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0 - SOP Sampling General Recommendations V.1

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Abstract

The Standard Operating Procedures (SOPs) contain general guidance on processing specimen within the scope of the ATLASea program. The guidance specifically refers to station metadata (or collection metadata), the tissue samples destined for DNA extraction, and to specimen vouchering.

Materials

Lab material :
- Gloves
- Dissection tools (tweezers, scalpels, scissors)
- Petri dish with different size
- Tube rack
- Paper towel
- Ethanol, Bleach, Filtered sea water, Liquid nitrogen
- Wash bottle
- Scale
- Dewar
- Dissection table
- Ice pack
- Tooth brush

Tubes:
- CORNING® 1.2 ml conical-bottom cryotube, skirted with external thread and natural screw cap [ref Dutscher # 430658]
- CORNING® 2 ml Cryotube, skirted, external thread with natural screw cap [ref Dutscher # 430659]
- 5 ml screw tube sterile (Eppendorf) [ref Dutscher # 934683]
- 25 ml screw tube sterile (Eppendorf) [ref Dutscher #934685]
- 50 ml Conical Centrifuge Tubes (Greiner) [ref Dutscher #227261]
- 1.5 mL Safe-Lock Tubes (Eppendorf) [ref Dutscher #033290]
Bags:
- Nylon protection net, reusable with drawstring (15×10 cm) [Amazon #https://www.amazon.fr/Anti-Insectes-Protection-Plantes-R%C3%A9utilisables-Anti-Oiseaux/dp/B08XXJMY4C]
- Nylon protection net, reusable with drawstring (15×25 cm) [Amazon #https://www.amazon.fr/AMZMUKAUP-Protection-Raisins-R%C3%A9utilisables-Rangement/dp/B09N7PV2LD/ref=sr_1_1_sspa?crid=2VTI1EVYUW654&keywords=sachet+filet+nylon&qid=1690200116&sprefix=sachet+ny%2Caps%2C213&sr=8-1-spons&sp_csd=d2lkZ2V0TmFtZT1zcF9hdGY&psc=1]
- Twist attaches [Amazon #**Twist Attaches Or, 800 Pcs Métallique Pince pour Fermeture Sachet Alimentaire, Attache Sac pour Paquet de Bonbon, Sachet Plastique, Transparent Cello**]
- Zip-Seal Bags (grands sachets) 350×250 mm [ref VWR #129-0307]
- Zip-Seal Bags (petits sachets) 170×120 mm [ref VWR #129-0297]

Scan:
- Bluetooth QR & Barcode to PC application to scan labels with your phone and import the code to the Excel sheet via Bluetooth: https://play.google.com/store/apps/details?id=dev.fabik.bluetoothhid
- Honeywell Voyager Extreme Performance 1470g-2D [Ref. Fabricant #1470G2D-2USB-1-R]

Photography equipment : see section C.

Before start

Beyond the present general recommendations, taxon-specific SOPs are also available, and describe more specific procedures for each taxon (see list below). Other taxonomic groups may be added in the future.

1. Anthozoa
2. Bryozoa
3. Medusozoa and Ctenophora
4. Tunicata
5. Echinodermata
6. Crustacea
7. Mollusca
8. Porifera
9. Annelida
10. Others worms
11. Macro-algae
12. Phytoplancton cultures
13. Zooplankton
14. Osteichthyes and Chondrichthyes

Those SOPs apply for MNHN field trips and Marine Stations. SOP dedicated to Ambassadors will also be published.

Future plans for this SOP
This SOP will be reviewed on a regular basis by ATLASea team members to incorporate feedback from the community. If you have any advice, comments, techniques, or lessons learned that you would like to contribute, we would greatly appreciate it (please contact: **ambassadors@atlasea.fr**).

ATLASea sampling selection
ATLASea collects marine organisms of ecological, endangered, and economical interest observed in the French EEZ. The **GoaT database** (Genomes on a Tree) must be consulted before a species enters the ATLASea program, to avoid overlaps with other genomic projects. Theoretically, only species that have not yet been sampled or sequenced by other programs will enter the ATLASea program. For any question or clarifications please write to **ambassadors@atlasea.fr**

****Please ensure that you hold sampling permits if these are required, please see the ATLASea Statement**

General procedure

Sampling and conditioning a specimen to be sequenced by ATLASea will generally involve the following 5 steps:

1. Sampling in the field and entry of collection metadata for traceability (section A)
2. Taxonomic identification and status verification in the GoaT database (section B)
3. Photographing the specimen live with labels provided by ATLASea (section C)
4. Flash freezing tissues for sequencing (section D), and preserving a sample for a voucher (section E)
5. Shipping the samples and voucher to Genoscope and MNHN (section F)

Before starting the specimen sampling, please ensure that you have the 2 types of labels (ATLASea and MNHN) and the screw cap cryotubes in sufficient quantity. Both can be sent to you by ATLASea, please ask Melanie van Weddingen at ambassadors@atlasea.fr. You will need one MNHN label per specimen (individual), one ATLASea label per batch of specimen(s) (one batch corresponds to a sampling event at the same time and the same place for a single species), and one ATLASea label per cryotube.

Please do not use any other tube than the recommended model (see Appendix).

Note:

The separator between data in the same column, such as locations, collector names, or institution names, is " ; ".
MNHN: Muséum national d'Histoire naturelle

A. Station metadata entry

1 **Definition**

A **collection station** is a **collection event** at **time t**, a **location XYZ**, the **people collecting** in the field, a **single collection method and a UNIQUE station code**. A station cannot have multiple different collection methods. If several collection methods are used at the same time and location, a separate station must be created for each collection method.

2 **Metadata**

All metadata fields are mandatory. If certain columns cannot be completed due to lack of knowledge or
information, enter the missing metadata in the "NOT_COLLECTED" column. Some columns correspond to "trailing" collection methods, such as dredging or trawling. Data from trawling methods must have the "start" and "end" columns completed to provide transect data from point A to point B.

List of metadata to complete:

- Mission name
- Station code
- Collection method
- Locality
- Coordinates
- Depth
- Datetime
- Names of collectors and their institutions
- Habitats and station photos

Mission name and station codeEach frame corresponds to a mission name defined by the Genoscope. Station codes are defined by the MNHN (National Museum of Natural History) upon data publication. In the field, each collection event must have a unique station code to identify it and link it to the collected species, thus maintaining complete traceability.

MNHN mission

For MNHN missions, predefined codes established by Tatiana Gauche are used. These codes are characterized by the acronym of the mission and the collection method, incremented by the method's replica. For more information, please contact tatiana.gauche@mnhn.fr.

Marine station mission

Outside of MNHN missions, when entering data, a unique temporary code must be assigned to each station. The official code is assigned after data processing by Tatiana Gauche according to the following nomenclature.

Collection method

The sampling method is mandatory so that the appropriate tool used to collect a given species can be identified. The method must be as precise as possible, as there is a wide variety of dredges and trawls, each with specific characteristics and different capture objectives. **Refer to the list in Table 1 and/or add new methods to bevalidated by Tatiana Gauche via tatiana.gauche@mnhn.fr.**

Table 1 : List of
station codes according to collection methods

	A	B	C	D
	METHOD FAMILY	**COLLECTION METHOD (EN)**	**COLLECTION METHOD (FR)**	**DETAILS**
	Grab	Van Veen grab	Benne Van Veen	
	Grab	OKEAN grab	Benne OKEAN	
	Bottle	Niskin bottle	Bouteille Niskin	
	Bottle	Bottle	Bouteille	(if no additional information)
	Trawl	Bottom trawl	Chalut de fond	
	Trawl	Pelagic trawl	Chalut pélagique	
	Trawl	GOC73 Demersal Trawler	Chalut démersal GOC73	
	Trawl	GOV 36/47 Demersal Trawler	Chalut démersal GOV 36/47	
	Trawl	GOV 36/49 Demersal Trawler	Chalut démersal GOV 36/49	
	Trawl	Panel trawl	Chalut à panneaux	
	Trawl	Beam trawl	Chalut à perche	
	Dredge	Rosado dredge	Drague Rosado	
	Dredge	Hand dredge	Drague à main	
	Dredge	Triangular dredge	Drague triangulaire	
	Dredge	Warén dredge	Drague Warén	
	Net	WP2 triple plankton net	Filet à plancton WP2 triple	

	A	B	C	D
	Intertidal	Picking up in littoral	Récolte à vue en marée	Rake ; Hooks ; Shore fishing with a dredge ; Crustacean pump
	Trap	Trap	Nasse	
	Scuba diving	Brushing in scuba diving	Brossage en plongée	
	Scuba diving	Picking up in scuba diving	Récolte à vue en plongée	
	Scuba diving	Vacuum cleaner in scuba diving	Aspirateur sous-marin en plongée	

Locality

Country: Refer to the list in the frame.

Sea: Refer to the list in the frame.

Region or locality: This field allows for quick identification of a species' locality. It relates to the dive site, for example, or to a nearby location that is easily identifiable or noteworthy.

Coordinates

Coordinates must be entered in decimal degrees (DD) as precisely as possible (10^{-6}). If it is a single point, the user enters the end points; if it is a transect (from point A to point B), the user must provide the two points, i.e., the start and end of the transect. **Example:**

	A	B	C	D	E
	POINT	**LATITUDE_START**	**LONGITUDE_START**	**LATITUDE_END**	**LONGITUDE_END**
	Unique			48.68755	-2.05053
	Transect	48.25369	-1.48229	48.02500	-1.78956

Datetime

The date and time of sampling are required in order to correctly identify a sampling event. You must provide the sampling date (format dd/mm/yyyy) and the start and end times (format hh:mm) for both single points and transects (at the moment of contact with the seabed/substrate).

Depth

Depth in meter (m) must be completed according to the type of sampling method. If the method involves scuba diving or shore-based sampling, the minimum and maximum sampling depths are mandatory, even if the depth is the same. For so-called “towed” sampling methods, the starting depth of the transect corresponds to the minimum depth, and the ending depth corresponds to the maximum depth. In the table, you can complete it as follows: “***0-15***” (for min-max) or “***12-10***” (for start-end).

Names of collectors and their institutions
Institute: Institution or organization of the collector. If several people are present during the sampling, in the same order as the collector’s names. Even if it's the same institute for both collectors, the information must be added.

Example: *Institute A ; Institute A ; Institute B ; Institute C*

Collector: This column identifies the people present during the sampling. It must follow the format “SURNAME Firstname” (real names and in **alphabetical order of the surnames** of divers and/or the people on board the vessel). **Don't forget to include accents in the participants' names.**

Example: *SURNAME Firstname A ; SURNAME Firstname B ; SURNAME Firstname C*

This procedure is the same for participants in the "taxonomists", "institution taxonomist" and "tube operators" columns.

Habitats and station photos
Within a single sampling event, several habitats may be present. In this context, the INPN provides the reference system for habitat, environment, and vegetation typologies (Habref). For greater practicality in the field, there are also SOPs for NatHab-Mediterranean and NatHab-Atlantic at broader habitat scales. For more detailed habitat descriptions, you may use the full habitat typologies, namely **NatHab-Mediterranean** and **NatHab-Atlantic**.
During MNHN missions, it is required to take photographs of grab or dredge samples, as well as habitat photos during shore-based or scuba diving sampling. Each photo must be sorted by the authors (blurry images, duplicates, relevance), renamed according to the MNHN nomenclature (code_station_context_author-name_replica.jpeg), and sent back to Tatiana Gauche via **tatiana.gauche@mnhn.fr**. The context in the filename specifies what should be highlighted in the photo; there are four categories (station, habitat, method, and organism).

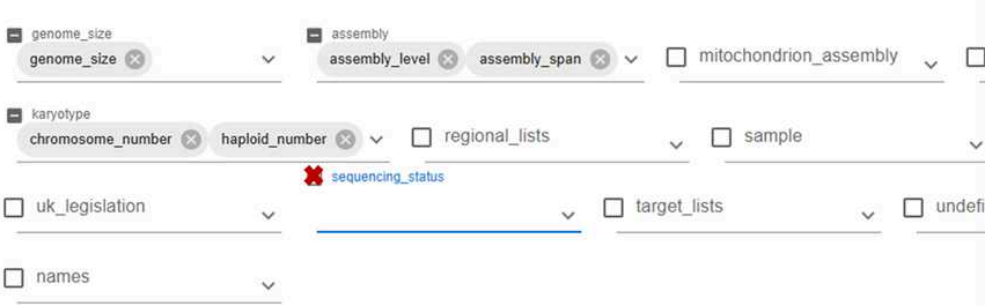
B. Taxonomic identification and status verification

3 The Genome on a Tree (GoaT) database centralises information generated by various genome sequencing projects. It enables researchers to monitors the evolution of the

status of the species that are being sequenced worldwide and deposited in the INSDC (International Nucleotide Sequence Database Collaboration) repositories (Genbank, ENA, DDBJ). All projects affiliated to the Earth Biogenome Project (EBP), including ATLASea, update GoaT regularly with the status of the species they are proceeding with. This ensures transparency, facilitates tracking of genomic progress, and helps prevent overlaps or duplication of effort. It is crucial to confirm the taxonomic identification of the species by a qualified taxonomist familiar with its distinctive morphological traits. The name of the taxonomist responsible for identifying the species will need to be recorded later. Once the specimen's name is confirmed, please verify in the World Register of Marine Species (**WoRMS**) that you are using the accepted name, not a synonym. Following this, you may verify its status in GoaT (**https://goat.genomehubs.org/**):

1. Type the name of the species (*Binomial nomenclature*) in the "Type to search GoaT taxon index" box.

2. Select the option "results columns" and ensure that the "sequencing status" option is activated. Update your option



3. Click on "TAXON" on the pulldown menu to the right of the entry box.
4. If no results are returned (0 hits), you may have misspelled the species name. GoaT contains ~1.5 million species described to date and their synonyms, so you should find your species. However, some genus may be poorly represented, especially for overseas species.
5. Click on the name of your species of interest in the table containing the results. If the genome is already sequenced at "reference" of "chromosome" level, a yellow badge

"EBP standard" will be shown above a "snail plot", when it is present, summarising the assembly's characteristics. Next to the plot, there should be at least "1 chromosomal" assembly shown.
6. If the genome is not sequenced at chromosome level, it may be sequenced at a lower level of contiguity. Look further down the table and check the "assembly_level" attribute, which may show "Scaffold" or "Contig".
7. If the genome is not sequenced at all, it may however be underway in a sequencing centre. Look further down the table and check the "sequencing_status" attribute, which shows the status at the centre that is the furthest advanced in the sequencing process. Statuses include, from least to most advanced in the sequencing process, "sample collected", "sample acquired", "in progress", "in assembly", "insdc open".

By default, ATLASea will only sequence the genome of species for which no high-quality genomic data has been produced (EBP Standard), or those not already marked as "in progress" by other projects. Exception will be made for species who have been sequenced at low contiguity levels (Scaffold or Contig) but this will be decided by the ATLASea Species Selection Committee. The ATLASea SSC will systematically verify the status of a species before proceeding with DNA extraction.

C. Standard Operating Procedures for Specimen Photography

4 Why take photos of specimen? Photos of specimen in ATLASea are extremely important for several reasons. First, for logistical reasons, they connect a recognisable physical specimen with its labels, which greatly facilitates traceability later on in the procedure. Second, when individuals are too small to be dissected and kept as voucher in MNHN collections, the photo is the only way to go back to the sample and perform detailed taxonomical identification. In effect, the photo becomes the Museum voucher. Finally, the genome that will be sequenced from the sample will probably become the reference genome for all genomic studies involving this species. Metadata accompanying the sample therefore become crucially important, including its photo. Taking photos of specimen is becoming standard practice in all projects that sample specimen from biodiversity for reference genome sequencing. A specimen with no photo voucher weakens the taxonomic assignation/hypothesis.

4.1 **General Guidelines**

- Specimens should be photographed while alive or under anesthesia for specific groups such as annelids, crustaceans, molluscs and fishes (refer to their sections in relevant SOPs).
- Seawater must be changed between each specimen and must be clean.
- Avoid using transparent plastic containers, instead use glass container on a black background or solid black containers. If the animal is dark, use a white background.
- It is possible to place the specimen directly on a black/white background without a container, for example Asteroidea, Echinoidea, Ophiuroidea. Return the specimen to

seawater from time to time (between adjustments, information collection, etc.) to avoid animal stress and deterioration (refer to their sections in relevant SOPs).
- The duration of the photography process may vary depending on the activity level of the specimen.
- Save all photos in JPEG format with the highest possible resolution (varies depending on the camera type, e.g., phone, professional camera).
- Name photos using the MNHN identifier assigned to the specimen (see taxon-specific SOP), with incremental numbering if there is more than one photo.

Example:
- Reference photo: MNHN-IM-2019-515655_01
- Specimen photo: MNHN-IM-2019-515655_02
- Photo 02: MNHN-IM-2019-515655_03
- Photo 03: MNHN-IM-2019-515655_04

Photography Planning:
If you are processing specimen, you need to take one Reference Photo (see Section C.4.3), one Specimen photo (without labels) and possibly several others (without labels) to focus on anatomical details that are critical for taxonomic identification.

Reference Photo: Specimen with labels (ATLASea, MNHN).
Specimen photo: Entire specimen in greatest possible details / resolution.
Anatomical Detail Photos: Close-ups of specific anatomical features.

If you are processing several specimens from the same species, the Reference Photo (see Section C.4.3) should contain all specimen together. For the Specimen Photo, if possible, take a photo of each individual, one by one, making sure to respect their MNHN code. Otherwise, designate one as the voucher and focus on that one.
Once the photos are taken, the specimen can proceed to cold-chain processing.

4.2 **Photography Equipement**

Ideally, please use high quality material used for scientific photography, with a flash, installed on a stand and with dedicated lightning. If this equipment is not available where you are, you can also use a smartphone attached to a support for stability, and good *ad hoc* lightning.
Always use a scale, such as a ruler graduated in mm and cm, and ensure that it is visible on the photo (no reflection, blurry, etc.) across the length of the specimen.
If using professional cameras, here are some general guidelines:
- **Shutter Speed (1/100)**: Use fast speeds for live specimens to freeze motion, especially when using flashes.
- **Aperture (F14)**: Higher values decrease light entry but increase depth of field, resulting in sharper images.
- **ISO (125)**: Adjusts brightness. Higher values increase brightness but add noise, reducing image sharpness.

- Avoid lenses that cause distortion, such as wide-angle lenses.
- Use **50 mm or 100 mm macro lenses** for specimens larger than 1 cm.
- Use a **65 mm macro lens** for specimens smaller than 1 cm.

4.3 **Reference Photos**

Single Specimen

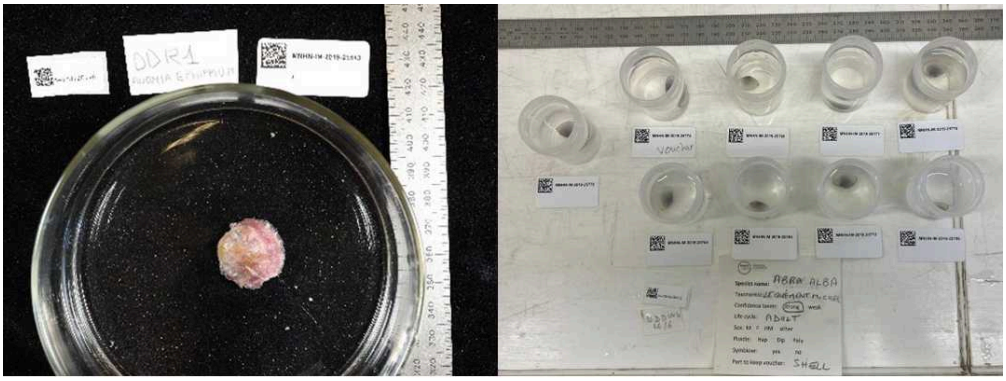
If you are processing a single specimen, you need to take one Reference Photo, which will be used to connect the specimen with its identification labels in case of doubt later in the procedure. The specimen need not be photographed in great details, but the photo MUST include a ruler, an ATLASea label and an MNHN label corresponding to the correct phylum (see taxon-specific SOP for more details).

Multiple Specimens

When multiple specimens represent the same species, designate one as the voucher for the Specimen Photography if it's not possible to take a photo of each individual.

Procedure for the Reference Photo:

- Separate specimens into containers.
- Assign an MNHN label **to each specimen**.
- Assign **a single** ATLASea label to the entire collection.
- Mark the MNHN label of the voucher specimen with "Voucher" or a cross for identification.
- Include a ruler.



Typical Reference Photos for single specimen (left) and multiple specimen (right). Additional labels (Station labels e.g. DDR1, species identification labels) are shown but are only relevant for ATLASea field missions.

Proceed with further photos of the voucher specimen (Specimen Photo and additional clos-ups).

After the reference photo, you can take photo of the specimen and some close up for details without the labels. But the photo should be name with the right ID. See taxon-

specific SOP for more details.

4.4 **Sending photos**

All photos should be sent by email to **ambassadors@atlasea.fr** in one or several batches, or made available on a local server for download with the link sent to the above address. Please remember to use JPEG format, and to name the photos with the MNHN ID of the Reference Photo with an incremented suffix for all ensuing photos.

D. Preparation of tissues

5 Prior to the preparation of tissues, the operations carried out on the Vertebrata and Cephalopoda (collection, anesthesia, euthanasia) must be carried out in accordance with European directive n°2010/63/UE, transposed in France under decree **n°2013-118** of February 1, 2013 relating to the protection of animals used for scientific purposes.

Regardless the organism, the steps for tissues preparation are as follow:

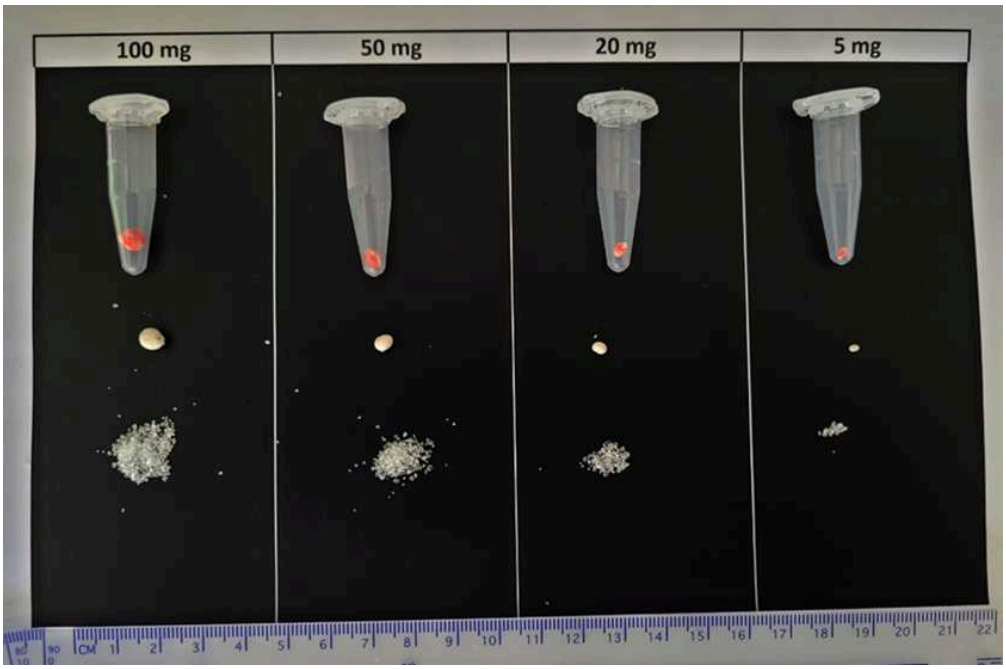
1. **Fresh material** is critical for obtaining HMW-DNA. If possible, specimens should be sampled **alive**. However, specimens will deteriorate even in these conditions so **sampling should occur as soon as possible once the specimen is out of its natural environment.**
2. Anaesthetic methods can be applied to calm animals. See specifics SOPs for more details.
3. Before dissection and preservation remove all visible contaminants and epibionts as much as possible (washes, brushing... with stereomicroscope).
4. **Dissection** should be done as **quickly** as possible, maintaining the cold chain until flash-freezing (for example, by dissecting individuals on a glass board placed on an ice tray).
5. **Decontaminate** instruments (forceps, scalpels, etc.) between **EACH** organism by wiping with wet absorbent paper, then immersing them for 1 min in sterile water, transferred for 5 minutes in a bleach bath (2.6% active chlorine solution diluted ¼), then rinsing them for 5 minutes in a sterile water bath, finish with ethanol immersion to dry the instrument quickly. **Wash surfaces** (Aniospray + water...) and change gloves between each organism.
6. Always handle input material in a manner that minimizes nuclease exposure and activity, e.g. wear clean gloves (change regularly) when handling input material, storage tubes etc., use nuclease-free buffers and filtered and autoclaved seawater bottles and keep the input material as cold as possible during handling.
7. For each taxon, provide enough aliquots :

- one for taxonomic identification vouchering (see taxon-specific SOP)
- at least 15 for High Molecular Weight (HMW) DNA extraction, RNA extraction and long-range data production (Flash-frozen or in ethanol depending on the organisms, see taxon-specific SOP)

8. For **large specimen**, dissect **at least 10 pieces** (approx. **300 mg** each for animals, ideally **1 g** each for algae and plants) to be used for DNA extraction. For RNA extraction, also prepare **2 to 3 additional tubes** containing a mixture of all recommended tissues, for a total weight of approximately **50 mg per tube**. Cut each piece into smaller fragments before putting them in separate tubes (with unique identification labels). More details for each phylum in dedicated SOPs.
9. Collect “fleshy” parts when possible (avoiding shell, digestive contents, embryos/brooded progeny, ...).
10. For **small individuals**, put **1 specimen** per **conical-bottom** tube. In the case of very small specimens, make sure that it is placed in the bottom of the tube.
11. Avoid compacting the sample in the bottom of the tube, and never fill the tube to the top (to facilitate sample recovery for subsequent handling and to prevent the cap from popping off during thawing).
12. **Never pool different individuals** (even from the same species) in the same tube.
13. Each vial should be handled with gloves and correctly labelled:

- Only use labels provided by ATLASea:
- **Labels must be placed lengthwise along the tube, not wrapped around it.**
- Be sure that tubes and gloves are dry before handling the labels (the labels can detach from the tubes during the flash freezing if wet).

14. After conditioning the sample in the tubes, screw the cap of the tube properly (to prevent the cap from opening when immersed in liquid nitrogen), then weigh the tube with the cap. Use a tare with the same model of tube already labelled to deduce the weight of the sample inside the tube. For small individuals, estimate their weight using the scale below:



15. Scan the labels on the vials and fill in the log sheet dedicated to the ATLASea sampling. Ask **ambassadors@atlasea.fr** for the latest version. The **barcode** must be **scanned** (before flash freezing) to avoid typos. Ensure that all tissues from the same individual are correctly identified on the log sheet.
16. Samples should be flash-frozen in several **aliquots as soon as they are prepared**.
17. Once scanned, the sample must be immediately preserved. Most biological samples should be flash frozen (FF) in liquid nitrogen to minimize nucleic acid degradation by nucleases, then stored at -80°C and shipped on dry ice (see Section D). For the voucher, depending on the sample, it can also be preserved in ethanol 80%, stored at -20°C and shipped in cold box. More details for each phylum in dedicated SOPs
18. Vials should be grouped (around 10 tubes) and placed in a nylon bag identified with a unique number. When possible, place tubes corresponding to the same taxon in the same bag. Bags should be properly sealed using twist-ties to avoid loss of tubes during the transportations. Sealed bags should be then immersed in liquid nitrogen (in Dewar).

(Left) typical nylon bag used to group samples from the same species, if several species will be provided. (Right) Dewar container used to hold liquid nitrogen and flash freeze samples.

19. Avoid freeze–thaw cycles at all costs, as they can cause unwanted cell disruption and DNA degradation.
20. Transfer sealed bags in a -80°C freezer for longer storage. If immediate storage of the samples in a -80°C freezer is not feasible due to field conditions, an alternative is to place them in a larger liquid nitrogen container specifically designed for storage. This container should have a large opening to facilitate sample retrieval. The samples can then be transported to a facility where they can be stored under ultra-freezer conditions.
21. Place the nylon bags into a Zip-Seal bag, label it with the campaign information, and prepare it for shipping (on dry ice).

E. Voucher

6

1. It is very important to have as many taxonomic vouchers as possible (for post-mission correction/validation of identification and collection duty). These vouchers must ideally be minimally damaged and include taxonomically relevant parts.
2. Once the specimen dissection is finished, never throw away anything, all parts of the animal is still relevant as a voucher after sampling. The rest of the animal must be fixed, for example in ethanol 85%. See taxon-specific SOP for more details for conservation.
3. Fish must be frozen at -80°C and sent frozen at the same temperature when stored.
4. Vouchers must be labelled properly. Labels must be ethanol resistant if put inside the container. The MNHN Labels are ethanol resistant, put them with the corresponding specimen. A specimen must always have a label to be able to identify it.
5. If the specimen is too small and nothing is left after dissection and sample preservation, another specimen can be fixed as species representative. WARNING : ensure that they have the same morphological traits of the preserved specimen and that they come from the same station.
6. If nothing remains of the specimen after dissection and there is no other specimen from the same batch to be designated as voucher, you need to keep the labels

(ATLASea, MNHN). These labels should be placed in a bag labelled “ATLASea specimen labels GHOST VOUCHER”. Never throw away a label. Send them to the ATLASea team with or without the others vouchers.

7. All the permits are mandatory; we cannot include a species in the MNHN collection without the permit. Send them with the samples and vouchers.

F. Shipment of Genomic Samples and Vouchers

7

1. The samples and vouchers can be sent all at once.
2. Always arrange shipping details with a staff member of Genoscope SeqLab and MNHN manager collection send the ATLASea log sheet via e-mail.
3. Please contact:

- **Janaina RIGONATO**: jrigonat@genoscope.cns.fr
- Karine LABADIE: **klabadie@genoscope.cns.fr**
- Pedro OLIVEIRA: **pcoutool@genoscope.cns.fr**
- Mélanie VAN WEDDINGEN: melanie.van-weddingen@mnhn.fr

4. Shipment of **frozen samples** should be performed either in dry-shippers or on dry ice via a suitable carrier (e.g.: Transportéo, Cryoexpress, etc).
5. The samples preserved in -80°C should be placed in the **middle of dry ice** and the **box completely filled with dry ice**, samples preserved in ethanol -20°C should be placed on top of dry ice.
6. Separate the sample and the vouchers.
7. Shipment should be favoured for a delivery on Mondays or Tuesdays between 8.30 a.m. and 4.00 p.m. Outside this time frame, please contact **Janaina RIGONATO** to arrange for the reception.
8. The sample package should be sent to the following address:

SITE CEA EVRY
Réception Marchandises
To : **Janaina Rigonato**,
Emmanuelle Petit or Pedro H Oliveira
31, Boulevard des Coquibus
91000 Évry, France

9. The voucher package should be sent to the following address :

Muséum national d’Histoire naturelle
Mélanie Van Weddingen
55 rue Buffon, CP51
75005, Paris, France

10. Each shipment should include a letter mentioning:

- The name ATLASea
- The name of the sender
- A partial description of the samples
- Permits for species requiring CITES permits

- Printed copy of the email which was sent to **ambassadors@atlasea.fr** prior to the shipment of the samples, and that had the ATLASea log sheet as attached file (do not print the actual log sheet).