



## The Gnatwork

Intended use of resource / data

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### Title of resource

GN\_15: Identification of blood meal source from dipteran specimens

### Authored by

When using this protocol, the following should be referenced:

Garros, C., Gardès, L., Allène, X., Rakotoarivony, I., Viennet, E., Rossi, S. and Balenghien, T. (2011). Adaptation of a species-specific multiplex PCR assay for the identification of blood meal source in *Culicoides* (Ceratopogonidae: Diptera): applications on Palaearctic biting midge species, vectors of Orbiviruses. *Infection, Genetics and Evolution*, 11(5): 1103-1110.

### DOI

10.1016/j.meegid.2011.04.002

### Description

Three multiplex species-specific PCR-based assays to identify the blood meal source of engorged female dipteran specimens for veterinary interest. Protocol from the Gnatwork Brazil workshop, November 4-8<sup>th</sup> 2019.

### Intended use

Scientific research use and training purposes.

### Restrictions on use

Content is not to be redistributed in the public domain (e.g. presentation, lecture, online or in publications).

### Resource history

Protocol taken from Garros *et al.* (2011) for identifying the blood meal source of *Culicoides* females.



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## GN\_15: Identification of blood meal source from dipteran specimens

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### A. Introduction

This method details the protocol for the Identification of blood meal source from dipteran specimens.

### B. Materials required

#### Equipment

- PCR laminar flow cabinet (or microbiological safety cabinet Class II) (ideally two cabinets, to allow separation of mastermix preparation and template addition activities)
- Thermal cycler
- Fridge (+4°C)
- Freezer (-20°C)
- PCR reaction tubes either as individual tubes, tube strips or PCR plates
- Reaction tube spinner, plate spinner, or centrifuge with plate rotor (appropriate to the plasticware to be used)
- Vortex
- Pipettes (0.1-2.0 µl, 1-20 µl, 20-200 µl, 100-1000 µl)
- Disposable pipette tips containing hydrophobic filters (2µl, 20µl, 200µl, 1000µl)
- For primers: 1.5 ml screw cap or flip-tops (e.g. Eppendorf® Safe Lock Tubes #0030 123.328) microcentrifuge tubes
- For mastermix preparation: 1.5 ml flip-top microcentrifuge tube or 15ml centrifuge tubes (dependent upon volume of mastermix required to be prepared)
- PCR adhesive plate sealers (\*only if using 96-well PCR plates)
- Blue roll
- 96 well PCR tube rack
- Microcentrifuge tube rack

#### Reagents

- DNAZap™ (AM9890, ThermoFisher Scientific, UK) (or equivalent)
- Nuclease free water (NFW)
- Forward & reverse primers (see Table 1)
- NucleoSpin Tissue Extraction Kit (740952, Magerey-Nagel, Düren, Germany)
- Selected Mastermix Components (see below)

#### Taq DNA Polymerase

- 10 mM dNTP Mix (e.g. D7295 Sigma, UK; 18427-088: ThermoFisher Scientific, UK)
- Taq DNA Polymerase (201203: Qiagen; kit contains 10x PCR Buffer, 10x CoralLoad PCR Buffer, 5x Q-Solution, 25 mM MgCl<sub>2</sub>)



## C. Method

- C.1 Separate the abdomens of engorged female specimens from the body.
- C.2 Extract the DNA from the abdomen using NucleoSpin Tissue kit, following the manufacturer's instructions.
- C.3 Ultraviolet (UV) sterilise the PCR laminar flow hood (or microbiological safety cabinet (MSC)) which is designated for mastermix preparation and if required also clean the working area, pipettes etc. with DNAZap™ (or equivalent). Once cleaned complete the following steps within the PCR laminar flow hood (or MSC).
- C.4 Make a working stock of each primer at the concentration required by the mastermix by briefly vortexing resuspended 100µM primers, then make an appropriate dilution in a second appropriately labelled 1.5ml microcentrifuge tube [store both re-suspended 100µM primer and working stock 10µM primer at -20°C when not in use].
- C.5 Because multiplexing numerous primer sets can lead to cross-reactivity, this protocol defines three multiplex combination assays (see Table 1 for primers, Table 2 for assay conditions):
  - Multiplex combination 1: dog, pig.
  - Multiplex combination 2: chamois, red deer, roe deer, cow, goat, sheep.
  - Multiplex combination 3: cat, horse.

**Table 1** Primer set used for the identification of blood meal origin in dipteran abdomens

| Reverse primers                     | Oligo Name | Sequence (5'-3')                  | Size (bp) |
|-------------------------------------|------------|-----------------------------------|-----------|
| <b>Multiplex combination 1</b>      |            |                                   |           |
| Forward primer UNIV1                |            | GACCAATGATATGAAAAACCATCGTTGT      |           |
| Dog <i>Canis lupus familiaris</i>   | CANIS      | CAAGCATACTCCTAGTAAGGATCCG         | 170       |
| Pig <i>Sus scrofa</i>               | SUS        | TCTGATGTGTAATGTATTGCTAAGAAC       | 219       |
| <b>Multiplex combination 2</b>      |            |                                   |           |
| Forward primer UNIV2                |            | TGAGGACAAATATCATTYTGAGGRGC        |           |
| Chamois <i>Rupicapra rupicapra</i>  | RUPI       | TGAGGGTAGCCTTGCTACCGAGAAGCCT      | 90        |
| Red deer <i>Cervus elaphus</i>      | CERVUS     | AGTAAGTGTACTATAGCGAGTGCTGCG       | 188       |
| Roe deer <i>Capreolus capreolus</i> | CAPREOLUS  | TTGTCCGCGTTTGATGGGATTCCTATC       | 220       |
| Cow <i>Bos taurus</i>               | BOS        | TAAGATGTCCTTAATGGTATAGTAG         | 287       |
| Goat <i>Caprus hircus</i>           | CAPRA      | TTAGAACAAGAATTAGTAGCATGGCG        | 313       |
| Sheep <i>Ovis aries</i>             | OVIS       | GGCGTGAATAGTACTAGTAGCATGAGGATGA   | 336       |
| <b>Multiplex combination 3</b>      |            |                                   |           |
| Forward primer UNIV3                |            | TTTTTTTTTTTCGVTCHATYCCHAAAYAACTAG |           |
| Cat <i>Felis catus</i>              | FELIS      | GATTCATGTTAGGGTTAGGAGATCC         | 180       |
| Horse <i>Equus caballus</i>         | EQUUS      | TACGTATGGGTGTTCCACTGGC            | 208       |

- C.6 Thaw if needed, then vortex briefly forward and reverse primers and other mastermix components.
- C.7 Make sufficient of the mastermix (Table 2) for the number of wells required for samples and positive and negative controls (volume per reaction x number of reactions required +10% [to account for wastage during pipetting, use of reagent reservoirs etc.]).



- C.8 Vortex the mastermix and aliquot into each well.
- C.9 If separate mastermix preparation and template addition areas/hood are not available proceed directly to step C.10, if separate areas are available seal tubes/plates containing mastermix and transfer the plate/tubes containing mastermix to the designated template addition area then proceed to step C.10.
- C.10 Thaw if needed, then briefly gently mix/vortex DNA extractions (caution excessive vortexing can increase DNA fragment shearing decreasing the quality of the DNA extraction).
- C.11 Using a new pipette tip per well to prevent cross-contamination transfer DNA template into the reaction wells.
- C.12 Using a new pipette tip per well transfer the nominated positive control sample into the designated positive control well(s). See troubleshooting tip one for an appropriate positive control.
- C.13 Using a new pipette tip per well transfer nuclease free water into the designated negative control well(s).
- C.14 If using PCR plates seal the plate securely with PCR adhesive film/foil. Or if using individual reaction tubes or tube strips ensure they are all sealed securely.
- C.15 Briefly vortex tubes/plate.
- C.16 Spin reaction tubes/plate for approximately 10s in the reaction tube spinner / centrifuge to concentrate reaction mix at the base of the wells.
- C.17 Place reaction tubes in the thermal cycler and carry out the appropriate PCR amplification using the thermal profile appropriate to the primers used (see Table 2).  
Note. For Multiplex combination 2 primer set, touchdown PCR cycles are used to reduce nonspecific amplification.

**Table 2** PCR master mix and thermal profiles

| Component           | Initial Concentration | Final Concentration          | Volume Per Reaction in $\mu$ l |
|---------------------|-----------------------|------------------------------|--------------------------------|
| 10x Reaction Buffer | 10x                   | 1x                           | 2.5                            |
| dNTPs               | 10 mM                 | 200 $\mu$ M each             | 0.5                            |
| Toptaq              | 5 units/ $\mu$ l      | 1.25 U/rxn                   | 0.25                           |
| Primers             | 10 $\mu$ M stock      | 0.4 $\mu$ M (10 $\mu$ M/rxn) | 1                              |
| Host DNA            |                       |                              | 25 – 50 ng                     |
| Nuclease free water |                       |                              | To 25 $\mu$ l final volume     |



| <b>Multiplex combination 1 or 3 primer set</b> |            |      |
|--|------------|------|
| Initial denaturation                           | 5 minutes  | 94°C |
| <b>3-step Cycling (40 Cycles)</b>              |            |      |
| Denaturation                                   | 30 seconds | 94°C |
| Annealing                                      | 30 seconds | 53°C |
| Extension                                      | 30 seconds | 72°C |
| Final Extension                                | 10 minutes | 72°C |
| Hold   | ∞          | 4°C  |

| <b>Multiplex combination 2 primer set</b>                            |            |                                     |
|--|------------|-------------------------------------|
| <b>Touchdown PCR cycles used to reduce nonspecific amplification</b> |            |                                     |
| Initial denaturation   | 5 minutes  | 94°C                                |
| <b>3-step Touchdown PCR Cycling (20 Cycles)</b>                      |            |                                     |
| Denaturation   | 30 seconds | 94°C                                |
| Annealing  | 30 seconds | 61°C, decrease by 0.5 °C each cycle |
| Extension  | 30 seconds | 72°C                                |
| <b>3-step Cycling (15 Cycles)</b>                                    |            |                                     |
| Denaturation   | 30 seconds | 94°C                                |
| Annealing  | 30 seconds | 53°C                                |
| Extension  | 30 seconds | 72°C                                |
| Final Extension  | 10 minutes | 72°C                                |
| Hold   | ∞          | 4°C                                 |

- C.18 UV Sterilise the PCR Laminar flow hood(s)/MSCs and other working areas used and if required also clean working area, pipettes etc. with DNAzap™ (or equivalent).
- C.19 When the thermal cycle is finished, remove reaction tubes from the thermal cycler and store PCR product at 4°C if to be used with 24 hours or store at -20°C until required for downstream analysis.
- C.20 Visualise PCR products on a 2% (w/v) agarose gel (see Gnatwork protocol GN\_11: Agarose Gel Electrophoresis using SYBR Safe DNA gel stain).

## **D. Results**

- D.1 Where appropriate associated experiment results should be recorded in the relevant laboratory notebook.
- D.2 Confirm successful amplification via agarose gel electrophoresis on a 2% (w/v) agarose gel. If using the 2% 96-well E-Gel™ run the gel for 8 minutes on program EG. Successful amplification using this protocol is indicated by the presence of a band at the appropriate size for the target amplicon plus the primer size (Table 1), results are recorded as the presence or absence of a band at the correct size. No band should be present in the negative control lane(s).



## E. Tips and troubleshooting

- For positive controls, where possible use EDTA-blotted blood collected in vet clinics or by wildlife institutions and extract DNA using a commercial kit (DNeasy Tissue & Blood, Qiagen [see GN\_09: DNA extraction from dipteran specimens, whole blood and cultured cells using Qiagen DNeasy spin columns]).
- Addition of between 25 – 50 ng of DNA template per reaction is optimal, hence depending on the DNA yield of the DNA extractions the volume of DNA template added to each reaction may need to be increased or decreased as required, increasing or decreasing the volume of NFW to ensure the total volume including template is constant at 25 $\mu$ l to maintain the concentration of other reagents in the mastermix.
- This protocol may be adapted for use with a variety of other mastermixes and Taq DNA polymerases from other suppliers. Care must be taken, however, when selecting alternative