SWAMP DATA MANAGEMENT PLAN

Tissue Template

Surface Water Ambient Monitoring Program

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www.waterboards.ca.gov/swamp

TABLE OF CONTENTS

A. Analytical Data

The typical method for submitting Laboratory Analytical Data to the SWAMP Database is electronically through the online data checker. This section will focus on the tools and steps involved in submitting these data.

The following information should be used in conjunction with the SWAMP QAPrP for complete compliance with the SWAMP program including measurement quality objectives and required quality assurance (QA) samples.

1. Analysis Authorization Forms

2. Tissue Data

Tissue Data consists of Tissue ByCatch, Collection, Composite, SuperComposite, Results and Batch data. The tissue composite data is submitted to the SWAMP database in two worksheets; TissueComposite and TissueSuperComposite. The tissue results data is submitted to the SWAMP database in two worksheets; TissueResults and TissueBatch.

a. Tissue Data Template

The Tissue Data Templates are available online at http://swamp.mpsl.mlml.calstate.edu/resources-and-downloads/database-management-systems/swamp-25-database/templates-25/tissue-data-templates.

b. Formatting the Data

Several Microsoft Excel template exists for laboratories to use to format the tissue laboratory data in a manner that can be easily loaded into the SWAMP database. As previously discussed, for many labs working under the SWAMP master contract, the composite information can be obtained from the Analysis Authorization form through the project's tissue coordinator. This section will discuss each of the fields in the template and how to populate them.

All valid LookUp list values are available at http://ftp.mpsl.mlml.calstate.edu/LookUpLists.php. At any time, if the necessary field does not appear in the LookUp list, the SWAMP Data Management Team (DMT) must be contacted to have it added.

i. ByCatch

This data is generally entered into the database through the forms. If it cannot be entered using the forms, this worksheet holds information specific to the ByCatch data. This worksheet should be named **ByCatch** (with no spaces) in its worksheet tab. The fields in this sheet are and should be completed as follows:

ii. Collection

This data is generally entered into the database through the forms. If it cannot be entered using the forms, this worksheet holds information specific to the Tissue Collection. This worksheet should be named **Collection** in its worksheet tab. The fields in this sheet are and should be completed as follows:

iii. Composite

The first worksheet to travel with the Tissue Composite data holds information specific to the composited samples. This worksheet should be named **Composite** in its worksheet tab. The fields in this sheet are and should be completed as follows. Examples of special types of samples are listed in the Special Circumstances section.

Template Field Name	LookUp List	Description & Business Rules
EventCode	EventLookUp	EventCode represents the initial intent of the sampling event at a particular station. BR: The EventCode will be in a hierarchical order as follows: BA – If the initial intent of sampling is for Bioassessment (Tissue and/or WaterQuality samples may or may not also be collected) TI – If the initial intent of sampling is for Tissue (WaterQuality samples may or may not also be collected; no associated Bioassessment samples collected) WQ – If the initial intent of sampling is for WaterQuality (no associated Bioassessment or Tissue samples collected) For example, if the initial intent of sampling on Day 1 was for Tissue and WaterQuality, the EventCode would be TI. If for some reason the WaterQuality had to be re-sampled the next day, on Day 2, the event for the re-sampling would still be TI because Tissue was the initial intent of sampling on Day 1 even though the WaterQuality was sampled on Day 2.

ProtocolCode	ProtocolLookUp	ProtocolCode represents the sampling protocol used, which includes the set of methods, methodology and/or specifications, such as MPSL-DFG_Field_v1.0. Established protocols may be used or Regions may document their own sampling protocols. BR: It is preferable to combine protocols per StationCode and date so that all WaterQuality, Bioassessment and Tissue data are combined under the same EventCode. For example, if Tissue and WaterQuality are sampled at a station, the EventCode would be TI. If the protocols are different for Tissue and WaterQuality, the Tissue protocol would be used and the WaterQuality protocol would be listed in the SampleComments. If that is not preferable, separate EventCodes may be used with each individual protocol. Default value is Not Recorded.
StationCode	StationLookUp	StationCode represents a unique sampling site in a sampling design. A single waterbody may have multiple stations. BR: The format for the unique alphanumeric description of the station is ###ABC123, where ### is the Hydrologic Unit number and ABC123 is an alphanumeric description of the Station. An example is 111EELBRN which is Hydrologic Unit 111 and an abbreviated code to indicate “Eel River - South Fork near Branscomb”.
SampleDate		SampleDate refers to the date the sample was collected in the field. BR: The format for date in the templates is dd/mmm/yyyy, such as 10/Nov/2007. For samples with collection times that last longer than one day, like autosamplers, the sample date is the date sampling began. When entering data using the forms, the format is mm/dd/yy. For transplanted bivalves, the SampleDate is the date the transplanted organisms were collected, removed, or retrieved from the field.

AgencyCode	AgencyLookUp	AgencyCode refers to the organization or agency that collected the sample. This should be listed on the Chain of Custody (COC) document that accompanies the samples from the field. BR: If an environmental sample is used to perform laboratory QC, i.e. a matrix spike or lab duplicate, the AgencyCode still refers to the agency that collected the native sample, not the agency that created the QC sample. See 'Special Circumstances' for LABQA business rules.
ProjectCode	ProjectLookUp	ProjectCode references the project that is associated with the sample. BR: The formatting for a ProjectCode is as follows Program_Project. For example, the format for a SWAMP Regional Board project is SWAMP_RBX where SWAMP is the program, RB indicates it is a Regional Board sample and X is the Regional Board number. The format for a SWAMP State Board project is SWAMP_SB_XXX where SWAMP is the program, SB indicates it is a State Board sample and XXX represents the State Board project. For example, the ProjectCode for the Bioaccumulation Oversight Group would be SWAMP_SB_BOG. For a project other than SWAMP such as the Friends of the Los Angeles River, the project is FLAR_XXX where FLAR indicates it is a Friends of the Los Angeles River program and XXX represents the Friends of the Los Angeles River project. In some cases, there may not be a specific project but only a program. In this case the ProjectCode would be just the program; e.g. UMD.
SampleComments (Not Required)		SampleComments records any comments related to the sampling event at a particular station. BR: When a PurposeFailureCode of Other is used, a SampleComment is required.

LocationCode	LocationLookUp	LocationCode describes the physical location in the waterbody where the sample was collected. One sampling event may have a single or multiple locations. BR: For a single point of sampling, the physical location in the waterbody can be used such as Bank, Thalweg, Midchannel, OpenWater. The LocationCode for field results should be the same as the location for the WaterQuality collection method. For TI EventType sampling, the physical location plus the CollectionMethod is used such as BankNet1, BankShock1, OpenWaterTrawl1, OpenWaterNet1. For resident mussel or clam collections, the LocationCode would be the physical location in the water body plus the generic CollectionMethod, e.g. BankTissue_Grab1. OpenWater sampling with multiple sub-locations within a single water body or station could have locations of OpenWaterTrawl1, OpenWaterTrawl2 describing one large location with two smaller areas of sampling within the OpenWater Location. Multiple physical locations within a single station could consist of a LocationCode such as BankShock1, BankNet1, OpenWaterHook1. If recording specific locations within a station are necessary for the project, a LocationCode such as Location1Net1, Location1Net2, Location2Shock1 may be used.
GeometryShape (Not Required)	VariableCodesLookUp	GeometryShape is the physical shape of the location; e.g. Line, Point, Line Centroid, Polygon, Polygon Centroid
CollectionMethodCode	CollectionMethodLookUp	CollectionMethodCode refers to the general method of collection such as Net, Shock, Trap, Trawl, Bag, Cage. BR: The SWAMP tissue default (fish and bivalves) is Tissue_Grab if a specific method of collection was not used.

CollectionDeviceName	CollectionDeviceLookUp	CollectionDeviceName refers to the specific device used in the collection of the sample such as MPSL-Eboat_(BigE), WPCL-DFG Gill Net 1(50m,1.5").
CollectionTime		CollectionTime refers to the time when the first sample of a sampling event at a specific station was collected in the field. BR: If the sampling crew collects 18 fish at a single station, the CollectionTime for each would be the start time of the first fish collected. By doing so, the samples can easily be linked and any holding time issues will be consistent, and conservative, for the laboratory work. For transplanted bivalves, the CollectionTime refers to the retrieval time the organisms were collected in the field after deployment. The CollectionTime format should be expressed as xx:xx in 24 hour time, such as 13:30 for 1:30 pm.
TisSource	VariableCodesLookUp	TisSource or Tissue Source references the original source of the collected organism; e.g. resident, transplant BR: Bivalves could be Res (Resident) or Trans (Transplant) while fish are NA (Not Applicable)
Replicate		The Replicate number is used to distinguish between replicates created at a single collection in the field. BR: The default is 1.
TissueCollectionComments (Not Required)		TissueCollectionComments is intended to record any comments relating to the collection of the tissue sample for laboratory analysis.

OrganismID		OrganismID is a unique identifier assigned to the organism by the field crew or the agency that has possession of the field data sheets and of the fish to begin. BR: The OrganismID can be made unique by following this order: StationCode, project abbreviation, project year, organism abbreviation, bag number, -, fish number; e.g. 901SJATC5SW01RES02-6 where 901SJATC5 is the StationCode, SW is the project abbreviation for SWAMP, 01 is the project year, RES is the organism abbreviation for Redear Sunfish, 02 is the bag number (meaning it's the second bag of Redear Sunfish at this station), -, 6 is the fish number (meaning it is the 6th fish in the second bag). It is preferable to add -Dup to the end of the ID to help confirm the that the collection is a Field Duplicate of the native sample.
TagNumber (Not Required)		TagNumber references the individual tag number assigned to and placed on the organism (usually only fish). BR: Not required but recommended
OrganismName	OrganismLookup	OrganismName refers to the common name of the organism collected.
LifeStageCode	LifeStageLookUp	LifeStage is a unique code referencing the stage of life of the organism; e.g. adult, juvenile
TotalCount (Not Required)		TotalCount is the total count of alive organisms in the tissue sample associated with the same OrganismID. BR: For bivalves, if you have a bag of 45 mussels but 10 are dead, the TotalCount would be 35 and a comment regarding the 10 dead mussels would be recorded in the ProcessedOrganismsExpandedBivalvesComments.

PartCreated **(Not Required)**		PartCreated references whether a subsequent part was created from the OrganismID, i.e. Yes would be populated if any portion of the processed organism was taken for analysis.
ForkLength **(Not Required)**		ForkLength is the measured length of the organism from the most forward point, with mouth closed, to the center of the fork in the tail.
TotalLength **(Not Required)**		Total Length is the measured length of the organism from the most forward point of the head, with mouth closed, to the farthest tip of the tail.
UnitLengthFish **(Not Required)**	VariableCodesLookUp	UnitLengthFish refers to the units used in measuring the length of the fish. BR: SWAMP prefers mm.
LengthSource **(Not Required)**	VariableCodesLookUp	LengthSource is the physical location where the length measurements were recorded; e.g. field, lab
Weight **(Not Required)**		Weight is the weight of the entire fish.
UnitWeightFish **(Not Required)**	VariableCodesLookUp	UnitWeightFish refers to the units used in measuring the weight of the fish. BR: SWAMP prefers g.
WeightSource **(Not Required)**	VariableCodesLookUp	WeightSource is the physical location where the weight measurements were recorded; e.g. field, lab
SizeDescr **(Not Required)**		SizeDescr or Size Description is a description of the grouping of organisms by size; e.g. small, large, 100-150cm BR: This field is to be used at discretion of the project as a grouping characteristic. Used only when sizes are estimated. Not populated if individual fish measurements are recorded.

Age **(Not Required)**		Age describes the age of the organism. BR: This field is to be used at discretion of the project as an age descriptor. If required by the project and the age is not recorded, enter -88.
Sex **(Not Required)**	VariableCodesLookUp	Sex refers to the sex of the organism; e.g. M, F, Unk
Anomaly **(Not Required)**	VariableCodesLookUp	Anomaly describes any anomalies that may be on or in the organism; e.g. Deformity-skeletal, Lesion, Parasite
ProcessedOrganismsExpandedFishComments **(Not Required)**		ProcessedOrganismsExpandedFishComments records any comments relating to the ProcessedOrganismsExpandedFish, e.g. the location of the anomaly.
BivalveID		BivalveID is a unique identifier (when combined with OrganismID) that is assigned to the organism. BR: Default is 1.
Count **(Not Required)**		Count is the actual number of organisms represented by the BivalveID. BR: Default is 1.
ShellLength **(Not Required)**		ShellLength is the actual measured length of the shell of the individual organism. BR: When a group of organisms are measured and averaged, enter the average length of the shell.
ShellWidth **(Not Required)**		ShellWidth is the actual measured width of the shell of the individual organism. BR: When a group of organisms are measured and averaged, enter the average width of the shell.

UnitShellLengthWidth (Not Required)	VariableCodesLookUp	UnitShellLengthWidth refers to the units used in measuring the length and width of the organism. BR: When a group of organisms are measured and averaged, enter the unit as avg xx where xx refers to the unit.
LengthWidthType (Not Required)	VariableCodesLookUp	LengthWidthType describes the type of length or width measurement recorded; e.g. Ca (Carapace), Ab (Abdomen), TL (Total Length) BR: If two different types of measurements were recorded, enter the primary type here and the secondary type in the ProcessedOrganismsExpandedBivalvesComments field.
BeginWeight (Not Required)		BeginWeight is the weight of the bivalve organism at the start date.
EndWeight (Not Required)		EndWeight is the weight of the bivalve organism at the end date.
UnitWeightBivalve (Not Required)	VariableCodesLookUp	UnitWeightBivalve refers to the units used in measuring the weight of the bivalve.
BivalveSex (Not Required)	VariableCodesLookUp	Sex refers to the sex of the organism; e.g. M, F, Unk
SizeDescrBivalve (Not Required)		SizeDescrBivalve or Size Description Bivalve is a description of the grouping of organisms by size; e.g. small, large, 100-150cm BR: This field is to be used at discretion of the project as a grouping characteristic. Used only when sizes are estimated. Not populated if individual shell measurements are recorded.
ProcessedOrganismsExpandedBivalvesComments (Not Required)		ProcessedOrganismsExpandedBivalvesComments records any comments relating to the ProcessedOrganismsExpandedBivalves. BR: Include the number of animals involved in the weight and length measurements if it is different from the count number.

TissueID		TissueID is a unique identifier that is assigned to the tissue part and is used to differentiate between different parts of the same fish or composited fish vs. an individual fish. BR: For fish, a suggested format is fundingcode_tag number_part initial (I-indivdual, O-otolith, C-composite, etc.), e.g. SW01_2435_I. For bivalves, a suggested format is OrganismID_part initial, e.g. 901SJATC5SW01RCM01_C
TissueName	TissueLookUp	TissueName is the name of the tissue part used in the composite and analysis.
PreparationPreservation	PrepPreservationLookUp	PreparationPreservation references the preparation or preservation method performed on the tissue part in order to create the composite. BR: If no preparation or preservation method was performed the default value is None.
EntryDateTime (Not Required)		EntryDateTime reflects the date and time when the template is filled out and can be used as a way to group data entry.
TissueWeight		TissueWeight is the measured weight of the tissue part included in the composite.
UnitTissueWeight	VariableCodesLookUp	UnitTissueWeight refers to the units used in measuring the weight of the tissue part.
PartsComments (Not Required)		PartsComments records any comments relating to the tissue parts.

CompositeID		CompositeID is a unique identifier supplied by the Compositing Agency to identify the composited tissue parts. It can refer to either the original Composite or the SuperComposite where multiple Composites are combined to create a SuperComposite. BR: This CompositeID will be listed on the analysis authorization. For an individual fish, a suggested format is I_OrganismID, where I references an individual fish, e.g. I_901SJATC5SW01RES02-6. One fish composite of different fish from one or more bags would be C1_OrganismID (minus bag and fish number), e.g. C1_901SJATC5SW01RES. If there is a second fish composite from one or more bags, the CompositeID would be C2_OrganismID (minus bag and fish number), e.g. C2_901SJATC5SW01RES. For bivalves, a suggested format is C1_OrganismID (minus the bag number)_analysis acronym (if needed to make unique), e.g. C_901SJATC5SW01RCM_TM where TM references trace metals. For a non-muscle part of a fish such as liver, otolith, scale, gonads, etc., a suggested format is Part Initial (from TissueID)_OrganismID (minus bag and fish number), e.g. L_901SJATC5SW01RES for a liver composite. For SuperComposites, a suggested format is SC_OrganismID (minus bag and fish number), where SC means SuperComposite.
CompositeType	VariableCodesLookUp	CompositeType indicates the type of composite, e.g. Normal, SuperComposite. BR: In the Composite template, only Normal will be recorded. In the SuperComposite template, only SuperComposite will be recorded. In the Results template, Normal and SuperComposite is recorded for samples and LABQA is recorded for LABQA.
CompositeReplicate		CompositeReplicate is the composite replicate number used to distinguish between replicate composites. BR: Default value is 1.

CompositeWeight		CompositeWeight is the weight of the total Composite or SuperComposite used in the analysis. BR: Default value is -88.
UnitCompositeWeight	VariableCodesLookUp	UnitCompositeWeight refers to the units used in measuring the weight of the Composite or SuperComposite.
HomogDate		HomogDate is the date the Composite or SuperComposite was homogenized. BR: Date format is dd/mmm/yyyy.
OrganismGroup	VariableCodesLookUp	OrganismGroup is the organism group of the sample, e.g. Fish, Bivalves, Crustacean, Mammal, Bird or Amphibian. BR: The default for LABQA is Not Applicable except for CRMs. The CRM should reflect the correct organism group.
CompAgencyCode	AgencyLookUp	CompAgencyCode is the agency that physically created the Composite or SuperComposite.
CompositeComments (Not Required)		CompositeComments are any comments related to the Composite or SuperComposite.

(a) Special Circumstances

There is one type of special circumstance discussed in this section. This type includes samples that are generated or created by the compositing laboratory.

(i) Compositing Lab-Generated QA samples

There is one type of sample discussed in this section that is generated by the compositing laboratory which is the laboratory-generated blind duplicate of a composite sample.

(a) Blind Duplicate Samples

For these samples, all fields describing the Sample, Location, Collection, Processed Organism, Processed Organism Expanded and Parts remain the same as the native sample.

CompositeID	Will appear blind to analyzing laboratory. Should be renamed similar to native composite sample at project management level after all associated results have been loaded into the database.
Composite Replicate	1
OrganismGroup	Provided by compositing laboratory. Same as native composite sample
CompositeType	Provided by compositing laboratory. Same as native composite sample
SampleTypeCode	CompBLDup
LabReplicate	1
Matrix	Provided by compositing laboratory. Same as native field sample or composite

iv. SuperComposite

The second worksheet to travel with the Tissue Composite data holds information specific to the super-composited samples. This worksheet should be named **SuperComposite** in its worksheet tab. The fields in this sheet are and should be completed as follows:

Template Field Name	LookUp List	Description & Business Rules
SuperCompositeID		CompositeID is a unique identifier supplied by the Compositing Agency to identify the composited tissue parts. It can refer to either the original Composite or the SuperComposite where multiple Composites are combined to create a SuperComposite. BR: This CompositeID will be listed on the analysis authorization. For an individual fish, a suggested format is I_OrganismID, where I references an individual fish, e.g. I_901SJATC5SW01RES02-6. One fish composite of different fish from one or more bags would be C1_OrganismID (minus bag and fish number), e.g. C1_901SJATC5SW01RES. If there is a second fish composite from one or more bags, the CompositeID would be C2_OrganismID (minus bag and fish number), e.g. C2_901SJATC5SW01RES. For bivalves, a suggested format is C1_OrganismID (minus the bag number)_analysis acronym (if needed to make unique), e.g. C_901SJATC5SW01RCM_TM where TM references trace metals. For a non-muscle part of a fish such as liver, otolith, scale, gonads, etc., a suggested format is Part Initial (from TissueID)_OrganismID (minus bag and fish number), e.g. L_901SJATC5SW01RES for a liver composite. For SuperComposites, a suggested format is SC_OrganismID (minus bag and fish number), where SC means SuperComposite.
CompositeType	VariableCodesLookUp	CompositeType indicates the type of composite, e.g. Normal, SuperComposite. BR: In the Composite template, only Normal will be recorded. In the SuperComposite template, only SuperComposite will be recorded. In the Results template, Normal and SuperComposite is recorded for samples and LABQA is recorded for LABQA.
CompositeReplicate		CompositeReplicate is the composite replicate number used to distinguish between replicate composites. BR: Default value is 1.

CompositeWeight		CompositeWeight is the weight of the total Composite or SuperComposite used in the analysis. BR: Default value is -88.
UnitCompositeWeight	VariableCodesLookUp	UnitCompositeWeight refers to the units used in measuring the weight of the Composite or SuperComposite.
HomogDate		HomogDate is the date the Composite or SuperComposite was homogenized. BR: Date format is dd/mmm/yyyy.
OrganismGroup	VariableCodesLookUp	OrganismGroup is the organism group of the sample, e.g. Fish, Bivalves, Crustacean, Mammal, Bird or Amphibian. BR: The default for LABQA is Not Applicable except for CRMs. The CRM should reflect the correct organism group.
CompAgencyCode	AgencyLookUp	CompAgencyCode is the agency that physically created the Composite or SuperComposite.
CompositeComments (Not Required)		CompositeComments are any comments related to the Composite or SuperComposite.
CompositeSourceID		CompositeSourceID is a unique identifier supplied by the Compositing Agency to identify the composited tissue parts in the SuperComposite. BR: This CompositeID must match the original CompositeID used in the SuperComposite.
CompositeSourceWeight		CompositeSourceWeight is the weight of the portion of the original Composite used to create the SuperComposite.
UnitCompositeSourceWeight	VariableCodesLookUp	UnitCompositeSourceWeight refers to the units used in measuring the weight of the SuperComposite.

v. Tissue Results Worksheet

There are two worksheets that must travel with the Tissue Results data for the data package to be considered complete. The first holds all chemistry results, including QC data, and should be named **Results** in a worksheet tab. The second worksheet to travel with the Tissue Results data holds information specific to the laboratory batch in which data is analyzed. Each record in the Tissue Results sheet represents a result from a specific analysis for a particular parameter of a single composite or for a single QC sample. This worksheet will also contain all supporting QC sample results. If beginning with an Analysis Authorization, the following fields will likely be pre-populated in the **Data** worksheet: *CompositeID, CompositeReplicate, OrganismGroup, CompositeType, SampleTypeCode, PreparationPreservation, and PreparationPreservationDate.* Please note that all fields are required to have data except when otherwise noted below. Examples of special types of samples are listed in the Special Circumstances section.

Template Field Name	LookUp List	Description & Business Rules
LabSampleID		The LabSampleID is a recommended field intended to provide lab specific identification for an analyzed sample. BR: The format and content is determined by the lab. It is preferable to add -Dup, -MS, -MSD to the end of the ID to help confirm the SampleType and the LabSampleID of the native sample.
CompositeID		CompositeID is a unique identifier supplied by the Compositing Agency to identify the composited tissue parts. It can refer to either the original Composite or the SuperComposite where multiple Composites are combined to create a SuperComposite. BR: This CompositeID will be listed on the analysis authorization. For an individual fish, a suggested format is I_OrganismID, where I references an individual fish, e.g. I_901SJATC5SW01RES02-6. One fish composite of different fish from one or more bags would be C1_OrganismID (minus bag and fish number), e.g. C1_901SJATC5SW01RES. If there is a second fish composite from one or more bags, the CompositeID would be C2_OrganismID (minus bag and fish number), e.g. C2_901SJATC5SW01RES. For bivalves, a suggested format is C1_OrganismID (minus the bag number)_analysis acronym (if needed to make unique), e.g. C_901SJATC5SW01RCM_TM where TM references trace metals. For a non-muscle part of a fish such as liver, otolith, scale, gonads, etc., a suggested format is Part Initial (from TissueID)_OrganismID (minus bag and fish number), e.g. L_901SJATC5SW01RES for a liver composite. For SuperComposites, a suggested format is SC_OrganismID (minus bag and fish number), where SC means SuperComposite.

CompositeReplicate		CompositeReplicate is the composite replicate number used to distinguish between replicate composites. BR: Default value is 1.
OrganismGroup	VariableCodesLookUp	OrganismGroup is the organism group of the sample, e.g. Fish, Bivalves, Crustacean, Mammal, Bird or Amphibian. BR: The default for LABQA is Not Applicable except for CRMs. The CRM should reflect the correct organism group.
CompositeType	VariableCodesLookUp	CompositeType indicates the type of composite, e.g. Normal, SuperComposite. BR: In the Composite template, only Normal will be recorded. In the SuperComposite template, only SuperComposite will be recorded. In the Results template, Normal and SuperComposite is recorded for samples and LABQA is recorded for LABQA.
CompositeComments (Not Required)		CompositeComments are any comments related to the Composite or SuperComposite.
SampleTypeCode	SampleTypeLookUp	SampleTypeCode refers to the type of sample collected or analyzed. BR: Some commonly used SampleTypeCode choices include Grab, Integrated, MS1, CRM, LCS, LabBlank, CNEG, Composite.
PreparationPreservation	PrepPreservationLookUp	PreparationPreservation references the preparation or preservation method performed on the organism prior to processing. BR: If no preparation or preservation method was performed the default value is None. Tissue should be fieldfrozen or labfrozen.
PreparationPreservationDate		PreparationPreservationDate is the date and time the preparation or preservation was started. BR: The format is dd/mmm/yyyy hh:mm. If there is no preparation or preservation method performed (None) then the PreparationPreservationDate should be listed as 01/Jan/1950 00:00 (the SWAMP default date/time value for none). If a composite has multiple preparation or preservation dates, enter the earliest date.

DigestExtractMethod	DigestExtractLookUp	DigestExtractMethod references the digestion or extraction method performed on the sample prior to analysis. BR: If no digestion or extraction method was performed the default value is None.
DigestExtractDate		DigestExtractDate is the date and time the digestion or extraction was started. BR: The format is dd/mmm/yyyy hh:mm. If there is no digestion or extraction performed on the sample (None) then the DigestExtractDate should be listed as 01/Jan/1950 00:00 (the default value for none).
LabBatch		The LabBatch is a unique code, provided by the laboratory, that represents a group of samples processed together. It groups all environmental samples with their supporting QC samples and will be used to verify completeness based on the SWAMP QAPrP. BR: The LabBatch is assigned to and identifies all samples digested or extracted together in one batch. When a digestion or extraction is not performed as part of the method, the LabBatch represents all samples within a unique analysis run. Please see the File and Batch Naming Convention to correctly format the LabBatch name. All lab batches listed in the Results worksheet need to be listed one time only in the LabBatch worksheet.
AnalysisDate		AnalysisDate is the date and time the sample was processed on the analytical instrument. BR: This date/time should be expressed as dd/mmm/yyyy hh:mm.
LabReplicate		The LabReplicate number is used to distinguish between replicates created in the laboratory. It differentiates the original field sample that was analyzed from all subsequent laboratory duplicates. BR: The default is 1 for the first sample and increases by one for each successive replicate analyzed in the laboratory.

MatrixName	MatrixLookUp	MatrixName refers to the sample matrix. BR: Water - For field-generated water samples, the MatrixName is samplewater. For lab-generated QC samples, the matrix should be the type of water that was used for the analysis of the sample, either labwater or blankwater. Labwater is water coming either directly from the tap in the laboratory or purchased spring water. Blankwater is laboratory Type I or Type II water, purchased reagent water or water that is run through a filtration process in a laboratory, such as Deionized (DI) or Milli-Q (MQ) water. Sediment - For field-generated sediment samples, the MatrixName is sediment. For lab-generated QC samples, blankmatrix could be used as the MatrixName which is a matrix used to identify a commercial- or lab-produced medium in tissue or sediment QC samples. If this is not the case then the MatrixName for lab-generated QC samples would be sediment which would include samples where water, solvent or nothing was used as a matrix. Tissue - For field-generated tissue samples, the MatrixName is tissue. For lab-generated QC samples, blankmatrix could be used as the MatrixName which is a matrix used to identify a commercial- or lab-produced medium in tissue or sediment QC samples. If this is not the case then the MatrixName for lab-generated QC samples would be tissue which would include samples where water, solvent or nothing was used as a matrix.
MethodName	MethodLookUp	MethodName refers to the analysis method used by the laboratory to analyze the sample. BR: Methods are expressed with a MethodName such as SM 4500-NH3 C or EPA 600/R-99-064 and must be fully described in the Method Lookup list and in the laboratory records. If a laboratory has modified an EPA or Standard Method, the laboratory agency needs to add “M” to end of the MethodName. In such situations, the modification should be documented and communicated to the SWAMP DMT for notation in the database. For instance, a lab would report a modified EPA 600/R-99-064 as EPA 600/R-99-064M accompanied by a description of the modification made. Any method for the SWAMP Project which is not in the current SWAMP database lookup list must be approved by the SWAMP QA Team prior to being added to the database.
AnalyteName	AnalyteLookUp	The AnalyteName is the name of the analyte or parameter for which the analysis is conducted and result is reported. The lookup list includes the acceptable abbreviation or name of the variable used by the database, enabling consistency across reporting.

FractionName	FractionLookUp	FractionName is a specific descriptor of the Analyte. BR: For instance, metals are often expressed as Total or Dissolved, each of which would be expressed as the Fraction, distinguishing the appropriate Analyte. If there is no need for further description of the analyte, type 'None' in this field.
Unit	UnitLookUp	Unit refers to how the chemistry result is measured or expressed. BR: Each combination of Analyte and Matrix requires that a specific Unit be used in the SWAMP database to ensure comparability across data. This listing can be found in the SWAMP QAPrP, online at http://www.waterboards.ca.gov/water_issues/programs/swamp/tools.shtml#qa. Water units are indicated by weight/volume, i.e. ng/L. Sediment and tissue units are indicated by weight/weight and includes whether the sample result is reported as wet weight (ww) or dry weight (dw). For example, ng/g ww for ng/g wet weight. Surrogates recovery results will use a unit of %.
DilFactor		DilutionFactor is the factor by which a sample was diluted and is reported as a whole number. BR: Default value is 1. A dilution other than 1 is recorded when a sample requires an additional dilution to fit into the standard curve of the instrument. It does not apply to dilutions that are standard in the method being used for analysis. Final reported results, along with the MDL and RL, must be corrected for dilution that was carried out during the process of analysis. 1 part sample plus 9 parts blank is a DilutionFactor of 10. A 50% dilution is equivalent to a DilutionFactor of 2. A QACode of D is required when a dilution is performed on the sample.

Result		Final numeric result of a given analyte, stored as text to retain trailing zeros BR: The chemistry Result is expressed as a real number rather than a calculation. The result should be reported with appropriate number of significant figures. A result of 3.7266945 with 3 significant figures should be reported as 3.73. A result of 1.350 with 4 significant figures must display 1.350 in the Excel file. If you only see 1.35, that is the result that will be loaded to the database and the 4th significant figure will be dropped.
ResultQualCode (Not Required)	ResQualLookUp	The Result Qualifier Code or ResultQualCode qualifies the analytical result of the sample. BR: This field may be left blank for results that are considered detected. The database will be populated with an equal sign (=) when the data are loaded. When a result is Not Detected (ND) or Detected Not Quantified (DNQ) a ResultQualCode is required and the appropriate code would be applied. When the result is -88, a ResultQualCode is required. If the ResultQualCode value is NR for Not Recorded, then a reason for this code must be written into the TissueResultComments field and/or an appropriate QACode would be applied.
MDL		Method Detection Limit (MDL) is the minimum concentration of an analyte that undergoes the entire measurement process and can be reported with a stated level of confidence that the analyte concentration is greater than zero. It is the detection limit associated with the method used to analyze the analyte, or parameter, in the sample. BR: If no MDL is used, enter -88. A value other than -88 must be used for either the MDL or the RL.
RL		Reporting Limit (RL) is the minimum value below which data are documented as nonquantifiable. It is the reporting limit for the sample analyzed, as determined by the laboratory. BR: If no RL is used, enter -88. A value other than -88 must be used for either the RL or the MDL.

QACode	QALookUp	QACode is applied to the result to describe any special conditions, situations or outliers that occurred during or prior to the analysis to achieve the result. BR: The default code, indicating no special conditions, is None. If more than one code should be applied to a record, the convention is to list them in alphabetical order separated by commas and no spaces; i.e. GB,SC
ExpectedValue (Not Required)		The ExpectedValue is the concentration of the analyte in a reference standard, laboratory control sample or matrix spike sample or the value expected to obtain from analysis of the QC Sample. This consists of the native sample result concentration plus the spike amount. BR: For surrogate samples, the expected value should be 100, representing 100%. This field is required for SampleTypeCodes of MS1, MS2, CRM and LCS.
TissueResultComments (Not Required)		TissueResultComments are any comments related to the TissueResult.

vi. Tissue Lab Batch Worksheet

The second worksheet to travel with the Tissue Results data holds information specific to the laboratory batch in which data is analyzed. This worksheet should be named **LabBatch** (with no spaces) in its worksheet tab. The fields in this sheet are and should be completed as follows:

Template Field Name	LookUp List	Description & Business Rules
LabBatch		The LabBatch is a unique code, provided by the laboratory, that represents a group of samples processed together. It groups all environmental samples with their supporting QC samples and will be used to verify completeness based on the SWAMP QAPrP. BR: The LabBatch is assigned to and identifies all samples digested or extracted together in one batch. When a digestion or extraction is not performed as part of the method, the LabBatch represents all samples within a unique analysis run. Please see the File and Batch Naming Convention to correctly format the LabBatch name. All lab batches listed in the Results worksheet need to be listed one time only in the LabBatch worksheet.
LabAgencyCode	AgencyLookUp	LabAgencyCode refers to the organization, agency or laboratory that performed the analysis on the sample.
LabSubmissionCode (previously BatchQualifierCode)	LabSubmissionLookUp	The LabSubmissionCode is a unique batch qualifier code assigned to the LabBatch as a whole by the analyzing laboratory which references the quality of the data in the LabBatch. BR: If the LabSubmissionCode of A is used, meaning Acceptable, the laboratory is ensuring that all SWAMP QAQC protocols were met for the lab batch. If anything other than A is used, a LabBatchComment is required.
SubmittingAgencyCode	AgencyLookUp	SubmittingAgencyCode is the organization or agency that is responsible for submission of the data to the database. This agency may be different from LabAgencyCode if the analytical data were subcontracted to another agency.
LabBatchComm (Not Required)		LabBatchComments records any comments relating to the LabBatch as a whole. BR: If the LabSubmissionCode is anything other than "A", a LabBatchComment is required.

c. Special Circumstances

There are two types of special circumstances discussed in this section. The first type includes samples that are generated or created by the laboratory (LABQA). The second type includes environmental samples that are modified by the laboratory.

For a list of QA sample types required for each type of chemical analysis, please see the QAPrPC:\Projects\SWAMP\Swamp Database\2.5 New Database\Documentation\~~~IM Plan~~~\2.5 Draft IM Plan_06.10.09.doc - _SWAMP_Laboratory_QA#_SWAMP_Laboratory_QA.

i. Laboratory-generated QA samples (LABQA)

All samples generated from within the laboratory, such as LabBlank, LCS, CRM, etc. have specific alternative rules, which are as follows:

(b) TissueResult

LabSampleID	Recommended - provide lab specific identification for an analyzed sample
CompositeID	UniqueLabBatchIdentifier_UniqueName LabBlank: UniqueLabBatchIdentifier_Method Blank# Only include # of blank if there is more than one blank analyzed e.g. L-487-07_BS494_Method Blank or 2006HgDig07_Blank3 LCS: UniqueLabBatchIdentifier_LCS# Only include # of blank if there is more than one LCS analyzed e.g. L-487-07_BS494_LCS or 2006HgDig07_LCS2 CRM: UniqueLabBatchIdentifier_CRM Name e.g. L-487-07_BD 494_SRM1588b or 2006HgDig07_Dorm-2
Composite Replicate	1
OrganismGroup	LabBlank: Not Applicable LCS: Not Applicable CRM: Organism group of the CRM, e.g. Fish, Bivalves, Crustacean, Mammal, Bird, or Amphibian
CompositeType	LABQA
SampleTypeCode	Select from SampleTypeLookup list
Matrix	tissue (if laboratory is using solvent, water or nothing) blankmatrix (commercially generated product)
LabReplicate	1 2, 3, etc. only if it is truly a replicate of the LABQA sample

The following information will be loaded into the database by the data management team. Laboratories are not required to submit this information.

(c) Sample

EventCode	TI
ProtocolCode	Not Applicable
StationCode	LABQA
SampleDate	01/01/1950
AgencyCode	Not Recorded
ProjectCode	Not Applicable

(d) Location

LocationCode	Not Applicable

(e) Collection

CollectionMethodCode	Not Applicable
CollectionDevice	None
CollectionTime	00:00
TisSource	NA
Replicate	1

(f) Processed Organisms

OrganismID	LABQA
OrganismName	Not Applicable
LifeStageCode	NR
PartCreated	Yes

(g) Parts

TissueCode	NA
PreparationPreservation	None
TissueID	LABQA
TissueWeight	-88
UnitTissueWeight	g

(h) Composite

CompositeID	see above from TissueResult
Composite Replicate	1
CompositeType	LABQA

CompositeWeight	-88
UnitCompositeWeight	g
AgencyCode	Organization or agency that analyzed the sample
HomogDate	01/01/1950

ii. Laboratory-modified QA samples

There are several types of samples discussed in this section that are generated or modified within the laboratory. The first is a Matrix Spike, which is a modified or analyte-spiked field sample. The second is a laboratory-generated duplicate of a field sample. At times, laboratories use samples not generated through the SWAMP program to satisfy SWAMP batch QC requirements. This third type is a Non-Project sample.

(i) Matrix Spike (MS) and Laboratory Duplicate Samples

For these samples, all fields describing the sample (*CompositeID*, *OrganismGroup*, *CompositeType*) remain the same as the native sample. For Matrix Spike samples, the only fields that are different than the native field sample are the *SampleTypeCode*, which should be MS1, MS2 or MSBLDup and potentially the *CompositeReplicate*. For laboratory-generated Duplicate samples, the only field that is different than the native field sample is the *LabReplicate*.

LabSampleID	Recommended - provide lab specific identification for an analyzed composite sample. It is preferable to add -Dup, -MS, -MSD to the end of the Lab ID to help confirm the *SampleTypeCode* and the *LabSampleID* of the native composite sample.
CompositeID	Same as native composite sample
CompositeReplicate	1
OrganismGroup	Same as native composite sample
CompositeType	Same as native composite sample
SampleTypeCode	Same as native field sample - laboratory-generated Duplicates MS1 - Matrix Spike performed on a composite with a composite replicate of 1 MS2 - Matrix Spike performed on a composite with a composite replicate of 2 MSBLDup - Matrix Spike performed on a CompBLDup
LabReplicate	2 - lab-generated Duplicates 1 - Matrix Spike 2 - Matrix Spike Duplicate
Matrix	Same as native field sample or composite

(i) Matrix Spike Samples performed on Field Duplicates

Following is a table that describes the way to format matrix spike samples performed on field duplicates, field blind duplicates and composite blind duplicates in both the v2.2 and v2.5 SWAMP databases. The SampleTypeCode MS represents an MS/MSD pair.

v2.2 SWAMP Database			**v2.5 SWAMP Database**	
SampleTypeCode	*Sample Replicate*		*SampleTypeCode*	*Replicate*
One sample - sampled or split in triplicate - blind				
Grab	1	=	Grab	1
FieldBLDup	1	=	FieldBLDup or CompBLDup	1
FieldBLTrip	1	=	FieldBLDup or CompBLDup	2
One sample - sampled or split in triplicate				
Grab	1	=	Grab	1
FieldDup	1	=	Grab	2
FieldTrip	1	=	Grab	3
One pair of MS/MSD associated to one grab				
Grab	1	=	Grab	1
MS	1	=	MS1	1
One pair of MS/MSD associated to one grab - FieldDup present				
Grab	1	=	Grab	1
FieldDup	1	=	Grab	2
MS	1	=	MS1	1
One pair of MS/MSD associated to one FieldDup				
Grab	1	=	Grab	1
FieldDup	1	=	Grab	2
MSFDup	1	=	MS2	1
One pair of MS/MSD associated to one FieldBLDup				
Grab	1	=	Grab	1
FieldBLDup	1	=	FieldBLDup or CompBLDup	1
MSFBLDup	1	=	MSBLDup	1
Two pairs of MS/MSD, one associated to the Grab and one associated to the FieldDup				
Grab	1	=	Grab	1
FieldDup	1	=	Grab	2
MS	1	=	MS1	1
MSFDup	1	=	MS2	1

(ii) Calculating Matrix Spike Percent Recovery

The reported LabResult is the number gathered from the instrument and is the net amount recovered from the sample including the spike concentration. For spiked samples, the ExpectedValue is the total concentration of the analyte in the native sample plus the spiked concentration. Matrix Spike Percent Recovery is calculated by subtracting the native result from both the MS LabResult and the MS ExpectedValue, then dividing the two by each other and multiplying by 100. To illustrate:

$$\frac{\textbf{MS Lab Result – Native}}{\textbf{MS Expected – Native}} \textbf{ x 100} \qquad \textbf{or} \qquad \frac{\textbf{5 – 1}}{\textbf{10 – 1}} = \frac{\textbf{4}}{\textbf{9}} \textbf{ x 100} = \textbf{44\%}$$

If the sample being used for the matrix spike requires a dilution, the reported values for the MS and the native sample are the dilution corrected values, not the actual values from the instrument.

(j) Non-Project Matrix Spike and Duplicate Samples (000NONPJ)

At times, laboratories use samples not generated through the SWAMP program to satisfy SWAMP batch QA requirements. These samples have different formatting rules, as follows:

(iii) TissueResult

LabSampleID	Recommended - provide lab specific identification for an analyzed sample. It is preferable to add -Dup, -MS, -MSD to the end of the Lab ID to help confirm the SampleType and the LabSampleID of the native sample.
CompositeID	NPJC_UniqueLabSampleID_AgencyCode (analyzing laboratory agency) e.g. NPJC_2002-1910_MPSL-DFG
Composite Replicate	1
OrganismGroup	Organism group of the sample, e.g. Fish, Bivalves, Crustacean, Mammal, Bird, or Amphibian, or Not Recorded if it is not known
CompositeType	Normal
SampleTypeCode	Composite
Matrix	tissue
LabReplicate	2 - lab-generated Duplicates 1 - Matrix Spike 2 - Matrix Spike Duplicate
QACode	QAX, when the native sample is not included in the batch reported

The following information will be loaded into the database by the data management team. Laboratories are not required to submit this information.

(iv) Sample

EventCode	TI
ProtocolCode	Not Applicable
StationCode	000NONPJ

SampleDate	01/01/1950
AgencyCode	Not Recorded
ProjectCode	Not Applicable

(v) Location

LocationCode	Not Recorded

(vi) Collection

CollectionMethodCode	Not Recorded
CollectionDevice	Not Recorded
CollectionTime	00:00
TisSource	NA
Replicate	1

(vii) Processed Organisms

OrganismID	000NONPJ
OrganismName	Not Applicable
LifeStageCode	NR
PartCreated	Yes

(viii) Parts

TissueCode	NA
PreparationPreservation	None
TissueID	000NONPJ
TissueWeight	-88
UnitTissueWeight	g

(ix) Composite

CompositeID	see above from TissueResult
Composite Replicate	1
CompositeType	Normal
CompositeWeight	-88
UnitCompositeWeight	g

AgencyCode	Organization or agency that analyzed the sample
HomogDate	01/01/1950

d. Converting the Data

Analysis results in many laboratories are produced in a format that does not easily fit into the format described above. Many labs' instruments provide reports in a vertical, rather than horizontal format, for instance. The SWAMP DMT has developed a program to assist in the conversion of data from the analysis instrument-provided format to that required by the SWAMP Database. While this conversion program does not complete all of the work for the lab personnel, it greatly reduces the effort involved. Because each situation is unique, the SWAMP DMT should be contacted to make arrangements.