the Silt-Clay fraction in the sample and has been calculated independently for the two PS exercises. The process of assigning the flags for each component is described below. The target standards and recommended protocols may be modified in the future. A single standard 'averaged' value calculated across several components was found to be impracticable.

Own Sample - Extraction efficiency - Total Taxa target

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

Own Sample - Extraction efficiency - Total Individuals target

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

Own Sample - Total Biomass target

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

Own Sample - Bray-Curtis comparison

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

Own sample - Overall flag

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

Because of the considerable variation in the estimation of biomass (as discussed in earlier reports; (NMBAQC Scheme Annual report 1996/97, Section 3.2.5) the flag for this component has not been included in the determination of the overall flag for the OS

exercises. This is the same approach as applied for the previous year. Laboratories failing to supply OS or PS data have automatically been assigned a fail flag by default.

Particle Size Analysis - Silt-Clay fraction

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

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

Appendices

APPENDIX 1

NATIONAL MARINE BIOLOGICAL AQC CO-ORDINATING COMMITTEE

Dr. M. Service (Chair)	Department of Agriculture, Northern Ireland
Mrs. E. Hamilton (Secretary)	SEPA East
Mrs. A. Henderson (Contract Manager)	SEPA West
Dr. M. Elliott	University of Hull
Mr. D. Moore	FRS
Dr. H. Rees	CEFAS
Mr. R. Proudfoot	Environment Agency
Ms. S. White*	Environment Agency
Mr. J. Breen	IRTU/Industrial Science Centre
Mr. D. Connor	JNCC

(* to be replaced by Mr. A. Robinson of the Environment Agency Wales - October 1999)

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 NMMP.
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 1998/99

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