NATIONAL MARINE BIOLOGICAL ANALYTICAL QUALITY CONTROL SCHEME

NATIONAL MARINE BIOLOGICAL AQC REPORT 1997 / 1998

ANNUAL REPORT

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National Marine Biological AQC Co-ordinating Committee
Unicomarine Ltd

NATIONAL MARINE BIOLOGICAL ANALYTICAL QUALITY CONTROL SCHEME

Annual Report 1997 / 1998

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- **Addendum**

National Marine Biological AQC Scheme : Flagging of Own Samples 1996/97

1. The OS data supplied by Laboratory 4 in 1996/97 has been re-examined and the committee have agreed to amend the overall flag to a PASS.

2. The OS data supplied by Laboratory 17 in 1996/97 has been re-examined and the committee have agreed to apply a cautious PASS to be verified pending additional analysis.

1. OVERALL SUMMARY

- The National Marine Biological AQC Scheme (NMBAQC Scheme) has completed its fourth year in 1997/98. The background to the scheme is described in previous annual reports.
- Components of the scheme continued to be based on Ring Tests (RT), 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, screening data for the UK NMP programme.
- Participation in the scheme remained high with a total of twenty seven laboratories participating. Seventeen of these laboratories submitted data for NMP, six were consultants or private contractors and the remainder non NMP government labs. Interest had been expressed by some non NMP labs in 'selective' participation where particular components of the scheme could be excluded/included for them. NMP 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.
- Scheme components (Own Sample and Laboratory Reference) in 1997/98 appeared to be approached with different philosophies by different laboratories, plus 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 3) where individual laboratory performance is described and standards of achievement against the targets tabulated.
- Problems with biomass analysis were again evident in relation to the level of accuracy reported plus also the variation in results from the contractor and labs choosing not to report data.
- Major problems appear to exist in sorting accuracy.
- Particle size tests highlighted the variability in fine fraction analysis.
- Efforts to achieve better data feedback to participants were hindered by late returns and non returns of data plus format problems.
- NMP Laboratories achieved only 50% overall pass mostly due to non returns of OS data.
- Failure of some NMP laboratories to achieve the necessary overall standards may affect the inclusion of their data submissions to the NMP database.
- A workshop on field AQC sampling techniques (commencing in Spring 1997) was completed in the Autumn of 1997. The proceedings will be published in 1998. The review of NMP I and the way ahead for NMP II were the subject of a workshop in September 1997 at Newcastle.
- The Regional and Holistic NMP reports have been published during 1998.
- A new MCS Directory has been published . Coding problems are still under review.
- The quality of the NMP data base has been reviewed and a SNIFFER research project will use the data base to develop predictive benthic models.
- A Scheme Statement of Quality has been developed for issue to participants.
- The scheme has undergone a formal retendering exercise for 1998/99 - 2001/02

- Unicomarine Ltd. continued to successfully operate the scheme bringing added value to it again in its fourth year.

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

2. SCOPE OF THE SCHEME

The fourth year of the scheme was designed to build on last year's data and better reflect the standards being achieved continuing the emphasis on participant supplied samples. In total seven participant supplied samples have now been judged against the standards derived in 1996/97. To this end the format of the scheme in 1997/98 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) 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 3.

3. ISSUES ARISING

3.1 The composition and aims of the scheme

The statements made in last year's report hold true for 1997/98.

- **Ring tests** are generally accepted as a method of improving learning skills relating to taxonomy. Laboratories generally achieved good results. Areas of difficulty emerged with particular faunal groups which were tackled by the targeted RT and individual feedback. The standard ring test formed part of the core programme. It is recognised that the contractor supplied ring tests do not necessarily reflect the skills of individual laboratories and for this reason RT's have not been used to set a pass / fail standard for NMP 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 in 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 were 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 NMP 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 NMP data base have been applied only to OS samples for enumeration and taxon extraction as representing the true reflection of local lab 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 NMP determinand, this analysis has been assigned a pass / fail standard and must be completed by NMP labs. Most labs in the scheme carried out the analysis by one of the two preferred techniques in common use.

3.2 Participation

The twenty seven participants in 1997/98 comprised private contractors, university labs and Government labs in Scotland Ireland and England. Seventeen laboratories provide data or analytical services for NMP components and submit data to the NMP 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, clearly private contractors and non NMP labs, may favour completing certain components over others which will be compatible with their commercial interests or their budgets. This is their choice provided no contractual agreement is broken. For these labs, participation in selected components *eg.* only RTs is acceptable. However, labs submitting data to the NMP should complete the whole programme whether pass / fail standards have been devised or not for individual components.

3.3 Submission of data

Time scales for data return were lengthened in this last year. However there were still problems with late or non returns, use of formats different from contractor needs and inappropriate accuracy for biomass. Only seven NMP labs supplied all the data from all relevant components. Two supplied no data at all (1 less than 1996/97 but the two concerned also failed to supply any data last year) while the remainder 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

Insufficient feedback of results to participants was recognised last year as an important issue. Concern was recognised about releasing results in a staggered manner thus allowing knowledge of 'the answer' into the community but it was agreed that the need for faster feedback outweighed the risk of 'cheating' . However, considerable problems in achieving this data assessment/ reporting and feedback of data was encountered again this year due to the late or non return of data, use of differing formats or incorrect accuracy. Laboratories therefore have been issued this year with individual results from circulations (not comparative lab results) to allow labs to review their own performance.

3.5 Targets and standards

As in 1996/97, it was agreed that the separate components of the Own Samples and PS only would be scored against the targets. Thus for those labs returning data, 9 separate components can be assigned as pass or fail. The committee agreed it would be reasonable that in order to achieve an overall pass, the standards should be achieved or exceeded on >=6/9 components.

While individually very few laboratories had consistent problems, applying the agreed level of pass, eight out of sixteen NMP labs failed overall, **seven of which supplied insufficient or no OS data** (these are deemed to have failed) .

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

Achievement of the biological standards appear to be posing a challenge for a number of laboratories. It is intended that the standards will be re-assessed (not necessarily relaxed) and peer reviewed in 1998/99.

Particle size analysis poses less of a challenge to laboratories although a number of laboratories failed to return data and thus do not achieve a pass.

4. SCHEME PROPOSAL FOR 1998/99

The core programme for the scheme in the coming year 1998/99 will contain the following components:
1. Own samples;
2. Ring Tests including a targeted ring test
3. Macrobenthic 'Bucket' sample.
4. PSA samples.

Options for workshops to be held during the year include beginners invertebrate taxonomy, epibenthic surveys, biological survey techniques. The scheme may also address some problems of access to literature and relevant keys

5. CO-ORDINATING COMMITTEE ACTIVITIES AND PROJECTS

As well as the projects assigned to the contractor, committee members undertook specific tasks on behalf of the scheme.

5.1 Workshops

5.1.1 Workshop on comparative sampling and analytical methods.

This was held in March 1997 but is detailed below for completeness; there was a follow up in September 1997. A workshop was held on 17-21st March at Hull University sponsored by the Environment Agency, NMBAQC, ECSA and IECS. The workshop aimed to determine best practice and set standards for field and laboratory sampling of macro-invertebrates. More specifically, the following activities were carried out:

- Subtidal intercomparison of methods
- Intertidal review and demonstration
- Laboratory handling of procured samples
- Sub-sampling techniques comparison
- Biomass worker comparisons
- Subtidal sampling equipment demonstration

A follow-up meeting was held at Hull University to discuss the findings of the workshop on the 18th of September 1998. Proceedings are currently being written up.

- **Subtidal Intercomparison**

Eleven laboratories took part in this exercise, which aimed to compare the results from two standards sites in the Humber Estuary (one sandy, one muddy) sampled by each laboratory using as near as possible their standard procedures (0.1m² Day grab, 0.5mm mesh).

In general, there was little statistical difference in the results between laboratories with the exception of two laboratories. One laboratory used a 1 mm sieve as opposed to 0.5 mm. Not surprisingly, a significant difference was found between this laboratory and the rest. The second laboratory which deviated was testing an automatic sieving device supplied for demonstration by Guardline Ltd. Significantly fewer

individuals were retained by this method. However, a condition index derived in the laboratory indicated the automatic sieving device caused least damage to the invertebrates. The method was the only means of processing utilised on the workshop which conformed to all International Council for the Exploration of the Sea standards (Rumohr, 1990).

A detailed questionnaire was also taken regarding individual laboratories' field sampling and handling procedures. The questionnaire also included a detailed assessment of sampling equipment dimensions. A full account will be given in the proceedings, comparing the questionnaires with the detailed statistical assessment of the samples.

- **Intertidal Review and Demonstration**

Participants were requested to fill out a questionnaire describing their standard intertidal methods. It was found that in general the Environment Agency's standard methodology did not differ significantly from those of other laboratories.

- **Laboratory Handling of Samples** - Sub-Sampling Techniques Comparison

A standard sample, containing a known number of the small polychaete *Polydora sp.* was processed using a variety of sub-sampling techniques, with a wide variety of outcomes. It was found that the simpler, less labour intensive methods gave the most reliable estimates and were generally capable of achieving the NMBAQC standard of +/- 10% individuals. Standard methods for sub-sampling requires further consideration. More specific recommendations will be made in the proceedings.

- **Biomass Intercomparison**

A variety of approaches were demonstrated by participants for wet weight biomass determination. Significant differences were encountered particularly with soft bodied animals where varying pressure applied during blotting significantly affected the results. A standard protocol requires precise definition to minimise such bias.

- **Sub-Tidal Equipment Demonstration**

A variety of equipment was demonstrated namely: Multi-corer, 0.05m² van Veen grab, 0.1m² Day grab, Haps corer (0.0143 m²), Box corer (0.025 m²), Shipek grab, Hamon grab.

This exercise was aimed at participants experiencing the use of equipment which they otherwise might not have come across. There was some discussion at the follow up workshop regarding the length of time required to procure a core sample compared to a grab. However, the box corer is generally recommended by ICES in preference to a grab sampler. In practice the grab tends to be more cost effective due to sample turn around time whereas the box core reduces sampling bias. Further research should focus on an optimal design for a benthic sampler which combines both features. The Shipek grab and Hamon grabs were also demonstrated and tend to be used for gravelly substrates. The multicorer is an effective sampler for meiofauna and sediment studies.

Reference:

Rumohr, H. (1990). Soft bottom macrofauna: Collection and treatment of samples. In: Techniques in Marine Environmental Sciences No. 8. ICES ISSN 0903-2606

5.1.2 Workshop on NMP Phase I and II (see 5.3 NMP Developments, below)

5.2 NODC Codes and MCS Species Directory

Funding of the new MCS species directory was supported by the NMB AQC scheme and it has been published during the year. Problems of incompatible codes however has not yet been resolved. The committee is striving to have these issues resolved for the release of the CDROM version.

5.3 NMP Developments

Phase 1 of NMP (the spatial survey) is now completed. Several members of the committee and the steering group attended a workshop at Newcastle in September 1997 to review, assess and determine data gaps and finalise reporting plus form a view for the way ahead for Phase II. It was agreed that significant gaps in the data were to be filled between 1998-1999. The workshop identified biological systems and biological effects as the prime drivers for targeting future chemistry programmes and identifying trends

thus establishing the triad approach to examine long term trends. The criteria for the selection of sites for assessing temporal trends which will be addressed by NMP II, were explored extensively. A need for pristine sites and locations to assess diffuse pollution sources was highlighted.

During the year members of the committee met to determine the criteria for quality, completion and format of the data for the NMP marine biological data base, examine the data and agree the text for the holistic report. The regional reports for Northern Ireland and Scotland were published in 1997. The data from English coastal waters will be reported in the Holistic UK report.

After much discussion through 1997/98 regarding the need for specialised handling of marine biological data for the NMP data base, it was agreed that use be made of an existing system at Unicomarine .

The preparation of the guidance for NMP II : Temporal trends (The Green Book) is underway and will be to a higher spec than for Phase I in anticipation of a more co-ordinated and complete approach.

5.4 Data Quality and SNIFFER

During the year during discussions were ongoing surrounding the use of the NMP data for a 'RIVPACS' type project funded by Scotland and Northern Ireland Forum For Environmental Research (SNIFFER) - **Predictive Models of Benthic Community Features using NMP data.** As a precursor to the main project to be carried out by the University of Hull, the data base for NMP I would be assessed for its weaknesses and problems in achieving consistent data quality including the issues surrounding juveniles, singletons and qualitative data . This required that all participating NMP laboratories be approached for their specimens and sediment residues where still available, prior to decisions on merging taxa etc and any impact this might have on interpretation techniques.

5.5 Standards and Reporting Performance

A further year of applying the standards and targets devised and outlined in earlier reports, has been completed. Standards have not been set for biomass or the RT component. The latter remains critical to the taxonomic learning process but not as a quality testing ground. During 1998/99, the existing NMBAQC standards are likely to be reviewed (see 4.3 above) 'internally' taking into account standards in use in Canada and California and also by peer review within the UK

One member of the committee attended an OSPAR / ICES group which considers QA relating to macro and microphytobenthos.

Work proceeded during the year to progress the issue of a form of quality 'statement' for participating laboratories as this had been an important point of feed back during the previous year. Options explored through UKAS and the Institute of Biology proved not to be viable, so it was agreed that the Committee would issue these Statements indicating both participation and achievement for each scheme component for issue in the year. The statement will bear the date, the name of the participating laboratory and the level of achievement gained during the year. Individual arrangements can be made between participating labs and their subcontractors to use this performance statement but their name will not appear on the document as they are not contracted into the scheme.

5.6 Retendering of NMB AQC Contract 1998/9 - 2001/2

This contract for the scheme has been renewed informally year on year (after 1994) on the basis of contractor performance, value for money, and with a view to continuity.

It was the view of the Contract Manager and the committee that a formal retendering exercise should be completed prior to the commencement of the scheme in 1998/99. Consequently documentation was drawn up and formal invitations to tender sent to six UK contractors. The four respondents were invited to give presentations to the committee and were then judged against the compliance criteria laid down in the tender.

It was the unanimous view that on the grounds of
⇒ cost
⇒ value for money
⇒ added value which will be brought to the project
⇒ proven capability to run the contract
⇒ commitment to the NMBAQC scheme

that Unicomarine be awarded the contract till 2001/2.

6. Financial summary 1997/1998

The Fourth year of the scheme has been completed..

Twenty-seven laboratories participated during the year, two greater than last year due to the inclusion of the EA National Laboratory Service, Llanelli and University College, Cork.

Fees in 1997/98 remained the same as 1996/97. Non NMP laboratories were eligible to take advantage of the 'split fee' according to the components required. Laboratories participating in workshops held during the year were subsidised through the scheme to encourage and develop taxonomic and sampling skills.

The contract continued to be administered by Unicomarine on the basis of their experience, good management and reasonable cost.

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

Financial Summary 1997/1998

	INCOME	*EXPENDITURE*
Participant Fees	*42383.00*	
Interest	*2816.00*	
Consultant fees		*43588.96*
Management fee		*2780.00*
Workshop fees		*6918.00*
Hospitality		*129.50*
Travel & Subsistence		*342.66*
TOTALS	*45199.55*	*53760.04*
BALANCE B/F FROM BANK AC (94-98) £67341.00		
Available funds at 31st March 1998 £ 58781.13		
*All above figures **include VAT but exclude fees** received before year end for participation in year five.*		

Report from Contractor

7. REPORT FROM THE CONTRACTOR

List of Tables and Figures

Tables

List of Tables and Figures (contd.)

Figures

Appendices

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 fourth year of the Scheme (1997/98) followed the format of the third 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 twenty-seven laboratories participated in the Scheme. (The number of participants remains the same at the start of the fifth year (May 1998).)

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. NMP 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 fourth 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 for the first three years were maintained and details may be found in the report for 1994 / 95 and 1995/96.

With the increase in the use of e-mail and provision of internet access within organisations it is intended that, where possible in future, these channels will be used for data transfer. There are several issues to be addressed before this can be fully implemented but it is likely that e-mail transfer will be available during the course of the 1998/99 year.

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 v.5.00 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 November 1996 and new codes assigned. **In the present report all references to Laboratory Codes are the new (post-November 1996) codes.**

In April 1998 a second code change was implemented. These are in use for 1998/99 but do not appear in this current report.

2.2 Macrobenthic Samples (MB)

A single unsorted grab sample from coastal 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 MB05 was collected off Balfour Pier south-west Shapinsay, Orkney, in an area of sandy 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 1.00mm, 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 contained macrobenthic fauna 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.

Sixteen weeks were allowed for completion of the sample analysis (6 more than in 1996/97) 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 was 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. NMP laboratories were advised to use NMP 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 1997 / 98. 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 1997/98. The first of the year's RT circulations (RT10) 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 11) 'targeted' a single family of polychaetes (Syllidae) and the smaller crustacean orders (Tanaidacea,

Cumacea and Isopoda). These faunal groups had been identified from earlier RT circulations and MB exercises as causing laboratories significant problems with identification. Multiple examples of some species were included in the circulation, adult and juvenile specimens were also included.

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 (RT10) and the 'targeted' RT (RT11) 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 1997/98 (LR02). 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 1997/98 were undertaken by approximately twenty-seven 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 (MB05) was from a sandy substratum taken from a depth of approximately 6m. The samples were very diverse with an average of fifty-four species and six hundred and forty-four individuals, covering a variety of phyla. The composite list from all samples was approximately one hundred and seventy-five species. A number of samples had been stained with Rose Bengal. Overall, of the twenty-four laboratories participating in this exercise, fourteen laboratories returned samples and data; ten did not.

3.1.2 Efficiency of sample sorting

Table 1 presents for sample MB05, 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 eight taxa (22% of the total 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 90 individuals were not extracted from the samples (9.4% of the total in the sample). The average number of un-picked individuals was twenty-seven, however over two thirds of the laboratories missed less than this figure.

The values presented for the number of taxa not extracted (column 10) represent taxa not recorded or extracted (even if mis-identified) elsewhere in the results *ie.* these were taxa completely missed by the laboratory. Of those laboratories that provided their residue for re-analysis, only three laboratories extracted representatives of all the species present in their samples and in the worst instance six 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 (*ie.* 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 (8 out of 13 comparable laboratories), though 8.6% and 9.4% were missed in the worst instances. A breakdown of the missed individuals by taxonomic group is presented in Table 2.

3.1.2.3 *Uniformity of identification*

Although most of the species in the distributed sample were identified correctly by the participating laboratories there were some problems with approximately 17% of all identifications. The major problem areas appeared to be Maldanidae and Ampeliscidae, these included *Heteroclymene robusta* (often identified as *Euclymene oerstedii*), *Ampelisca tenuicornis* and *Ampelisca typica* (often found as mixtures in taxa vials or identified as either *A. diadema, A. armoricana* or *A. spinipes*). Some problems were evident among the smaller bivalve mollusc specimens including *Abra alba* (often identified as *A. nitida* or *A. tenuis*), *Nucula nucleus* (identified as *Nucula nitidosa* or *Nucula sulcata*) and *Mytilus edulis* (as *Modiolus*). Also commonly mis-identified were *Tryphosella sarsi* (mostly recorded as *Orchomene nana*) and *Akanthophoreus gracilis*. The molluscs *Lucinoma borealis* juv. and *Onoba aculeus* were also mis-identified. Some of the smaller molluscs such as *Crenella decussata*, *Onoba aculeus* and *Lucinoma borealis* juv. were frequently missed in the sample residue.

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 72% to 95%, with an average value of 85%. The index for the majority of laboratories (11 of 14) was in excess of 80%. The variation and relatively low average Bray-Curtis similarity indices can be attributed to several factors. In many cases, new taxa (*ie.* 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 several 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 MB05 circulation is presented in Table 3. The average difference between the two values was +32%, with the measurement made by Unicomarine Ltd. typically being less (*ie.* lighter) than that made by the participating laboratory. In half of the eleven instances the difference in measurements was less than +40%. The range was -9% (measurements by laboratory were greater than those made by Unicomarine Ltd.) to +53% (measurements by laboratory were less 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 samples were received from fourteen laboratories, together with descriptions of their origin and the collection and analysis procedures employed. Samples were identified as OS05, OS06 and OS07 on receipt. Ten laboratories did not participate in this component, only three informed us as such. 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 3l of residue. The associated fauna of the samples was also very varied; the number of taxa recorded ranged from 1 to 58, and the number of individuals from 1 to 1253. All NMP labs were required to participate in this exercise. Overall, of the twenty-one laboratories participating in this exercise, thirteen laboratories returned all three Own Samples and one laboratory provided a single sample. Two laboratories did not send any of their samples (although they had indicated their intention to do so), and 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 twenty-two cases (over half 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 eighteen exceptions, the difference was at most six taxa and the average difference was less than 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 40%. The average difference is 3.6% (only ten samples exceeded this average). Twenty-two of the samples received showed 100% extraction of fauna from residue (Table 4, column 12), and in seven samples various numbers of individuals (but no new taxa) were missed during sorting (Table 4, column 11). The remaining eleven samples contained taxa in the residue which were not previously extracted, the worst example being four new taxa found in the residue (Table 4, column 10).

3.2.3 *Uniformity of identification*

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

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

The procedure for the calculation of the similarity index was as used for the MB exercise. The Bray-Curtis similarity index figures (Table 4, column 14) ranged from 60% to 100%, with an average of 94%. This indicates that, with the exception of two samples, there was a generally high degree of similarity between the data-sets produced separately from the same sample by the participating laboratories and Unicomarine Ltd. Nine samples gave similarity figures of 100%, these included two of the three supplied samples from LB01, LB13 and LB18. 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. Only twenty-five of the forty samples received could be used in this comparative exercise. The total biomass values obtained by the participating laboratories were generally higher than those obtained by Unicomarine Ltd. The average was a 16% difference between the two sets of results, the range was from -167% to 67%. 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 22% for polychaetes, 12% for crustaceans and 15% for molluscs. These figures are markedly different to those produced by this same exercise last year , this emphasises the variability caused by not only duration and method of drying but also the consistency of results.

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. In both PS10 and PS11, samples were circulated to twenty-five participating laboratories. For PS10, sixteen laboratories returned data (including labs with grouped results); nine did not. For PS11, twelve out of the twenty-five participating laboratories returned data and thirteen 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.

The replicate samples from PS10, which were analysed by laser showed considerably more variation than those analysed by sieve. This sample had a very high fine fraction (average of 91% <63μm, by laser) and such samples frequently cause problems for the laser technique. Results for the individual replicates are provided in Table 6 and are displayed in Figure 1.

Sample PS11 was coarser and agreement between the replicates was much better. The shape of the distribution curves was similar for the two analytical techniques and they were more closely grouped. The spread of results for laser analysis was still 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 PS10 and PS11 respectively, only a single line is shown though it applies to four laboratories (the sub-contractor and the three laboratories utilising their results. In Tables 8 and 9, which present the summary statistics for PS10 and PS11 respectively, although the results are displayed for all four 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 *PS10*

There was considerable spread in the results from the participating laboratories and the separation between the analytical techniques was much less obvious than has been observed in other circulations. This is likely to have been due to the very fine nature of the sediment distributed; the sample had over 91% in the silt-clay fraction. It may be seen from Figure 1 that the data resulting from laser analysis of the replicate samples had considerably more spread than those from analysis by sieve. This is a common observation with laser analysis.

3.3.3.2 *PS11*

Agreement between laboratories was better for this sample with all but two laboratories falling into a broad group. The difference between the analytical techniques was apparent, but rather less marked than has been observed in other circulations.

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 three years. A number of labs use this part of the scheme as a training exercise and have selected it preferentially over other components. NMP 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 RT10 the species were from a variety of Phyla (as for previous years) while for RT11 fifteen specimens were

from the polychaete family Syllidae, and the remaining ten specimens came from the smaller crustacean orders. Other aspects of the two circulations, in particular the method of scoring results, were the same as for previous circulations. Overall twenty-six laboratories were distributed with both RT10 and RT11 specimens. For RT10, twenty-two laboratories returned samples and data; four did not. For RT11, nineteen laboratories returned samples and data; seven 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 three main reasons for these differences

- Variation in the 'accepted' spellings, e.g. *Nepthys*, *Nephtys*, *hombergi & hombergii.*
- Use of a different synonym for a species, e.g. *Nucula turgida* for *Nucula nitidosa.*
- Simple mis-spelling of a name, e.g. *Erichonius* for *Ericthonius.*

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 RT10 and RT11. 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 1996/97 as there was only a single 'standard' exercise (RT10). RT11 was targeted on a single polychaete family, the Syllidae, and three orders of crustaceans. The circulation was designed as more of a learning exercise to discover where particular difficulties lie within these groups.

3.4.3.1 *Tenth distribution – RT10*

Table 10 presents the results for the RT10. 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 (*Mytilus edulis* juv., *Paranais litoralis*, *Dendrodoa grossularia* and *Apherusa jurinei*) accounted for 56% of the differences at the level of genus. Four species (*Idotea granulosa*, *Lacuna parva*, *Mytilus edulis* juv. and *Ampharete lindstroemi*) accounted for 61 of 139 differences (44%) at the level of species. The majority of participating laboratories recorded the *Idotea granulosa* juv. as *Idotea pelagica.* This highlights the inability of current literature to correctly deal with juvenile specimens of *Idotea,* and the necessity of using, where available, all relevant keys and descriptions in conjunction with referenced specimens. Small specimens may be difficult to identify without a satisfactory growth series with which to compare animals.

3.4.3.2 *Eleventh distribution – RT11*

RT11 contained fifteen Syllidae and ten specimens from the smaller crustacean orders. 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 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 fifteen syllid species were relatively well identified throughout. One distinctive specimen, *Eurysyllis tuberculata,* was as expected identified correctly by all laboratories. The only generic differences recorded involved the *Streptosyllis websteri, Eusyllis blomstrandi, Exogone naidina* and *Exogone hebes* specimens, although there were only seven generic differences in total. *Sphaerosyllis taylori* appears to cause the most problems at the specific level (15 differences), with difficult splits resulting in them being incorrectly recorded as *S. thomasi* (no longer in the MCS), *S. hystrix* (several species confused under this name) and in single instances *S. pirifera, S. bulbosa* and *S. magnidentata* (no longer in MCS). The five examples of *Exogone* caused two generic and thirteen specific differences, with *E. naidina* being variously identified as *E. dispar*, *E. verugera* and *Spermosyllis sp.*

The ten specimens from the smaller crustacean orders of Tanaidacea, Cumacea and Isopoda produced 79% of the generic differences recorded and 53% of the specific differences. The three tanaids and single isopod caused the most generic differences (nineteen in total). The cumacean, *Diastylis rathkei* was a juvenile specimen and was identified by seventeen laboratories as *D. lucifera*, presumably because of the few spines on its telson (a diagnostic feature for *D. lucifera* but also a feature of all juvenile *Diastylis*). Another cumacean, *Vaunthompsonia cristata* was correctly identified by all participating laboratories.

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 RT10 and RT11 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 RT10 were of molluscs, with approximately 31% of the total number of generic differences and 30% of specific differences being attributable to Mollusca. Polychaeta were responsible for 28% of the total number of generic differences and 25% of specific differences. Crustaceans although only responsible for 14% of total generic differences accounted for 32% of specific differences, mainly due to the alternate identification of *Idotea granulosa* juv. by twenty laboratories at specific level.

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-

four laboratories participating in this exercise, fifteen 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 to date 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 MB05 posed rather different problems to participating laboratories compared to the samples of previous circulations. The extraction of fauna from the sediment was relatively straightforward but time consuming due its fine sandy consistency and high numbers of 'floating' amphipods and 'non-floating' small molluscs. However, many laboratories failed to extract all the countable material. Identification also caused several problems, probably partly due to unfamiliarity with the fauna but mostly due to the presence of recognised problem groups such as Ampeliscidae, Maldanidae and *Bathyporeia.* As a consequence, only four out of the fourteen returning laboratories attained a Bray-Curtis similarity index greater than 90%, however the average Bray-Curtis figure of 85% is slightly higher than that recorded for 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 53% heavier. In one instance (Laboratory 11) the measurement was lighter (-9%). Overall the average difference between the values determined by the participating laboratories Unicomarine Ltd. was 34% (i.e. laboratory measurements were heavier than those made by Unicomarine Ltd.).

It seems likely that the main reason for the observed difference 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 MB05 was +32%, while for MB04 it was +20%. There are likely to be several reasons for the difference between years, though the nature of the fauna in the distributed samples is likely to of particular importance. Sample MB05 had large numbers of crustacea and polychaeta and it has been found that these groups, particularly the former, tend to have much more variation in the weights than mollusca.

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. 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.

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 far better in the OS exercises than in the MB05 exercise. The average value of the index was 94% for the OS, compared with 85% for MB05. The average values of the other individual measures of processing performance (% of taxa extracted and identified, % individuals extracted) were also better than those obtained for the MB05 exercise by up to 32%. 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 MB05 exercise was more than eight 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 the 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.

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 PS10 appeared from an analysis of replicates (Figure 1) to be very uniform and indeed the results from participating laboratories (Figure 3) were quite closely grouped.

The agreement between the PS11 replicates analysed by sieve was also good though there was more scatter in the results from the laser for replicates from the same sample. This sample appeared to pose relatively few problems for the participating laboratories though the curve for a single analysis by sieve was clearly depressed.

Given the obvious difference between the analytical techniques as illustrated in these and earlier PS circulations it is clear 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 three 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.

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 1.0, and in most cases (11 of 15) laboratories had no differences or only a single difference. The situation was similar for identification at the level of species where at most a single difference in identification was recorded (10 of 15 laboratories). The average number of specific differences was 1.6. In the majority of instances identifications made by the participating laboratories were in agreement with those made by Unicomarine Ltd. A single laboratory had a rather larger number of differences (7 of 23 specimens). 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 13 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 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 only the OS and PS exercise have been used in 1997/98 for 'flagging' for the purposes of assessing data for the National 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 90% of the comparisons were considered to have passed the enumeration of taxa standard; 95% exceeded the enumeration of individuals standard and 83% passed the Bray-Curtis comparison standard.

Performance with respect to the biomass standard was much less good however with less than half of the participating laboratories (40%) 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 ten laboratories failed to meet the standard in PS10 (one Fail, nine Deemed Fails) and fifteen laboratories failed to meet the standard in PS11 (two Fail, thirteen Deemed Fails).

5.2 Comparison with results from previous year

A comparison of the 1996/97 and 1997/98 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 two years. For the OS component, there has been a slight increase in the percentage of laboratories achieving a Pass flag (48% to 57%, considering all participants). The situation is reversed for the PS component where a small fall is apparent (96% to 89%). 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 RT10 and RT11 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 four 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 'centralised analysis data'.

Laboratory - LB01

Macrobenthos

No sample returned due to time restraints.

Own Sample

OS05 – One spelling error and one name change. Bray-Curtis similarity index of 100%. Biomass on average 4% heavier than Unicomarine Ltd.
OS06 – Bray-Curtis similarity index of 100%. Biomass on average 25% heavier than Unicomarine Ltd.
OS07 – One individual not picked from residue (*Mytilus edulis* juv.). Bray-Curtis similarity index of 98.67%. Biomass on average 33% heavier than Unicomarine Ltd.

Particle size

PS10 – Centralised analysis data: Size distribution curve slightly elevated compared to majority of laboratories.
PS11 – Centralised analysis data: No major differences in size distribution curve.

Ring Test

RT10 – Three specific differences. Number of AQC identifications in Low group.
RT11 – One generic and five specific differences. Number of AQC identifications in Mid group.

Laboratory Reference

All specimens correctly identified.

Laboratory - LB02

Macrobenthos

Five taxonomic differences (one maldanid and four spionids). Count variance of seven individuals. Three vials contained mixtures of species. Five individuals not picked from residue,

including one previously un-picked taxon (*Mysella bidentata*). Bray-Curtis similarity index of 94.78%. Biomass not comparable due to lower level of precision (3 decimal places).

Own Sample

OS05 – Nematodes not picked from residue (assumed deliberate so therefore ignored in reanalysis). Bray-Curtis similarity index of 100%. Biomass not comparable due to lower level of precision (3 decimal places).
OS06 – One quarter sub-sample analysed. Nematodes not picked from residue (assumed deliberate so therefore ignored in reanalysis). One vial contained a mixture of species. Twenty-nine individuals not picked from sub-sample residue (seventeen were *Abra alba*) including one previously un-picked taxon (Insect larvae). Count variance of twenty-two individuals. Bray-Curtis similarity index of 98.8%. Biomass not comparable due to lower level of precision (3 decimal places).
OS07 – One taxonomic difference (*Abra*). One vial contained a mixture of species. One individual not extracted from residue (*Mangelia brachystoma*). Bray-Curtis similarity index of 98.04%. Biomass not comparable due to lower level of precision (3 decimal places).

Particle size

PS10 – No data received.
PS11 – No data received.

Ring Test

RT10 – One generic and three specific differences. Number of AQC identifications in Low group.
RT11 – One generic and two specific differences. Number of AQC identifications in Low group.

Laboratory Reference

Two generic and two specific differences. One spelling error.

Laboratory - LB03

Macrobenthos

No sample returned.

Own Sample

OS05 – No response to initial sample selection form.
OS06 – No response to initial sample selection form.
OS07 – No response to initial sample selection form.

Particle size

PS10 – No data received.
PS11 – No data received.

Ring Test

RT10 – No results received.
RT11 – No results received.

Laboratory Reference

No specimens received.

Laboratory - LB04

Macrobenthos

Twelve taxonomic differences (mostly maldanids and Ampeliscidae). Six vials contained mixtures of species. Forty-four individuals not picked from residue (including twenty-two *Onoba aculeus*). Count variance of forty individuals. Bray-Curtis similarity index of 84.68%. Biomass on average 52% heavier than Unicomarine Ltd.

Own Sample

OS05 – Not participating in this exercise this year.
OS06 – Not participating in this exercise this year.
OS07 – Not participating in this exercise this year.

Particle size

PS10 – Size distribution curve slightly elevated compared to majority of laboratories.
PS11 – No data received.

Ring Test

RT10 – Three generic and four specific differences. Number of AQC identifications in Low group.
RT11 – Two generic and seven specific differences. Number of AQC identifications in High group.

Laboratory Reference

One generic and one specific difference (cirratulid worm). One name change.

Laboratory - LB05

Macrobenthos

No sample returned.

Own Sample

OS05 – Two vials contained mixtures of species. Four taxonomic differences (spionids, cirratulids and lumbrinerids). No individuals missed during faunal extraction. Low numbers of individuals and taxa, therefore only a Bray-Curtis similarity index of 60% achieved. No biomass data supplied.
OS06 – Two taxonomic differences (molluscs: *Spisula* and *Nucula*). Two individuals not picked from residue including one previously un-picked taxon. Low numbers of individuals and taxa, therefore only a Bray-Curtis similarity index of 62.5% achieved. No biomass data supplied.
OS07 – Two vials contained mixtures of species. Bryozoans not extracted or identified (assumed deliberate so therefore ignored in reanalysis). Seven taxonomic differences. Ten individuals not picked from the residue including one previously un-picked taxon (*Goodallia triangularis*). Count variance of one individual. Bray-Curtis similarity index of 83.82%. No biomass data supplied.

Particle size

PS10 – No data received.
PS11 – No data received.

Ring Test

RT10 – No results received.
RT11 – No results received.

Laboratory Reference

No specimens received.

Laboratory - LB06

Macrobenthos

Ten taxonomic differences. Count variance of eighty-two individuals (PL enumeration of *Ampelisca tenuicornis* was 77 individuals higher than Unicomarine Ltd.). Three vials contained mixtures of species. Eighteen individuals not picked from residue (mostly *Crenella decussata* and *Onoba aculeus*). Bray-Curtis similarity index of 83.23%. Biomass on average 28% heavier than Unicomarine Ltd.

Own Sample

OS05 – Bray-Curtis similarity index of 100%. Biomass on average 48% heavier than Unicomarine Ltd.
OS06 – Count variance of one individual (Unicomarine Ltd. counted one extra *Pygospio elegans*). Bray-Curtis similarity index of 99.31%. Biomass on average 43% heavier than Unicomarine Ltd.
OS07 – Count variance of three individuals (Unicomarine Ltd. counted three less *Bathyporeia pilosa*). Bray-Curtis similarity index of 99.75%. Biomass on average 13% heavier than Unicomarine Ltd.

Particle size

PS10 – Centralised analysis data: Size distribution curve slightly elevated compared to majority of laboratories.
PS11 – Centralised analysis data: No major differences in size distribution curve.

Ring Test

RT10 – Three generic and seven specific differences. Number of AQC identifications in Mid group.
RT11 – Two generic and seven specific differences. Number of AQC identifications in High group.

Laboratory Reference

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

Laboratory - LB07

Macrobenthos

Maldanidae tails counted by PL; heads counted by Unicomarine Ltd. Six taxonomic differences. Count variance of twenty-eight individuals (this is influenced in some respect by the maldanid enumeration). One vial contained a mixture of species. Five individuals not picked from residue including two previously un-picked taxa (Nematoda and *Mytilus edulis* juv.). Bray-Curtis similarity index of 90.24%. No biomass data supplied.

Own Sample

OS05 – Taxa not split (reasons given). Five taxonomic differences (four mollusca and one cirratulid). Six individuals not picked from residue. Bray-Curtis similarity index of 95.75%. No biomass data supplied.
OS06 – Taxa not split (reasons given). Count variance of four individuals. Three individuals not picked from residue including one previously un-picked taxon (*Spiophanes bombyx*). Bray-Curtis similarity index of 92.56%. No biomass data supplied.
OS07 – Taxa not split (reasons given). One taxonomic difference (*Retusa umbilicata*). Count variance of two individuals. Seven individuals not picked from residue including four previously

un-picked taxa (*Pholoe minuta*, *Harpinia crenulata*, *Epitonium trevelyanum* and *Arctica islandica* juv.). Bray-Curtis similarity index of 96.37%. No biomass data supplied.

Particle size

PS10 – Distribution curve depressed compared to majority of laboratories, though similar to that resulting from analysis of replicates samples.
PS11 – No major differences in size distribution curve.

Ring Test

RT10 – Two generic and five specific differences. Number of AQC identifications in Mid group.
RT11 – Two specific differences. Number of AQC identifications in Low group.

Laboratory Reference

No specimens received.

Laboratory - LB08

Macrobenthos

Seven taxonomic differences. Count variance of one individual. One vial contained a mixture of species. Thirty-two individuals not picked from residue including four previously un-picked taxa (Nematoda, *Modiolus sp.* juv., *Retusa obtusata* and *Arenicola sp.* juv.). Bray-Curtis similarity index of 87.05%. Biomass on average 53% heavier than Unicomarine Ltd.

Own Sample

OS05 – No response to initial sample selection form.
OS06 – No response to initial sample selection form.
OS07 – No response to initial sample selection form.

Particle size

PS10 – No data received.
PS11 – No data received.

Ring Test

RT10 – Four specific differences. Number of AQC identifications in Low group.
RT11 – One generic and four specific differences. Number of AQC identifications in Mid group.

Laboratory Reference

No specimens received.

Laboratory - LB09

Macrobenthos

Not participating in this exercise.

Own Sample

Not participating in this exercise.

Particle size

PS10 – Not participating in this exercise.
PS11 – Not participating in this exercise.

Ring Test

RT10 – One generic and four specific differences. Number of AQC identifications in Low group.
RT11 – Three generic and five specific differences. Number of AQC identifications in Mid group.

Laboratory Reference

Not participating in this exercise.

Laboratory - LB10

Macrobenthos

Eight taxonomic differences. Count variance of nine individuals. One vial contained a mixture of species. Ninety individuals not picked from residue (approximately half were *Crenella decussata* and *Onoba aculeus*) including six previously un-picked taxa (*Anoplodactylus petiolatus*, *Cumella pygmaea*, *Abra alba*, Nematoda, *Rissoella globularis* and *Gibbula cineraria*). Bray-Curtis similarity index of 89.91%. Biomass on average 53% heavier than Unicomarine Ltd.

Own Sample

OS05 – Two vials contained mixtures of species. Sixty-three individuals not picked from residue (57 were *Hydrobia ulvae*) including two previously un-picked taxa (*Mediomastus fragilis* and *Mytilus edulis* juv.). Bray-Curtis similarity index of 75.29%. Biomass on average 56% heavier than Unicomarine Ltd.
OS06 – Three taxonomic differences. Count variance of one individual. Two vials contained mixtures of species. Eight individuals not picked from residue including two previously un-picked taxa (*Harpinia crenulata* and *Hiatella arctica*). Bray-Curtis similarity index of 95.44%. Biomass on average 30% heavier than Unicomarine Ltd.
OS07 – Eleven taxonomic differences. Count variance of twenty-seven individuals, fifteen countable individuals found within 'Polychaete fragments' vial. Five vials contained mixtures of species. Twenty-one individuals not picked from residue including two previously un-picked taxa (Rissoidae and *Pholoe minuta*). Bray-Curtis similarity index of 74.89%. Biomass on average 19% heavier than Unicomarine Ltd.

Particle size

PS10 – No major differences in size distribution curve.
PS11 – No major differences in size distribution curve.

Ring Test

RT10 – Three generic and seven specific differences. Number of AQC identifications in Mid group.
RT11 – One generic and three specific differences. Number of AQC identifications in Low group.

Laboratory Reference

All specimens correctly identified.

Laboratory - LB11

Macrobenthos

Sixteen taxonomic differences (seven involving molluscs). Count variance of seven individuals. Seven vials contained mixtures of species. Nineteen individuals not picked from residue (including seventeen molluscs) including two previously un-picked taxa (*Tanaopsis graciloides* and *Mytilus edulis* juv.). Bray-Curtis similarity index of 88.77%. Biomass on average 9% lighter than Unicomarine Ltd.

Own Sample

OS05 – One taxonomic difference (*Bathyporeia sarsi*). Count variance of one individual. One vial contained a mixture of species. Bray-Curtis similarity index of 96.64%. One specimen was not found, its vial was received without a lid. Some specimens were in poor condition, probably due to over drying during biomass determination. Biomass on average 10% lighter than Unicomarine Ltd.
OS06 – Count variance of one individual (*Nephtys hombergii* found by Unicomarine Ltd. to be headless). One specimen not found, its vial was received without a lid. Bray-Curtis similarity index of 96.55%. Biomass on average 19% lighter than Unicomarine Ltd.
OS07 – Count variance of two individuals. Two individuals not picked from residue from a previously un-picked taxa (*Mytilus edulis* juv.). Bray-Curtis similarity index of 91.89%. Biomass on average 18% lighter than Unicomarine Ltd.

Particle size

PS10 – No major differences in size distribution curve.
PS11 – No major differences in size distribution curve.

Ring Test

RT10 – Three generic and four specific differences. Number of AQC identifications in Low group.
RT11 – Three specific differences. Number of AQC identifications in Low group.

Laboratory Reference

All specimens correctly identified. One name change.

Laboratory - LB12

Macrobenthos

No sample returned.

Own Sample

OS05 – Selected sample not received.
OS06 – Selected sample not received.
OS07 – Selected sample not received.

Particle size

PS10 – Centralised analysis data: Size distribution curve slightly elevated compared to majority of laboratories.
PS11 – Centralised analysis data: No major differences in size distribution curve.

Ring Test

RT10 – Nine generic and sixteen specific differences. Number of AQC identifications in High group.
RT11 – Four generic and seven specific differences. Number of AQC identifications in High group.

Laboratory Reference

Three generic and three specific differences. Three spelling errors. One name change.

Laboratory - LB13

Macrobenthos

Six taxonomic differences. Count variance of one individual. Five individuals not picked from residue (one *Ampelisca* and four molluscs) including one previously un-picked taxon (*Mytilus*

edulis juv.). Bray-Curtis similarity index of 89.13%. Biomass on average 52% heavier than Unicomarine Ltd.

Own Sample

OS05 – Count variance of one individual (*Tubificoides amplivasatus* found within *Phoronis muelleri* vial). Bray-Curtis similarity index of 98.88%. Biomass on average 60% heavier than Unicomarine Ltd.
OS06 – Only one individual in whole sample. Bray-Curtis similarity index of 100%. Biomass on average 67% heavier than Unicomarine Ltd.
OS07 – Sample comprised two Oligochaetes (two taxa). Bray-Curtis similarity index of 100%. Biomass on average 167% lighter than Unicomarine Ltd.

Particle size

PS10 – Distribution curve depressed compared to majority of laboratories, though similar to that resulting from analysis of replicates samples.
PS11 – Size distribution curve depressed relative to other laboratories .

Ring Test

RT10 – One generic and four specific differences. Number of AQC identifications in Low group.
RT11 – One generic and four specific differences. Number of AQC identifications in Mid group.

Laboratory Reference

One generic and two specific differences. Three name changes.

Laboratory - LB14

Macrobenthos

Ten taxonomic differences. Count variance of five individuals. Four vials contained mixtures of species. Fifteen individuals not picked from residue. Bray-Curtis similarity index of 80.91%. Biomass on average 17% heavier than Unicomarine Ltd.

Own Sample

OS05 – Count variance of six individuals (Unicomarine Ltd. counted six extra *Hydrobia ulvae*). One individual not picked from residue (*Hydrobia ulvae*). Bray-Curtis similarity index of 99.45%.Biomass on average 5% heavier than Unicomarine Ltd.
OS06 – One vial contained a mixture of species. Two taxonomic differences (*Ophiura sp.* juv. and *Euspira catena* juv.). *Bathyporeia* found to be headless by Unicomarine Ltd. Count variance of one individual. Bray-Curtis similarity index of 99.03%. Biomass on average 2% heavier than Unicomarine Ltd.
OS07 – One taxonomic difference (*Chaetozone setosa* agg.). Count variance of six individuals. Two vials contained mixtures of species. Bray-Curtis similarity index of 95.72%. Biomass on average 17% heavier than Unicomarine Ltd.

Particle size

PS10 – No major differences in size distribution curve.
PS11 – No major differences in size distribution curve.

Ring Test

RT10 – Four generic and six specific differences. Number of AQC identifications in Mid group.
RT11 – Two generic and six specific differences. Number of AQC identifications in Mid group.

Laboratory Reference

One generic and one specific difference.

Laboratory - LB15

Macrobenthos

No sample returned.

Own Sample

OS05 – Seven taxonomic differences. Count variance of ten individuals. Two vials contained a mixture of species. Five individuals not picked from residue including two previously un-picked taxa (*Arctica islandica* juv. and *Mangelia nebula*). Bray-Curtis similarity index of 89.9%. Biomass on average 37% heavier than Unicomarine Ltd.
OS06 – Sample received; awaiting data.
OS07 – Selected sample not received.

Particle size

PS10 – No major differences in size distribution curve.
PS11 – No data received.

Ring Test

RT10 – No results received.
RT11 – No results received.

Laboratory Reference

No specimens received.

Laboratory - LB16

Macrobenthos

Five taxonomic differences. Count variance of seven individuals. Three vials contained a mixture of species. Twenty-four individuals not picked from residue including one previously un-picked taxon (*Onoba aculeus*). Bray-Curtis similarity index of 93.92%. No biomass data supplied.

Own Sample

OS05 – Selected sample not received.
OS06 – Selected sample not received.
OS07 – Selected sample not received.

Particle size

PS10 – No data received.
PS11 – No data received.

Ring Test

RT10 – One generic and five specific differences. Number of AQC identifications in Mid group.
RT11 – Six generic and eight specific differences. Number of AQC identifications in High group.

Laboratory Reference

One generic and one specific difference.

Laboratory - LB17

Macrobenthos

Four taxonomic differences (notably *Aricidea*, with approximately sixty individuals). Count variance of one individual. Seven vials contained mixtures of species. Sixteen individuals not picked from the residue (all molluscs) including two previously un-picked taxa (*Retusa obtusata* and *Modiolus sp.* juv.). Bray-Curtis similarity index of 71.54%. Biomass on average 22% heavier than Unicomarine Ltd.

Own Sample

OS05 – Half of vials received were labelled incorrectly. Count variance of two individuals. Bray-Curtis similarity index of 96.43%. Biomass on average 10% heavier than Unicomarine Ltd.
OS06 – Two taxonomic differences (one generic and one specific). Count variance of six individuals. Two vials contained a mixture of species. Bray-Curtis similarity index of 94.64%. Biomass on average 39% heavier than Unicomarine Ltd.
OS07 – Four taxonomic differences (notably *Chamelea gallina* with thirty individuals). Count variance of eight individuals. Two vials contained a mixture of species. Bray-Curtis similarity index of 74.34%. Biomass on average 13% heavier than Unicomarine Ltd.

Particle size

PS10 – No major differences in size distribution curve.
PS11 – No major differences in size distribution curve.

Ring Test

RT10 – Four generic and eight specific differences. Number of AQC identifications in High group.
RT11 – One generic and four specific differences. Number of AQC identifications in Mid group.

Laboratory Reference

One generic and one specific difference. One name change.

Laboratory - LB18

Macrobenthos

No sample returned.

Own Sample

OS05 – Sample contained only two individuals of the same species. Bray-Curtis similarity index of 100%. Biomass on average 17% heavier than Unicomarine Ltd.
OS06 – Sample contained only five individuals and three taxa. Bray-Curtis similarity index of 100%. Biomass on average 47% heavier than Unicomarine Ltd.
OS07 – One taxonomic difference (*Mysella bidentata*). Count variance of one individual. One individual not picked from residue (*Chaetozone setosa* agg.). Bray-Curtis similarity index of 94.74%. Biomass on average 36% heavier than Unicomarine Ltd.

Particle size

PS10 – No major differences in size distribution curve.
PS11 – No data received.

Ring Test

RT10 – Four specific differences. Number of AQC identifications in Low group.
RT11 – Two generic and four specific differences. Number of AQC identifications in Mid group.

Laboratory Reference

One specific difference.

Laboratory - LB19

Macrobenthos

Not participating in this exercise.

Own Sample

OS05 – Not participating in this exercise.
OS06 – Not participating in this exercise.
OS07 – Not participating in this exercise.

Particle size

PS10 – Not participating in this exercise.
PS11 – Not participating in this exercise.

Ring Test

RT10 – Three generic and six specific differences. Number of AQC identifications in Mid group.
RT11 – One generic and two specific differences. Number of AQC identifications in Low group.

Laboratory Reference

Not participating in this exercise.

Laboratory - LB20

Macrobenthos

Eleven taxonomic errors (notably *Urothoe*, with ninety individuals). Count variance of seven individuals. Seven vials contained mixtures of species. Seventy-one individuals not picked from residue (forty-eight being crustaceans) including four previously un-picked taxa (*Ophryotrocha sp.*, *Modiolus sp.* juv, *Nucula nucleus* and *Retusa obtusata*). Bray-Curtis similarity index of 77.18%. Biomass on average 46% heavier than Unicomarine Ltd.

Own Sample

OS05 – Taxa not split. One vial contained a mixture of species. Oligochaetes only identified to family level. Three individuals not picked from residue including one previously un-picked taxon (*Mytilus edulis* juv.). Bray-Curtis similarity index of 98.31%. No biomass data supplied.
OS06 – Sample contained just four taxa. Bray-Curtis similarity index of 100%. No biomass data supplied.
OS07 – Count variance of one individual. Bray-Curtis similarity index of 97.56%. No biomass data supplied.

Particle size

PS10 – Size distribution curve slightly elevated compared to majority of laboratories.
PS11 – No major differences in size distribution curve.

Ring Test

RT10 – Four generic and nine specific differences. Number of AQC identifications in High group.
RT11 – One generic and eight specific differences. Number of AQC identifications in High group.

Laboratory Reference

One generic and one specific difference. One name change.

Laboratory - LB21

Macrobenthos

No sample returned.

Own Sample

OS05 – No response to initial sample selection form.
OS06 – No response to initial sample selection form.
OS07 – No response to initial sample selection form.

Particle size

PS10 – No data received.
PS11 – No data received.

Ring Test

RT10 – No results received.
RT11 – No results received.

Laboratory Reference

No specimens received.

Laboratory - LB22

Macrobenthos

Five taxonomic differences. Count variance of twelve individuals. Three vials contained mixtures of species. Seven individuals not picked from residue including two previously un-picked taxa (*Onoba aculeus* and *Modiolus sp.* juv.). Bray-Curtis similarity index of 91.38%. Biomass on average 6% heavier than Unicomarine Ltd.

Own Sample

OS05 – Not participating in this exercise this year; no suitable samples.
OS06 – Not participating in this exercise this year; no suitable samples.
OS07 – Not participating in this exercise this year; no suitable samples.

Particle size

PS10 – No data received.
PS11 – No major differences in size distribution curve.

Ring Test

RT10 – Three generic and six specific differences. Number of AQC identifications in Mid group.
RT11 – Two specific differences. Number of AQC identifications in Low group.

Laboratory Reference

One specific error.

Laboratory - LB23

Macrobenthos

No sample returned.

Own Sample

OS05 – Two taxonomic differences (*Polydora caeca?* and *Potamopyrgus antipodarum)*. Bray-Curtis similarity index of 99.68%. Biomass not comparable due to lower level of precision (3 decimal places).
OS06 – Count variance of one individual. One individual not picked from residue (*Heterochaeta costata*). Bray-Curtis similarity index of 99.87%. Biomass not comparable due to lower level of precision (3 decimal places).
OS07 – Two taxonomic differences (*Abra alba* and *Bathyporeia elegans*). Count variance of two individuals. One vial contained a mixture of species. Four individuals not picked from residue (*Mysella bidentata*). Bray-Curtis similarity index of 90.2%. Biomass not comparable due to lower level of precision (3 decimal places).

Particle size

PS10 – No data received.
PS11 – No data received.

Ring Test

RT10 – Six generic and nine specific differences. Number of AQC identifications in High group.
RT11 – No results received.

Laboratory Reference

No specimens received.

Laboratory - LB24

Macrobenthos

No residue supplied for re-analysis. Fifteen taxonomic differences (notably maldanids and amphipods). Count variance of four individuals. Eight vials contained mixtures of species. Bray-Curtis similarity index of 71.5%. Biomass on average 36% heavier than Unicomarine Ltd.

Own Sample

OS05 – No response to initial sample selection form.
OS06 – No response to initial sample selection form.
OS07 – No response to initial sample selection form.

Particle size

PS10 – No data received.
PS11 – No data received.

Ring Test

RT10 – Five generic and ten specific differences. Number of AQC identifications in High group.
RT11 – Four generic and twelve specific differences. Number of AQC identifications in High group.

Laboratory Reference

No specimens received.

Laboratory - LB25

Macrobenthos

No sample returned.

Own Sample

OS05 – Not participating in this exercise this year.
OS06 – Not participating in this exercise this year.
OS07 – Not participating in this exercise this year.

Particle size

PS10 – No major differences in size distribution curve.
PS11 – No data received.

Ring Test

RT10 – Four generic and nine specific differences. Number of AQC identifications in High group.
RT11 – No results received.

Laboratory Reference

Two generic and seven specific differences. Five name changes.

Laboratory - LB26

Macrobenthos

No sample returned.

Own Sample

OS05 – Not participating in this exercise; no 'normal' sampling programme.
OS06 – Not participating in this exercise; no 'normal' sampling programme.
OS07 – Not participating in this exercise; no 'normal' sampling programme.

Particle size

PS10 – Size distribution curve slightly elevated compared to majority of laboratories.
PS11 – No data received.

Ring Test

RT10 – Four generic and six specific differences. Number of AQC identifications in Mid group.
RT11 – No results received.

Laboratory Reference

No specimens received.

Laboratory - LB27

Macrobenthos

Not participating in this exercise.

Own Sample

OS05 – Not participating in this exercise.
OS06 – Not participating in this exercise.
OS07 – Not participating in this exercise.

Particle size

PS10 – Size distribution curve slightly elevated compared to majority of laboratories.
PS11 – No major differences in size distribution curve.

Ring Test

RT10 – Not participating in this exercise.
RT11 – 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. The recent introduction of e-mail as an option for correspondence facilitates data transfer and its use is strongly recommended where practicable.
2. Laboratories involved in NMP 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.
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 NMP biomass data. Biomass procedures should not render the specimens indistinguishable.
4. There is still considerable variation in the format used to submit results for the PS exercises. This will need to be addressed to improve analysis of this component of the Scheme.
5. Clear differences in the results obtained by different analytical methods make it essential that the technique employed (*eg.* 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.
6. 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.
7. Some of the problems with identification included certain Amphipoda, these are to be the subject of a targeted RT. Other groups under consideration are Mollusca, and Spionidae.
8. There are still some serious problems of individuals and taxa missed at the sorting stage. However, the figures for these sorting errors are lower than in previous years exercises. In the MB exercise up to 6 taxa (9% of the actual total taxa in the sample) were not extracted. All laboratories missed individuals in the residue. In the worst instance 90 individuals (9% of total individuals in the sample) were not extracted from the residue. The situation was slightly worse, but still improved upon last years results, for some of the OS samples where a maximum of 4 taxa (11% of total) were not extracted. In the worst instance 63 individuals were not picked from the residue (39% of total). On average for the OS exercise, only 0.45 taxa were not extracted compared with 1.39 taxa from last years data. Enumeration of 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 (*eg.* 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.

9. 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 mis-interpreting a low index in terms of quality of service.

10. Protocols should be developed to standardise the approach to headless and partial specimens. MB05 illustrated that for Maldanidae there are problems with enumeration due to each laboratories 'normal' working methods of either counting heads or tails. This may influence enumeration and biomass estimations.

12. Implementation of an improved learning structure to the scheme through detailed individual exercise reports. For the LR, OS and MB future exercises, detailed results to be forwarded to each laboratory as soon as practicable, such as is done for RT exercises. After each RT exercise a bulletin should be 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).

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 MB05 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	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB02	44	46	-2	4.3	492	504	-12	2.4	1	5	1.0	-7	94.78	5
LB03	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB04	46	50	-4	8.0	608	692	-84	12.1	0	44	6.4	-40	84.68	12
LB05	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB06	67	66	1	1.5	655	591	64	9.8	0	18	3.0	82	83.23	10
LB07	51	49	2	3.9	570	547	23	4.0	2	5	0.9	28	90.24	6
LB08	49	50	-1	2.0	552	585	-33	5.6	4	32	5.5	-1	87.05	7
LB09	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB10	64	69	-5	7.2	876	957	-81	8.5	6	90	9.4	9	89.91	8
LB11	63	68	-5	7.4	1011	1037	-26	2.5	2	19	1.8	-7	88.77	16
LB12	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB13	57	56	1	1.8	685	689	-4	0.6	1	5	0.7	1	89.13	6
LB14	52	53	-1	1.9	744	754	-10	1.3	0	15	2.0	5	80.91	10
LB15	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB16	51	47	4	7.8	442	459	-17	3.7	1	24	5.2	7	93.92	5
LB17	29	37	-8	21.6	328	343	-15	4.4	2	16	4.7	1	71.54	4
LB18	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB19	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB20	49	57	-8	14.0	761	825	-64	7.8	4	71	8.6	7	77.18	11
LB21	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB22	59	60	-1	1.7	502	497	5	1.0	2	7	1.4	12	91.38	5
LB23	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB24	40	44	-4	9.1	529	533	-4	0.8	-	-	-	-	71.50	15
LB25	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB26	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LB27	-	-	-	-	-	-	-	-	-	-	-	-	-	-

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 MB05.

LabCode		Polychaeta	Oligochaeta	Crustacea	Echinodermata	Mollusca	Other	Overall
LB01	UM count	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-
LB02	UM count	172	0	263	0	16	53	504
	PL missed	3	0	1	0	1	0	5
	%missed	1.7	-	0.4	-	6.3	0.0	1.0
LB03	UM count	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-
LB04	UM count	95	0	539	0	51	7	692
	PL missed	6	0	12	0	26	0	44
	%missed	6.3	-	2.2	-	51.0	0.0	6.4
LB05	UM count	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-
LB06	UM count	243	3	287	0	54	4	591
	PL missed	2	0	0	0	16	0	18
	%missed	0.8	0.0	0.0	-	29.6	0.0	3.0
LB07	UM count	262	1	271	1	11	1	547
	PL missed	3	0	0	0	1	1	5
	%missed	1.1	0.0	0.0	0.0	9.1	100.0	0.9
LB08	UM count	142	1	408	1	29	4	585
	PL missed	10	0	6	0	15	1	32
	%missed	7.0	0.0	1.5	0.0	51.7	25.0	5.5
LB09	UM count	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-
LB10	UM count	333	1	514	1	89	19	957
	PL missed	24	0	8	0	46	12	90
	%missed	7.2	0.0	1.6	0.0	51.7	63.2	9.4
LB11	UM count	507	1	429	0	99	1	1037
	PL missed	1	0	2	0	16	0	19
	%missed	0.2	0.0	0.5	-	16.2	0.0	1.8
LB12	UM count	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-
LB13	UM count	209	0	428	2	47	3	689
	PL missed	0	0	1	0	4	0	5
	%missed	0.0	-	0.2	0.0	8.5	0.0	0.7
LB14	UM count	217	0	436	1	77	23	754
	PL missed	9	0	4	0	1	1	15
	%missed	4.1	-	0.9	0.0	1.3	4.3	2.0

Table 2. Comparison of the efficiency of extraction of fauna by the participating laboratories for the major taxonomic groups present in sample MB05.

LabCode		Polychaeta	Oligochaeta	Crustacea	Echinodermata	Mollusca	Other	Overall
LB15	UM count	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-
LB16	UM count	114	0	311	1	29	4	459
	PL missed	1	0	10	0	13	0	24
	%missed	0.9	-	3.2	0.0	44.8	0.0	5.2
LB17	UM count	187	0	98	5	50	3	343
	PL missed	0	0	0	0	16	0	16
	%missed	0.0	-	0.0	0.0	32.0	0.0	4.7
LB18	UM count	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-
LB19	UM count	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-
LB20	UM count	199	0	586	0	35	5	825
	PL missed	12	0	48	0	11	0	71
	%missed	6.0	-	8.2	-	31.4	0.0	8.6
LB21	UM count	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-
LB22	UM count	205	0	264	2	21	5	497
	PL missed	0	0	2	0	5	0	7
	%missed	0.0	-	0.8	0.0	23.8	0.0	1.4
LB23	UM count	-	-	-	-	-	-	0
	PL missed	-	-	-	-	-	-	0
	%missed	-	-	-	-	-	-	-
LB24	UM count	207	0	315	0	8	3	533
	PL missed	n/a	n/a	n/a	n/a	n/a	n/a	0
	%missed	n/a	n/a	n/a	n/a	n/a	n/a	0.0
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 MB05. Values are in grams (g).

LabCode		Nemertea	Polychaeta	Oligochaeta	Crustacea	Echinodermata	Mollusca	Other	Overall
LB01	PL	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-
LB02	PL	0	0.887	0	0.505	0	0.102	0.041	1.535
	UM	0	0.458	0	0.192	0	0.079	0.025	0.754
	%diff.	-	48.4	-	62.0	-	22.5	39.0	50.9
LB03	PL	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-
LB04	PL	0.0098	0.58776	0	1.0509	0	0.0799	0.0002	1.72856
	UM	0.005	0.334	0	0.423	0	0.074	0.0002	0.8362
	%diff.	49.0	43.2	-	59.7	-	7.4	0.0	51.6
LB05	PL	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-
LB06	PL	1.608	0.983	0.0001	0.307	0	0.21	0.0438	3.1519
	UM	1.2686	0.6288	0.0001	0.1739	0	0.1846	0.0201	2.2761
	%diff.	21.1	36.0	0.0	43.4	-	12.1	54.1	27.8
LB07	PL	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-
LB08	PL	0.0006	0.1904	0.0005	0.7273	0.008	0.1825	0.0334	1.1427
	UM	0.0004	0.1277	0.0004	0.189	0.005	0.1775	0.0318	0.5318
	%diff.	33.3	32.9	20.0	74.0	37.5	2.7	4.8	53.5
LB09	PL	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-
LB10	PL	0.0448	0.4371	0.0003	1.1098	0.1771	0.2777	0.0016	2.0484
	UM	0.016	0.1829	0.0001	0.4157	0.1011	0.2526	0.0007	0.9691
	%diff.	64.3	58.2	66.7	62.5	42.9	9.0	56.3	52.7
LB11	PL	0	0.397	0.0003	0.1645	0	9.4787	0.0001	10.0406
	UM	0	0.3747	0.0002	0.2966	0	10.266	0.0004	10.9379
	%diff.	-	5.6	33.3	-80.3	-	-8.3	-300.0	-8.9
LB12	PL	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-
LB13	PL	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-
LB14	PL	0	0.202	0	0.342	0.0002	0.836	0.001	1.3812
	UM	0	0.168	0	0.2687	0.0002	0.705	0.0006	1.1425
	%diff.	-	16.8	-	21.4	0.0	15.7	40.0	17.3

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 MB05. Values are in grams (g).

LabCode		Nemertea	Polychaeta	Oligochaeta	Crustacea	Echinodermata	Mollusca	Other	Overall
LB15	PL	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-
LB16	PL	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-
LB17	PL	0	0.6911	0	0.0528	0.0743	0.2782	0	1.0964
	UM	0	0.4802	0	0.0437	0.064	0.2726	0	0.8605
	%diff.	-	30.5	-	17.2	13.9	2.0	-	21.5
LB18	PL	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-
LB19	PL	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-
LB20	PL	0.0103	1.2564	0	0.9124	0	0.5747	0.0004	2.7542
	UM	0.0062	0.668	0	0.3544	0	0.4608	0.0002	1.4896
	%diff.	39.8	46.8	-	61.2	-	19.8	50.0	45.9
LB21	PL	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-
LB22	PL	0	0.2631	0	0.2339	0.0009	7.7762	0.0004	8.2745
	UM	0	0.1908	0	0.1367	0.0011	7.4415	0.0005	7.7706
	%diff.	-	27.5	-	41.6	-22.2	4.3	-25.0	6.1
LB23	PL	-	-	-	-	-	-	-	0
	UM	-	-	-	-	-	-	-	0
	%diff.	-	-	-	-	-	-	-	-
LB24	PL	0.0032	1.3186	0	0.2326	0	0.5918	0	2.1462
	UM	0.0026	0.7991	0	0.1506	0	0.4131	0	1.3654
	%diff.	18.8	39.4	-	35.3	-	30.2	-	36.4
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 (OS05 to OS07) 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_OS05	20	20	0	0.0	156	156	0	0.0	0	0	0.0	0	100.00	0	
LB01_OS06	11	11	0	0.0	63	63	0	0.0	0	0	0.0	0	100.00	0	
LB01_OS07	8	8	0	0.0	37	38	-1	2.6	0	1	2.6	0	98.67	0	
LB02_OS05	5	5	0	0.0	26	26	0	0.0	0	0	0.0	0	100.00	0	
LB02_OS06	20	21	1	4.8	789	796	-7	0.9	1	29	3.6	22	98.80	0	
LB02_OS07	34	35	1	2.9	76	77	-1	1.3	0	1	1.3	0	98.04	1	
LB03_OS05	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB03_OS06	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB03_OS07	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB04_OS05	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB04_OS06	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB04_OS07	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB05_OS05	12	14	2	14.3	50	50	0	0.0	0	0	0.0	0	60.00	4	
LB05_OS06	6	7	1	14.3	7	9	-2	22.2	1	2	22.2	0	62.50	2	
LB05_OS07	45	47	2	4.3	113	124	-11	8.9	1	10	8.1	-1	83.82	7	
LB06_OS05	2	2	0	0.0	3	3	0	0.0	0	0	0.0	0	100.00	0	
LB06_OS06	5	5	0	0.0	72	73	-1	1.4	0	0	0.0	-1	99.31	0	
LB06_OS07	7	7	0	0.0	603	606	-3	0.5	0	0	0.0	-3	99.75	0	
LB07_OS05	59	58	1	1.7	608	614	-6	1.0	0	6	1.0	0	95.75	5	Taxa not split
LB07_OS06	32	29	3	9.4	155	154	1	0.6	1	3	1.9	4	92.56	0	Taxa not split
LB07_OS07	31	35	4	11.4	147	156	-9	5.8	4	7	4.5	-2	96.37	1	Taxa not split
LB08_OS05	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB08_OS06	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB08_OS07	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB09															not participating in this component

Table 4. Results from the analysis of Own Samples (OS05 to OS07) 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
LB10_OS05	5	9	4	44.4	96	159	-63	39.6	2	63	39.6	0	75.29	0	
LB10_OS06	35	38	3	7.9	183	190	-7	3.7	2	8	4.2	1	95.44	3	
LB10_OS07	40	46	6	13.0	211	259	-48	18.5	2	21	8.1	-27	74.89	11	Taxa & individuals in fragments vial
LB11_OS05	8	8	0	0.0	75	74	1	1.3	0	0	0.0	1	96.64	1	
LB11_OS06	9	8	1	11.1	15	14	1	6.7	0	0	0.0	1	96.55	0	
LB11_OS07	11	12	1	8.3	37	37	0	0.0	1	2	5.4	2	91.89	0	
LB12_OS05	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB12_OS06	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB12_OS07	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB13_OS05	13	13	0	0.0	43	44	-1	2.3	0	0	0.0	-1	98.88	0	
LB13_OS06	1	1	0	0.0	1	1	0	0.0	0	0	0.0	0	100.00	0	
LB13_OS07	2	2	0	0.0	2	2	0	0.0	0	0	0.0	0	100.00	0	
LB14_OS05	5	5	0	0.0	635	642	-7	1.1	0	1	0.2	-6	99.45	0	
LB14_OS06	29	28	1	3.4	258	257	1	0.4	0	0	0.0	1	99.03	2	
LB14_OS07	43	43	0	0.0	611	605	6	1.0	0	0	0.0	6	95.72	1	
LB15_OS05	43	47	4	8.5	156	151	5	3.2	2	5	3.3	10	89.90	7	Some specimens missing
LB15_OS06	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB15_OS07	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB16_OS05	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB16_OS06	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB16_OS07	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB17_OS05	13	13	0	0.0	56	54	2	3.6	0	0	0.0	2	96.43	0	
LB17_OS06	18	18	0	0.0	501	507	-6	1.2	0	0	0.0	-6	94.64	2	
LB17_OS07	34	35	1	2.9	156	148	8	5.1	0	0	0.0	8	74.34	4	
LB18_OS05	1	1	0	0.0	2	2	0	0.0	0	0	0.0	0	100.00	0	
LB18_OS06	3	3	0	0.0	5	5	0	0.0	0	0	0.0	0	100.00	0	
LB18_OS07	15	15	0	0.0	38	38	0	0.0	0	1	2.6	1	94.74	1	

Table 4. Results from the analysis of Own Samples (OS05 to OS07) 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
LB19															not participating in this component
LB20_OS05	8	10	2	20.0	87	90	-3	3.3	1	3	3.3	0	98.31	0	Taxa not split, Oligochaete identification to family
LB20_OS06	4	4	0	0.0	12	12	0	0.0	0	0	0.0	0	100.00	0	
LB20_OS07	8	8	0	0.0	20	21	-1	4.8	0	0	0.0	-1	97.56	0	Taxa not split
LB21_OS05	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB21_OS06	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB21_OS07	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB22															not participating in this component
LB23_OS05	14	14	0	0.0	1253	1253	0	0.0	0	0	0.0	0	99.68	2	
LB23_OS06	10	10	0	0.0	763	763	0	0.0	0	1	0.1	1	99.87	0	
LB23_OS07	13	14	1	7.1	101	103	-2	1.9	0	4	3.9	2	90.20	2	
LB24_OS05	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB24_OS06	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB24_OS07	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
LB25															not participating in this component
LB26															not participating in this component
LB27															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 OS05-OS07.

		Sample OS05								
LabCode		Nemertea	Polychaeta	Oligochaeta	Pycnogonida	Crustacea	Echinodermata	Mollusca	Other	Overall
LB01	PL	0.0093	0.6991	0.0000	0.0000	0.1531	0.0000	4.8483	0.0000	5.7098
	UM	0.0054	0.4628	0.0000	0.0000	0.1046	0.0000	4.8854	0.0000	5.4582
	%diff.	41.9	33.8	-	-	31.7	-	-0.8	-	4.4
LB02	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB03	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB04	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB05	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB06	PL	0.0000	0.0003	0.0000	0.0000	0.0020	0.0000	0.0000	0.0000	0.0023
	UM	0.0000	0.0002	0.0000	0.0000	0.0010	0.0000	0.0000	0.0000	0.0012
	%diff.	-	33.3	-	-	50.0	-	-	-	47.8
LB07	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB08	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB09	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB10	PL	0.0000	0.0072	0.0147	0.0000	0.0002	0.0000	0.0227	0.0000	0.0448
	UM	0.0000	0.0022	0.0049	0.0000	0.0001	0.0000	0.0127	0.0000	0.0199
	%diff.	-	69.4	66.7	-	50.0	-	44.1	-	55.6
LB11	PL	0.0000	0.0541	0.0000	0.0000	0.0002	0.0000	18.8176	0.0000	18.8719
	UM	0.0000	0.0922	0.0000	0.0000	0.0003	0.0000	20.7027	0.0000	20.7952
	%diff.	-	-70.4	-	-	-50.0	-	-10.0	-	-10.2
LB12	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB13	PL	0.0000	0.3073	0.0003	0.0000	0.0000	0.0000	0.0089	0.0001	0.3166
	UM	0.0000	0.1250	0.0002	0.0000	0.0000	0.0000	0.0027	0.0001	0.1280
	%diff.	-	59.3	33.3	-	-	-	69.7	0.0	59.6
LB14	PL	0.0000	0.3053	0.0000	0.0000	0.0000	0.0000	4.5491	0.0001	4.8545
	UM	0.0000	0.2531	0.0000	0.0000	0.0000	0.0000	4.3781	0.0001	4.6313
	%diff.	-	17.1	-	-	-	-	3.8	0.0	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 OS05-OS07.

		Sample OS06								
LabCode		Nemertea	Polychaeta	Oligochaeta	Pycnogonida	Crustacea	Echinodermata	Mollusca	Other	Overall
LB01	PL	0.0000	0.0645	0.0004	0.0000	0.0090	0.0000	0.2167	0.0001	0.2907
	UM	0.0000	0.0423	0.0009	0.0000	0.0047	0.0000	0.1691	0.0001	0.2171
	%diff.	-	34.4	-125.0	-	47.8	-	22.0	0.0	25.3
LB02	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB03	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB04	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB05	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB06	PL	0.0000	0.0082	0.0036	0.0000	0.0000	0.0000	0.0000	0.0000	0.0118
	UM	0.0000	0.0044	0.0023	0.0000	0.0000	0.0000	0.0000	0.0000	0.0067
	%diff.	-	46.3	36.1	-	-	-	-	-	43.2
LB07	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB08	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB09	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB10	PL	0.0194	1.9789	0.00003	0.0000	1.4704	1.9831	7.5398	2.941	15.9326
	UM	0.0220	1.3186	0.0001	0.0000	1.3478	1.1229	5.5478	1.7735	11.1327
	%diff.	-13.4	33.4	-233.3	-	8.3	43.4	26.4	39.7	30.1
LB11	PL	0.0000	0.0003	0.0001	0.0000	0.0016	0.0000	0.2418	0.0000	0.2438
	UM	0.0000	0.0003	0.0002	0.0000	0.0036	0.0000	0.2858	0.0000	0.2899
	%diff.	-	0.0	-100.0	-	-125.0	-	-18.2	-	-18.9
LB12	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB13	PL	0.0000	0.0018	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0018
	UM	0.0000	0.0006	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0006
	%diff.	-	66.7	-	-	-	-	-	-	66.7
LB14	PL	0.0000	0.3381	0.0000	0.0000	0.0000	0.1921	0.8625	0.0011	1.3938
	UM	0.0000	0.3605	0.0000	0.0000	0.0000	0.1592	0.8420	0.0007	1.3624
	%diff.	-	-6.6	-	-	-	17.1	2.4	36.4	2.3

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 OS05-OS07.

Sample OS07

LabCode		Nemertea	Polychaeta	Oligochaeta	Pycnogonida	Crustacea	Echinodermata	Mollusca	Other	Overall
LB01	PL	0.0000	0.0486	0.0000	0.0000	0.0023	0.0000	0.0030	0.0001	0.0540
	UM	0.0000	0.0317	0.0000	0.0000	0.0017	0.0000	0.0026	0.0001	0.0361
	%diff.	-	34.8	-	-	26.1	-	13.3	0.0	33.1
LB02	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB03	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB04	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB05	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB06	PL	0.0000	0.0002	0.0000	0.0000	0.6517	0.0000	1.3696	0.0000	2.0215
	UM	0.0000	0.0002	0.0000	0.0000	0.5154	0.0000	1.2505	0.0000	1.7661
	%diff.	-	0.0	-	-	20.9	-	8.7	-	12.6
LB07	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB08	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB09	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB10	PL	0.0399	7.5682	0.0000	0.0000	0.1781	0.1129	7.8200	0.0244	15.7435
	UM	0.0210	5.0185	0.0000	0.0000	0.0801	0.098	7.4578	0.0103	12.6857
	%diff.	47.3	33.7	-	-	55.0	13.2	4.6	57.8	19.4
LB11	PL	0.0000	0.0324	0.0005	0.0000	0.0001	0.0000	0.3515	0.0000	0.3845
	UM	0.0000	0.0640	0.0006	0.0000	0.0002	0.0000	0.3900	0.0000	0.4548
	%diff.	-	-97.5	-20.0	-	-100.0	-	-11.0	-	-18.3
LB12	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB13	PL	0.0000	0.0000	0.0003	0.0000	0.0000	0.0000	0.0000	0.0000	0.0003
	UM	0.0000	0.0000	0.0008	0.0000	0.0000	0.0000	0.0000	0.0000	0.0008
	%diff.	-	-	-166.7	-	-	-	-	-	-166.7
LB14	PL	0.0000	0.2498	0.0000	0.0000	0.0010	0.0153	0.5067	0.0000	0.7728
	UM	0.0000	0.2129	0.0000	0.0000	0.0010	0.0153	0.4086	0.0000	0.6378
	%diff.	-	14.8	-	-	0.0	0.0	19.4	-	17.5

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 OS05-OS07.

Sample OS05

LabCode		Nemertea	Polychaeta	Oligochaeta	Pycnogonida	Crustacea	Echinodermata	Mollusca	Other	Overall
LB15	PL	0.0010	0.1138	0.0000	0.0000	0.0863	1.6593	0.2511	0.1178	2.2293
	UM	0.0001	0.0465	0.0000	0.0000	0.0390	1.0488	0.1604	0.1098	1.4046
	%diff.	90.0	59.1	-	-	54.8	36.8	36.1	6.8	37.0
LB16	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB17	PL	0.0000	0.2618	0.0002	0.0000	0.0051	0.0000	0.0000	0.0000	0.2671
	UM	0.0000	0.2341	0.0014	0.0000	0.0050	0.0000	0.0000	0.0000	0.2405
	%diff.	-	10.6	-600.0	-	2.0	-	-	-	10.0
LB18	PL	0.0000	0.0000	0.0000	0.0000	0.0006	0.0000	0.0000	0.0000	0.0006
	UM	0.0000	0.0000	0.0000	0.0000	0.0005	0.0000	0.0000	0.0000	0.0005
	%diff.	-	-	-	-	16.7	-	-	-	16.7
LB19	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB20	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB21	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB22	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
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	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-

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 OS05-OS07.

Sample OS06

LabCode		Nemertea	Polychaeta	Oligochaeta	Pycnogonida	Crustacea	Echinodermata	Mollusca	Other	Overall
LB15	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB16	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB17	PL	0.0000	4.2141	0.0196	0.0000	0.0016	0.0000	0.0516	0.0013	4.2882
	UM	0.0000	2.5537	0.0165	0.0000	0.0007	0.0000	0.0464	0.0023	2.6196
	%diff.	-	39.4	15.8	-	56.3	-	10.1	-76.9	38.9
LB18	PL	0.0000	0.0032	0.0001	0.0000	0.0000	0.0000	0.0001	0.0000	0.0034
	UM	0.0000	0.0016	0.0001	0.0000	0.0000	0.0000	0.0001	0.0000	0.0018
	%diff.	-	50.0	0.0	-	-	-	0.0	-	47.1
LB19	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB20	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB21	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB22	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
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	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-

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 OS05-OS07.

		Sample OS07								
LabCode		Nemertea	Polychaeta	Oligochaeta	Pycnogonida	Crustacea	Echinodermata	Mollusca	Other	Overall
LB15	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB16	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB17	PL	0.0001	0.0649	0.0001	0.0000	0.0139	0.1044	0.2595	0.0000	0.4429
	UM	0.0001	0.0510	0.0001	0.0000	0.0111	0.1084	0.2133	0.0000	0.3840
	%diff.	0.0	21.4	0.0	-	20.1	-3.8	17.8	-	13.3
LB18	PL	0.0000	0.0927	0.0001	0.0000	0.0017	0.0000	0.0034	0.0102	0.1081
	UM	0.0000	0.0608	0.0001	0.0000	0.0007	0.0000	0.0021	0.0058	0.0695
	%diff.	-	34.4	0.0	-	58.8	-	38.2	43.1	35.7
LB19	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB20	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB21	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
LB22	PL	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-
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	-	-	-	-	-	-	-	-	0.0000
	UM	-	-	-	-	-	-	-	-	0.0000
	%diff.	-	-	-	-	-	-	-	-	-

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 PS10.

PS10	% Clay & Silt	Median (phi)	Mean (phi)	Sorting	Skew
PS10 - 38 - laser	89.13	5.56	4.90	1.66	0.219
PS10 - 39 - laser	89.33	5.55	5.06	1.64	0.238
PS10 - 40 - laser	98.44	7.18	6.17	1.55	-0.100
PS10 - 41 - laser	92.16	5.78	5.19	1.62	0.195
PS10 - 42 - laser	93.05	6.53	5.53	1.72	-0.030
PS10 - 43 - laser	91.34	5.98	5.20	1.69	0.115
PS10 - 44 - laser	93.51	6.86	5.59	1.78	-0.104
PS10 - 31 - sieve	*	*	*	*	*
PS10 - 32 - sieve	*	8.90	*	*	*
PS10 - 33 - sieve	*	8.90	*	*	*
PS10 - 34 - sieve	*	8.75	*	*	*
PS10 - 35 - sieve	*	8.89	*	*	*
PS10 - 36 - sieve	*	8.76	*	*	*
PS10 - 37 - sieve	*	8.32	*	*	*

* Statistic unavailable as 50%-ile falls in Clay fraction

Table 7. Summary of the results of particle size analysis of the replicate samples from sediment circulation PS11.

PS11	% Clay & Silt	Median (phi)	Mean (phi)	Sorting	Skew
PS11 - 01A - laser	53.07	4.09	2.66	2.48	0.211
PS11 - 02A - laser	58.69	4.23	4.08	1.92	0.532
PS11 - 03A - laser	56.48	4.20	3.92	2.01	0.472
PS11 - 04A - laser	50.28	4.00	3.30	2.07	0.371
PS11 - 05A - laser	42.92	3.81	3.49	1.72	0.448
PS11 - 06A - laser	60.00	4.31	4.14	1.95	0.502
PS11 - 07A - laser	50.57	4.01	3.62	1.90	0.443
PS11 - 01B - sieve	61.01	4.33	5.38	1.80	0.583
PS11 - 02B - sieve	61.60	4.33	5.49	1.91	0.606
PS11 - 03B - sieve	61.90	4.35	5.54	1.96	0.607
PS11 - 04B - sieve	60.17	4.32	5.51	1.95	0.609
PS11 - 05B - sieve	56.74	4.21	5.27	1.61	0.658
PS11 - 06B - sieve	58.87	4.29	5.24	1.68	0.564
PS11 - 07B - sieve	59.78	4.32	5.53	1.97	0.613

Table 8. Summary of the particle size information received from participating laboratories for the tenth particle size distribution - PS10.

Lab	Method	%<63µm	Median	Mean	Sort	IGS (SKi)
LB01	L*	81.76	6.13	4.42	1.39	-0.675
LB02	-	-	-	-	-	-
LB03	-	-	-	-	-	-
LB04	L	81.38	6.13	4.35	1.38	-0.676
LB05	-	-	-	-	-	-
LB06	L*	81.76	6.13	4.42	1.39	-0.675
LB07	S, P, CC	96.36	n/c	7.70	1.48	-2.190
LB08	-	-	-	-	-	-
LB09	not participating in this component					
LB10	L	91.48	6.79	5.19	1.76	-0.163
LB11	S	84.03	4.40	3.95	1.52	-2.910
LB12	L*	81.76	6.13	4.42	1.39	-0.675
LB13	DS, L	98.94	7.10	6.91	1.21	-0.220
LB14	L	95.10	7.13	5.94	1.83	-0.044
LB15	WS, DS, L	78.75	5.40	5.77	2.13	0.270
LB16	-	-	-	-	-	-
LB17	FD, L	100.00	7.00	7.07	1.35	0.090
LB18	L	89.42	6.15	5.22	1.36	-0.268
LB19	not participating in this component					
LB20	S, P	98.70	5.94	5.93	0.60	-0.150
LB21	-	-	-	-	-	-
LB22	-	-	-	-	-	-
LB23	-	-	-	-	-	-
LB24	-	-	-	-	-	-
LB25	WS	94.06	n/c	n/c	n/c	n/c
LB26	WS?	98.11	5.77	n/c	1.12	0.397
LB27	L	81.76	6.13	4.42	1.39	-0.675

Key to methods:

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

Summary	%<63µm	Median	Mean	Sort	IGS (SKi)
Number of values	13	11	11	12	12
Mean of laboratories	91.39	6.18	5.68	1.43	-0.54
Mean of 7 replicates (laser)	92.42	6.21	5.38	1.67	0.08
Mean of 7 replicates (sieve)	#N/A	8.75	#N/A	#N/A	#N/A
Laboratory minimum	78.75	4.40	3.95	0.60	-2.91
Laboratory maximum	100.00	7.13	7.70	2.13	0.40

#N/A statistic not calculable

Table 9. Summary of the particle size information received from participating laboratories for the eleventh particle size distribution - PS11.

Lab	Method	%<63µm	Median	Mean	Sort	IGS (SKi)
LB01	L*	60.76	4.25	1.28	0.42	n/c
LB02	-	-	-	-	-	-
LB03	-	-	-	-	-	-
LB04	-	-	-	-	-	-
LB05	-	-	-	-	-	-
LB06	L*	60.76	4.25	1.28	0.42	n/c
LB07	S, P, L	67.72	4.70	5.33	1.84	0.480
LB08	-	-	-	-	-	-
LB09	not participating in this component					
LB10	L	62.76	4.50	4.14	2.01	0.412
LB11	S	62.59	4.20	4.03	0.75	-2.360
LB12	L*	60.76	4.25	1.28	0.42	n/c
LB13	DS, L ?	87.10	6.01	6.01	1.88	-0.070
LB14	L	62.47	4.38	4.27	2.08	0.555
LB15	-	-	-	-	-	-
LB16	-	-	-	-	-	-
LB17	FD, L	65.00	4.50	4.80	1.47	0.330
LB18	-	-	-	-	-	-
LB19	not participating in this component					
LB20	S	56.50	3.71	3.96	1.49	4.110
LB21	-	-	-	-	-	-
LB22	L	48.64	n/c	n/c	n/c	n/c
LB23	-	-	-	-	-	-
LB24	-	-	-	-	-	-
LB25	-	-	-	-	-	-
LB26	-	-	-	-	-	-
LB27	L	60.76	4.25	1.28	0.42	n/c

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	9	8	8	8	7
Mean of laboratories	63.73	4.53	4.23	1.49	0.49
Mean of 7 replicates (laser)	53.14	4.09	3.60	2.01	0.43
Mean of 7 replicates (sieve)	60.01	4.31	5.42	1.84	0.61
Laboratory minimum	48.64	3.71	1.28	0.42	-2.36
Laboratory maximum	87.10	6.01	6.01	2.08	4.11

Table 10. The identifications of the fauna made by participating laboratories for RT10. Names are given only where different from the AQC identification.

RT10	Taxon	LB01	LB03	LB05	LB07	LB09	LB11	LB13
RT1001	Arenicola marina	--	n/d	n/d	--	--	--	--
RT1002	Paranais litoralis	--	n/d	n/d	--	Tubificoides pseudogaster	--	--
RT1003	Manayunkia aestuarina	--	n/d	n/d	?Fabriciola cf. berkleyi	--	Fabriciola baltica	--
RT1004	Nymphon brevirostre	--	n/d	n/d	--	- [rubrum]	--	--
RT1005	Musculus discors	--	n/d	n/d	--	--	--	- costulatus
RT1006	Mytilus edulis	--	n/d	n/d	Modiolula phaseolina	--	Modiolus modiolus	Modiolus modiolus
RT1007	Skeneopsis planorbis	--	n/d	n/d	--	--	--	--
RT1008	Eatonina fulgida	[Coriandria] -	n/d	n/d	[Coriandria] -	[Cingulopsis] -	[Coriandria] -	[Coriandria] -
RT1009	Idotea granulosa	- pelagica	n/d	n/d	- pelagica	- pelagica	- pelagica	- pelagica
RT1010	Mediomastus fragilis	--	n/d	n/d	--	--	--	--
RT1011	Ampharete lindstroemi	--	n/d	n/d	--	- baltica	--	--
RT1012	Cyathura carinata	--	n/d	n/d	--	--	--	--
RT1013	Tubificoides benedii	--	n/d	n/d	--	- [benedeni]	--	- [benedeni]
RT1014	Donax vittatus	--	n/d	n/d	--	--	--	--
RT1015	Lacuna parva	- pallidula	n/d	n/d	- pallidula	--	--	- pallidula
RT1016	Dendrodoa grossularia	--	n/d	n/d	--	--	n/d n/d	--
RT1017	Lanice conchilega	--	n/d	n/d	--	--	--	--
RT1018	Flabelligera affinis	--	n/d	n/d	--	--	--	--
RT1019	Spio decorata	--	n/d	n/d	--	--	--	--
RT1020	Malacoceros fuliginosus	--	n/d	n/d	--	--	--	--
RT1021	Capitella capitata	- [capitata spp comp]	n/d	n/d	--	--	--	--
RT1022	Apherusa jurinei	[Epherusa] -	n/d	n/d	- [jurinei/cirrus]	--	--	--
RT1023	Corophium volutator	--	n/d	n/d	- arenarium	--	--	--
RT1024	Nucula nitidosa	--	n/d	n/d	--	--	--	--
RT1025	Corophium insidiosum	- bonnellii	n/d	n/d	--	- acherusicum	--	--

RT10	Taxon	LB02	LB04	LB06	LB08	LB10	LB12	LB14
RT1001	Arenicola marina	--	Micromaldane ornithochaeta	--	--	- [marina?]	n/d n/d	--
RT1002	Paranais litoralis	--	Tubificoides pseudogaster	Tubificoides psuedogaster	--	--	Tubificoides pseudogaster	--
RT1003	Manayunkia aestuarina	--	- [aesturarina]	[Manyunkia] [aesturina]	--	--	Fabriciola cf berkeleyi	--
RT1004	Nymphon brevirostre	--	--	- [rubrum]	--	--	- gracile	- [rubrum]
RT1005	Musculus discors	--	--	- costulatus	--	- costulatus?	- n/d	Modiolarca tumida
RT1006	Mytilus edulis	Modiolus modiolus	--	--	--	Modiolus modiolus	Modiolus phaseolinus	Modiolus modiolus
RT1007	Skeneopsis planorbis	--	--	--	--	--	[Skenopsis] -	--
RT1008	Eatonina fulgida	[Coriandria] -	[Cingulus] -	[Cingulopsis] -	[Cingulopsis] -	Hydrobia ulvae?	n/d n/d	[Eatonia] -
RT1009	Idotea granulosa	- pelagica	Zenobiana prismatica	- pelagica	- pelagica	- neglecta?	- pelagica	- pelagica
RT1010	Mediomastus fragilis	[Mediomatus] -	--	--	--	--	- [fragilus]	--
RT1011	Ampharete lindstroemi	- baltica	--	- finmarchia	- grubei	- [lindstroemi?]	- finmarchia	--
RT1012	Cyathura carinata	--	--	--	--	--	--	--
RT1013	Tubificoides benedii	--	--	- [benedeni]	- [benedeni]	- [benedeni]	--	--
RT1014	Donax vittatus	--	--	--	--	--	--	--
RT1015	Lacuna parva	--	- pallidula	--	- pallidula	- pallidula	- pallidula	- pallidula
RT1016	Dendrodoa grossularia	--	--	Fam: Ascidiidae	--	Styela coriacea	Aplidium pallidum	Corella parallelogramma
RT1017	Lanice conchilega	[Lanica] -	--	- [concheliga]	--	--	Eupolymnia nebulosa	--
RT1018	Flabelligera affinis	--	--	--	--	--	n/d n/d	--
RT1019	Spio decorata	--	--	- filicornis	--	--	- filicornis	--
RT1020	Malacoceros fuliginosus	--	--	--	- [fulginosus]	--	--	--
RT1021	Capitella capitata	- [capitata species complex]	--	--	--	--	--	- [capitata (Agg.)]
RT1022	Apherusa jurinei	--	--	n/d n/d	- cf. cirrus	--	n/d n/d	Hyale nilssoni
RT1023	Corophium volutator	--	--	--	--	--	--	--
RT1024	Nucula nitidosa	--	- [turgida]	--	--	--	- [turgida]	--
RT1025	Corophium insidiosum	[Corphium] -	--	--	--	- acherusicum	- acutum	--

Table 10. The identifications of the fauna made by participating laboratories for RT10. Names are given only where different from the AQC identification.

RT10	Taxon	LB15	LB17	LB19	LB21	LB23	LB25	LB27
RT1001	Arenicola marina	n/d	- [Spp. juv.]	--	n/d	--	--	
RT1002	Paranais litoralis	n/d	Amphichaeta sannio	--	n/d	--	Tubifex sp.	
RT1003	Manayunkia aestuarina	n/d	Fabriciola balyica	--	n/d	Fabriciola berkeleyi	--	
RT1004	Nymphon brevirostre	n/d	- [rubrum]	- [rubrum]	n/d	--	--	
RT1005	Musculus discors	n/d	--	--	n/d	--	--	
RT1006	Mytilus edulis	n/d	Modiolula phaseolina	Modiolus modiolus	n/d	--	Modiolus barbatus	
RT1007	Skeneopsis planorbis	n/d	--	--	n/d	--	--	
RT1008	Eatonina fulgida	n/d	[Cingulopsis] -	[Coriandria] -	n/d	Rissoella opalina	[Cingulopsis] -	
RT1009	Idotea granulosa	n/d	- pelagica	- pelagica	n/d	- pelagica	- baltica	
RT1010	Mediomastus fragilis	n/d	--	--	n/d	Capitella hermaphrodita	Tubifex sp.	
RT1011	Ampharete lindstroemi	n/d	- finmarchica	- balthica	n/d	- falcata	- baltica	
RT1012	Cyathura carinata	n/d	--	Anthura gracilis	n/d	--	--	
RT1013	Tubificoides benedii	n/d	- [benedeni]	--	n/d	--	- [benedeni]	
RT1014	Donax vittatus	n/d	--	--	n/d	--	--	
RT1015	Lacuna parva	n/d	- pallidula	- pallidula	n/d	Velutina undata	Littorina obtusata	
RT1016	Dendrodoa grossularia	n/d	Styela coriacea	--	n/d	--	--	
RT1017	Lanice conchilega	n/d	--	--	n/d	--	--	
RT1018	Flabelligera affinis	n/d	--	--	n/d	Pherusa plumosa	--	
RT1019	Spio decorata	n/d	--	--	n/d	--	- filicornis	
RT1020	Malacoceros fuliginosus	n/d	--	--	n/d	- [fuliginosa]	- vulgaris	
RT1021	Capitella capitata	n/d	[Capitola] -	--	n/d	--	--	
RT1022	Apherusa jurinei	n/d	- cirrus	Atylus swammerdami	n/d		--	
RT1023	Corophium volutator	n/d	--	--	n/d	--	--	
RT1024	Nucula nitidosa	n/d	--	--	n/d	--	- nucleus	
RT1025	Corophium insidiosum	n/d	--	--	n/d	- acutum	--	

RT10	Taxon	LB16	LB18	LB20	LB22	LB24	LB26
RT1001	Arenicola marina	--	- [marina / sp. (juvenile)]	Boguea sp.	--	Capitella sp. indet	Lumbriclymene cylindricauda
RT1002	Paranais litoralis	--	--	? Amphichaeta sannio	Chaetogaster langi	n/d n/d	Tubificoides cf. crenacoleus
RT1003	Manayunkia aestuarina	--	--	Fabriciola cf bekeleyi	--	--	--
RT1004	Nymphon brevirostre	--	- [rubrum]	--	--	- [rubrum]	--
RT1005	Musculus discors	--	--	- costulatus	- costulatus	--	- [cf discors]
RT1006	Mytilus edulis	--	--	--	--	Modiolus barbatus	Modiolus modiolus
RT1007	Skeneopsis planorbis	--	--	--	--	--	--
RT1008	Eatonina fulgida	[Cingulopsis] -	--	[Cingulopsis] -	n/d n/d	[Coriandria] -	--
RT1009	Idotea granulosa	- pelagica	- pelagica	- chelipes	- pelagica	- pelagica	--
RT1010	Mediomastus fragilis	--	[Medimastus] -	--	Capitomastus minimus	--	--
RT1011	Ampharete lindstroemi	- baltica	- baltica	--	--	- [lindsroemi]	--
RT1012	Cyathura carinata	--	--	--	--	[Cyanthura] -	--
RT1013	Tubificoides benedii	--	--	- [benedeni]	- [benedeni]	- swirencoides	--
RT1014	Donax vittatus	--	--	--	--	--	--
RT1015	Lacuna parva	Velutina plicatilis	- pallidula	- pallidula	- pallidula	- sp. indet	--
RT1016	Dendrodoa grossularia	--	--	--	--	--	n/d n/d
RT1017	Lanice conchilega	--	--	--	--	--	--
RT1018	Flabelligera affinis	--	--	--	--	Poecilochaetus serpens	--
RT1019	Spio decorata	--	--	--	- ["decorata"]	- armata	- armata
RT1020	Malacoceros fuliginosus	--	--	--	--	--	--
RT1021	Capitella capitata	--	--	- [agg.]	--	--	- [capitata agg.]
RT1022	Apherusa jurinei	--	--	Amphipoda Sp A	--	Amphipod indet	- sp.
RT1023	Corophium volutator	- arenarium	- arenarium	- sextonae	--	--	--
RT1024	Nucula nitidosa	--	--	--	--	--	--
RT1025	Corophium insidiosum	- acherusicum	--	- volutator	--	- acutum	--

Not participating in this component

Table 11. The identifications of the fauna made by participating laboratories for RT11. Names are given only where different from the AQC identification.

RT11	Taxon	LB01	LB03	LB05	LB07	LB09	LB11	LB13
RT1101	Sphaerosyllis taylori	--	n/d	n/d	--	--	--	- hystrix
RT1102	Eurysyllis tuberculata	--	n/d	n/d	--	--	--	--
RT1103	Streptosyllis websteri	--	n/d	n/d	--	--	--	--
RT1104	Exogone naidina	- verugera	n/d	n/d	--	--	--	Spermosyllis sp.
RT1105	Sphaerosyllis taylori	- thomasi	n/d	n/d	--	- thomasi	--	--
RT1106	Exogone hebes	--	n/d	n/d	--	--	--	--
RT1107	Eusyllis blomstrandi	--	n/d	n/d	--	Syllides articulocirrata	--	--
RT1108	Sphaerosyllis bulbosa	--	n/d	n/d	--	--	--	--
RT1109	Streptosyllis bidentata	--	n/d	n/d	--	--	--	--
RT1110	Exogone verugera	--	n/d	n/d	--	--	- naidina	--
RT1111	Typosyllis variegata	[Syllis] -	n/d	n/d	- [cf variegata]	--	--	[Syllis] -
RT1112	Sphaerosyllis bulbosa	--	n/d	n/d	--	--	--	--
RT1113	Exogone naidina	--	n/d	n/d	--	--	- verugera	- verugera
RT1114	Exogone hebes	--	n/d	n/d	--	--	--	--
RT1115	Streptosyllis websteri	--	n/d	n/d	--	--	--	--
RT1116	Tanaopsis graciloides	--	n/d	n/d	--	--	--	--
RT1117	Pseudoparatanais batei	--	n/d	n/d	--	--	--	--
RT1118	Tanaissus lilljeborgi	Pseudotanais jonesi	n/d	n/d	- elongatus	Leptognathia gracilis	--	--
RT1119	Iphinoe trispinosa	--	n/d	n/d	--	--	--	--
RT1120	Eudorella truncatula	--	n/d	n/d	--	--	--	--
RT1121	Vaunthompsonia cristata	--	n/d	n/d	--	[Vauntompsonia] -	[Vauntompsonia] -	[Vautompsonia] -
RT1122	Nannastacus unguiculatus	- brevicaudatus	n/d	n/d	--	--	--	--
RT1123	Diastylis rathkei	- lucifera	n/d	n/d	- lucifera	- lucifera	- lucifera	- lucifera
RT1124	Cumella pygmaea	--	n/d	n/d	--	--	--	--
RT1125	Cymodoce truncata	--	n/d	n/d	--	Sphaeroma rugicauda	--	--

RT11	Taxon	LB02	LB04	LB06	LB08	LB10	LB12	LB14
RT1101	Sphaerosyllis taylori	--	- hystrix	--	--	--	- magnidentata	--
RT1102	Eurysyllis tuberculata	--	--	--	--	--	--	--
RT1103	Streptosyllis websteri	--	--	--	--	--	Opisthodonta pterochaeta	--
RT1104	Exogone naidina	--	--	--	--	--	--	--
RT1105	Sphaerosyllis taylori	- thomasi	--	- hystrix	--	--	--	- thomasi
RT1106	Exogone hebes	--	--	--	--	--	--	- dispar
RT1107	Eusyllis blomstrandi	--	--	--	- assimilis	--	--	Typosyllis armillaris
RT1108	Sphaerosyllis bulbosa	--	--	--	--	--	--	--
RT1109	Streptosyllis bidentata	--	--	--	--	--	--	--
RT1110	Exogone verugera	--	--	--	--	--	--	--
RT1111	Typosyllis variegata	[Syllis] -	[Syllis] -	- hyalina	--	--	[Syllis] -	- hyalina
RT1112	Sphaerosyllis bulbosa	--	- thomasi	--	--	--	--	--
RT1113	Exogone naidina	--	- dispar	- dispar	--	--	--	--
RT1114	Exogone hebes	--	--	--	--	--	- dispar	--
RT1115	Streptosyllis websteri	--	--	--	--	--	[Streblosyllis] -	--
RT1116	Tanaopsis graciloides	--	Tanaissus lilljeborgi	Typhlotanais brevicornis	--	--	Tanaissus lilljeborgi	--
RT1117	Pseudoparatanais batei	--	--	--	--	--	--	--
RT1118	Tanaissus lilljeborgi	--	--	--	--	Akanthophoreus gracilis	--	--
RT1119	Iphinoe trispinosa	--	--	--	--	--	--	--
RT1120	Eudorella truncatula	--	--	--	- emarginata	--	Pseudocuma similis	--
RT1121	Vaunthompsonia cristata	--	--	[Vauntompsonia] -	--	--	--	[Vauntompsonia] -
RT1122	Nannastacus unguiculatus	--	- brevicaudatus	- brevicaudatus	--	- brevicaudatus	--	--
RT1123	Diastylis rathkei	--	- lucifera	- lucifera	- lucifera	- lucifera	- lucifera	- lucifera
RT1124	Cumella pygmaea	--	--	--	--	--	--	--
RT1125	Cymodoce truncata	Dynamene bidentata	Dynamene bidentata	Dynamene bidentata	Dynamene bidentata	--	Sphaeroma hookeri	Sphaeroma rugicauda

Table 11. The identifications of the fauna made by participating laboratories for RT11. Names are given only where different from the AQC identification.

RT11	Taxon	LB15	LB17	LB19	LB21	LB23	LB25	LB27
RT1101	Sphaerosyllis taylori	n/d	- hystrix	--	n/d	n/d	n/d	
RT1102	Eurysyllis tuberculata	n/d	--	--	n/d	n/d	n/d	
RT1103	Streptosyllis websteri	n/d	--	--	n/d	n/d	n/d	
RT1104	Exogone naidina	n/d	--	--	n/d	n/d	n/d	
RT1105	Sphaerosyllis taylori	n/d	--	--	n/d	n/d	n/d	
RT1106	Exogone hebes	n/d	--	--	n/d	n/d	n/d	
RT1107	Eusyllis blomstrandi	n/d	--	--	n/d	n/d	n/d	
RT1108	Sphaerosyllis bulbosa	n/d	--	--	n/d	n/d	n/d	
RT1109	Streptosyllis bidentata	n/d	--	--	n/d	n/d	n/d	
RT1110	Exogone verugera	n/d	--	--	n/d	n/d	n/d	
RT1111	Typosyllis variegata	n/d	--	--	n/d	n/d	n/d	
RT1112	Sphaerosyllis bulbosa	n/d	--	--	n/d	n/d	n/d	
RT1113	Exogone naidina	n/d	--	--	n/d	n/d	n/d	
RT1114	Exogone hebes	n/d	--	--	n/d	n/d	n/d	
RT1115	Streptosyllis websteri	n/d	--	--	n/d	n/d	n/d	
RT1116	Tanaopsis graciloides	n/d	--	--	n/d	n/d	n/d	
RT1117	Pseudoparatanais batei	n/d	--	--	n/d	n/d	n/d	
RT1118	Tanaissus lilljeborgi	n/d	- elongatus	Leptognathia manca	n/d	n/d	n/d	
RT1119	Iphinoe trispinosa	n/d	--	--	n/d	n/d	n/d	
RT1120	Eudorella truncatula	n/d	--	--	n/d	n/d	n/d	
RT1121	Vaunthompsonia cristata	n/d	[Vauntompsonia] -	--	n/d	n/d	n/d	
RT1122	Nannastacus unguiculatus	n/d	--	--	n/d	n/d	n/d	
RT1123	Diastylis rathkei	n/d	- lucifera	- lucifera	n/d	n/d	n/d	
RT1124	Cumella pygmaea	n/d	--	--	n/d	n/d	n/d	
RT1125	Cymodoce truncata	n/d	Sphaeroma rugicauda	--	n/d	n/d	n/d	

Not participating in this component

RT11	Taxon	LB16	LB18	LB20	LB22	LB24	LB26
RT1101	Sphaerosyllis taylori	--	- pirifera	- ?thomasi	- sp. indet	- hystrix	n/d
RT1102	Eurysyllis tuberculata	--	--	--	--	--	n/d
RT1103	Streptosyllis websteri	--	--	--	--	Syllides sp. indet	n/d
RT1104	Exogone naidina	--	--	--	--	--	n/d
RT1105	Sphaerosyllis taylori	--	[Spaerosyllis] tetralyx	- [?taylori]	--	- bulbosa	n/d
RT1106	Exogone hebes	--	--	- dispar	--	n/d n/d	n/d
RT1107	Eusyllis blomstrandi	--	--	--	--	--	n/d
RT1108	Sphaerosyllis bulbosa	--	--	- ?pirifera	--	- tetralix	n/d
RT1109	Streptosyllis bidentata	--	--	- sp	--	- sp. indet	n/d
RT1110	Exogone verugera	--	--	--	--	--	n/d
RT1111	Typosyllis variegata	[Typosyllis (Syllis)] sp.	--	- [cf. variegata]	--	--	n/d
RT1112	Sphaerosyllis bulbosa	--	[Spaerosyllis] -	- ?pirifera	--	- sp. indet	n/d
RT1113	Exogone naidina	--	--	--	--	- dispar	n/d
RT1114	Exogone hebes	--	--	--	--	[Exogoninae] sp. indet	n/d
RT1115	Streptosyllis websteri	--	--	- bidentata	--	Syllides sp. indet	n/d
RT1116	Tanaopsis graciloides	Leptognathia gracilis	[Tanopsis] -	--	--	--	n/d
RT1117	Pseudoparatanais batei	Tanaopsis graciloides	--	[Pseuoparatanais] -	--	--	n/d
RT1118	Tanaissus lilljeborgi	Leptognathia breviremis	--	--	--	--	n/d
RT1119	Iphinoe trispinosa	--	--	--	--	Vaunthompsonia cristata	n/d
RT1120	Eudorella truncatula	--	--	--	--	--	n/d
RT1121	Vaunthompsonia cristata	--	--	[Vauntompsonia] -	[Vauntompsonia] -	--	n/d
RT1122	Nannastacus unguiculatus	Bodotria arenosa	Eocuma dollfusi	--	--	--	n/d
RT1123	Diastylis rathkei	- lucifera	--	- lucifera	- lucifera	- lucifera	n/d
RT1124	Cumella pygmaea	Petalosarsia declivis	Pseudocuma similis	--	--	--	n/d
RT1125	Cymodoce truncata	Sphaeroma rugicauda	--	Sphaeroma rugicauda	--	--	n/d

Table 12. Summary results from the identification of specimens supplied by participating laboratories for Laboratory Reference exercise LR02.

	Differences	
LabCode	Generic	Specific
01	0	0
02	2	2
03	-	-
04	1	1
05	-	-
06	2	3
07	-	-
08	-	-
09	-	-
10	0	0
11	0	0
12	3	3
13	1	2
14	1	1
15	-	-
16	1	1
17	1	1
18	0	1
19	-	-
20	1	1
21	-	-
22	0	1
23	-	-
24	-	-
25	2	7
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 / NMP 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.	Target	Flag	Target	Lab.	Flag	NMP Flag
LB01_OS05	20	18.0 - 22.0	PASS	156	140.4 - 171.6	PASS	5.7098	4.3666 - 06.549	PASS	90.0	100.00	PASS	
LB01_OS06	11	09.0 - 13.0	PASS	63	56.7 - 69.3	PASS	0.2907	0.1737 - 00.260	**Fail**	90.0	100.00	PASS	PASS
LB01_OS07	8	06.0 - 10.0	PASS	37	34.2 - 41.8	PASS	0.0540	0.0289 - 00.043	**Fail**	90.0	98.67	PASS	
LB02_OS05	5	03.0 - 07.0	PASS	26	23.4 - 28.6	PASS	-	-	Deemed fail	90.0	100.00	PASS	
LB02_OS06	20	18.9 - 23.1	PASS	789	716.4 - 875.6	PASS	-	-	Deemed fail	90.0	98.80	PASS	PASS
LB02_OS07	34	31.5 - 38.5	PASS	76	69.3 - 84.7	PASS	-	-	Deemed fail	90.0	980.04	PASS	
LB03_OS05	-	-	Deemed fail	-	-	Deemed fail	-	-	Deemed fail	90.0	-	Deemed fail	
LB03_OS06	-	-	Deemed fail	-	-	Deemed fail	-	-	Deemed fail	90.0	-	Deemed fail	**Fail**
LB03_OS07	-	-	Deemed fail	-	-	Deemed fail	-	-	Deemed fail	90.0	-	Deemed fail	
LB04_OS05	-	-	Deemed fail	-	-	Deemed fail	-	-	Deemed fail	90.0	-	Deemed fail	
LB04_OS06	-	-	Deemed fail	-	-	Deemed fail	-	-	Deemed fail	90.0	-	Deemed fail	**Fail**
LB04_OS07	-	-	Deemed fail	-	-	Deemed fail	-	-	Deemed fail	90.0	-	Deemed fail	
LB05_OS05	12	12.0 - 16.0	PASS	50	45.0 - 55.0	PASS	-	-	Deemed fail	90.0	60.00	**Fail**	
LB05_OS06	6	05.0 - 09.0	PASS	7	7.0 - 11.0	PASS	-	-	Deemed fail	90.0	62.50	**Fail**	PASS
LB05_OS07	45	42.3 - 51.7	PASS	113	111.6 - 136.4	PASS	-	-	Deemed fail	90.0	83.82	**Fail**	
LB06_OS05	2	00.0 - 04.0	PASS	3	1.0 - 5.0	PASS	0.0023	0.0010 - 00.001	**Fail**	90.0	100.00	PASS	
LB06_OS06	5	03.0 - 07.0	PASS	72	65.7 - 80.3	PASS	0.0118	0.0054 - 00.008	**Fail**	90.0	99.31	PASS	PASS
LB06_OS07	7	05.0 - 09.0	PASS	603	545.4 - 666.6	PASS	2.0215	1.4129 - 02.119	PASS	90.0	99.75	PASS	
LB07_OS05	59	52.2 - 63.8	PASS	608	552.6 - 675.4	PASS	-	-	Deemed fail	90.0	95.75	PASS	
LB07_OS06	32	26.1 - 31.9	**Fail**	155	138.6 - 169.4	PASS	-	-	Deemed fail	90.0	92.56	PASS	PASS
LB07_OS07	31	31.5 - 38.5	**Fail**	147	140.4 - 171.6	PASS	-	-	Deemed fail	90.0	96.37	PASS	
LB08_OS05	-	-	Deemed fail	-	-	Deemed fail	-	-	Deemed fail	90.0	-	Deemed fail	
LB08_OS06	-	-	Deemed fail	-	-	Deemed fail	-	-	Deemed fail	90.0	-	Deemed fail	**Fail**
LB08_OS07	-	-	Deemed fail	-	-	Deemed fail	-	-	Deemed fail	90.0	-	Deemed fail	
LB09	not participating in this component												

Table 13. Summary of the performance of participating laboratories in the Own Sample (OS) exercises with respect to the NMBAQC / NMP 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.	Target	Flag	Target	Lab.	Flag	NMP Flag
LB10_OS05	5	7.0 - 11.0	**Fail**	96	143.1 - 174.9	**Fail**	0.0448	0.0159 - 00.023	**Fail**	90.0	75.29	**Fail**	
LB10_OS06	35	34.2 - 41.8	PASS	183	171.0 - 209.0	PASS	15.9326	8.9062 - 13.359	**Fail**	90.0	95.44	PASS	**Fail**
LB10_OS07	40	41.4 - 50.6	**Fail**	211	233.1 - 284.9	**Fail**	15.7435	0.1486 - 15.222	**Fail**	90.0	74.89	**Fail**	
LB11_OS05	8	6.0 - 10.0	PASS	75	66.6 - 81.4	PASS	18.8719	6.6362 - 24.954	PASS	90.0	96.64	PASS	
LB11_OS06	9	6.0 - 10.0	PASS	15	12.0 - 16.0	PASS	0.2438	0.2319 - 00.347	PASS	90.0	96.55	PASS	PASS
LB11_OS07	11	10.0 - 14.0	PASS	37	33.3 - 40.7	PASS	0.3845	0.3638 - 00.545	PASS	90.0	91.89	PASS	
LB12_OS05	-	-	Deemed fail	-	-	Deemed fail	-	-	Deemed fail	90.0	-	Deemed fail	
LB12_OS06	-	-	Deemed fail	-	-	Deemed fail	-	-	Deemed fail	90.0	-	Deemed fail	**Fail**
LB12_OS07	-	-	Deemed fail	-	-	Deemed fail	-	-	Deemed fail	90.0	-	Deemed fail	
LB13_OS05	13	11.0 - 15.0	PASS	43	39.6 - 48.4	PASS	0.3166	0.1024 - 00.153	**Fail**	90.0	98.88	PASS	
LB13_OS06	1	-1.0 - 3.0	PASS	1	-1.0 - 3.0	PASS	0.0018	0.0005 - 00.000	**Fail**	90.0	100.00	PASS	PASS
LB13_OS07	2	0.0 - 4.0	PASS	2	0.0 - 4.0	PASS	0.0003	0.0006 - 00.001	**Fail**	90.0	100.00	PASS	
LB14_OS05	5	3.0 - 7.0	PASS	635	577.8 - 706.2	PASS	4.8545	3.7050 - 05.557	PASS	90.0	99.45	PASS	
LB14_OS06	29	25.2 - 30.8	PASS	258	231.3 - 282.7	PASS	1.3938	1.0899 - 01.634	PASS	90.0	990.03	PASS	PASS
LB14_OS07	43	38.7 - 47.3	PASS	611	544.5 - 665.5	PASS	0.7728	0.5102 - 00.765	**Fail**	90.0	95.72	PASS	
LB15_OS05	43	42.3 - 51.7	PASS	156	135.9 - 166.1	PASS	2.2293	1.1237 - 01.685	**Fail**	90.0	89.90	**Fail**	
LB15_OS06	-	-	Deemed fail	-	-	Deemed fail	-	-	Deemed fail	90.0	-	Deemed fail	**Fail**
LB15_OS07	-	-	Deemed fail	-	-	Deemed fail	-	-	Deemed fail	90.0	-	Deemed fail	
LB16_OS05	-	-	Deemed fail	-	-	Deemed fail	-	-	Deemed fail	90.0	-	Deemed fail	
LB16_OS06	-	-	Deemed fail	-	-	Deemed fail	-	-	Deemed fail	90.0	-	Deemed fail	**Fail**
LB16_OS07	-	-	Deemed fail	-	-	Deemed fail	-	-	Deemed fail	90.0	-	Deemed fail	
LB17_OS05	13	11.0 - 15.0	PASS	56	48.6 - 59.4	PASS	0.2671	0.1924 - 00.288	PASS	90.0	96.43	PASS	
LB17_OS06	18	16.0 - 20.0	PASS	501	456.3 - 557.7	PASS	4.2882	2.0957 - 03.143	**Fail**	90.0	94.64	PASS	PASS
LB17_OS07	34	31.5 - 38.5	PASS	156	133.2 - 162.8	PASS	0.4429	0.3072 - 00.460	PASS	90.0	74.34	**Fail**	

Table 13. Summary of the performance of participating laboratories in the Own Sample (OS) exercises with respect to the NMBAQC / NMP 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.	Target	Flag	Target	Lab.	Flag	NMP Flag
LB18_OS05	1	-1.0 - 3.0	PASS	2	00.0 - 4.0	PASS	0.0006	0.0004 - 00.000	PASS	90.0	100.00	PASS	
LB18_OS06	3	1.0 - 5.0	PASS	5	3.0 - 7.0	PASS	0.0034	0.0014 - 00.002	**Fail**	90.0	100.00	PASS	PASS
LB18_OS07	15	13.0 - 17.0	PASS	38	34.2 - 41.8	PASS	0.1081	0.0556 - 00.083	**Fail**	90.0	94.74	PASS	
LB19	not participating in this component												
LB20_OS05	8	8.0 - 12.0	PASS	87	81.0 - 99.0	PASS	-	-	Deemed fail	90.0	98.31	PASS	
LB20_OS06	4	2.0 - 6.0	PASS	12	10.0 - 14.0	PASS	-	-	Deemed fail	90.0	100.00	PASS	PASS
LB20_OS07	8	6.0 - 10.0	PASS	20	18.9 - 23.1	PASS	-	-	Deemed fail	90.0	97.56	PASS	
LB21_OS05	-	-	Deemed fail	-	-	Deemed fail	-	-	Deemed fail	90.0	-	Deemed fail	
LB21_OS06	-	-	Deemed fail	-	-	Deemed fail	-	-	Deemed fail	90.0	-	Deemed fail	**Fail**
LB21_OS07	-	-	Deemed fail	-	-	Deemed fail	-	-	Deemed fail	90.0	-	Deemed fail	
LB22	not participating in this component												
LB23_OS05	14	12.0 - 16.0	PASS	1253	1127.7 - 1378.3	PASS	-	-	Deemed fail	90.0	99.68	PASS	
LB23_OS06	10	8.0 - 12.0	PASS	763	686.7 - 839.3	PASS	-	-	Deemed fail	90.0	99.87	PASS	PASS
LB23_OS07	13	12.0 - 16.0	PASS	101	92.7 - 113.3	PASS	-	-	Deemed fail	90.0	90.20	PASS	
LB24_OS05	-	-	Deemed fail	-	-	Deemed fail	-	-	Deemed fail	90.0	-	Deemed fail	
LB24_OS06	-	-	Deemed fail	-	-	Deemed fail	-	-	Deemed fail	90.0	-	Deemed fail	**Fail**
LB24_OS07	-	-	Deemed fail	-	-	Deemed fail	-	-	Deemed fail	90.0	-	Deemed fail	
LB25	not participating in this component												
LB26	not participating in this component												
LB27	not participating in this component												

Key: "-" - 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.

PS10 Target range = 81.4 - 101.4

	PS10	
LabCode	Actual	Flag
LB01*	81.8	PASS
LB02	-	Deemed Fail
LB03	-	Deemed Fail
LB04	81.4	PASS
LB05	-	Deemed Fail
LB06*	81.8	PASS
LB07	96.4	PASS
LB08	-	Deemed Fail
LB09	not particpating in component	
LB10	91.5	PASS
LB11	84.0	PASS
LB12*	81.8	PASS
LB13	98.9	PASS
LB14	95.1	PASS
LB15	78.8	**Fail**
LB16	-	Deemed Fail
LB17	100.0	PASS
LB18	89.4	PASS
LB19	not particpating in component	
LB20	98.7	PASS
LB21	-	Deemed Fail
LB22	-	Deemed Fail
LB23	-	Deemed Fail
LB24	-	Deemed Fail
LB25	94.1	PASS
LB26	98.1	PASS
LB27	81.8	PASS

PS11 Target range = 53.7 - 73.7

	PS11	
LabCode	Actual	Flag
LB01*	60.8	PASS
LB02	-	Deemed Fail
LB03	-	Deemed Fail
LB04	-	Deemed Fail
LB05	-	Deemed Fail
LB06*	60.8	PASS
LB07	67.7	PASS
LB08	-	Deemed Fail
LB09	not particpating in component	
LB10	62.8	PASS
LB11	62.6	PASS
LB12*	60.8	PASS
LB13	87.1	**Fail**
LB14	62.5	PASS
LB15	-	Deemed Fail
LB16	-	Deemed Fail
LB17	65.0	PASS
LB18	-	Deemed Fail
LB19	not particpating in component	
LB20	56.5	PASS
LB21	-	Deemed Fail
LB22	48.6	**Fail**
LB23	-	Deemed Fail
LB24	-	Deemed Fail
LB25	-	Deemed Fail
LB26	-	Deemed Fail
LB27	60.8	PASS

"-" 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 and 1997/98 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
1996/97	PS	08, 09	27	1	20	56
1997/98		10, 11	25	3	22	50

Figures

Figure 1. Particle size distribution curves resulting from analysis of replicate samples of sediment distributed as PS10. Seven samples analysed by sieve-pipette and seven samples analysed by Laser.

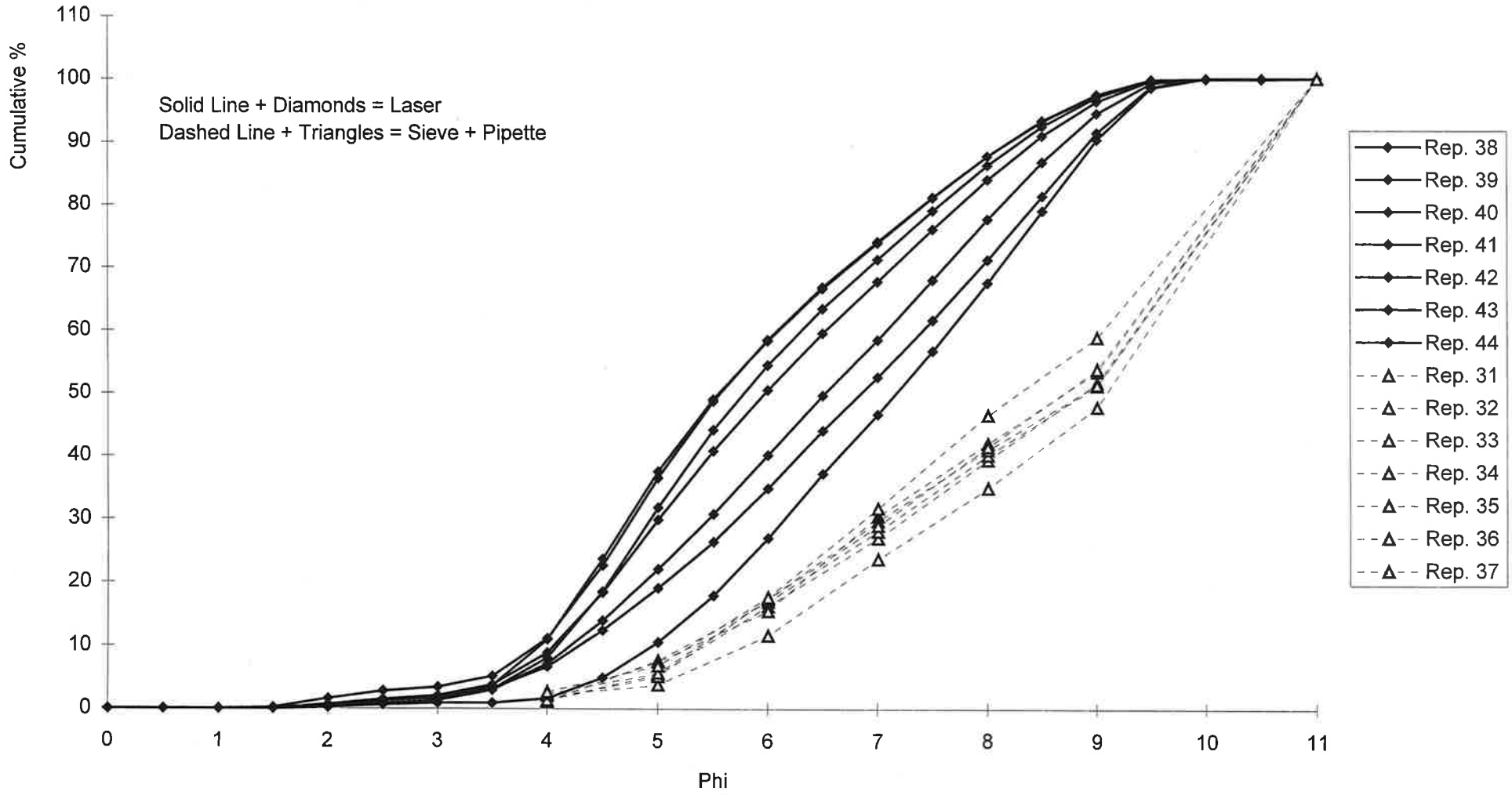


Figure 2. Particle size distribution curves resulting from analysis of replicate samples of sediment distributed as PS11. Seven samples analysed by sieve-pipette and seven samples analysed by Laser.

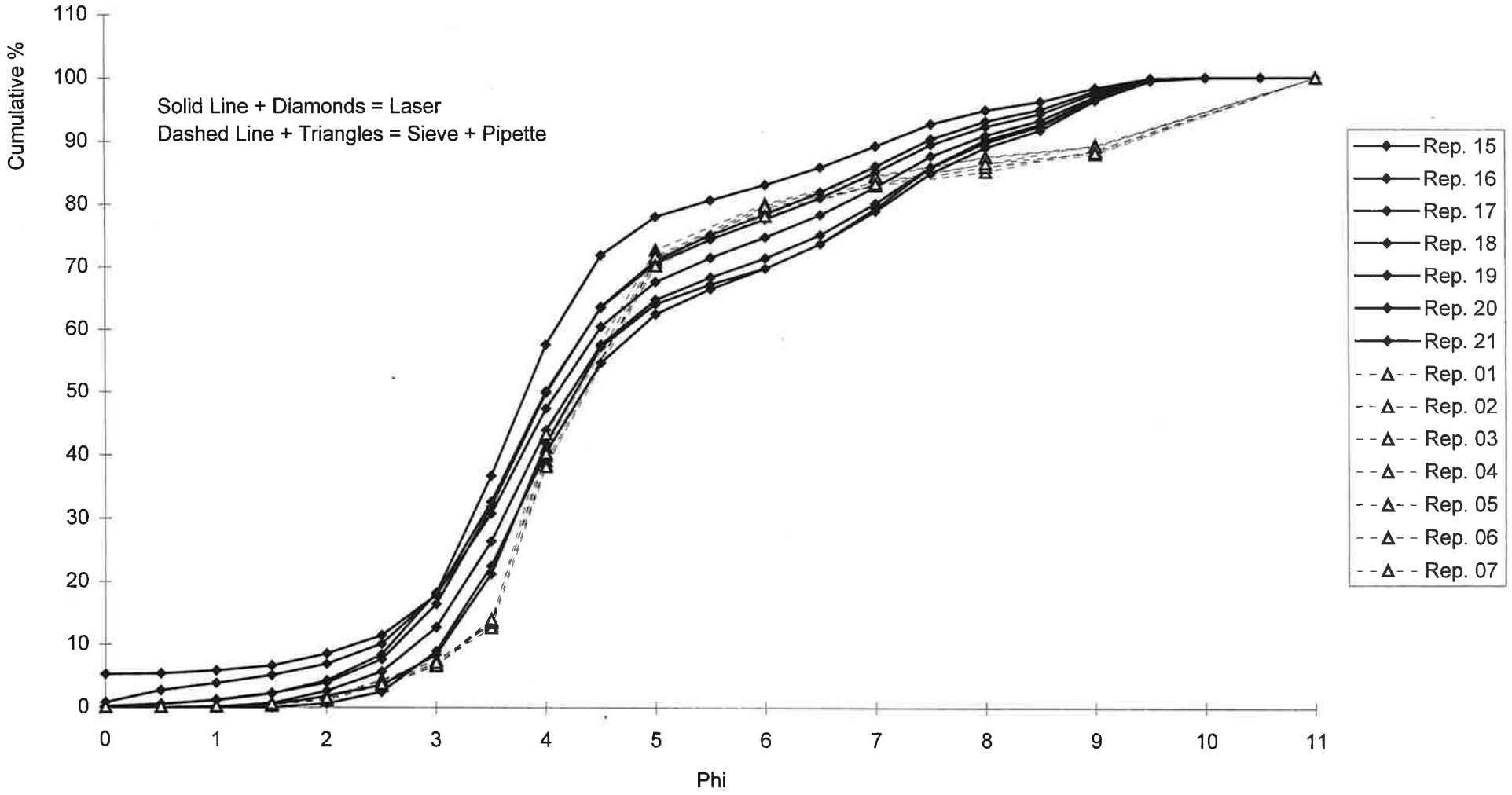


Figure 3. Particle size distribution curves from participating laboratories for sediment samples from PS10. The average values for the AQC analysis of replicates are included.

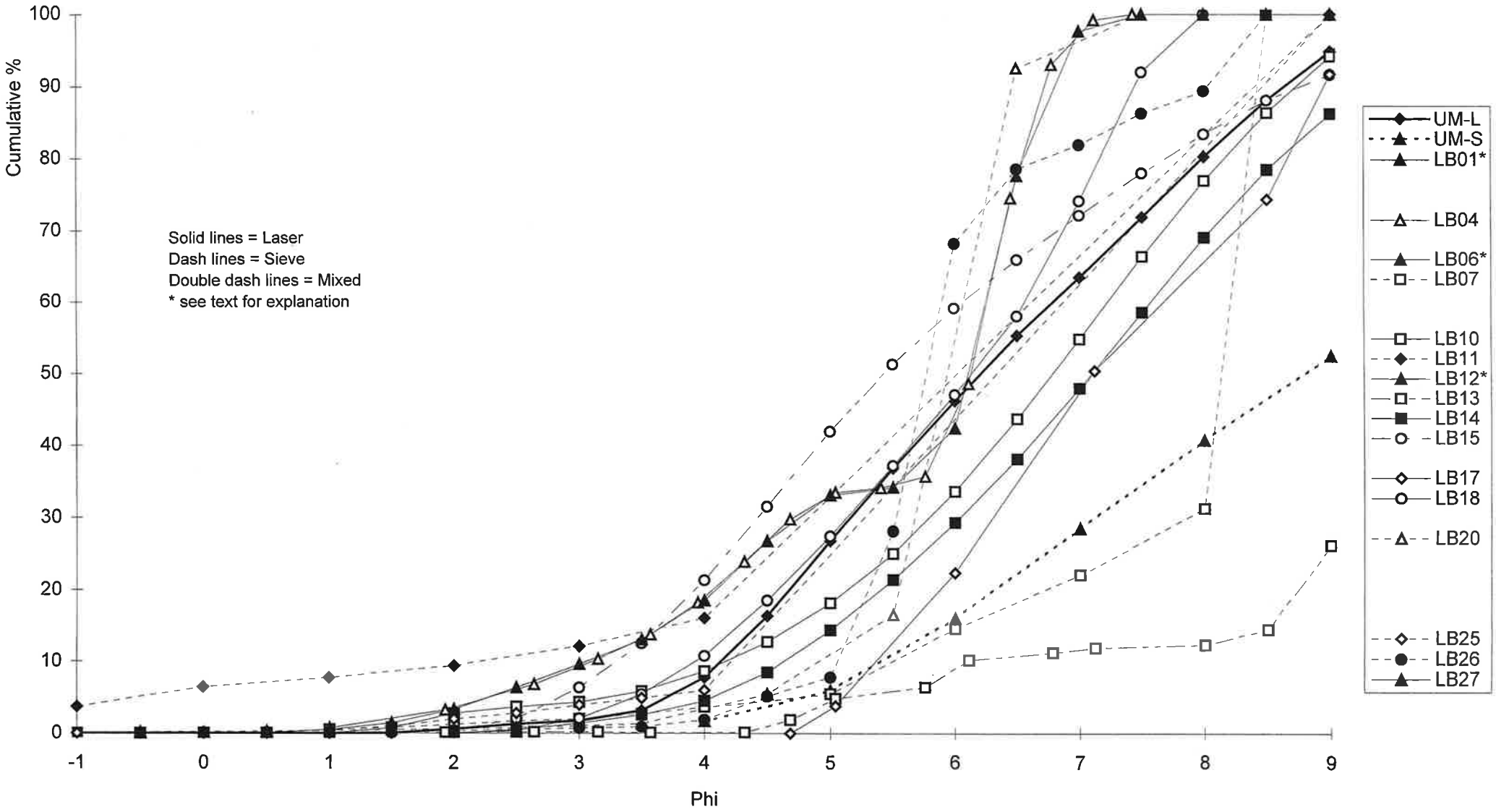


Figure 4. Particle size distribution curves from participating laboratories for sediment samples from PS11. The average values for the AQC analysis of replicates are included.

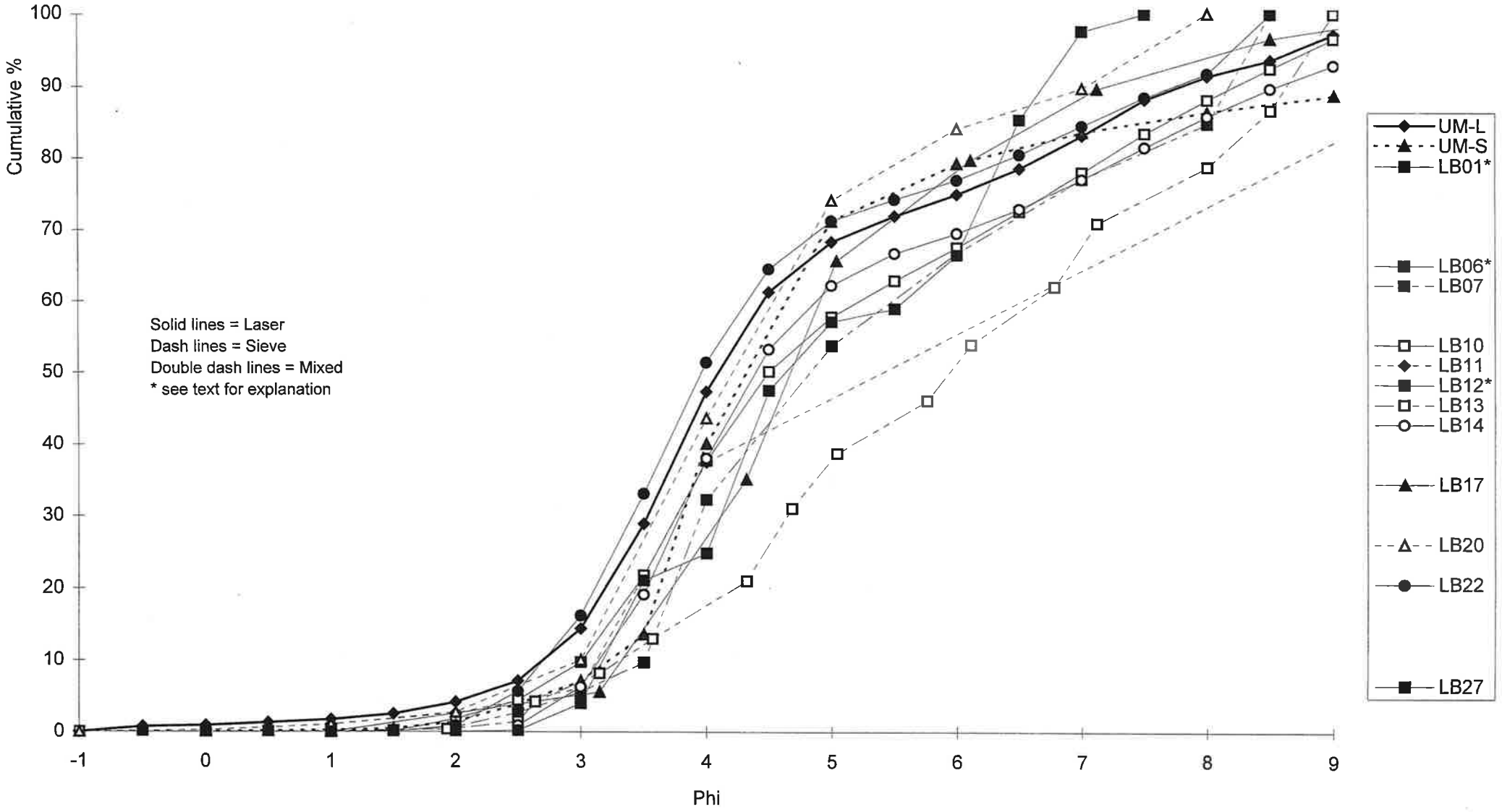


Figure 5. The number of differences at the level of genus and species recorded for each of the participating laboratories for RT10. Arranged in order of increasing number of differences at the level of species.

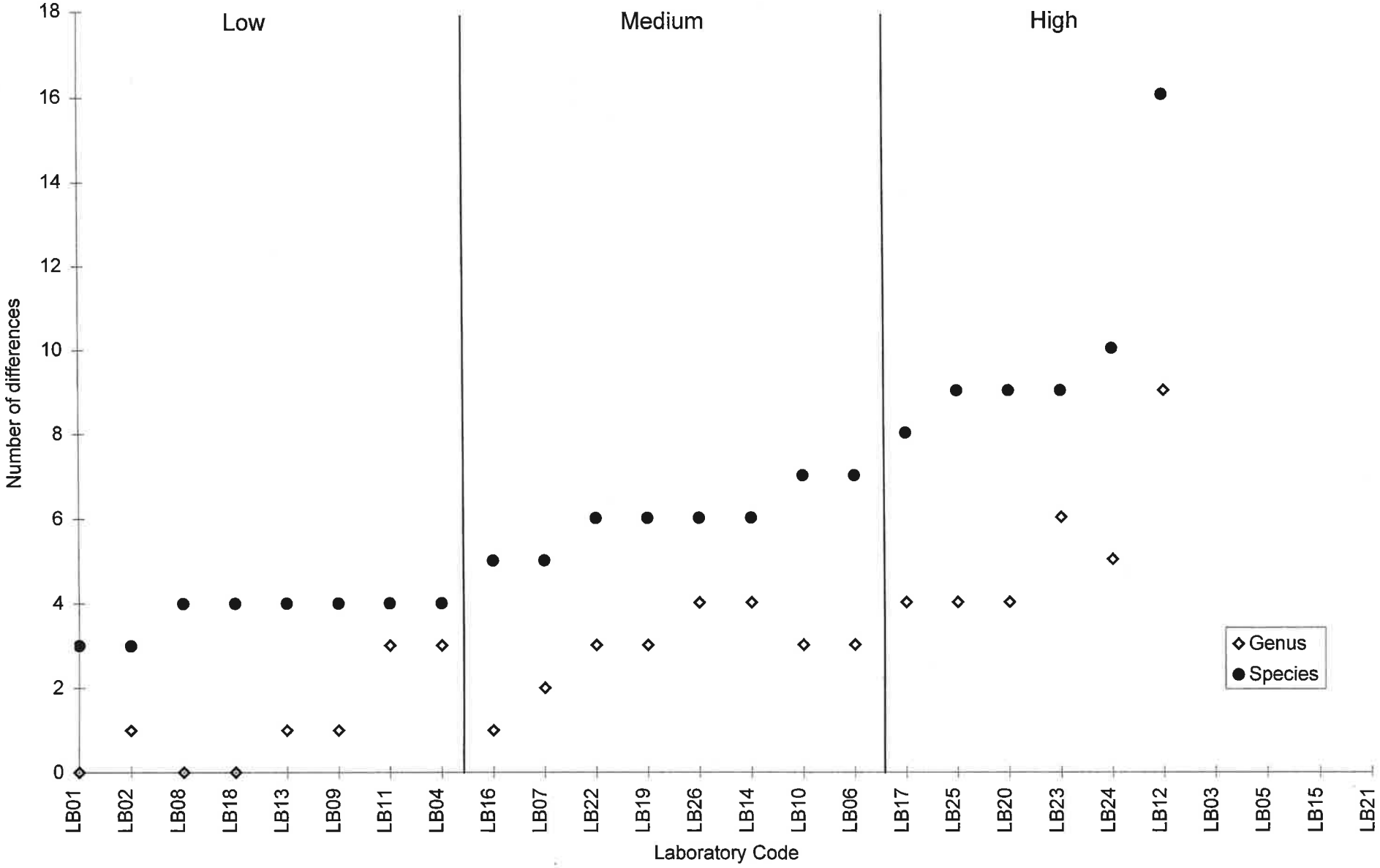
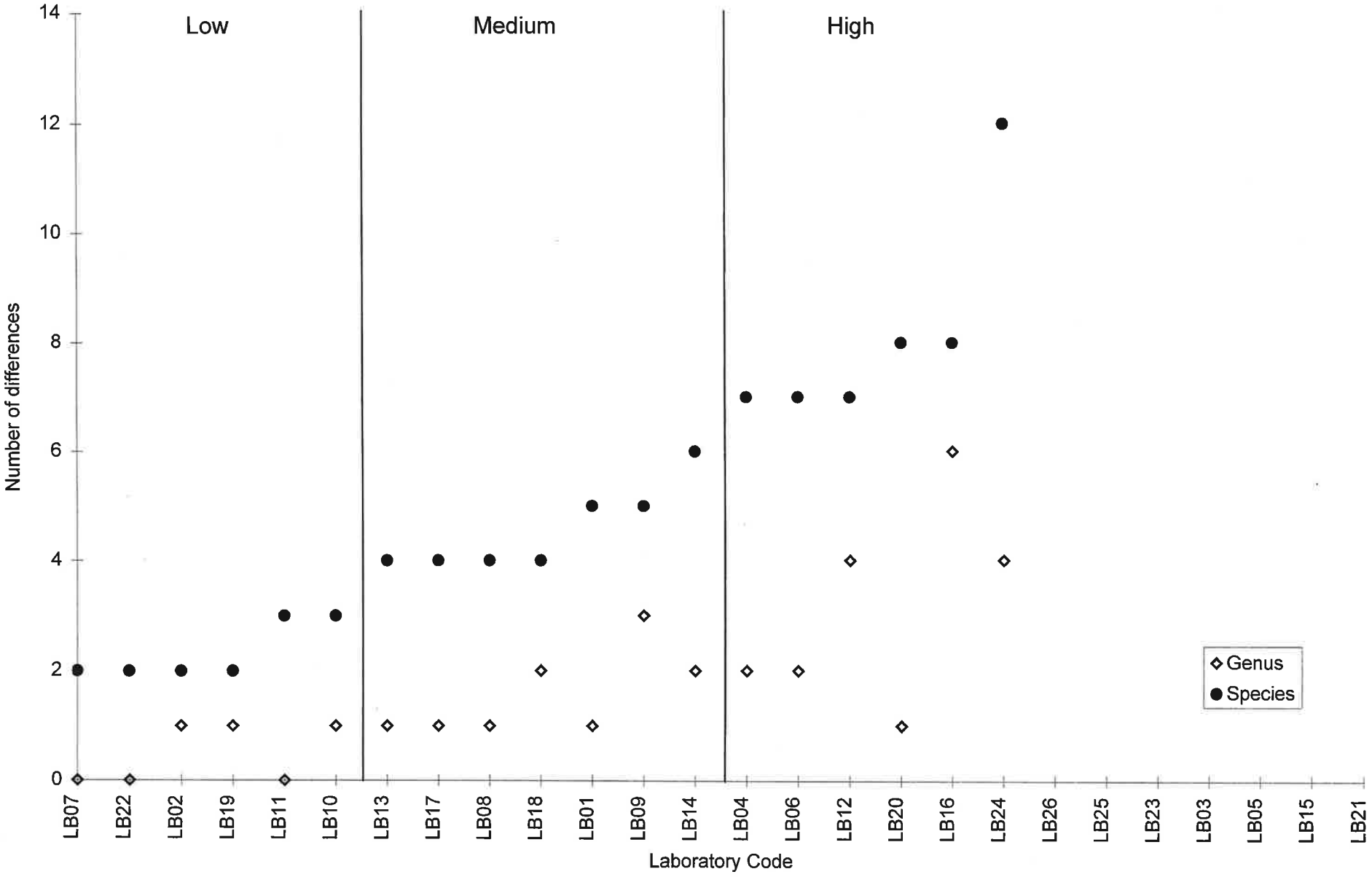


Figure 6. The number of differences at the level of genus and species recorded for each of the participating laboratories for RT11. Arranged in order of increasing number of differences at the level of species.



Appendix 1

List of groups from which specimens should be selected for LR02.

	Major Group	Group	Note
1	Oligochaeta	Tubificidae	
2	Polychaeta	Ampharetidae	
3	Polychaeta	Cirratulidae	
4	Polychaeta	Nephtyidae	
5	Polychaeta	Nereididae	
6	Polychaeta	Phyllodocidae	
7	Polychaeta	Sigalionidae or Polynoidae	Choose one
8	Polychaeta	Spionidae	
9	Polychaeta	Spionidae	
10	Polychaeta	Syllidae	
11	Polychaeta	Terebellidae	
12	Polychaeta	Hesionidae, Glyceridae, Goniadidae, Opheliidae, Sphaerodoridae, Eunicida, Paraonidae, Maldanidae	Choose one from the list
13	Crustacea	Ampeliscidae	
14	Crustacea	Oedicerotidae	
15	Crustacea	Another gammaridean amphipod family	Choose another family
16	Crustacea	Decapoda	
17	Crustacea	Cumacea	
18	Crustacea	Isopoda	
19	Mollusca	Gastropoda - Opisthobranchia	
20	Mollusca	Gastropoda - non Opisthobranchia	
21	Mollusca	Pelecypoda	
22	Mollusca	Pelecypoda	
23	Mollusca	Caudofoveata, Solenogastres or Polyplacophora	One specimen from one class
24	Echinodermata	Echinoidea, Holothurioidea or Ophiuroidea	One specimen from one class
25	Other	Sipuncula, Pycnogonida, Bryozoa, Cnidaria	

Appendix 2

Description of Scheme Standards

In the third year of the Scheme (1996/97) required levels of performance were set by the NMBAQC steering committee for the Own Sample and Particle Size Analysis exercises. The flags applied to the various exercises are based on a comparison of the results from sample analysis by Unicomarine Ltd. and those from the laboratory. The OS exercise has several aspects, each with a separate standard. Each of the standards has been calculated independently for 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.

1. 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.

1.1 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.

1.2 Own Sample - Total Biomass target

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

1.3 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%.

1.4 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.

2. 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
Ms. I. Baber (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	EA
Mr. J. Breen	IRTU/Industrial Science Centre

APPENDIX 2

ROLE OF THE NATIONAL MARINE BIOLOGICAL AQC COMMITTEE

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

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

APPENDIX 3

NATIONAL MARINE BIOLOGICAL AQC SCHEME

ROLE OF THE CONTRACT MANAGER

Objectives

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

2. To recommend quality materials where appropriate.

3. To manage the scheme's finances.

Schedule of Work

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

2. Implement the plan for 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 1997/98

AES Ltd: Aquatic Services Unit, University College, Cork: Centre for Environment, Fisheries and Aquaculture Science (CEFAS): Department of Agriculture Northern Ireland (DANI): Environment Agency (EA): Environmental Resources and Technology Ltd (ERT): Fawley Aquatic Research Laboratories Ltd.: Fisheries Research Science (FRS Marine Lab Aberdeen): Industrial Science Centre / Industrial Research and Technology Unit (IRTU Northern Ireland): SEAS Ltd: Scottish Environment Protection Agency (SEPA): Southern Science Ltd.: Institute of Estuarine and Coastal Sciences (IECS), Hull: Zeneca .