UNIVERSITÉ LAVAL
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Sampling Protocol

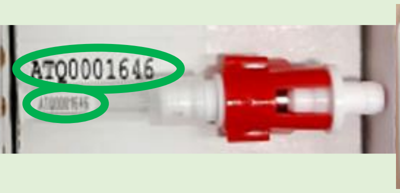
Genotyping sheep with Allflex pliers

Société des éleveurs de moutons de race pure du Québec
semrpq@semrpq.com

Important Information for Sampling

For collection

- Carefully read this sampling protocol.
- Complete the data sheet in .xlsx format (feuille_de_données) :
    - Always write the nine (9) digits of the sheep's digital ID in the "ATQ_sheep" column (or tatou if none);
    - Indicate the sheep's breed in the "Breed" column;
    - Indicate the sheep's sex in the "Sex" column;
    - If the sheep has a particular condition (e.g., cramping, color, horn, etc.), mention it in the "Comment" column.
    - If a sample collection fails, discard the tube and leave the corresponding line blank in the data file.
- The tube number (ATQ_tube) and box number (Box) are found on the sample box:



- Only sample purebred sheep registered in GenOvis for cofinancing category.
- Sample tubes (both new and used) must be stored at room temperature and kept out of direct sunlight.
- Sheep must be restrained before sampling to prevent injuries or improper sampling.

For returning samples

- Contact William Poisson by email (william.poisson.1@ulaval.ca) to receive a return label and provide the following information and documents:
    1. Your availability for collection.
    2. The data sheet in Excel format.
    3. The measure and weight of the return box.
- Once the samples are received, the university team will inform SEMRPQ of the number of samples received and send them for genotyping.
- Genotyping fees apply to all submitted samples. If genomic results cannot be obtained due to insufficient DNA or tissue absence, a $2 discount will be applied.
- Once the genotyping results are available, SEMRPQ will send you an invoice, payable upon receipt.
- After payment is received and genomic analyses are completed, results will be sent to you by the project team.

For any questions, feel free to contact us!
semrpq@semrpq.com
william.poisson.1@ulaval.ca

Required Equipment:

- Allflex pliers (blue).
- Sample tubes.
- Data sheet (feuille_de_données) in Excel format.

****Note: The data sheet must be returned in digital format (.XLSX) via email after sampling.*

Procedure

A. Loading a sample tube in the pliers

1. Remove an unused sample tube from the box (following data sheet tube order). The tube should be in one piece; if not, reassemble it (blade with white base, red intermediate piece, and tube)

2. Ensure the retention ring on the pliers is open (black piece at the bottom; if closed, turn it) and insert the sample tube as illustrated

3. Once the tube is inserted, turn the retention ring to the closed position.

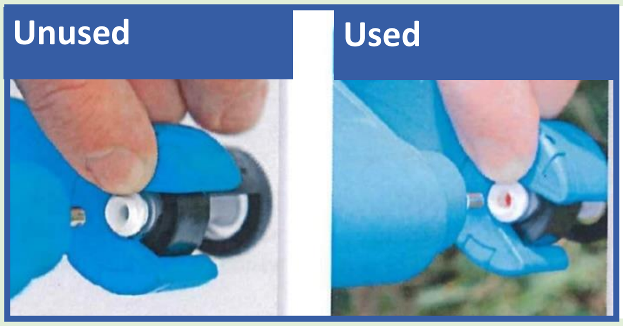
4. Align the tube with the piston (if not aligned) and squeeze the pliers until the piston is flush with the white base of the blade (yellow arrow on the image).

5. Release the pliers, ensuring the white base and blade move with the piston. If not, reapply pressure.

6. Remove the red intermediate piece by holding both tabs and **keep it** for later tube storage.

Warning: The blade is VERY sharp.

B. Sampling process



1. Verify that the inserted tube is unused.
   ➔ Used tubes are marked with a red dot on top and green marble **INSIDE** the tube (not on top).

2. Slide the sheep's ear into the pliers, avoiding the edges (<1cm), large veins, and cartilage folds.

Important: Restrain the animal to prevent injuries.

B. Sampling process

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3. Firmly and quickly squeeze the pliers, then release.

Important: Follow the animal's movements to avoid tears.

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4. Turn the retention ring and remove the tube.

Important: Ensure the sample is present in the tube. If not, discard the tube, mark the missed sample on the data sheet, and retry with a new tube.

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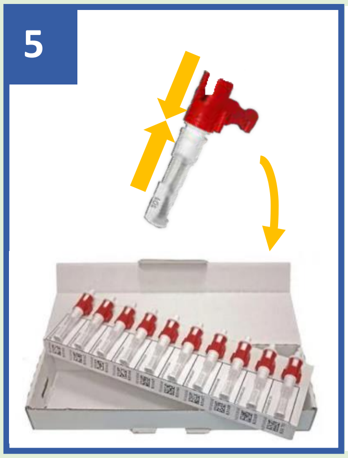

5. Replace the previously removed red intermediate piece on the tube, then store it in its designated slot (according to ATQ_tube number) in the box.

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6. Remove the blade by separating the pliers and discard it.

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7. Complete the corresponding tube row in the data sheet (**Excel format**):

- **ATQ_sheep** column: 9-digit ATQ (numeric ID) of the animal (tatou ID if none).
- **Breed column**: Breed code
- **Sex column**: Sex (M or F).
- **Anomaly column**: 1 if the animal has been classified as abnormal, else nothing.
- **Comment column**: Add any notes (e.g., different phenotype, parentage, etc.).

Final Notes:

- The **full ID of the animal must be recorded correctly** (9 digits for digital (ATQ) ID or full tatou ID) in the appropriate row, or the sample will not be processed.
- Report any discrepancies in data file to ensure accurate results.

For any questions, feel free to contact us!
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