APPENDIX B:

Quality Control and Assessment of Infaunal Identification and Enumeration: The SCBPP Experience

Quality Control and Assessment of Infaunal Identification and Enumeration: The SCBPP Experience

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ABSTRACT

While it is recognized that the quality of studies designed to measure anthropogenic impacts on marine benthic organisms fundamentally depends on the ability of taxonomists to consistently discriminate, identify, and count organisms, few attempts have been made to carry out formal quality control and assessment programs for infaunal identification and enumeration. In this paper, the quality control and assessment procedures for taxonomic identification that were developed for the Southern California Bight Pilot Project (SCBPP) are described and evaluated. Quality control and assessment were based upon the reanalysis of 10% of the samples processed by each of four laboratories. Overall error rates were 3.4% in number of taxa reported, 2.1% in total organism counts, and 4.7% in accuracy of identifications. Approximately 13% of the records examined contained an identification or counting error. The synoptic review of the data, along with sample reanalysis, revealed additional taxonomic problems that were resolved by combining taxa into higher taxonomic categories. Approximately 80% of the 92,570 specimens collected in the survey were identified to species level. The quality control procedures not only provided data for measurements of error in identification and enumeration, they also provided education and feedback that improved the quality of the taxonomy and thus the data for the project. The levels of error measured in this study provide the first data points for developing control limits around identification and abundance measures for multi-laboratory taxonomic analysis. The incorporation of these or similar procedures, having been proven successful for assessing the accuracy of the taxonomic analysis of infaunal samples, is recommended for subsequent regional surveys.

INTRODUCTION

In southern California, quality assurance procedures are routinely included in environmental monitoring programs. Standard protocols are used for sample handling (e.g., fixation, preservation, labeling and storage), counting, and identification. Quality assurance for identification is primarily based on cooperation and communication among taxonomists through participation in the Southern California Association of Marine Invertebrate Taxonomists (SCAMIT). SCAMIT, founded in 1982, holds monthly workshops on the taxonomy of the invertebrate fauna of the region. The minutes and products of these workshops are distributed to members in a monthly newsletter. In addition, SCAMIT maintains and distributes a taxonomic listing of soft-bottom species (SCAMIT 1996) that represents the consensus of its members for standard usage of taxa names in infaunal monitoring programs within the region.

While quality assurance for taxonomic identification is routine, quality control is less common. Environmental monitoring programs have long incorporated formal quality control procedures for analysis of chemical and physical samples. Calibration standards, blanks, and duplicates are standard quality control measures. Quality assessment is provided by analysis of performance evaluation samples, performance audits and, in some cases, participation in interlaboratory calibrations. However, while it has been recognized that the quality of studies designed to measure anthropogenic impacts on benthic organisms fundamentally depends on the ability of taxono-

mists to consistently discriminate, identify, and count organisms, few attempts have been made to carry out formal quality control and assessment programs for infaunal identification and enumeration.

Programs that have included quality control often use voucher material that is examined by an "expert" for confirmation of identifications. This approach assumes that the voucher material accurately represents all the specimens reported under that name. It does not allow assessment of the accuracy of identifications or counts and provides little information to characterize the quality of the data.

In some programs, 10% of the samples in each survey are reanalyzed. However, the results of the reanalysis are not used to formally assess data quality. The objective of these quality control activities has been to correct the detected errors rather than determine rates of error that may be used to characterize the accuracy of survey results.

Prior to the SCBPP program, measures to assess data quality had not been developed. Ellis (1985) suggested that quality control for biological surveys should measure accuracy and precision of taxonomic identification. Ellis defined accuracy as the allocation of a specimen to the correct taxon and precision as the allocation of all members of a taxon to the same taxon. However, Ellis did not suggest how accuracy and precision should be measured.

MATERIALS AND METHODS

Background

In 1994, 12 agencies began planning a cooperative regional survey called the Southern California Bight Pilot Project (SCBPP). The objective of the survey was to measure the ecological health of soft-bottom benthic fish and infaunal communities on the mainland shelf of southern California (see SCCWRP 1996 a,b for more information). Since data produced by taxonomists from four agencies would be integrated into a single data set, taxonomic accuracy and consistency was a major concern. The challenge of achieving accurate and consistent results, inherent in any large survey of infaunal organisms, was compounded by differences in the expertise, experience, and opinion of the many taxonomists involved in the analysis. Quality assurance procedures were needed to minimize the effects of these variables. Methods to characterize the effectiveness of the quality assurance program and quantify the resulting data quality (quality control and assessment) were also needed. In this paper, the quality control and quality assessment procedures for taxonomic identification that were developed and implemented for the SCBPP are described and evaluated.

Methods and Materials

Representatives of the agencies responsible for processing samples (Table 1) joined in a cooperative effort to design a quality assurance plan for the analysis of samples from the SCBPP. In a series of meetings, consensus was reached on goals, procedures (both analytical and quality control), measurement quality objectives (MQOs), and reporting requirements. The goal of taxonomic analysis for the SCBPP was species-level identification of all macrobenthic organisms collected and an accurate count of each species. Seventeen taxonomists participated in the analysis of SCBPP infaunal samples (Table 2). While the goal was species-level identification, it was understood that in some cases higher level identifications would be necessary because of difficulties in taxonomy. For these groups, the level of identification was specified in advance (Table 3). An MQO of 10%, representing the maximum allowable deviation from the "true" value, was established for number of taxa, total number of organisms, and identification accuracy. Identification accuracy was based upon the number of taxa misidentified expressed as a percentage of the total number of taxa present.

In order to determine whether the quality assurance procedures were effective (i.e., MQOs were met), a formal quality control and assessment exercise was designed based upon the reanalysis of a subset of infaunal samples. This exercise included five steps: (1) sample reanalysis, (2) discrepancy reporting, (3) discrepancy resolution, (4) error classification and tallying, and (5) calculation of the percent error of the analysis.

For the exercise, a randomly selected 10% of the samples (N = 26) processed by each lab were redistributed among the other three labs for reanalysis. However, records of the results from the reanalysis of six samples were lost prior to error classification and could not be included in this analysis. The 20 samples reanalyzed represented 7.9% (20/252) of the infaunal samples collected in the SCBPP. A total of 1,715 records (i.e., a taxon and its reported abundance) as originally reported were considered, or 8.2% of the 20,765 records as originally submitted to the SCBPP infaunal database.

The same procedures and rules employed in the original analysis were followed for the reanalysis. During reanalysis, the taxonomists were not given access to the original results. When the reanalysis was complete, differences between the first and second analyses were listed on a Quality Control Discrepancy Report.

Staff from the two labs then met to resolve the discrepancies. Discrepancies in counts of more than 5% were resolved by a recount by the reanalytical lab. If an agreement could not be reached on taxonomy, the issue was

TABLE 1. SCBPP Infaunal Group responsible for developing protocols for QA/QC of infaunal samples.

NAME	REPRESENTING
David Montagne, Chair	County Sanitation Districts of Los Angeles County
Donald Cadien	County Sanitation Districts of Los Angeles County
George Robertson	County Sanitation Districts of Orange County
Douglas Diener (MEC Analytical Systems, Inc.)	County Sanitation Districts of Orange County
Ann Dalkey	City of Los Angeles, Environmental Monitoring Division
Charles Phillips	City of Los Angeles, Environmental Monitoring Division
Ronald Velarde	City of San Diego, Metropolitan Wastewater Department
Dean Pasko	City of San Diego, Metropolitan Wastewater Department

TABLE 2. Taxonomists responsible for analysis of SCBPP infaunal samples.

ANNELIDS	ARTHROPODS	MOLLUSCS	ECHINODERMS	MISC. PHYLA
Kelvin Barwick [1]	Donald Cadien [2]	Kelvin Barwick [1]	Donald Cadien [2]	Donald Cadien [2]
Cheryl Brantley [2]	Douglas Diener [5]	Donald Cadien [2]	Nancy Carder [6]	John Ljubenkov [5]
Ann Dalkey [3]	Dean Pasko [1]	Megan Lilly [1]	Megan Lilly [1]	Dean Pasko [1]
Lawrence Lovell [4]	James Roney [3]	John Ljubenkov [5]	James Roney [2]	Charles Phillips [3]
Ricardo Martinez-Lara [1]	Timothy Stebbins [1]	Charles Phillips [3]		
Thomas Parker [2]				
Charles Phillips [3]				
Rick Rowe [1]				
Ronald Velarde [1]				

[1]City of San Diego, Metropolitan Wastewater Department
[2]County Sanitation Districts of Los Angeles County
[3]City of Los Angeles, Environmental Monitoring Division
[4]L. Lovell (for County Sanitation Districts of Orange County)
[5]MEC Analytical Systems, Inc. (for County Sanitation Districts of Orange County)
[6]N. Carder (for County Sanitation Districts of Orange County)

TABLE 3. Groups specified in the laboratory procedures that were to be identified to higher taxonomic classifications.

GROUP	LEVEL OF IDENTIFICATION
Nematodes	Phylum
Kinorhynchs	Phylum
Oligochaetes	Class
Hirudinean Annelids	Class
Podocopid Ostracods	Order
Harpacticoid Copepods	Order
Phoronids	Genus
Enteropneust Hemichordates	Class

presented to the Chairman of the Infaunal Group for resolution. To facilitate the process, four workshops were held in which the taxonomists jointly met for discrepancy resolution.

The results of the discrepancy resolution were reported on a Discrepancy Resolution Report. Discrepancies were classified as either errors or differences in taxonomic judgment. The report allowed all errors in the original results to be classified and their effects tallied. Inaccurate identifications and counts, specimens overlooked in the original analysis, and violations of counting or identification rules were classified as errors.

Discrepancies that were the result of differences in taxonomic judgment, while not considered an error on the part of the original analyst, were tallied. For instance, a discrepancy between a report of *Polydora* sp. and *Polydora narica* does not represent an error, but rather a decision by one taxonomist to identify the specimen only to genus level. This decision may be based on the taxonomist's judgment that the specimen's condition is too poor for species identification, or may reflect the taxonomist's lack of expertise in that particular group of organisms. Discrepancies resulting from nomenclatural inconsistencies, apparent specimen loss, or failure to note removal of specimens for vouchers were also noted but not included in the assessment of data quality as they were not considered to be errors. A discrepancy in nomenclature is easily corrected by data editing. Specimen loss and failure to note vouchers are post-processing procedural problems that do not affect the original results.

After the infaunal data were compiled into a database, the taxonomists synoptically reviewed the list of species identified by each laboratory for taxonomic consistency. Possible inconsistencies revealed by this review were investigated by examination of voucher specimens and, if necessary, sample material. When the taxonomists could not consistently identify specimens at the level reported, taxa names were changed to ensure consistency within the data. In most cases, a higher taxonomic classification was used. Taxa that were found to be problematic were not included in

the analysis because it was assumed the inability to identify specimens was caused by the general state of knowledge, not by individual performance.

For quality assessment of the final data set, the results of the sample reanalysis exercise were used to calculate the percent error of analysis for number of taxa ($\%Err_{No.\ Tax}$), total organism count ($\%Err_{No.Orgs}$), and identification accuracy ($\%_{ErrID}$). The percent error in the number of taxa and number of organisms counted provide measures of data quality for such metrics as species richness, abundance, and diversity. Identification accuracy, expressed as percent error in identification of individual taxa, provides a measure of how well the data represent community composition. The error rates were calculated as follows:

$$\%Err_{No.Tax} = 100 * \left(No.Tax_{Resolved} - No.Tax_{Original} / \ No.Tax_{Resolved} \right)$$

$$\%Err_{No.Orgs} = 100 * \left(No.Orgs_{Resolved} - No.Orgs_{Original} / \ No.Orgs_{Resolved} \right)$$

$$ID_{Accuracy} = 100 * \left(No.Tax_{Misid} / No.Tax_{Resolved} \right)$$

Percent error in the number of taxa and number of organisms may be either positive or negative. Mean percent error was calculated for each laboratory and for the overall project.

RESULTS

In the reanalysis of 20 samples (1,715 records), approximately 436 discrepancies between the two analyses were initially reported (Table 4), disregarding errors on the part of the reanalytical lab. Approximately 52% of the discrepancies were classified as errors. The remaining discrepancies were caused by factors that were not considered to be errors, including differences in the taxonomic level to which the analysts identified the specimen, apparent loss of specimens, failure to note removal of voucher specimens, or nomenclatural inconsistencies.

Errors were detected in approximately 13% of the records examined (Table 5). The incidence of miscounts and misidentifications was 5.0 and 4.5%, respectively. In the initial identification, 3.3% of the taxa were overlooked. A small number of records (0.3%) was included that should not have been because the records were specifically excluded by the counting and identification rules. Percent error of analysis in number of taxa, total organism count, and identification accuracy were 3.4, 2.1, and 4.7%, respectively (Table 6).

Taxa that were excluded from the calculation of error based on the reanalysis exercise and synoptic review of the data are shown in Table 7. In most instances, only two or three names were combined in one taxonomic category. However, 15 taxa were combined within the harmothinae polychaetes as well as within the polychaete genus *Lumbrineris*. Over 10 taxa were combined within lineid nermerteans and maldanid polychaetes, respectively.

DISCUSSION

The objective of the quality control and assessment procedures was to measure errors relative to measurement quality objectives. For the SCBPP, the goal of taxonomic analysis was species-level identification of all macrobenthic organisms collected and an accurate count of each species. To determine if this goal had been achieved, MQOs were established for the number of taxa, total number of organisms, and identification accuracy.

In practice, species-level identification of all specimens is not possible. A number of obstacles are always present, not the least of which is the state of knowledge of the taxonomy of infaunal species. Some groups in southern California are comparatively well known (e.g., bivalve molluscs), while others are relatively unknown (e.g., nemerteans). A substantial number of unrecognized species may be assumed to be present on the mainland shelf. In addition, the condition of many specimens will prevent species-level identification. These factors, along with differences in the levels of experience and areas of expertise among taxonomists, are present in any survey of this kind and will directly impact the survey results.

While it was recognized at the beginning of this study that some groups could not be identified to species (Table 3), the process of reanalysis and the synoptic review of survey results revealed more taxa that could not be accurately and consistently identified (Table 7). Anthozoans, nemerteans, holothurians, and ascidians, for the most part, could not be identified with the current state of knowledge. It was also discovered that some groups of polychaetes, particularly species in the genus *Lumbrineris*, some species of maldanids, and species in the genera *Malmgreniella* and *Harmothoe*, could not be consistently identified. These problems arose despite efforts by local taxonomists (through SCAMIT) to reach consensus on the treatment of most of these groups.

The cumulative result of all of these factors was that almost 20% of the specimens collected in the SCBPP survey could not be identified to species (Table 8). The inability to accurately identify to species leads to underestimates of community diversity and species richness. Wu (1982) demonstrated that genus or higher level identifications, which he referred to as taxonomic uncertainty, may be an important source of error in the calculation and interpretation of diversity indices.

The process of resolving discrepancies and classifying errors presented a number of difficulties. Measuring error in identification was complicated by the fact that there is no absolute benchmark in taxonomy. The identity of a speci-

TABLE 4. Classification and prevalence of discrepancies discovered during quality control reanalysis. An example of misapplication of identification rules is inclusion of epibionts in counts. Discrepancies classified as errors for purposes of data quality assessment are shown in boldface.

TYPE OF DISCREPANCY	# OF CASES	% OF DISCREPANCIES REPORTED
Judgmental Differences	131	30.0%
Miscount	**83**	**19.0%**
Misidentification	**78**	**17.9%**
Specimen(s) Overlooked	**57**	**13.1%**
Apparent Specimen Loss/ Voucher Removal	57	13.1%
Nomenclatural Inconsistency	23	5.3%
Misapplication of Id Rules	**5**	**1.1%**

TABLE 5. Classification and incidence of errors discovered during quality control reanalysis. A record is a taxon and its reported abundance. An example of misapplication of identification rules is inclusion of epibionts in counts. Percentages preceded by + or - are cases where net result of errors was an understatement (-) or overstatement (+) of the number of records in the original results.

TYPE OF ERROR	% OF RECORDS AFFECTED
Miscount	5.0%
Misidentification	4.5%
Specimen(s) Overlooked	-3.3%
Misapplication of ID Rules	+0.3%

TABLE 6. Summary of quality control results and calculation of error of analysis. MQO=Measurement Quality Objective.

Analytical Lab	# of Samples Receiving QC-Reanalysis		Analysis of Error: Mean % error *Range*			# of Samples Exceeding MQO of 10% in Error of Analysis		
	Planned	Actual	# of Taxa	Total Count	ID Accuracy	# of Taxa	Total Count	ID Accuracy
A	6	6	4.8% *2.9 - 5.9*	3.1% *2.2 - 6.1*	6.9% *4.3 - 10.5*	0	0	1
B	4	2	1.8% *1.2 - 2.3*	1.0% *0.3 - 1.5*	3.6% *2.3 - 5.0*	0	0	0
C	8	6	4.5% *1.0 - 9.2*	2.2% *0 - 3.1*	3.0% *0 - 4.3*	0	0	0
D	8	6	1.1% *0 - 2.0*	1.5% *-1.2 - 4.9*	4.6% *2.0 - 11.7*	0	0	1
All Labs	26	20	3.4% *0 - 9.2*	2.1% *-1.2 - 6.1*	4.7% *0 - 11.7*	0	0	2

men is not always clear and, to some degree, identifying a species involves judgment. In many cases, characteristics that are used to identify specimens develop with the growth of the organism; small juveniles can only be identified to genus or some higher taxonomic category.

The point at which a taxonomist is comfortable with a specific identification varies with experience and other factors. The characters that are used to identify species are, in some cases, variable. The literature is often ambiguous or incomplete. For these reasons, there may be cases where one taxonomist is comfortable with a species-level identification and another is not. In other words, differences between taxonomists may be caused by legitimate differences in opinion, and not by error or misjudgment. Thus, for quality control, it is necessary to discriminate such judgmental differences from error. While not considered errors, these differences in the level of identification are as important a cause of measurement variability as misidentification and miscounts. Furthermore, they create an unavoidable source of noise in the results. Almost 8% of the records in this study were affected by this factor.

To determine counting errors, it was necessary to develop ad hoc approaches to some of the more intractable difficulties. When slightly fewer specimens of a species were counted in the reanalysis than originally reported, it was particularly difficult to accurately classify and scale errors in counting. A lower count could be caused by an overcount by the original taxonomist; a commingling, in part, of two species; a difference in the level of identification applied to some of the specimens; failure to note

TABLE 7. Level of taxonomic identification resulting from reidentification of specimens and review of data.

TAXONOMIC GROUP	NAME ADOPTED AFTER QA/QC	TAXONOMIC LEVEL	# OF TAXA COMBINED
PHYLUM CNIDARIA			
Class Anthozoa	Ceriantharia	Order	4
Class Anthozoa	Actiniaria	Order	5
Class Anthozoa, Order Pennatulacea	*Acanthoptilum* spp.	Genus	3
PHYLUM NEMERTEA			
Class Anopla	Anopla	Class	7
Class Anopla	Palaeonemertea	Order	2
Class Enopla, Order Hoplonemertea	Hoplonemertea	Order	3
Class Enopla, Order Hoplonemertea	Lineidae	Family	12
Class Enopla, Order Hoplonemertea	*Amphiporus* spp.	Genus	4
Class Enopla, Order Hoplonemertea	*Tetrastemma* spp.	Genus	2
PHYLUM MOLLUSCA			
Class Aplacophora, Order Aplacophora	Chaetodermatidae	Family	5
Class Gastropoda, Order Megagastropoda	*Bittium* spp.	Genus	2
Class Gastropoda, Order Megagastropoda	*Asperiscala* spp.	Genus	2
Class Gastropoda, Order Megagastropoda	*Nitidiscala* spp.	Genus	2
Class Gastropoda, Order Megagastropoda	*Crepidula* spp.	Genus	4
Class Gastropoda, Order Neogastropoda	*Ophiodermella* spp.	Genus	3
Class Bivalvia, Order Veneroida	*Solen* spp.	Genus	2
Class Bivalvia, Order Myoida	*Corbula* spp.	Genus	2
Class Bivalvia, Order Septibranchida	*Cardiomya* spp.	Genus	2
PHYLUM ANNELIDA			
Class Polychaeta, Order Orbiniida	*Levinsenia* spp.	Genus	3
Class Polychaeta, Order Cossurida	*Cossura* spp.	Genus	2
Class Polychaeta, Order Spionida	*Protocirrineris* spp.	Genus	2
Class Polychaeta, Order Spionida	*Monticellina* spp.	Genus	5
Class Polychaeta, Order Capitellida	*Mediomastus* spp.	Genus	3
Class Polychaeta, Order Capitellida	*Clymenella* spp.	Genus	3
Class Polychaeta, Order Capitellida	Maldanidae	Family	11
Class Polychaeta, Order Opheliida	*Ophelina* spp.	Genus	2
Class Polychaeta, Order Phyllodocida	Harmothoinae	Subfamily	15
Class Polychaeta, Order Phyllodocida	*Sthenelais* spp.	Genus	3
Class Polychaeta, Order Phyllodocida	*Sphaerosyllis* spp.	Genus	2
Class Polychaeta, Order Eunicida	*Lumbrineris* spp.	Genus	15
Class Polychaeta, Order Eunicida	*Drilonereis* spp.	Genus	3
Class Polychaeta, Order Fauveliopsida	*Fauveliopsis* spp.	Genus	3
Class Polychaeta, Order Terebellida	*Terebellides* spp.	Genus	2
Class Polychaeta, Order Sabellida	*Demonax* spp.	Genus	2
PHYLUM ARTHROPODA			
Class Malacostraca, Order Leptostraca	*Nebalia* spp.	Genus	3
Class Malacostraca, Order Isopoda	*Edotia* spp.	Genus	2
Class Malacostraca, Order Isopoda	*Synidotea* spp.	Genus	2
Class Malacostraca, Order Amphipoda	*Aorides* spp.	Genus	6
Class Malacostraca, Order Amphipoda	*Photis* spp.	Genus	4
Class Malacostraca, Order Amphipoda	*Protomedeia* spp.	Genus	2
PHYLUM ECHINODERMATA			
Class Holothuroidea	Holothuroidea	Class	2
PHYLUM CHORDATA			
Class Ascidiacea	Ascidiacea	Class	4

TABLE 8. Performance relative to goal of species-level identification of all macrobenthic organisms collected. 781 species-level taxa were reported in the survey.

LEVEL OF IDENTIFICATION	# OF ORGANISMS	% OF TOTAL ORGANISMS
Species-Level Identification	74746	80.7%
Higher Level Identification	17824	19.3%

removal of specimens to a voucher collection; or loss in handling. The first two reasons (miscounting and misidentification) would be evidence of error, while the latter three would not.

In practice, unless there was substantial difference in the count, making the magnitude of loss implausible, or the species was one not easily lost in handling (e.g. large species), or there was evidence of commingling under another name (e.g., an offsetting undercount of a closely related or similar species or taxon), the original count was accepted and the discrepancy attributed to specimen loss. The effect of this rule is that specimen loss is probably substantially overstated and errors from miscounts understated. If the reanalysis found more specimens than originally reported, in the absence of plausible evidence of misidentification, the higher count was accepted and the original analysis was credited with a counting error. The effect of these rules was a bias towards acceptance of the original count if it was more than the reanalytical count. The result was that most miscount errors were undercounts rather than overcounts.

The problem with differentiating specimen loss and miscounts cannot be eliminated. Taking steps to ensure closer adherence to sample processing rules can eliminate un-annotated voucher-specimen removal as a source of confusion and minimize specimen loss. Such measures would allow all cases of apparent overcount by the original analysts to be treated as counting error (in the absence of strong evidence to the contrary). This approach would slightly overstate counting error, which would result in a more conservative estimate.

To assess data quality, error rates were calculated for three community characteristics central to the analytical use of the data: number of taxa, number of organisms, and the identity of the organisms reported. The analysis of error indicates that overall the MQOs of 10% were met for all three types of error (Table 6). In 2 of 20 samples, the rate of error in identification accuracy exceeded the MQO (10.5 and 11.7%).

It is difficult to put these error rates into context. As this was the first attempt to use reanalysis results to assess rates of error in taxonomic analysis of infaunal samples, the MQO of 10% in the laboratory manual was arbitrarily chosen. However, careful attention was given to the quality of the taxonomy throughout the program. The taxonomists involved had long-term involvement in SCAMIT's efforts to standardize regional infaunal taxonomy. Prior to sampling, the taxonomists agreed to standardized protocols for nomenclature and orthography. For some groups, taxonomic keys were developed for use in the project. Cooperative training and assistance in taxonomy was provided by a series of workshops jointly sponsored by the SCBPP and SCAMIT. Twenty-three workshops were held between June 1994 and August 1995. Given the experience of the taxonomists and the attention given to taxonomy, it is reasonable to assume that the error rate was low.

More importantly, the results provide a standard against which subsequent efforts within the region may be judged. Integration of these or similar measures into the quality assurance plans for regional monitoring will greatly increase the likelihood of producing results that are accurate and comparable. The levels of error measured in this study provide the first data points that can be used to develop control limits around identification and abundance measures for multi-laboratory taxonomic analysis in subsequent regional surveys. As additional measures of error are accumulated and control limits defined, participating laboratories could be held responsible for maintaining data quality within those limits.

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