

MULTIPLE SCENARIOS OF GENETIC SAMPLES IN ENTOMOLOGY:

Best Practices

Scenario 1: Genetic sample is a whole specimen

Scenario 2: Genetic sample is a leg/other part from a specimen in collection

Scenario 3: Genomics Sample

SCENARIO 1.-

Description: In this scenario you collected specimens here and there for genetic analysis.

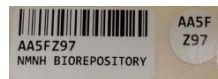
Best practices:

1. **Place one specimen per cryo-vial.** There are legacy collections with multiple specimens per vial; this will pose more work down the road if the identification proves incorrect and there are more than one species in the lot. When this is the case, the specimen has to be moved to a new vial and processed independently.
2. **Each cryo-vial is assigned a BioRep# (BioRepository number).** At the time of making preparations for your trip, request BR# labels from the BR and affix these labels to the cryo-vials to have them ready to use in the field.
3. **Each sample is assigned a USNMENT#.** At the time of making preparations for your trip, request these labels from CIMU and affix these labels to the cryo-vials to have them ready to use in the field.
4. **Create one record per cryo-vial.** This will be a stand-alone Genetic Sample record. Use the provided FIMS Template to capture information in the field. Upon return to the office, complete the record and provide the dataset to appropriate staff for import into EMu

Scenario 1.- Stand Alone Genetic Sample



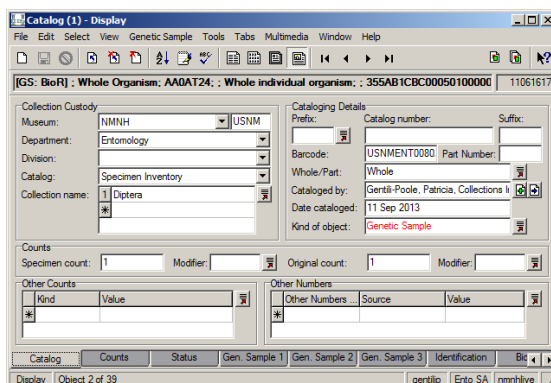
1 cryo-vial containing 1 whole specimen. Many specimens is not recommended



1 BioRep# assigned; label affixed to cryo-vial



1 USNMENT # (barcode) assigned; label affixed to cryo-vial



The screenshot shows the EMu Catalog (1) - Display window. The main title bar reads "Catalog (1) - Display". The menu bar includes File, Edit, Select, View, Genetic Sample, Tools, Tabs, Multimedia, Window, and Help. The toolbar contains various icons for file operations and navigation. The main content area displays the following information:

- Collection Custody: Museum: NMNH, Department: Entomology, Division: Specimen Inventory, Catalog: 1 Diptera, Collection name: *
- Cataloging Details: Prefix: USNM, Catalog number: USNM0000, Part Number: Whole, Cataloged by: Gentil-Poole, Patricia, Collections I, Date cataloged: 11 Sep 2013, Kind of object: Genetic Sample
- Counts: Specimen count: 1, Original count: 1
- Other Counts: A table with columns Kind and Value.
- Other Numbers: A table with columns Other Numbers, Source, and Value.

The bottom status bar shows "Display | Object 2 of 39" and "gentilp | Ento SA | nmnhhive".

1 Record in EMu, kind of object = Genetic Sample


SCENARIO 2.-

Description: In this scenario you took a leg/other part from a specimen in the collection.


Best Practices:

1. The specimen in the collection and the cryo-vial are assigned a **USNM#** each. Place the labels in/on them.
2. The **cryo-vial** is assigned a **BioRep#**. At the start of the project request BR# for the cryo-vials with the leg/other part and affix the labels to the cryo-vial
3. Create two records in EMu:
 - a. A **Specimen/Lot** record for the specimen in the collection, indicate that the specimen is a Voucher to the leg/other part and that the record is the Parent of the Genetic Sample record
 - b. A **Genetic Sample** record for the leg/other part, derive this record from the previous one indicating the Parent/Child relationship; establish a link to the FreezerPro through the BR#; indicate that the sample has a Voucher in the collection.

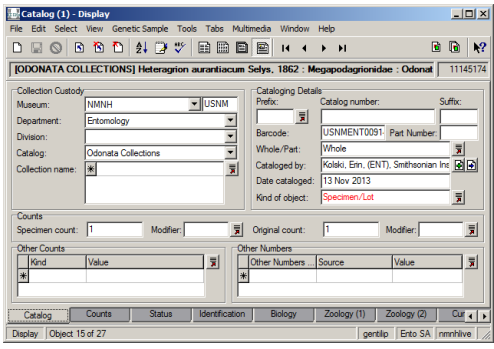
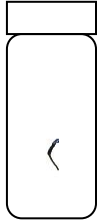
Scenario 2.- Genetic Sample with Voucher in Collection



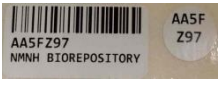
1 specimen in collection




1 USNM # (barcode) assigned; label on pin or in fluid vial or slide or envelope

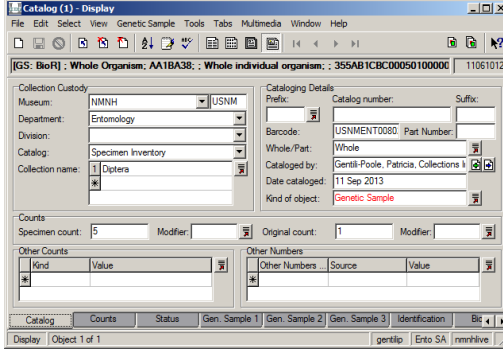
1 cryo-vial containing a piece of the specimen (most commonly a leg)



1 BioRep # assigned, label affixed to cryo-vial



1 USNM # (barcode) assigned; label on cryo-vial



1 Parent Record in EMu; kind of object = Specimen/Lot



1 Child Record in EMu; kind of object = Genetic Sample

IMPORTANT NOTES ABOUT GENOMICS SAMPLES

We are still experimenting and finding the best way to handle this new type of material, not only for Entomology but at the Museum level. Keep this in mind as we work through the process

'Nomenclatorial Schema' for the unidentified taxa

It is a fact of life that in Entomology we will have unidentified taxa collected. Final identification may happen many years after the collecting event and cataloguing effort. How we name those unidentified samples will have an impact on maintenance and future retrieval of the records.

Our natural tendency will be to go with Genus_01 species_01 for a particular family, if the collector can identify the family. There is the potential that many different collectors or even the same one in a later collecting event will identify different taxa with the same 'name'. These will then be retrieved from the system together, and users will need to 'dig up' in the system for the information to find the one they are looking for.

We are then recommending the following

Best Practices:

1. **Use the following fields:**
 - a. Family = *Family_01_BioRep#* [if family is not known]
 - b. Genus= *Genus_01_BioRep#*
 - c. Species = *species_01_BioRep#*
2. **Include leading zeroes** as a necessity for alphabetizing and grouping records in list view to check and revise.
3. **Include one of the BioRep#s** in the Genomics Sample to secure uniqueness. Pick any one you want from the series you assigned to each record in the sample.

Identification of a Genomics Sample

If we start with a set of 9 specimens collected for one species to sequence the full genome, there will be a set of 18 records representing one Genomics Sample. Processing DNA extractions will generate even more records to keep track of.

For many reasons we will want to be able to retrieve all the records in the database that comprise a single Genomics Sample, as easy and as quickly as possible.

EMu, using the relationships between the records, will compile a hierarchical grid for all the records involved in a Voucher Sampling Tree without having to generate a new identifier number.

We are then recommending the following

Best Practices:

1. **Designate an Exemplar Voucher** located in the main collection. Indicate this fact in the corresponding record
2. **For each record in the sample**, indicate it has an Exemplar Voucher by establishing this relationship in the record
3. **Establish proper Parent/Child relationships** between the records for the specimens and the leg/other part

SCENARIO 3.-

Description: In this scenario you are collecting specimens for full genome sequencing. You should collect an Exemplar Voucher specimen for the collection and as many specimens for grinding up for sequencing as necessary depending on the size of the specimen, these will be your Genomics Sample. Processing these samples takes two steps.

Step 1. In this first step you are processing the Exemplar Voucher and a leg/other part for confirmation of identification using CO1 analysis.

Best Practices:

1. **Prepare the Exemplar Voucher** according to the collection standards for the group; and place the leg/other part in a cryo-vial.
2. **The cryo-vial is assigned a BioRep#.** At the time of making preparations for your trip, request BioRep# labels from the BR and affix these labels to the cryo-vials to have them ready to use in the field.
3. **The Exemplar Voucher and the cryo-vial are assigned a USNMENT# each.** Place the labels on the specimen according to standards, and attach the label to the exterior of the cryo-vial. At the time of making preparations for your trip, request these labels from CIMU and affix these labels to the cryo-vials to have them ready to use in the field.
4. **Create two records in EMu:**
 - a. **A Specimen/Lot record for the specimen in the collection,** indicate that the specimen is an Exemplar Voucher and that the record is the Parent of the Genetic Sample record
 - b. **A Genetic Sample record for the leg/other part,** derive this records from the previous one so it becomes its Child; establish a link to the FreezerPro record through the BR#, indicate that the sample has an Exemplar Voucher in the collection.

Step 2. In this second step you are processing the rest of the Genomics Sample, the multiple specimens collected for the full genome extraction. For confirmation of the identification you will also need to process a leg/other part for CO1 analysis.

Best Practices:

1. **Prepare the specimens** according to standards; and place them and the leg/other part in a cryo-vial each.
2. **Each cryo-vial is assigned a BioRep#.** At the time of making preparations for your trip, request BioRep# labels from the BioRepository and affix these labels to the cryo-vials to have them ready to use in the field.
3. **Each cryo-vial is assigned a USNMENT#.** Attach the labels to the exterior of the cryo-vial. At the time of making preparations for your trip, request these labels from CIMU and affix these labels to the cryo-vials to have them ready to use in the field.
4. **Create Genetic Sample records in EMu for each cryo-vial:**
 - a. **One Genetic Sample record for each specimen in a cryo-vial,** each individual record will be the Parent of the record for the leg/other part. Indicate that the sample has an Exemplar Voucher.
 - b. **One Genetic Sample record for each leg/other part,** derive this record from the record for the specimen providing the leg so it becomes its child; establish a link to the FreezerPro record through the BioRep#, the link to the Exemplar Voucher record will transfer from the Parent.

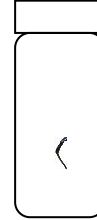
Scenario 3.- Genetic Samples for Genomics – Step 1



1 specimen in collection (Exemplar Voucher)



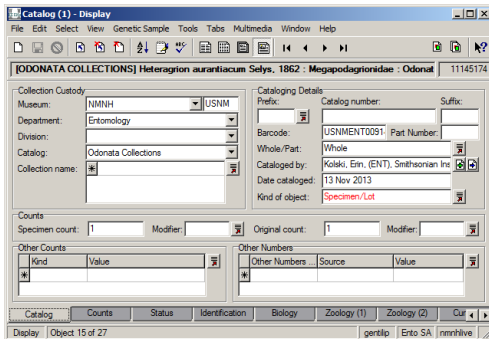
1 USNMMENT # (barcode) assigned; label on specimen or in fluid vial or slide or envelope



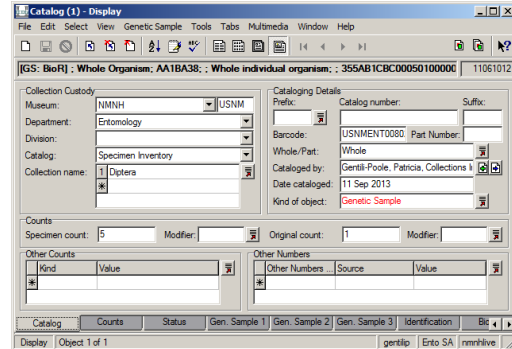
1 cryo-vial containing a piece of the specimen (most commonly a leg)



1 BioRep # assigned; label affixed to cryo-vial
1 USNMMENT # (barcode) assigned; label on cryo-vial



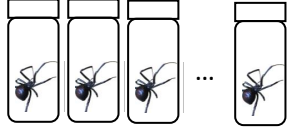
1 Parent Record in EMu; kind of object = Specimen/Lot



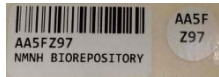
1 Child Record in EMu; kind of object = Genetic Sample



Scenario 3.- Genetic Samples for Genomics- Step 2



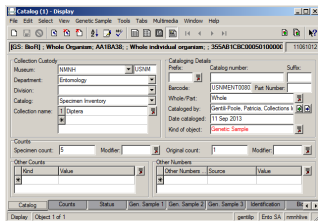
1 to n cryo-vials containing 1 whole specimen each (as necessary for sequencing complete Genome)



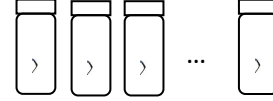
1 BioRep # assigned to each cryo-vial; label affixed to cryo-vial



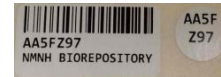
1 USNMENT # (barcode) assigned to each cryo-vial; label affixed to cryo-vial



1 Record in EMu per cryo- vial; kind of object = Genetic Sample; each linked to exemplar voucher record



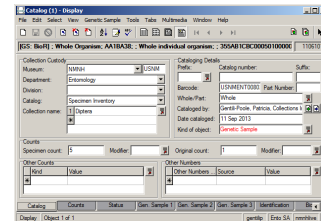
1 cryo-vial containing a piece of the specimen (most commonly a leg) for each specimen in collecting event



1 BioRep # assigned to each cryo-vial; label affixed to cryo-vial



1 USNMENT # (barcode) assigned to each cryo-vial; label affixed to cryo-vial



1 Child Record in EMu per cryo-vial; kind of object = Genetic Sample; each a child of the record for the rest of the specimen; each linked to exemplar voucher record