

**Deepwater Horizon Oil Spill (DWHOS)
Water Column Technical Working Group**

NRDA Offshore Fish and Nekton Sample Processing Plan

**Principal Investigator: Dr. Tracey Sutton
Virginia Institute of Marine Science**

May 25, 2012

Prepared by:

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Proposed Work Period

February 1, 2012 – July 1, 2013 (18-months of effort is budgeted in this plan)

1.0 Project Description

The purpose of the NRDA Fish and Nekton Sample Processing Plan is to establish a protocol for the analysis of fish and large invertebrate samples collected during the Natural Resource Damage Assessment (NRDA) associated with the Deepwater Horizon Oil Spill (DWHOS). The samples to be analyzed under this plan include those collected as part of the cruises listed in Table 1 and depicted in Figures 1-3. The first sample processing priority will be completion of family-level identification (Table 2) and associated counts. After this initial processing, full taxonomic identification is prioritized by cruise, gear type and timing of sampling (Table 1). Dr. Tracey Sutton (Virginia Institute of Marine Science, VIMS) will be the project Principal Investigator (PI).

Due to the large number of NRDA fish and nekton samples and the projected timing for the completing species-level identifications, the priority is to (i) compile counts for midwater trawl samples sorted to the family level onboard the ship, (ii) sort the 10 m² MOCNESS samples to the family level and conduct counts, and (iii) sort and conduct family-level counts for the epipelagic trawl samples. After family-level counts have been completed, all specimens will be identified to the lowest possible taxonomic level. Priorities for completing species-level identification will be assigned based on two categories: month sampled (priority on April-July) and gear type (midwater trawls, epipelagic trawl, and 10 m² MOCNESS). Priorities by cruise are listed in Table 1. The prioritization scheme may be updated via amendments to this plan as the sample processing ensues.

The data products to be prepared for specimens identified to family- and species-level will be: (i) quarterly progress reports (see Section 7), (ii) electronic data reports (prepared upon completion of family-level identification for all samples from a cruise and upon completion of full taxonomic identifications for all samples from a cruise), and (iii) a final, comprehensive data report with summaries of data generated as part of this plan. At the species level, data products include taxonomic identifications, biomass measurements, counts, and length/width measurements of the nekton samples listed in this plan. At the family level, data products include taxonomic identifications and counts of the nekton samples listed in this plan. As has been the case in all other processing plans, the data report will not include any analysis, evaluations, or interpretations of the data.

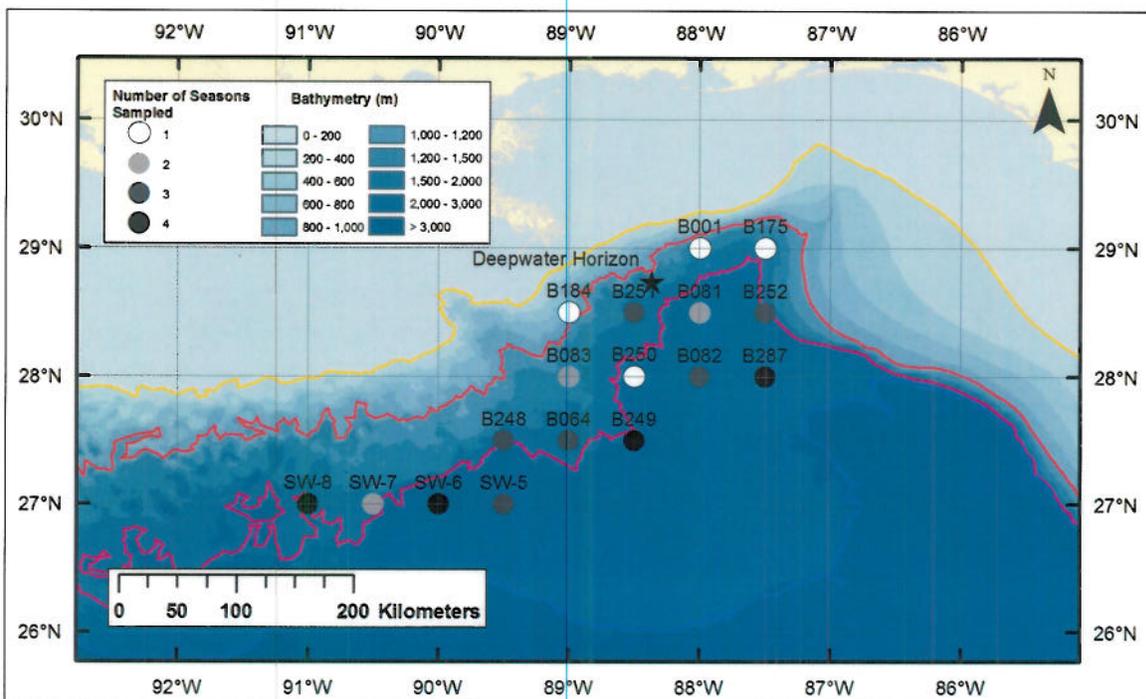


Figure 1. *Pisces* Sampling Stations – stations sampled during the December 2010, March-April 2011, June-July 2011 and September 2011 midwater trawl surveys. Symbols are colored based on the number of seasons (up to 4) each location was sampled.

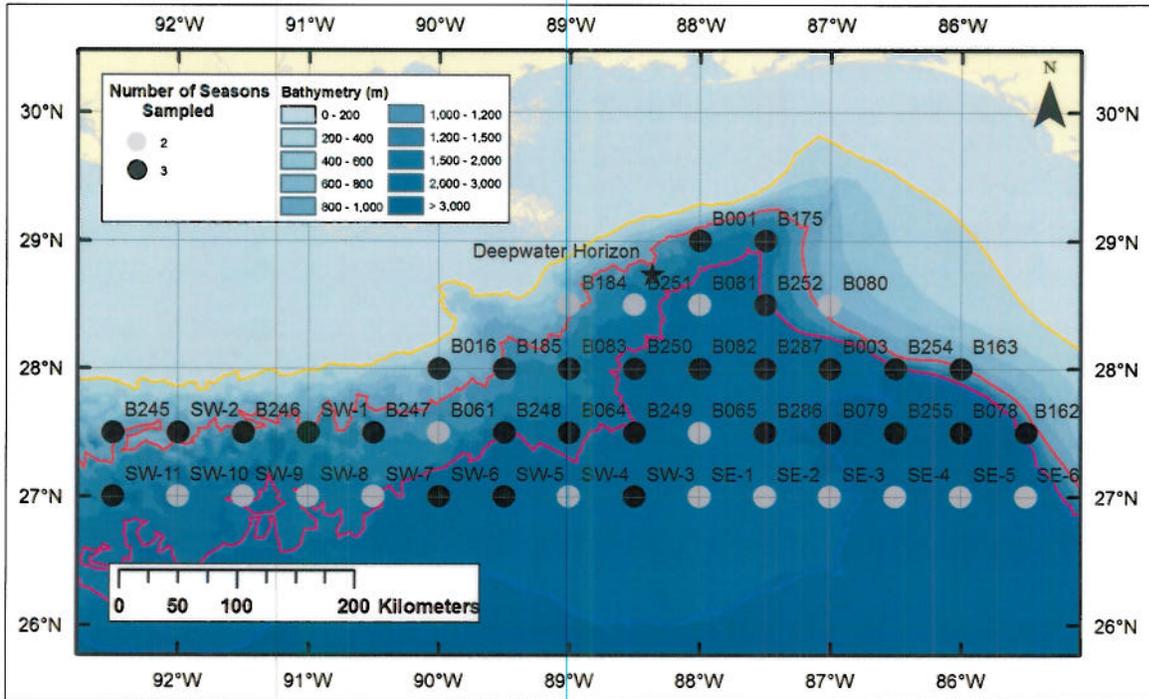


Figure 2. *Meg Skansi* Sampling Stations – stations sampled during the Winter, Spring, and Summer 2011 10m² MOCNESS surveys. Symbols are colored based on the number of seasons (up to 3) each location was sampled.

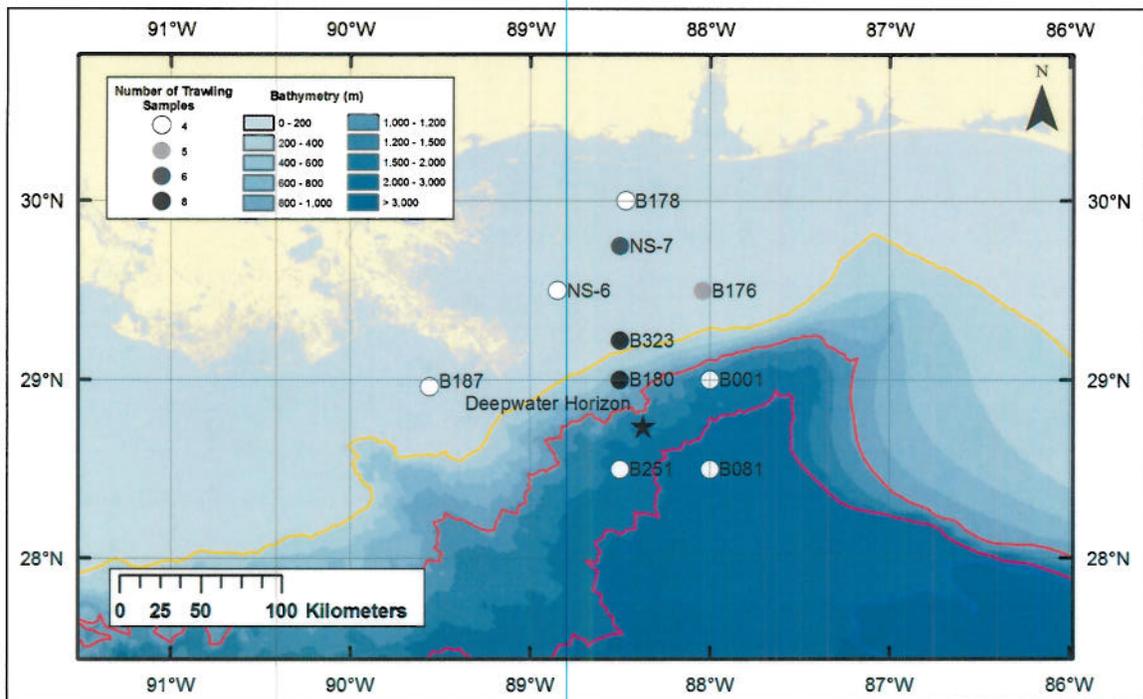


Figure 3. *McArthur II* Small Pelagics Cruise – number of epipelagic trawl deployments at each station sampled during the surveys. Symbols are colored based on the number of deployments at each location.

Table 1. Priorities for Species-Level Identifications: NRDA Water Column Technical Working Group fish and nekton sampling cruises in 2010 and 2011. All sampling occurred in the northeast Gulf of Mexico near the wellhead and in surrounding waters (see Figures 1-3). All cruises were cooperative BP/Trustee surveys.

Priority	Cruise Name	Dates	Gear Type(s) / Deployment	Sample Location as of March 2012
1	<i>Pisces</i> Summer 2011	June 21 – July 14, 2011	Mid-water Trawl Net (Deep 1500m, day/night)	VIMS
2	<i>Meg Skansi</i> Spring 2011	April 14 – June 30, 2011	10 m ² MOCNESS (Deep 1500m, day/night)	Archived at Alpha Analytical until delivery to VIMS
3	<i>McArthur II</i> Fall 2011	September 12 – October 7, 2011	Epipelagic Trawl Net (Shallow <25m, day/night)	Archived at Alpha Analytical until delivery to VIMS
4	<i>Pisces</i> Spring 2011	March 22 – April 11, 2011	Mid-water Trawl Net (Deep 1500m, day/night)	Archived at Alpha Analytical until delivery to VIMS
5	<i>Meg Skansi</i> Summer 2011	July 18 – September 30, 2011	10 m ² MOCNESS (Deep 1500m, day/night)	Archived at Alpha Analytical until delivery to VIMS
6	<i>Pisces</i> Fall 2011	September 7 – 29, 2011	Mid-water Trawl Net (Deep 1500m, day/night)	Archived at Alpha Analytical until delivery to VIMS
7	<i>Pisces</i> Winter 2010	December 1 - 20, 2010	Mid-water Trawl Net (Deep 1500m, day/night)	Archived at Alpha Analytical until delivery to VIMS
8	<i>Meg Skansi</i> Winter 2011	January 25 – April 1, 2011	10 m ² MOCNESS (Deep 1500m, day/night)	Archived at Alpha Analytical until delivery to VIMS

Table 2. Priorities for Family-Level Identifications: NRDA Water Column Technical Working Group fish and nekton sampling cruises for which samples will be processed at the family-level. Priority order indicates processing order.

Priority	Cruise Name	Dates	Gear Type(s) / Deployment
1	<i>Pisces</i> All	December 2010; Mar-Apr 2011; Jun-Jul 2011; September 2011	Mid-water Trawl Net (Deep 1500m, day/night)
2	<i>Meg Skansi</i> All	January 25 – April 1, 2011; April 14 – June 30, 2011; July 18 – September 30, 2011	10 m ² MOCNESS (Deep 1500m, day/night)
3	<i>McArthur II</i> Fall 2011	September 12 – October 7, 2011	Epipelagic Trawl Net (Shallow <25m, day/night)

2.0 Project Organization and Responsibilities

Multiple individuals will be involved in processing the samples. Dr. Tracey Sutton is the project PI and is responsible for coordination with others involved in the project and for submission of the data from each cruise and the final data products. Dr. Sutton and his Research Associates at VIMS will be the primary persons sorting the samples. In addition, Dr. Sutton's lab will be primarily responsible for the generation of abundance, biomass, size frequency, and metadata and its upload to the NOAA NRDA Content Management System. For details on data distribution, please see the distribution section below.

All work is expected to be conducted at the VIMS laboratories except for the full taxonomic identifications of the macrocrustacea portion which will be conducted by Drs. Tamara Frank (Nova Southeastern University) and Martha Nizinski (NOAA NMFS National Systematics Laboratory). Dr. Sutton's lab will sort out the macrocrustacea, as part of the initial sample sorting, and send that portion under NOAA chain of custody (COC) to Dr. Frank's laboratory at Nova Southeastern University for further processing. For more specifics, see the sample handling and COC section. Samples may also be sent to laboratories of the other expert taxonomists identified in this plan (including experts selected in the future by the Trustees, as discussed below) if determined by the Trustees that use of such laboratories will facilitate the processing of samples pursuant to this work plan. Samples shall be shipped following NOAA COC protocols and stored in secure locations under Trustee control. Laboratories receiving samples will follow the protocols of this plan.

Dr. Tracey Sutton will lead the team identifying the fishes. Dr. Sutton has an extensive background in taxonomic identification, life history, food web interaction, and habitat use of deep-sea fishes and invertebrates. He has over sixteen years of experience in the marine science discipline and deep-sea research. During this time he has published over 40 journal articles and conference proceedings, many of which deal with deep-sea species. Dr. Sutton ran the NRDA midwater trawl program on the *Pisces* for all 4 cruises and helped to develop the NRDA 10 m² MOCNESS program on the *Meg Skansi*.

Dr. Jon Moore (Florida Atlantic University), who has an extensive background in deep-sea fish taxonomy, will assist in the identification of the fishes. His research focuses around the ecology, evolution, and the conservation of marine organisms and their habitats. He has over twenty contributions to books and has published over fifty journal articles in his field.

Dr. Michael Vecchione (NOAA NMFS, National Systematics Laboratory) will oversee the identification of pelagic mollusks (cephalopod, pteropod, heteropod). Dr. Vecchione is the Director of the NOAA Fisheries National Systematics Laboratory and his current research focuses on the natural history of cephalopods and marine biodiversity. His cephalopod systematics work includes characterization of fauna in US waters, in addition to polar and deep sea environments, and life history specifics.

Dr. Heather Judkins (University of South Florida) will lead the identification effort for the cephalopod taxonomic group. Dr. Judkins' doctoral research provided the first comprehensive study of the distribution, abundance, and ecological importance of cephalopods in the Gulf of

Mexico and South Atlantic region. Dr. Judkins has numerous publications in peer-reviewed journals on cephalopod distribution, abundance, and species richness.

Dr. Marsh Youngbluth (Harbor Branch Oceanographic Institution) will lead the effort for the gelatinous species, including pyrosomes. With over 30 years in the field, Dr. Youngbluth has investigated the gelatinous fauna of open water systems around the world.

Dr. Bruce Collette (NOAA NMFS, National Systematics Laboratory) will provide consultation regarding the identification of larval and juvenile epipelagic fishes. Dr. Collette has over 30 years of experience in the field, his expertise is in economically important scombroid fishes, including tunas, mackerels, and bonitos. His work also extends to other epipelagic fishes and bottom fishes.

Dr. Heidi Banford (University of West Georgia) will provide additional consultation regarding the identification of larval and juvenile epipelagic fishes, working in concert with Dr. Collette.

Dr. Tamara Frank (Nova Southeastern University) will coordinate and lead the identification of macrocrustacea (decapods, large euphausiids, mysidaceans, large amphipods). Dr. Frank has over 30 years of experience researching pelagic macrozooplankton. Her most recent research has centered on the visual physiology of pelagic and benthic crustaceans, vertical migrations of macrozooplankton, development of *in situ* sampling instrumentation, and linkages between benthic and pelagic ecosystems.

Dr. Martha Nizinski (NOAA NMFS, National Systematics Laboratory) will assist Dr. Frank with the identification of the macrocrustacea group. Dr. Nizinski has been a zoologist with the National Systematics Laboratory for over 20 years. Her work there has been focused on research relating to biodiversity, ecology, and systematics of marine crustaceans, mollusks, and fishes.

The organization of taxonomic experts is depicted in Figure 4. As mentioned, Dr. Sutton is ultimately responsible for the execution of the work outlined in this plan. The other experts, working in concert with Dr. Sutton, cover the range of organisms likely to be found in these samples. All experts will consult each other on taxonomic identifications, follow the same processing protocols, and use the same data sheets.

Additional expert taxonomists may be used as necessary to assist with species identification and/or confirmation and will be selected by the Trustees from among individuals recommended by either the Trustees or BP. Funding from BP for expenses of any expert taxonomist not identified in this sample processing plan is conditioned on BP's approval of the selection prior to initiation of work by the expert(s). All expert taxonomists that are consulted will be referenced in the final data product along with area of expertise, affiliation, and species identified/confirmed. Notwithstanding any other provision of this plan, the Trustees reserve the right to withhold from BP all information provided by an expert not approved by BP (and supporting documentation related to the expert's work).

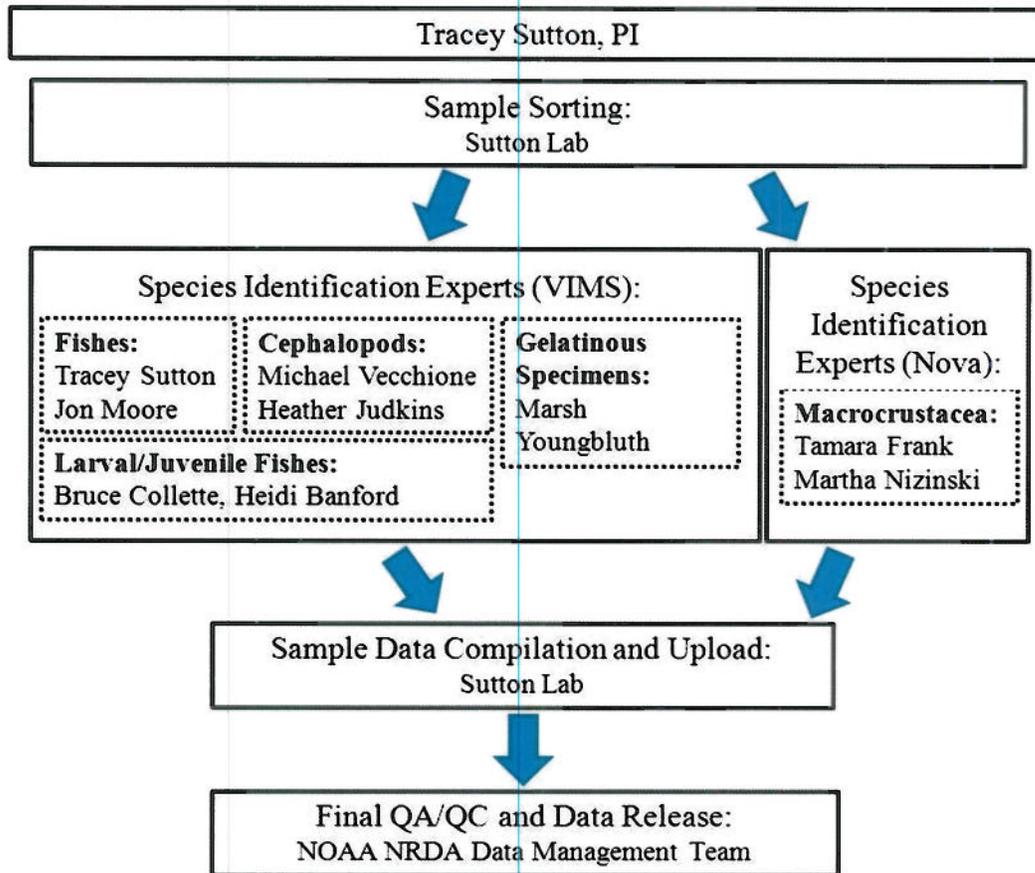


Figure 4. Organization of Experts involved in the Taxonomic Identification Process for NRDA Fish and Nekton.

3.0 Sample Handling, Chain of Custody, and Prioritization Procedures

All 10-m² MOCNESS, midwater trawl, and epipelagic trawl samples collected as part of the MC252 spill NRDA program (Table 1) will be archived at Alpha Analytical under Trustee custody. As needed, samples will be transported to Dr. Tracey Sutton at the Virginia Institute of Marine Science, under NOAA chain of custody (COC) for processing. Samples will be stored using formaldehyde, isopropanol, or ethanol at room temperature (i.e. between 12 degrees C and 32 degrees C). Upon arrival at a laboratory, the label on the lid and the internal label will be checked against the sample ID listed on the NOAA COC form and any differences will be noted on the COC form. Samples will also be checked for condition and their status noted at the time of receipt (i.e., any breakages, loss of sample, etc.). Samples will be kept in a locked, climate-controlled (room temperature) containment space, and key access will be granted directly by Dr. Sutton or a designated individual in his absence. An inventory of all samples will be conducted and samples will be prioritized (by cruise, see Table 1) prior to analysis.

Each laboratory receiving samples is equipped with locking cabinets or a lockable room where the samples will be stored at any time that they are not being actively handled for processing. At the end of each work day and when samples have been fully processed they will then be returned to the original storage location in the lockable cabinet or storage room to which access is limited

to Dr. Sutton or a designated individual. For long-term storage, specimens will generally be transferred to either 70% ethanol:water (fishes and crustaceans) or 50% isopropanol:water (other invertebrates) for long-term storage at Alpha Analytical. Sample sorting data sheets will be used to document processing of the samples in the laboratory (Attachment 5 and 6).

Subsamples may be generated as part of the initial sort and subsequent analyses. In cases of subsample generation, all new sample names will be noted in addition to the sample name of the parent sample, as directed by the NOAA NRDA Data Management Team (see Section 4). All subsamples will be held under NOAA COC. Additional comments, such as fixation medium (e.g., formalin, ethanol, isopropanol; percent dilution listed), new container size/location/sample number, container contents (species ID), etc. will be noted. The processing of samples will be tracked on the sample sorting data sheets (Attachments 5 and 6).

The macrocrustacea portion sorted from the samples by VIMS personnel will be shipped to Dr. Frank (Nova) following NOAA COC protocols. All samples will be stored in locked cabinets or rooms at the destination lab. Key access to the room with the samples will be limited to Dr. Frank or a designated individual. All sample handling will be conducted in the same manner as described for Dr. Sutton's lab. Upon completion of the identification process, samples will be returned to Alpha Analytical under NOAA COC to ensure macrocrustacea samples are archived with the other sample portions. Dr. Frank will report results to Dr. Sutton's lab where all data will be compiled for uploading to the NOAA NRDA Content Management System.

4.0 Laboratory Procedures

Samples sorted may require separation into a series of sample jars for further taxonomic analysis. As needed, sample IDs will be created and tracked for samples that are split into separate jars by having original sample IDs with suffixes added (e.g., TF### for samples split for identification in Dr. Frank's lab, or PC### for samples split for taxonomic confirmation in Dr. Sutton's lab) in conjunction with naming conventions and documentation procedures approved by the NOAA NRDA Data Management Team.

4.1 Family-Level Taxonomic Identification

All specimens collected in midwater trawl, epipelagic trawl, and 10 m² MOCNESS samples will initially be identified to the family level. For the midwater trawl samples these identifications occurred during the cruises and were completed by Dr. Sutton and Dr. Moore. For the epipelagic trawl and 10 m² MOCNESS samples, family level sorting, identification and counting will be conducted primarily by Dr. Sutton.

4.2 Species-Level Taxonomic Identification

All specimens collected in midwater trawl, epipelagic trawl, and 10 m² MOCNESS samples will be identified to the lowest possible taxonomic level, in most cases expected to be the species level. Taxonomic identification will focus on the fishes and mollusks (squids and octopods), as the former numerically dominate the deepwater nekton of the Gulf of Mexico (Hopkins and Sutton, 1998) and the latter represent an important link between deepwater nekton and higher trophic levels (e.g., endangered marine mammals). Damaged specimens will be identified to the lowest identifiable level.

In both the Sutton (VIMS) and Frank (Nova) laboratories, all specimens will be sorted into the lowest taxonomic group feasible. For groups that contain only a few specimens, all specimens will be identified to the lowest taxonomic classification possible and measured (fishes: mm standard length; crustaceans: carapace or body length). Size frequency distributions will be generated for dominant taxa (i.e., dominant taxa are those defined as contributing at least 5% of total numbers or biomass per cruise) by measuring at least 25 individuals (or all specimens if fewer than this number are found in the sample). For groups that are comprised of large numbers of specimens (~>1,000), all specimens in the groups will be identified to the lowest taxonomic classification possible and a size range will be established for each species/taxon by measuring at least 25 individuals. Additionally for fishes, life stages of each specimen will be noted for three categories: larva (pre-flexion, or metamorphosis in the case of leptocephali), juvenile (post-flexion to pre-adult form), or adult.

Representative specimens of all lowest identifiable taxa will be photographed as a digital reference for taxonomic identification. Photograph metadata will include (i) the specimen number, (ii) the sample containing the voucher specimen, and (iii) the taxonomic designation given to the specimen. The original digital record of the photographic images will be saved, backed up and stored pursuant to NOAA NRDA data management protocols. An identical copy of all images will be made available to LOSCO, on behalf of the State of Louisiana, and to BP (or Cardno ENTRIX on behalf of BP) as part of the information provided to the parties pursuant to section 6.3.

Biomass of all taxa will be determined using the preferred method by taxa either by direct weighing (with fixation adjustment; e.g., Sutton and Hopkins, 1996) or via taxon-specific length/weight regression (e.g., Sutton et al., 2010). Fresh wet weight biomass data for some taxonomic categories will be available from some cruises (NOAA ship *Pisces* via motion-compensated scales).

A list of species/taxa counts per location/time (station, depth, time of day) for all species/taxa will be generated as part of the data deliverables. Additionally, density estimates for abundance and biomass per cubic meter (m³) for each species will be generated via standardization by sampling effort. For a description of sampling effort calculations (volume filtered and/or distance towed) for the midwater trawl see Attachment 2. For the 10 m² MOCNESS, volume will be taken from the electronic data files produced by the gear. For the epipelagic trawl, standardizing calculations have not yet been developed. All metadata for each station and sample will be included in the information labs will upload to the NOAA NRDA Content Management System, along with comments or ancillary data and be released to LOSCO, on behalf of the state of Louisiana, and to BP (or Cardno ENTRIX on behalf of BP) at the conclusion of the electronic data reporting phase from each cruise.

5.0 Quality Assurance and Control Procedures

Quality assurance and quality control (QA/QC) measures will be implemented as part of this nekton processing plan. The primary evaluation of precision and accuracy (as measured by correct identification of organisms) will be conducted by comparisons of results of identification of a subset of samples by more than one taxonomic expert. All samples, subsamples, and representative specimen imagery will be maintained under NOAA COC procedures at all times.

All identification information, counts and measurements of nekton, and associated notes including corrections will be managed and retained by the labs under the direction of the NOAA NRDA Data Management Team. The NOAA NRDA Data Management Team will pair field sample metadata with the lab results and perform a completeness check to ascertain that the laboratory information matches up properly with field sample information and all field information has associated laboratory information. Additional details concerning the QA/QC procedures are described below.

5.1 Training of Laboratory Personnel

Any personnel working under the experts listed in this plan will go through a training period. During the initial training period, all specimens identified by the trained laboratory personnel will be checked by senior experts at the respective laboratories (VIMS, Nova) and this review will be documented (Attachment 4). Proficiency in identification will be attained as indicated by a 95% or higher agreement between the identifications by the trained laboratory personnel and the expert.

After the initial training period, laboratory personnel will be continuously evaluated for quality control. Five percent (5%) of the total number of nekton samples per cruise identified by any individual laboratory personnel will be verified for taxonomic quality control by one of the named experts in this plan. If a sample is returned by the expert with less than 95% taxonomic agreement, the laboratory individual responsible for that sample will repeat the training specifications where all samples are checked until a 95% agreement is again attained. If the identity of a taxon is corrected during QC, the corrected taxon name and specimen length will be recorded on the corresponding lab data record form along with reason(s) for the correction.

5.2 Family-Level Taxonomic Identification and Counts

Samples identified in the VIMS lab to the family level (by Dr. Sutton or another individual deemed by him to be experienced enough to identify all families common to the data set) will undergo a one percent (1%) quality control check. Samples will be randomly chosen and the quality control counts will be conducted by someone other than the individual who conducted the original counts. It is anticipated that this will occur for all 10m² MOCNESS and epipelagic trawl samples.

For samples that were identified to the family level by Dr. Sutton or Dr. Moore upon collection (midwater trawl samples) quality checks have already been completed. Specimens sorted aboard the vessel for family level taxonomic identification (midwater trawl cruises in December 2010 and March-April 2011) were reevaluated by Dr. Sutton as part of the process of reclassifying them for consistency with the family grouping developed for the June-July 2011 cruise. For the June-July 2011 cruise, 30% of the family level taxonomic identifications were reevaluated coincident with the species level identification. For the September 2011 cruise both Dr. Sutton and Dr. Moore were aboard and collaborated regarding family-level identifications, the details of which are being confirmed. Any additional data validation that the trustees determine is necessary for consistency with the quality checks which occurred for the other cruises discussed in this paragraph will be undertaken as part of the species level identification for specimens collected during the September 2011 cruise.

5.3 Species-Level Taxonomic Identification and Counts

Samples for quality control among experts identifying organisms to the species level will be randomly selected with additional samples exchanged as needed to ensure inclusion of all depth strata and gear types. For taxonomic identification and counts quality control, five percent (5%) of the total number of samples per cruise will be exchanged and verified by the other expert taxonomists responsible for the identification of each taxonomic group. If the identity of a taxon is corrected during QC, the corrected taxon name and specimen length will be recorded on the corresponding lab data record form along with reason(s) for the correction. If agreement cannot be reached on a given taxon, the specimen will be assigned to the lowest agreed upon taxonomic level. Specimens re-assigned to a different taxon during quality control will be properly labeled with an identifier (e.g., 'dot label' or 'X') to facilitate locating the specimen for re-examination, if necessary. Required corrections will be evaluated, and taxon and/or species potentially misidentified previous to the QC check will be reviewed. Reason for changes will be communicated to the laboratory personnel so future identifications are consistent with the final identifications.

5.4 Reference Image Collection

A reference collection of images of representative specimens will be maintained along with collection information and shared between researchers to help ensure uniformity in recognizing identification criteria and to facilitate communication among taxonomists.

5.5 Data Transcriptions

For the sorting and identification processes, upon transfer of data from paper data sheets to electronic media, a cross-check of 100% of all transcriptions will take place by an individual other than the individual that entered the original data. This cross-check can take place by individuals in the same lab. The individual conducting the data transcription cross-check and the date it takes place will be documented on the corresponding lab bench sheet. Cross-checks did not occur for the midwater trawl family-level data that were entered directly into the database aboard the sampling vessel at the time of collection.

6.0 Distribution of Laboratory Results

Data reporting and distribution will be accomplished as described below for both the family-level and species-level data.

6.1 Sample and Data Inventories

Each individual laboratory (VIMS, Nova), will coordinate with the NOAA NRDA Data Management Team to be registered for the NOAA NRDA Content Management System. The NOAA NRDA Content Management System will serve as a repository of information required by NOAA from each lab that is receiving and processing samples. Upon registration, labs will receive training on the NOAA NRDA Content Management System and more detailed instructions on the requirements for each of the categories of documentation, including "Confirmation", "Metadata", "Results", and "Sample Crosswalk."

Upon receipt of samples, each laboratory shall deliver an inventory and status review of all samples, including all necessary metadata and splitting or composite information, generated as part of this sample processing plan to the NOAA NRDA Data Management Team via the NOAA

NRDA Content Management System. There will be limited accessibility (limited to only lab and NOAA NRDA Data Management Team members) to the data until the full internal data review process has been completed for the priority level (i.e., by cruise, see Tables 1 and 2), as described in Sections 5 & 6. Data will be identified as to its level of review in the NOAA NRDA Content Management System and updated periodically as the review process proceeds.

The NOAA NRDA Data Management Team will coordinate with each lab to determine the appropriate format and required content for each type of data/results. As sample analyses and lab QA/QC processes (per Section 5) are completed, labs will upload results, additional metadata and quality control information, taxonomic images and metadata, and other information determined to be appropriate to support these data (i.e., sample tracking forms, lab data sheets, COC forms, and laboratory logs).

6.2 Data Review

There will be a final data review prior to the release of family-level or species-level data to all parties via the NOAA NRDA Content Management System. Throughout the QA/QC process completed by the lab, any changes made to taxonomic or other information will be documented on data sheets or forms for recording this information. All of this information will be maintained during all review steps in the process and stored in secure locations under Trustee control and will be made available to all parties upon request.

The final data review will be the marrying of the data provided by the labs (family-level or species-level) with the corresponding field information by the NOAA NRDA Data Management Team. The NOAA NRDA Data Management Team will perform a completeness check to ascertain that the laboratory information matches up properly with field sample information and all field information has associated laboratory information.

6.3 Data Release and Consensus Data Sets

Once processing of samples from an entire cruise at a specified taxonomic level (i.e., the family-level or species-level) is completed and reviewed, the data and supporting information referenced in Section 6.1 will be made available to the parties to this agreement via appropriate means (e.g., portable hard drives, etc.) as determined by the NOAA NRDA Data Management Team. NOAA and the Louisiana Oil Spill Coordinator's Office (LOSCO) on behalf of the State of Louisiana and BP (or Cardno ENTRIX on behalf of BP) will be alerted when these data become available.

In the interest of maintaining one consistent data set for use by all parties, only the verified and validated data set made available by the NOAA NRDA Data Management Team shall be considered the consensus data set. In order to ensure reliability of the consensus data and full review by the parties, no party shall publish consensus data until 14 days after such data have been made available to the parties. Any questions raised on the consensus data set as it was made available to the parties shall be handled consistent with the procedures in Section 7.2 of the Deepwater Horizon NRDA Analytical Quality Assurance Plan.

- The Trustees and BP shall each designate an individual responsible for raising questions, if any, on the consensus data set.

- If questions are raised, the two designated individuals will meet to determine the source of the difference and resolve.
- The questions raised and their resolution shall be distributed to all parties.
- No changes to the consensus data set will be made if the differences are considered immaterial by both designated individuals, acting on behalf of the parties.
- If the parties agree that changes to the dataset should be made, the dataset will be updated in accordance with the resolution and reposted with a notation that the dataset has been revised.
- If the designated individuals do not agree on how to resolve the difference concerning the consensus data set, the designated individuals shall request assistance from the Assessment Managers for the Trustees and BP.

Species-level identification will generally be completed subsequent to family-level identifications, and may lead to changes in some of the family-level identifications. To maintain a single consensus dataset, upon the release of the species-level data the family-level counts contained therein shall be considered the consensus family-level data, superceding any previously released data containing only family-level identifications. Relying on one data set will reduce the chance of error or confusion that arises when maintaining multiple data sets that contain the same information.

6.4 Retention of Materials

All information will be retained and maintained during all review steps in the process, stored in secure locations under Trustee control, and will be made available to all parties should a need for such supplemental information be identified.

All materials associated with the collection or analysis of samples under these protocols or pursuant to any approved work plan, including any remains of samples and including remains of extracts created during or remaining after analytical testing, must be preserved and disposed of in accordance with the preservation and disposal requirements set forth in Pretrial Orders (“PTOs”) # 1, # 30, #35, # 37, #39 and #43 and any other applicable Court Orders governing tangible items that are or may be issued in MDL No. 2179 IN RE: Oil Spill by the Oil Rig "DEEPWATER HORIZON" (E.D. LA 2010). Destructive analytical testing of oil, dispersant or sediment samples may only be conducted in accordance with PTO # 37, paragraph 11, and PTO # 39, paragraph 11. Circumstances and procedures governing preservation and disposal of sample materials by the trustees must be set forth in a written protocol that is approved by the state or federal agency whose employees or contractors are in possession or control of such materials and must comply with the provisions of PTOs # 1, # 30, # 35, 37, #39 and #43.

7.0 Progress Reporting Schedule

Progress reports will be submitted quarterly to the NRDA Water Column TWG by all laboratories and will include two major sections, one describing the status of sample processing in the laboratory and one describing the data uploading progress for the previous three-month reporting period. A standardized format will be used for all lab progress reports (Attachment 3). At a minimum, the laboratory operations section of the progress report should include the number of samples processed, general location of samples processed by station ID, gear and cruise information associated with the samples, date samples were archived,

operational/logistical issues, and planned activities for the next three months. The data uploading section of the progress report should include, at a minimum, when and what data were uploaded, when confirmation, metadata, results and sample cross-checks were completed, any logistical issues, and planned activities for the next three months. The actual results of the processing effort will not be summarized in the quarterly progress reports, but rather the status of the processing and data uploading effort.

8.0 Budget

Given the uncertainty in the rate at which labs can process samples, we have estimated an 18-month operating budget for VIMS (\$391,819) and Nova (\$186,840). Budgets for the other researchers listed in this plan are provided in Attachment 1, and are based on 12-month estimates. It should be noted that the number of samples listed in this plan exceed the number that can be completed in the time/budgets estimated here. The costs indicated in Attachment 1 and any additional reasonable costs within the scope of this workplan that may arise shall be reimbursed by BP upon receipt of written invoices submitted by the Trustees. The Trustees will make a good faith effort to notify BP in advance of any such increased costs.

The total budget for effort, as noted above (18-months for the PIs), is \$952,989.

9.0 References

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10.0 Attachments

- Attachment 1. Laboratory budgets
- Attachment 2. Trawl volume calculations
- Attachment 3. Standardized quarterly report template
- Attachment 4. Training record documentation form
- Attachment 5. Nova Lab data record form
- Attachment 6. VIMS Lab data record form

