**Minutes of the 1st Management Committee Meeting of the COST Action**

CA22108 – Wildlife Malaria Network (WIMANET)

*CSO approval date: 12/05/2023 - COST Action starting and meeting date: 28/09/2023*

*Online ZOOM meeting*

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# Agenda, Presentation and Polls

The Objectives of the MC1 meeting are:

* Take ownership of the Action challenge
* Networking and community building
* Bring everyone to the same level of knowledge on COST
* Develop Action structure, methodology and planning

The Agenda is available in Annex I, the full presentation as well as the outcomes of the polls, are available in Annex II.

# Participants and Hosting Team

* Science Officer assigned for this Action: Federica Ortelli
* Administrative Officer assigned to this Action: Aldona Gembalik
* Action Chair Candidate: Jenny Dunn

A group picture was taken with the participants (Annex III).

The attendance list is available in Annex IV.

# COST Action Café and debriefing

For four rounds of the discussion, the participants were invited to join online breakout rooms organised by Working Group topics listed here after:

* **WG1**: Coordinating genomics, transcriptomics, and molecular markers
* **WG2**: Incorporating molecular markers and morphology to assign wildlife malaria lineages to species
* **WG3**: Vector transmission success in wildlife malaria
* **WG4**: Impact of anthropogenic activities and wildlife malaria on host haematology
* **WG5**: Drivers of spatiotemporal variation in multi-host-parasite communities
* **WG6**: Coordinating and implementing the CBOs

In each breakout room, a volunteer from the MC was appointed as Rapporteur. The Management Committee will develop further the ideas by the MC2 meeting. The summary of the discussions is available in Annex V).

# Pre-requisites for the Decision Making

The minimum of 2/3 of the parties present (17 out of 19 Countries present) to reach the quorum was achieved allowing the Management Committee to take formal votes in accordance with the [Annotated Rules](https://www.cost.eu/Annotated_Rules_for_COST_Actions_C).

# Decisions by the Management Committee

Decisions taken at the meeting by the Management Committee are recorded in the ZOOM chat (Annex VI).

### Election of the Chair and Vice-Chair and selection of the Grant Holder (Scientific Representative)

Jenny Dunn (UK) was elected Chair

Alfonso Marzal (ES) was elected Vice Chair

The MC selected University of Lincoln as Grant Holder Institution, represented at the MC by Jenny Dunn.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Leadership Position** | **Name** | **Country** | **YRI (Y/N)** | **Gender** | **ITC (Y/N)** |
| **Action Chair** | Jenny Dunn | UK | Y | F | N |
| **Vice Chair** | Alfonso Marzal | ES | N | M | N |
| **Grant Holder Scientific Representative** | Jenny Dunn | UK | Y | F | N |

### Agreement on the Action Structure

The proposed members were approved unanimously.

* Grant Awarding Co-ordinator: Alexandra Corduneanu (Romania)
* Science Communication Co-ordinator: Tamara Emmenegger (Switzerland)

The following Action Management Structure for leading (L) and co-leading (CL) the Working Groups were proposed:

* WG1 (Genomics): Nayden Chakarov (Germany) (L).
* WG2 (Species): Melanie Duc (Lithuania) (L), Ravinder Sehgal (US) (CL).
* WG3 (Vectors): Josué Martínez-de la Puente (Spain) (L), Carolina Chagas (Lithuania) (CL).
* WG4 (Haematology): Swen Renner (Austria) (L), Diego Santiago-Alarcon (US) (CL).
* WG5 (Communities): Kasun Bodawatta (Denmark)
* WG6 (Communication): Martina Ferraguti (Spain)

The proposed members were approved unanimously.

Additional co-leads will be encouraged to self-nominate during the lifetime of the Action (especially YRIs and those from ITCs, and ensuring a gender balance), and will be voted in by the MC.

### Election of other leadership positions

The elected leadership positions are listed hereafter.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Leadership Position** | **Name** | **Country** | **YRI (Y/N)** | **Gender** | **ITC (Y/N)** |
| **WG1 Leader** | Nayden Chakarov | Germany | Y | M | N |
| **WG2 Leader** | Melanie Duc | Lithuania | Y | F | Y |
| **WG3 Leader** | Josué Martinez-de la Puente | Spain | N | M | N |
| **WG4 Leader** | Swen Renner | Austria | N | M | N |
| **WG5 Leader** | Kasun Bodawatta | Denmark | Y | M | N |
| **WG6 Leader** | Martina Ferraguti | Spain | Y | F | N |
| **Grant Awarding Coordinator** | Alexandra Corduneanu | Romania | Y | F | Y |
| **Science Communication Coordinator** | Tamara Emmenegger | Switzerland | Y | F | N |

### Core Group and mandates

The Core Group of the COST ACTION is composed by the Chair, Vice Chair and the six WG leads.

The following Core Group delegated responsibilities were presented and asked to be approved by the attendants:

* To invite participants for networking activities.
* To select participants who will be reimbursed.
* To select providers for dissemination and communication products (e.g. website).
* To approve changes to place or date of activities.

The presented responsibilities of the Core Group were approved unanimously.

### Discussions and decisions

1. **Working Group Structure**

The following rules of the structure and organization of the Working Groups (WGs) were presented:

* The meetings will be organised to allow WG members to contribute to as many WGs as they want.
* Additional co-leads for WGs are welcome. Younger researchers, female researchers and researchers from ITCs are particularly encouraged to participate as co-leads of the WGs.
* New co-leads should be confirmed by MC.
* Task leaders will be decided within WGs.

1. **Working Group Membership**

The following rules of the Working Groups membership were presented:

* All current applications will be accepted.
* All network proposers will be accepted.
* All MC Members will be accepted.

The attendants were asked to approve whether the agreement of new WG members should be delegated to Core Group. The attendants approved it unanimously.

1. **Objectives of the Grant Period 1**

The next milestones (M) and deliverables (D) to be achieved for each working group (WG) during the Grant Period 1 were presented:

* M1.1: Produce summary of target species and geographic regions to expand genomic/transcriptomic resources (WG1)
* M2.1: Identify species with morphological descriptions and attached molecular sequence information (WG2)
* M3.1: Summarise current knowledge on the vector competence of haemosporidians and the experimental designs and conditions used in previous studies (WG3)
* M4.1: Compile existing datasets from researchers and museums for analysis and reference (WG4)
* M5.1: Identify and summarise key variables and clarify statistical methods, structure of models, task allocation to compile multi-host-parasite community datasets (WG5)
* D6.1: Construct and publicise a WIMANET website (WG6)
* D6.2. Identify individuals who will be involved in decisions on grant and award allocation and approval, and implement unconscious bias training (WG6)
* D6.3. Advertise the Action and travel support across disciplines and encourage scientists and specialists from different disciplines to participate (WG6)

1. **Proposed activities for the Grant Period 1**

The following activities to be developed during the Grant Period 1 ((1/11/23 – 31/10/24) were presented:

* Meeting 1: WG and MC meeting. Online, provisionally 6/12/2023 – 8/12/2023, 3 days.
  + 60+ participants. Introductions, outline and assignation of initial tasks.
* Meeting 2: Workshop, Cluj-Napoca, Romania, provisionally 18/03/2024 – 21 /03/2024.
  + 55 in-person participants, hybrid meeting. Progress towards Grant Period Goals
* Training school: Czech Republic, 2/09/2024 - 6/09/2024
  + 25 participants, 8 trainers, 5 days (nominally 1 days training per research co-ordination objective (WGs 1-5))
* Short-Term Scientific Missions (prioritise for WG2 and WG4): 6 STSMs
* Website

1. **Proposed budget for the Grant Period 1**

The following budget for the activities to be carried out during the Grant Period 1 was presented:

|  |  |  |
| --- | --- | --- |
| **Activity** | **Participants** | **Budget** |
| Meeting 1 (online) | 60+ | €3,000.00 |
| Meeting 2 (hybrid) | 55 (in person) | €50,344.00 |
| Training School | 25 + 8 | €34,144.00 |
| STSMs | 6 | €12,000.00 |
| Website |  | €8,000.00 |
| FSAC @ 15% |  | €16,123.20 |
| Total |  | €123,611.20 |

The attendants were asked to approve whether the Core Group can move €10,000 between budget lines without the necessity of MC vote. The attendants approved it unanimously.

### AOB

Some other business were discussed during the meeting:

* design of WIMANET logo
* the use of cloud-based storage service (i.e. Google Drive, Slack) for asynchronous work between meetings)
* Website hosting

The science communication coordinator offered to liaise with the Chair and WG6 Lead to investigate options

**Minutes prepared by:** *Action Science Officer and Action Vice-Chair*

ANNEXES

### Agenda

* Purpose of the meeting
* Getting to know each other
* COST presentation + Q&A
* Action Chair Candidate presentation (Presentation of the Action) + Q&A
* Group Photo / **Break**
* COST Action Café (parallel discussion sessions)
* **Lunch**
* Debriefing from the COST Action Café
* Election of mandatory leadership positions / **Break**
* MC Discussion and Decisions (moderated by elected Chair)

### Presentation & polls

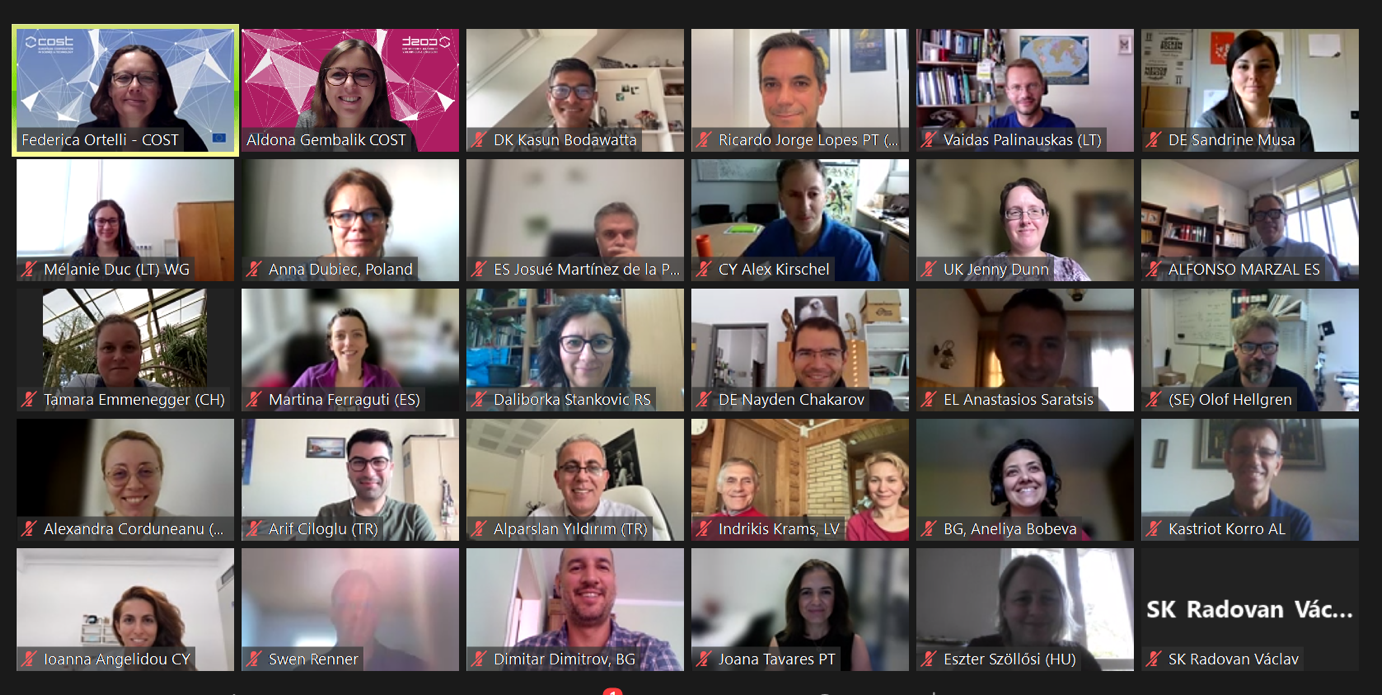








### Group photo



### Attendance list

|  |  |  |
| --- | --- | --- |
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| Jenny Dunn | JDunn@lincoln.ac.uk | United Kingdom |

### Breakout Room Discussions

|  |
| --- |
| **WG1: Coordinating genomics, transcriptomics, and molecular markers** |
| Rapporteur(s): Nayden Chakarov |
| **What is our main goal?**  Define what are we able, almost able to do, what are the aim, common protocols and open questions?  Define and make databases for levels of common interest – markers, genes, regions, complete genomes.  Identifying applicable methods to get rare data. – Consult practicing groups.  Identify avenues for co-analysis of host and parasite genomes. |
| **How can we achieve it?**  Conserved markers for phylogenies – doable with sequence capture.  Divergent genes – whole genomes needed. Exchange of protocols how to achieve it.  Joint analyses methods and go-to- people and groups for given exchange of research services, sequencing practices, exchange expeditions with these groups.  Increase coherence and synergies.  Identify joint analysis goals where every next reference meaningfully contributes to.  Cryobanks and sharable sample collections. |
| **Which resources do we need?**  Servers and databases. “MALAVI2.0”  Servers for storing available raw and semi-processed data for sharing +/- embargos.  Databanks with data available data for collaborations.  Databanks with labs where lineage or group-specific multiplictions in hosts is possible or otherwise can get highly parasitized hosts. |
| **What are the next steps?**  Identify the most successful techniques, where and how to apply them.  Solidify resources on model & reference lineages and create genomic resources on missing or focus links.  Seek and identify informative biomarkers from available genomic data. E.g. microRNA, copy variation, coverage variation |
| **WG2: Incorporating molecular markers and morphology to assign wildlife malaria lineages to species** |
| Rapporteur(s): Mélanie Duc |
| **What is our main goal?**  Maintaining the **databases** (MalAvi database for repository of avian haemosporidian molecular records; species identification on NRC webpage). But still many gaps between molecular and morphology. Other taxa databases?  Sharing **expertise** and **experience**: increasing the knowledge and skills on parasite identification.  Developing molecular tools (**markers**) for resolving mixed infections.  **Diversity** in parasites and hosts.  **Phylogenetic relationships**.  **Machine learning** development? |
| **How can we achieve it?**  Maintaining and updating **databases**; new contributions.  Including more parameters in the databases? Parasitemia? New databases for other taxa (as all in one seem complicated)?  Reviews of existing **protocols**. Then give **standardized method** papers for both molecular and morphological identification.  Not just on avian haemosporidians but also reptiles and bats.  Papers, pdf, videos of explanations and teaching.  How to sample the host (birds, bats, reptiles). How to prepare slides, stain them in the proper way. In which buffer to collect/conserve samples, etc. Guidelines; how to work when low parasitemia?  Protocols for identification of species.  ® make public how to work and co-operate with other fields.  **Training schools**: for species identification; genetic marker/tools.  Many slides available (parasites identified by molecular methods, but not morphologically).  Increase the **network** and **collaborations**. Share the knowledge and be able to use it even after.  **Sampling** in countries so far with no/very few samples. Increase of network (ornithologists; museums, etc).  Development of **machine learning**; pixel based? |
| **Which resources do we need?**  Protocols.  Training school on sampling: catching, identifying and sampling hosts: trainers, facilities.  Training school on parasite species identification: trainers (few), facilities (connected microscopes, or many microscopes); how many trainees?  Development of new markers: sequences (of specific regions)  Database: material available; people.  Network |
| **What are the next steps?**  To determine: Who can teach? On which topic? Who would like to attend a training? Where are the facilities for a training? Who has materials? Who has the skills to work with it? New methods to applied?  Broadcast standardized method papers for both molecular and morphological work and identification. |
| **WG3: Vector transmission success in wildlife malaria** |
| Rapporteur(s): Jenny Dunn/Josué Martinez-de la Puente |
| **What is our main goal?**  Identify factors that influence transmission success in wildlife malaria |
| **How can we achieve it?**  Collate data that exists currently, and summarise knowledge from both the field and from experimental infections.  Identify priorities for identifying vectors – mosquitoes and also across other taxa – recruit specialist entomologists into the Action and also as trainers for summer schools to help with training?  Understand specificity of lineage-vector relationships, and protocols for analysis of vectors – interpreting molecular data from different parts of the mosquito  Focussed day during training schools - Training on mosquitoes, but how to translate into other systems?  Use bioluminescent sporozoites from rodent models for training – possible applications to other systems?  Species bias from traps (e.g. different heights)? How to collect in a standardised and comparable manner  Molecular barcoding/metabarcoding techniques for vector ID |
| **Which resources do we need?**  Knowledge of availability of colonies to work with - Database of facilities/laboratories who have experimental capabilities  Training within summer schools, and agreement on protocols for summer schools  Entomological knowledge to identify vectors |
| **What are the next steps?**  Establish database of facilities/laboratories who have experimental capabilities, which species, and which techniques – on website, searchable?  Integrate vector protocols – sampling and processing, data interpretation – into summer schools |
| **WG4: Impact of anthropogenic activities and wildlife malaria on host haematology** |
| Rapporteur: **Swen Renner** |
| **What is our main goal?**  Impact of anthropogenic activities and wildlife malaria on host haematology  The main goal is to **understand the mechanism/impact of human activities on wildlife-malaria-systems under Global Change scenarios.** |
| **How can we achieve it?**  Collecting (tissue) samples, Road kill sampling, …  Use existing material from others studies (and collections)  Short time scientific missions (analysing slides in museums, crawl through databases, …)  **Literature research/meta-analysis**  on baseline models pre/post human activities  on clinical effects/outcome of infections on community aspects and ultimately conservation biology  **Historic changes** of anthropogenic activities and their interaction (last 2 or so decades; slides, specimens, tissue, blood?) |
| **Which resources do we need?**  Database access and screening  Training schools/summer schools to train next generation ecologists to collect wildlife malaria (globally)  **Join/Visit LTER to screen potential data availability and cooperation** |
| **What are the next steps?**  Define the human activities in more detail (global change or parts there off)  Outline the literature research ideas into tangible parts  Contact ornithologists with historic blood samples (and maybe tissues for antibodies)(O. Hellgren) |
| **WG5: Drivers of spatiotemporal variation in multi-host-parasite communities** |
| Rapporteur(s): Kasun Bodawatta |
| **What is our main goal?**  **What are the biotic and abiotic drivers influencing host-malaria associations (e.g., host switching, host specificity) across vertebrate clades on a global scale.**  Produce a review/perspective/metanalysis paper to highlight the trends and major gaps spatiotemporal patterns of wildlife-malaria associations, encouraging other vertebrate groups to create good malaria databases, point out the weaknesses and strengths of these databases (Learning from MalAvi).  Training workshops on technology on analysing community level data – providing standardized analytical methods.  Standardize protocols for abiotic and biotic parameters to collect from multi-host-parasites systems |
| **How can we achieve it?**  Step1:  Literature/database review on what are the available datasets on spatiotemporal patterns of malaria-wildlife interactions  Finding out how we can standardize these datasets?  Get an idea on what factors can we compare and how can we properly compare between different studies – Statistical methods  Identify the effects of different abiotic and biotic factors at local and global scales on host-parasite associations. How can we fill the missing gaps (under-sampled areas?)  Step 2:  How unique is data we find in one community to another community in a different region (How robust are the host-parasite links between communities – can we extrapolate these data?): Identify the drivers of host-parasite associations interactions at both global and local scales.  What type of data available – generated yet unpublished? (There are be available/unpublished datasets that can be compiled to compare between different communities across space and time.) – Reach out others to see if there are datasets available  We should also look at the host phylogenetic impacts on these associations too.  Include the community structures of hosts in the analyses  Need to identify main lineages associated with bird species – which can be used to make predictions on how parasites can be spread to new areas  Challenges:  The robustness of the links between hosts and parasites depends on the sampling sizes. Community based sampling can have smaller sampler sizes. |
| **Which resources do we need?**  - More information to include in available malaria databases (e.g., including both presence and absence of malaria) and discussion on improvement and expansion of databases to other vertebrate groups.  - Networking and contacting people around the world who might have generated malaria data  - Expertise from non-avian malaria systems (other vertebrate groups) |
| **What are the next steps?**  Division of labour among WG members |
| **WG6: Coordinating and implementing the CBOs** |
| Rapporteur(s): **Martina Ferraguti** |
| **What is our main goal?**  **Sharing** the increase **knowledge** and **skills** of the network.  **Disseminate the goals and outcomes** of the network. Clarify that Haemosporidians are a powerful model to study malaria parasites (it will depend on the target public). Avian malaria can be a bridge to know more about blood parasites.  **Promoting** the **Haemosporidian parasite Conferences** (maybe thinking about the one in 2026 if it will be held in Europe). |
| **How can we achieve it?**  **Social Media** (e.g., Twitter, others?).  Set a WIMANET **webpage**.  **Conceptual paper** about where is the gap in the knowledge (e.g., systematic review).  Topic:  Focus our attention on all the groups of Haemosporidian parasites, not only avian malaria parasites  If you study resident birds, you are losing info about other groups like migratory ones.  By stressing the attention on which malaria species (lineages) may be of a particular importance, maybe linked to specific regions. Potential traps: contaminations in your data: e.g., if a linage is only transmitted in Africa, is that true? We really need more data to deeply understand the transmission dynamics of a parasite.  **Questionnaire Report** to complete by the community during the first annual meeting and then analyse it over the following years of the Action (see for example *https://www.aedescost.eu/node/222*), and then publish a document with the output of the Questionnaire. As alternative, we could also think about perform an “**online survey**” follow the ‘Delphi process’ (a well-tested method which uses iterative rounds of anonymous scoring, with comments, to develop consensus). They are using formal expert elicitation methods to gather knowledge on the response of insects to different threats, especially for insect taxa and regions where they have not been able to find suitable empirical data. We should think about which research question we want to accomplish, but this is something nice and relatively easy to do as a Network.  Professional **videos:**  Training videos for general public (stakeholders, etc.), and for a scientific audience (to increase the skills of the network) on subject likes "working with avian malaria parasites”, field techniques, lab techniques (blood smear and PCR) (see for example: *https://www.aedescost.eu/videos*. We should carefully determine the focus and target audience, but it's certainly worth considering.  Explaining the goals of WIMANET. We think this can be a valuable endeavour, and we could consider creating a similar video for outreach (see for example *https://www.youtube.com/watch?v=BjQQeXGvYc4&list=PL-1YwbPvENS1qRjIsAEds-8\_ch4PlYh22&index=4&ab\_channel=Biodiversa%2B*).  Consider the **One Health** approach in relation to birds and livestock (chickens) or pets (parrots), while also taking into account integrated taxonomy within the **Biodiversity** to gain a deeper understanding of the living world around us.  Organize **Training School** (TS) locations. Up to 10-15 students for parasites study is enough (or a micro to connect it to a screen).  Vectors: mosquito and *Culicoides* sampling.  Birds: sampling, taking blood, etc.  Molecular tools focus on blood smears (microscopes), an affordable and relatively straightforward technique (or also include PCR, it depends on the involvement of participants and cost efforts they want to afford).  Statistical Modelling: how to use R software to model the collected data. Also think about specific cases such as phylogenetic studies.  Make a Standard Protocol with the learnings from the TS for parasite sampling and screening methods (blood sampling, blood-smears). This could result in collaborative data collection all over Europe from WIMANET COST countries, and then we can publish a collaborative paper (also including a standard sampling made with data from the TS teachers). |
| **Which resources do we need?**  - **Press release** about the main goal of the WIMANE, published in different language.  - Newsletter.  - Budget for doing internal calls for who can apply to the TS.  - Facilities for the TS (laboratories with microscope), field station. Usually, TS are free for the cost members, but we can think about offering some “places” to external people (mix system, ask for it). |
| **What are the next steps?**  - Looking for constructing the WIMANET webpage.  - Search for locations and facilities for the TS.  - Signing in the Social Media we want to start and think about collaborate with existing ones. |

### MC decisions Recoding

